Zhu-Hong You

List of Publications by Year
in descending order

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Version: 2024-02-01

91 papers	4,673 citations	117571 34 h-index	110317 64 g-index
93 all docs	93 docs citations	93 times ranked	2316 citing authors

#	Article	IF	Citations
1	Biomedical Knowledge Graph Embedding with Capsule Network for Multi-label Drug-Drug Interaction Prediction. IEEE Transactions on Knowledge and Data Engineering, 2022, , 1-1.	4.0	23
2	Multi-Neighborhood Learning for Global Alignment in Biological Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2598-2611.	1.9	12
3	A graph auto-encoder model for miRNA-disease associations prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	63
4	Prediction of lncRNA-disease associations via an embedding learning HOPE in heterogeneous information networks. Molecular Therapy - Nucleic Acids, 2021, 23, 277-285.	2.3	17
5	HiSCF: leveraging higher-order structures for clustering analysis in biological networks. Bioinformatics, 2021, 37, 542-550.	1.8	76
6	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.	1.1	7
7	A survey on computational models for predicting proteinâ€“protein interactions. Briefings in Bioinformatics, 2021, 22, .	3.2	92
8	SGANRDA: semi-supervised generative adversarial networks for predicting circRNAâ€“disease associations. Briefings in Bioinformatics, 2021, 22, .	3.2	33
9	DF-MDA: An effective diffusion-based computational model for predicting miRNA-disease association. Molecular Therapy, 2021, 29, 1501-1511.	3.7	12
10	A Novel Method to Predict Drug-Target Interactions Based on Large-Scale Graph Representation Learning. Cancers, 2021, 13, 2111.	1.7	31
11	MGRL: Predicting Drug-Disease Associations Based on Multi-Graph Representation Learning. Frontiers in Genetics, 2021, 12, 657182.	1.1	8
12	In silico drug repositioning using deep learning and comprehensive similarity measures. BMC Bioinformatics, 2021, 22, 293.	1.2	6
13	A structural deep network embedding model for predicting associations between miRNA and disease based on molecular association network. Scientific Reports, 2021, 11, 12640.	1.6	7
14	DANE-MDA: Predicting microRNA-disease associations via deep attributed network embedding. IScience, 2021, 24, 102455.	1.9	14
15	Learning from low-rank multimodal representations for predicting disease-drug associations. BMC Medical Informatics and Decision Making, 2021, 21, 308.	1.5	10
16	Identification of potential drugâ€“targets by combining evolutionary information extracted from frequency profiles and molecular topological structures. Chemical Biology and Drug Design, 2020, 96, 758-767.	1.5	8
17	LNRLMI: Linear neighbour representation for predicting lncRNAâ€“miRNA interactions. Journal of Cellular and Molecular Medicine, 2020, 24, 79-87.	1.6	27
18	Learning distributed representations of RNA and protein sequences and its application for predicting lncRNA-protein interactions. Computational and Structural Biotechnology Journal, 2020, 18, 20-26.	1.9	31

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19	Integrative Construction and Analysis of Molecular Association Network in Human Cells by Fusing Node Attribute and Behavior Information. Molecular Therapy - Nucleic Acids, 2020, 19, 498-506.	2.3	13
20	DBMDA: A Unified Embedding for Sequence-Based miRNA Similarity Measure with Applications to Predict and Validate miRNA-Disease Associations. Molecular Therapy - Nucleic Acids, 2020, 19, 602-611.	2.3	49
21	An efficient approach based on multi-sources information to predict circRNAâ€“disease associations using deep convolutional neural network. Bioinformatics, 2020, 36, 4038-4046.	1.8	105
22	MIPDH: A Novel Computational Model for Predicting microRNAâ€“mRNA Interactions by DeepWalk on a Heterogeneous Network. ACS Omega, 2020, 5, 17022-17032.	1.6	17
23	Learning Representations to Predict Intermolecular Interactions on Large-Scale Heterogeneous Molecular Association Network. IScience, 2020, 23, 101261.	1.9	16
24	iMDA-BN: Identification of miRNA-disease associations based on the biological network and graph embedding algorithm. Computational and Structural Biotechnology Journal, 2020, 18, 2391-2400.	1.9	11
25	NEMPD: a network embedding-based method for predicting miRNA-disease associations by preserving behavior and attribute information. BMC Bioinformatics, 2020, 21, 401.	1.2	6
26	Prediction of drug-target interactions from multi-molecular network based on LINEÂnetwork representation method. Journal of Translational Medicine, 2020, 18, 347.	1.8	26
27	iCDA-CGR: Identification of circRNA-disease associations based on Chaos Game Representation. PLoS Computational Biology, 2020, 16, e1007872.	1.5	63
28	GCNCDA: A new method for predicting circRNA-disease associations based on Graph Convolutional Network Algorithm. PLoS Computational Biology, 2020, 16, e1007568.	1.5	85
29	Incorporating chemical sub-structures and protein evolutionary information for inferring drug-target interactions. Scientific Reports, 2020, 10, 6641.	1.6	11
30	Prediction of Drugâ€“Target Interactions From Multi-Molecular Network Based on Deep Walk Embedding Model. Frontiers in Bioengineering and Biotechnology, 2020, 8, 338.	2.0	51
31	A learning based framework for diverse biomolecule relationship prediction in molecular association network. Communications Biology, 2020, 3, 118.	2.0	19
32	SAEROF: an ensemble approach for large-scale drug-disease association prediction by incorporating rotation forest and sparse autoencoder deep neural network. Scientific Reports, 2020, 10, 4972.	1.6	22
33	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.	1.5	64
34	Bioentity2vec: Attribute- and behavior-driven representation for predicting multi-type relationships between bioentities. GigaScience, 2020, 9, .	3.3	10
35	GNMFLMI: Graph Regularized Nonnegative Matrix Factorization for Predicting LncRNA-MiRNA Interactions. IEEE Access, 2020, 8, 37578-37588.	2.6	24
36	RPI-SE: a stacking ensemble learning framework for ncRNA-protein interactions prediction using sequence information. BMC Bioinformatics, 2020, 21, 60.	1.2	35

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37	Predicting miRNA-disease association from heterogeneous information network with GraRep embedding model. Scientific Reports, 2020, 10, 6658.	1.6	43
38	A Highly Efficient Biomolecular Network Representation Model for Predicting Drug-Disease Associations. Lecture Notes in Computer Science, 2020, , 271-279.	1.0	5
39	A MapReduce-Based Parallel Random Forest Approach for Predicting Large-Scale Protein-Protein Interactions. Lecture Notes in Computer Science, 2020, , 400-407.	1.0	2
40	NLPEI: A Novel Self-Interacting Protein Prediction Model Based on Natural Language Processing and Evolutionary Information. Evolutionary Bioinformatics, 2020, 16, 117693432098417.	0.6	3
41	Predicting Human Disease-Associated piRNAs Based on Multi-source Information and Random Forest. Lecture Notes in Computer Science, 2020, , 227-238.	1.0	3
42	MLMDA: a machine learning approach to predict and validate MicroRNAâ€“disease associations by integrating of heterogenous information sources. Journal of Translational Medicine, 2019, 17, 260.	1.8	68
43	Construction and Comprehensive Analysis of a Molecular Association Network via lncRNAâ€“miRNA â€“Diseaseâ€–Drugâ€–Protein Graph. Cells, 2019, 8, 866.	1.8	34
44	A Learning-Based Method for LncRNA-Disease Association Identification Combing Similarity Information and Rotation Forest. IScience, 2019, 19, 786-795.	1.9	70
45	CGMDA: An Approach to Predict and Validate MicroRNA-Disease Associations by Utilizing Chaos Game Representation and LightGBM. IEEE Access, 2019, 7, 133314-133323.	2.6	27
46	Predicting Drug-Disease Associations via Using Gaussian Interaction Profile and Kernel-Based Autoencoder. BioMed Research International, 2019, 2019, 1-11.	0.9	28
47	ACP-DL: A Deep Learning Long Short-Term Memory Model to Predict Anticancer Peptides Using High-Efficiency Feature Representation. Molecular Therapy - Nucleic Acids, 2019, 17, 1-9.	2.3	123
48	Sequence-based Prediction of Protein-Protein Interactions Using Gray Wolf Optimizerâ€“Based Relevance Vector Machine. Evolutionary Bioinformatics, 2019, 15, 117693431984452.	0.6	15
49	Age Is Important for the Early-Stage Detection of Breast Cancer on Both Transcriptomic and Methylomic Biomarkers. Frontiers in Genetics, 2019, 10, 212.	1.1	11
50	In Silico Prediction of Small Molecule-miRNA Associations Based on the HeteSim Algorithm. Molecular Therapy - Nucleic Acids, 2019, 14, 274-286.	2.3	54
51	LMTRDA: Using logistic model tree to predict MiRNA-disease associations by fusing multi-source information of sequences and similarities. PLoS Computational Biology, 2019, 15, e1006865.	1.5	111
52	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.	1.8	30
53	A High Efficient Biological Language Model for Predicting Proteinâ€“Protein Interactions. Cells, 2019, 8, 122.	1.8	56
54	Predicting circRNA-disease associations using deep generative adversarial network based on multi-source fusion information. , 2019, , .		16

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55	Global Vectors Representation of Protein Sequences and Its Application for Predicting Self-Interacting Proteins with Multi-Grained Cascade Forest Model. Genes, 2019, 10, 924.	1.0	10
56	Predicting drugâ˜disease associations via sigmoid kernel-based convolutional neural networks. Journal of Translational Medicine, 2019, 17, 382.	1.8	33
57	Identification of self-interacting proteins by integrating random projection classifier and finite impulse response filter. BMC Genomics, 2019, 20, 928.	1.2	4
58	Construction and Analysis of Molecular Association Network by Combining Behavior Representation and Node Attributes. Frontiers in Genetics, 2019, 10, 1106.	1.1	11
59	MicroRNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2019, 20, 515-539.	3.2	507
60	BNPMDA: Bipartite Network Projection for MiRNAâ€“Disease Association prediction. Bioinformatics, 2018, 34, 3178-3186.	1.8	307
61	A Deep Learning Framework for Robust and Accurate Prediction of ncRNA-Protein Interactions Using Evolutionary Information. Molecular Therapy - Nucleic Acids, 2018, 11, 337-344.	2.3	116
62	An improved efficient rotation forest algorithm to predict the interactions among proteins. Soft Computing, 2018, 22, 3373-3381.	2.1	34
63	HEMD: a highly efficient random forest-based malware detection framework for Android. Neural Computing and Applications, 2018, 30, 3353-3361.	3.2	47
64	DRMDA: deep representationsâ€based miRNAâ€“disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 472-485.	1.6	75
65	A Computational-Based Method for Predicting Drugâ€“Target Interactions by Using Stacked Autoencoder Deep Neural Network. Journal of Computational Biology, 2018, 25, 361-373.	0.8	140
66	RFDT: A Rotation Forest-based Predictor for Predicting Drug-Target Interactions Using Drug Structure and Protein Sequence Information. Current Protein and Peptide Science, 2018, 19, 445-454.	0.7	94
67	Novel Human miRNA-Disease Association Inference Based on Random Forest. Molecular Therapy - Nucleic Acids, 2018, 13, 568-579.	2.3	97
68	A heterogeneous label propagation approach to explore the potential associations between miRNA and disease. Journal of Translational Medicine, 2018, 16, 348.	1.8	41
69	Prediction of protein self-interactions using stacked long short-term memory from protein sequences information. BMC Systems Biology, 2018, 12, 129.	3.0	17
70	FMSM: a novel computational model for predicting potential miRNA biomarkers for various human diseases. BMC Systems Biology, 2018, 12, 121.	3.0	12
71	Accurate Prediction of ncRNA-Protein Interactions From the Integration of Sequence and Evolutionary Information. Frontiers in Genetics, 2018, 9, 458.	1.1	29
72	Using Two-dimensional Principal Component Analysis and Rotation Forest for Prediction of Protein-Protein Interactions. Scientific Reports, 2018, 8, 12874.	1.6	27

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73	Improving Prediction of Self-interacting Proteins Using Stacked Sparse Auto-Encoder with PSSM profiles. International Journal of Biological Sciences, 2018, 14, 983-991.	2.6	19
74	An Ensemble Classifier with Random Projection for Predicting Proteinâ€“Protein Interactions Using Sequence and Evolutionary Information. Applied Sciences (Switzerland), 2018, 8, 89.	1.3	24
75	A Systematic Prediction of Drug-Target Interactions Using Molecular Fingerprints and Protein Sequences. Current Protein and Peptide Science, 2018, 19, 468-478.	0.7	69
76	Distributed Winner-Take-All in Dynamic Networks. IEEE Transactions on Automatic Control, 2017, 62, 577-589.	3.6	109
77	Advancing the prediction accuracy of protein-protein interactions by utilizing evolutionary information from position-specific scoring matrix and ensemble classifier. Journal of Theoretical Biology, 2017, 418, 105-110.	0.8	50
78	Prediction of protein-protein interactions by label propagation with protein evolutionary and chemical information derived from heterogeneous network. Journal of Theoretical Biology, 2017, 430, 9-20.	0.8	17
79	In silico prediction of drug-target interaction networks based on drug chemical structure and protein sequences. Scientific Reports, 2017, 7, 11174.	1.6	62
80	MCMDA: Matrix completion for MiRNA-disease association prediction. Oncotarget, 2017, 8, 21187-21199.	0.8	189
81	Prediction of Drugâ€“Target Interaction Networks from the Integration of Protein Sequences and Drug Chemical Structures. Molecules, 2017, 22, 1119.	1.7	61
82	Detection of Interactions between Proteins by Using Legendre Moments Descriptor to Extract Discriminatory Information Embedded in PSSM. Molecules, 2017, 22, 1366.	1.7	28
83	NRDTD: a database for clinically or experimentally supported non-coding RNAs and drug targets associations. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	60
84	An ensemble approach for large-scale identification of protein-protein interactions using the alignments of multiple sequences. Oncotarget, 2017, 8, 5149-5159.	0.8	40
85	PBMDA: A novel and effective path-based computational model for miRNA-disease association prediction. PLoS Computational Biology, 2017, 13, e1005455.	1.5	387
86	Accurate prediction of protein-protein interactions by integrating potential evolutionary information embedded in PSSM profile and discriminative vector machine classifier. Oncotarget, 2017, 8, 23638-23649.	0.8	36
87	CIPPN: computational identification of protein pupylation sites by using neural network. Oncotarget, 2017, 8, 108867-108879.	0.8	16
88	Identification of self-interacting proteins by exploring evolutionary information embedded in PSI-BLAST-constructed position specific scoring matrix. Oncotarget, 2016, 7, 82440-82449.	0.8	24
89	Highly Accurate Prediction of Protein-Protein Interactions via Incorporating Evolutionary Information and Physicochemical Characteristics. International Journal of Molecular Sciences, 2016, 17, 1396.	1.8	35
90	Robust and accurate prediction of protein self-interactions from amino acids sequence using evolutionary information. Molecular BioSystems, 2016, 12, 3702-3710.	2.9	17

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91	Improved protein-protein interactions prediction via weighted sparse representation model combining continuous wavelet descriptor and PseAA composition. BMC Systems Biology, 2016, 10, 120.	3.0	25