

Zhu-Hong You

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1656994/publications.pdf>

Version: 2024-02-01

91
papers

4,673
citations

117625

34
h-index

110387

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. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2022, , 1-1.	5.7	23
2	Multi-Neighborhood Learning for Global Alignment in Biological Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2598-2611.	3.0	12
3	A graph auto-encoder model for miRNA-disease associations prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	63
4	Prediction of lncRNA-disease associations via an embedding learning HOPE in heterogeneous information networks. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 23, 277-285.	5.1	17
5	HiSCF: leveraging higher-order structures for clustering analysis in biological networks. <i>Bioinformatics</i> , 2021, 37, 542-550.	4.1	76
6	An Efficient Computational Model for Large-Scale Prediction of Protein-Protein Interactions Based on Accurate and Scalable Graph Embedding. <i>Frontiers in Genetics</i> , 2021, 12, 635451.	2.3	7
7	A survey on computational models for predicting protein-protein interactions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	92
8	SGANRDA: semi-supervised generative adversarial networks for predicting circRNA-disease associations. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	33
9	DF-MDA: An effective diffusion-based computational model for predicting miRNA-disease association. <i>Molecular Therapy</i> , 2021, 29, 1501-1511.	8.2	12
10	A Novel Method to Predict Drug-Target Interactions Based on Large-Scale Graph Representation Learning. <i>Cancers</i> , 2021, 13, 2111.	3.7	31
11	MGRL: Predicting Drug-Disease Associations Based on Multi-Graph Representation Learning. <i>Frontiers in Genetics</i> , 2021, 12, 657182.	2.3	8
12	In silico drug repositioning using deep learning and comprehensive similarity measures. <i>BMC Bioinformatics</i> , 2021, 22, 293.	2.6	6
13	A structural deep network embedding model for predicting associations between miRNA and disease based on molecular association network. <i>Scientific Reports</i> , 2021, 11, 12640.	3.3	7
14	DANE-MDA: Predicting microRNA-disease associations via deep attributed network embedding. <i>IScience</i> , 2021, 24, 102455.	4.1	14
15	Learning from low-rank multimodal representations for predicting disease-drug associations. <i>BMC Medical Informatics and Decision Making</i> , 2021, 21, 308.	3.0	10
16	Identification of potential drug targets by combining evolutionary information extracted from frequency profiles and molecular topological structures. <i>Chemical Biology and Drug Design</i> , 2020, 96, 758-767.	3.2	8
17	LNRLMI: Linear neighbour representation for predicting lncRNA-miRNA interactions. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 79-87.	3.6	27
18	Learning distributed representations of RNA and protein sequences and its application for predicting lncRNA-protein interactions. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 20-26.	4.1	31

#	ARTICLE	IF	CITATIONS
19	Integrative Construction and Analysis of Molecular Association Network in Human Cells by Fusing Node Attribute and Behavior Information. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 498-506.	5.1	13
20	DBMDA: A Unified Embedding for Sequence-Based miRNA Similarity Measure with Applications to Predict and Validate miRNA-Disease Associations. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 602-611.	5.1	49
21	An efficient approach based on multi-sources information to predict circRNA-disease associations using deep convolutional neural network. <i>Bioinformatics</i> , 2020, 36, 4038-4046.	4.1	105
22	MIPDH: A Novel Computational Model for Predicting microRNA-mRNA Interactions by DeepWalk on a Heterogeneous Network. <i>ACS Omega</i> , 2020, 5, 17022-17032.	3.5	17
23	Learning Representations to Predict Intermolecular Interactions on Large-Scale Heterogeneous Molecular Association Network. <i>IScience</i> , 2020, 23, 101261.	4.1	16
24	iMDA-BN: Identification of miRNA-disease associations based on the biological network and graph embedding algorithm. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2391-2400.	4.1	11
25	NEMPD: a network embedding-based method for predicting miRNA-disease associations by preserving behavior and attribute information. <i>BMC Bioinformatics</i> , 2020, 21, 401.	2.6	6
26	Prediction of drug-target interactions from multi-molecular network based on LINE network representation method. <i>Journal of Translational Medicine</i> , 2020, 18, 347.	4.4	26
27	iCDA-CGR: Identification of circRNA-disease associations based on Chaos Game Representation. <i>PLoS Computational Biology</i> , 2020, 16, e1007872.	3.2	63
28	GCNCDA: A new method for predicting circRNA-disease associations based on Graph Convolutional Network Algorithm. <i>PLoS Computational Biology</i> , 2020, 16, e1007568.	3.2	85
29	Incorporating chemical sub-structures and protein evolutionary information for inferring drug-target interactions. <i>Scientific Reports</i> , 2020, 10, 6641.	3.3	11
30	Prediction of Drug-Target Interactions From Multi-Molecular Network Based on Deep Walk Embedding Model. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 338.	4.1	51
31	A learning based framework for diverse biomolecule relationship prediction in molecular association network. <i>Communications Biology</i> , 2020, 3, 118.	4.4	19
32	SAEROF: an ensemble approach for large-scale drug-disease association prediction by incorporating rotation forest and sparse autoencoder deep neural network. <i>Scientific Reports</i> , 2020, 10, 4972.	3.3	22
33	A deep learning-based method for drug-target interaction prediction based on long short-term memory neural network. <i>BMC Medical Informatics and Decision Making</i> , 2020, 20, 49.	3.0	64
34	Bioentity2vec: Attribute- and behavior-driven representation for predicting multi-type relationships between bioentities. <i>GigaScience</i> , 2020, 9, .	6.4	10
35	GNMFLMI: Graph Regularized Nonnegative Matrix Factorization for Predicting LncRNA-MiRNA Interactions. <i>IEEE Access</i> , 2020, 8, 37578-37588.	4.2	24
36	RPI-SE: a stacking ensemble learning framework for ncRNA-protein interactions prediction using sequence information. <i>BMC Bioinformatics</i> , 2020, 21, 60.	2.6	35

#	ARTICLE	IF	CITATIONS
37	Predicting miRNA-disease association from heterogeneous information network with GraRep embedding model. <i>Scientific Reports</i> , 2020, 10, 6658.	3.3	43
38	A Highly Efficient Biomolecular Network Representation Model for Predicting Drug-Disease Associations. <i>Lecture Notes in Computer Science</i> , 2020, , 271-279.	1.3	5
39	A MapReduce-Based Parallel Random Forest Approach for Predicting Large-Scale Protein-Protein Interactions. <i>Lecture Notes in Computer Science</i> , 2020, , 400-407.	1.3	2
40	NLPEI: A Novel Self-Interacting Protein Prediction Model Based on Natural Language Processing and Evolutionary Information. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432098417.	1.2	3
41	Predicting Human Disease-Associated piRNAs Based on Multi-source Information and Random Forest. <i>Lecture Notes in Computer Science</i> , 2020, , 227-238.	1.3	3
42	MLMDA: a machine learning approach to predict and validate MicroRNA-disease associations by integrating of heterogenous information sources. <i>Journal of Translational Medicine</i> , 2019, 17, 260.	4.4	68
43	Construction and Comprehensive Analysis of a Molecular Association Network via lncRNA-miRNA-disease-Drug-Protein Graph. <i>Cells</i> , 2019, 8, 866.	4.1	34
44	A Learning-Based Method for lncRNA-Disease Association Identification Combing Similarity Information and Rotation Forest. <i>IScience</i> , 2019, 19, 786-795.	4.1	70
45	CGMDA: An Approach to Predict and Validate MicroRNA-Disease Associations by Utilizing Chaos Game Representation and LightGBM. <i>IEEE Access</i> , 2019, 7, 133314-133323.	4.2	27
46	Predicting Drug-Disease Associations via Using Gaussian Interaction Profile and Kernel-Based Autoencoder. <i>BioMed Research International</i> , 2019, 2019, 1-11.	1.9	28
47	ACP-DL: A Deep Learning Long Short-Term Memory Model to Predict Anticancer Peptides Using High-Efficiency Feature Representation. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 17, 1-9.	5.1	123
48	Sequence-based Prediction of Protein-Protein Interactions Using Gray Wolf Optimizer-Based Relevance Vector Machine. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431984452.	1.2	15
49	Age Is Important for the Early-Stage Detection of Breast Cancer on Both Transcriptomic and Methyloomic Biomarkers. <i>Frontiers in Genetics</i> , 2019, 10, 212.	2.3	11
50	In Silico Prediction of Small Molecule-miRNA Associations Based on the HeteSim Algorithm. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 14, 274-286.	5.1	54
51	LMTRDA: Using logistic model tree to predict MiRNA-disease associations by fusing multi-source information of sequences and similarities. <i>PLoS Computational Biology</i> , 2019, 15, e1006865.	3.2	111
52	Prediction of Self-Interacting Proteins from Protein Sequence Information Based on Random Projection Model and Fast Fourier Transform. <i>International Journal of Molecular Sciences</i> , 2019, 20, 930.	4.1	30
53	A High Efficient Biological Language Model for Predicting Protein-Protein Interactions. <i>Cells</i> , 2019, 8, 122.	4.1	56
54	Predicting circRNA-disease associations using deep generative adversarial network based on multi-source fusion information. , 2019, , .		16

#	ARTICLE	IF	CITATIONS
55	Global Vectors Representation of Protein Sequences and Its Application for Predicting Self-Interacting Proteins with Multi-Grained Cascade Forest Model. <i>Genes</i> , 2019, 10, 924.	2.4	10
56	Predicting drug-disease associations via sigmoid kernel-based convolutional neural networks. <i>Journal of Translational Medicine</i> , 2019, 17, 382.	4.4	33
57	Identification of self-interacting proteins by integrating random projection classifier and finite impulse response filter. <i>BMC Genomics</i> , 2019, 20, 928.	2.8	4
58	Construction and Analysis of Molecular Association Network by Combining Behavior Representation and Node Attributes. <i>Frontiers in Genetics</i> , 2019, 10, 1106.	2.3	11
59	MicroRNAs and complex diseases: from experimental results to computational models. <i>Briefings in Bioinformatics</i> , 2019, 20, 515-539.	6.5	507
60	BNPMDA: Bipartite Network Projection for miRNA-Disease Association prediction. <i>Bioinformatics</i> , 2018, 34, 3178-3186.	4.1	307
61	A Deep Learning Framework for Robust and Accurate Prediction of ncRNA-Protein Interactions Using Evolutionary Information. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 11, 337-344.	5.1	116
62	An improved efficient rotation forest algorithm to predict the interactions among proteins. <i>Soft Computing</i> , 2018, 22, 3373-3381.	3.6	34
63	HEMD: a highly efficient random forest-based malware detection framework for Android. <i>Neural Computing and Applications</i> , 2018, 30, 3353-3361.	5.6	47
64	DRMDA: deep representations-based miRNA-disease association prediction. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 472-485.	3.6	75
65	A Computational-Based Method for Predicting Drug-Target Interactions by Using Stacked Autoencoder Deep Neural Network. <i>Journal of Computational Biology</i> , 2018, 25, 361-373.	1.6	140
66	RFDT: A Rotation Forest-based Predictor for Predicting Drug-Target Interactions Using Drug Structure and Protein Sequence Information. <i>Current Protein and Peptide Science</i> , 2018, 19, 445-454.	1.4	94
67	Novel Human miRNA-Disease Association Inference Based on Random Forest. <i>Molecular Therapy - Nucleic Acids</i> , 2018, 13, 568-579.	5.1	97
68	A heterogeneous label propagation approach to explore the potential associations between miRNA and disease. <i>Journal of Translational Medicine</i> , 2018, 16, 348.	4.4	41
69	Prediction of protein self-interactions using stacked long short-term memory from protein sequences information. <i>BMC Systems Biology</i> , 2018, 12, 129.	3.0	17
70	FMSM: a novel computational model for predicting potential miRNA biomarkers for various human diseases. <i>BMC Systems Biology</i> , 2018, 12, 121.	3.0	12
71	Accurate Prediction of ncRNA-Protein Interactions From the Integration of Sequence and Evolutionary Information. <i>Frontiers in Genetics</i> , 2018, 9, 458.	2.3	29
72	Using Two-dimensional Principal Component Analysis and Rotation Forest for Prediction of Protein-Protein Interactions. <i>Scientific Reports</i> , 2018, 8, 12874.	3.3	27

#	ARTICLE	IF	CITATIONS
73	Improving Prediction of Self-interacting Proteins Using Stacked Sparse Auto-Encoder with PSSM profiles. <i>International Journal of Biological Sciences</i> , 2018, 14, 983-991.	6.4	19
74	An Ensemble Classifier with Random Projection for Predicting Protein-Protein Interactions Using Sequence and Evolutionary Information. <i>Applied Sciences (Switzerland)</i> , 2018, 8, 89.	2.5	24
75	A Systematic Prediction of Drug-Target Interactions Using Molecular Fingerprints and Protein Sequences. <i>Current Protein and Peptide Science</i> , 2018, 19, 468-478.	1.4	69
76	Distributed Winner-Take-All in Dynamic Networks. <i>IEEE Transactions on Automatic Control</i> , 2017, 62, 577-589.	5.7	109
77	Advancing the prediction accuracy of protein-protein interactions by utilizing evolutionary information from position-specific scoring matrix and ensemble classifier. <i>Journal of Theoretical Biology</i> , 2017, 418, 105-110.	1.7	50
78	Prediction of protein-protein interactions by label propagation with protein evolutionary and chemical information derived from heterogeneous network. <i>Journal of Theoretical Biology</i> , 2017, 430, 9-20.	1.7	17
79	In silico prediction of drug-target interaction networks based on drug chemical structure and protein sequences. <i>Scientific Reports</i> , 2017, 7, 11174.	3.3	62
80	MCMDA: Matrix completion for MiRNA-disease association prediction. <i>Oncotarget</i> , 2017, 8, 21187-21199.	1.8	189
81	Prediction of Drug-Target Interaction Networks from the Integration of Protein Sequences and Drug Chemical Structures. <i>Molecules</i> , 2017, 22, 1119.	3.8	61
82	Detection of Interactions between Proteins by Using Legendre Moments Descriptor to Extract Discriminatory Information Embedded in PSSM. <i>Molecules</i> , 2017, 22, 1366.	3.8	28
83	NRDTD: a database for clinically or experimentally supported non-coding RNAs and drug targets associations. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	60
84	An ensemble approach for large-scale identification of protein-protein interactions using the alignments of multiple sequences. <i>Oncotarget</i> , 2017, 8, 5149-5159.	1.8	40
85	PBMDA: A novel and effective path-based computational model for miRNA-disease association prediction. <i>PLoS Computational Biology</i> , 2017, 13, e1005455.	3.2	387
86	Accurate prediction of protein-protein interactions by integrating potential evolutionary information embedded in PSSM profile and discriminative vector machine classifier. <i>Oncotarget</i> , 2017, 8, 23638-23649.	1.8	36
87	CIPPN: computational identification of protein pupylation sites by using neural network. <i>Oncotarget</i> , 2017, 8, 108867-108879.	1.8	16
88	Identification of self-interacting proteins by exploring evolutionary information embedded in PSI-BLAST-constructed position specific scoring matrix. <i>Oncotarget</i> , 2016, 7, 82440-82449.	1.8	24
89	Highly Accurate Prediction of Protein-Protein Interactions via Incorporating Evolutionary Information and Physicochemical Characteristics. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1396.	4.1	35
90	Robust and accurate prediction of protein self-interactions from amino acids sequence using evolutionary information. <i>Molecular BioSystems</i> , 2016, 12, 3702-3710.	2.9	17

#	ARTICLE	IF	CITATIONS
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