Zhu-Hong You

List of Publications by Year
in descending order

186 papers	10,454 citations	31976 53 h-index	38395 95 g-index
190 all docs	190 docs citations	190 times ranked	4922 citing authors

#	Article	IF	Citations
1	Graph representation learning in bioinformatics: trends, methods and applications. Briefings in Bioinformatics, 2022, 23, .	6.5	64
2	Attention-based Knowledge Graph Representation Learning for Predicting Drug-drug Interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	46
3	SAWRPI: A Stacking Ensemble Framework With Adaptive Weight for Predicting ncRNA-Protein Interactions Using Sequence Information. Frontiers in Genetics, 2022, 13, 839540.	2.3	3
4	A deep learning method for repurposing antiviral drugs against new viruses via multi-view nonnegative matrix factorization and its application to SARS-CoV-2. Briefings in Bioinformatics, 2022, 23, .	6.5	56
5	HINGRL: predicting drugâ€“disease associations with graph representation learning on heterogeneous information networks. Briefings in Bioinformatics, 2022, 23, .	6.5	60
6	GraphTGI: an attention-based graph embedding model for predicting TF-target gene interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	7
7	Predicting Protein-Protein Interactions via Random Ferns with Evolutionary Matrix Representation. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-11.	1.3	1
8	A Novel Ensemble Learning-Based Computational Method to Predict Protein-Protein Interactions from Protein Primary Sequences. Biology, 2022, 11, 775.	2.8	2
9	BioChemDDI: Predicting Drugâ€“Drug Interactions by Fusing Biochemical and Structural Information through a Self-Attention Mechanism. Biology, 2022, 11, 758.	2.8	3
10	Combining K Nearest Neighbor With Nonnegative Matrix Factorization for Predicting Circrna-Disease Associations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, , 1-10.	3.0	2
11	Predicting Proteinâ€“Protein Interactions Based on Ensemble Learning-Based Model from Protein Sequence. Biology, 2022, 11, 995.	2.8	1
12	LDGRNMF: LncRNA-disease associations prediction based on graph regularized non-negative matrix factorization. Neurocomputing, 2021, 424, 236-245.	5.9	53
13	Self-Interacting Proteins Prediction from PSSM Based on Evolutionary Information. Scientific Programming, 2021, 2021, 1-10.	0.7	2
14	SEDMDroid: An Enhanced Stacking Ensemble Framework for Android Malware Detection. IEEE Transactions on Network Science and Engineering, 2021, 8, 984-994.	6.4	65
15	Efficient framework for predicting MiRNA-disease associations based on improved hybrid collaborative filtering. BMC Medical Informatics and Decision Making, 2021, 21, 254.	3.0	3
16	FWHT-RF: A Novel Computational Approach to Predict Plant Protein-Protein Interactions via an Ensemble Learning Method. Scientific Programming, 2021, 2021, 1-11.	0.7	2
17	A Novel Network-Based Algorithm for Predicting Protein-Protein Interactions Using Gene Ontology. Frontiers in Microbiology, 2021, 12, 735329.	3.5	11
18	SANE: A sequence combined attentive network embedding model for COVID-19 drug repositioning. Applied Soft Computing Journal, 2021, 111, 107831.	7.2	23

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19	Learning from low-rank multimodal representations for predicting disease-drug associations. BMC Medical Informatics and Decision Making, 2021, 21, 308.	3.0	10
20	A learning-based method to predict LncRNA-disease associations by combining CNN and ELM. BMC Bioinformatics, 2021, 22, 622.	2.6	1
21	Graph convolution for predicting associations between miRNA and drug resistance. Bioinformatics, 2020, 36, 851-858.	4.1	77
22	Combining High Speed ELM Learning with a Deep Convolutional Neural Network Feature Encoding for Predicting Protein-RNA Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 972-980.	3.0	43
23	LNRLMI: Linear neighbour representation for predicting lncRNAâ€miRNA interactions. Journal of Cellular and Molecular Medicine, 2020, 24, 79-87.	3.6	27
24	Privacy-Preserving Global Structural Balance Computation in Signed Networks. IEEE Transactions on Computational Social Systems, 2020, 7, 164-177.	4.4	7
25	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.	4.1	31
26	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.	5.1	13
27	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.	5.1	49
28	A survey of current trends in computational predictions of protein-protein interactions. Frontiers of Computer Science, 2020, 14, 1.	2.4	19
29	Prediction of Protein-Protein Interactions from Protein Sequences by Combining MatPCA Feature Extraction Algorithms and Weighted Sparse Representation Models. Mathematical Problems in Engineering, 2020, 2020, 1-11.	1.1	2
30	MIPDH: A Novel Computational Model for Predicting microRNAâ€“mRNA Interactions by DeepWalk on a Heterogeneous Network. ACS Omega, 2020, 5, 17022-17032.	3.5	17
31	Ensemble Learning Prediction of Drug-Target Interactions Using GIST Descriptor Extracted from PSSM-Based Evolutionary Information. BioMed Research International, 2020, 2020, 1-10.	1.9	5
32	FCGCNMDA: predicting miRNA-disease associations by applying fully connected graph convolutional networks. Molecular Genetics and Genomics, 2020, 295, 1197-1209.	2.1	23
33	RPI-SE: a stacking ensemble learning framework for ncRNA-protein interactions prediction using sequence information. BMC Bioinformatics, 2020, 21, 60.	2.6	35
34	Identification of Autistic Risk Genes Using Developmental Brain Gene Expression Data. Lecture Notes in Computer Science, 2020, , 326-338.	1.3	0
35	Prediction of LncRNA-Disease Associations Based on Network Representation Learning. , 2020, , .		2
36	Proteinâ€“Protein Interactions Prediction via Multimodal Deep Polynomial Network and Regularized Extreme Learning Machine. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 1290-1303.	6.3	30

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37	Discovery of Novel DPP-IV Inhibitors as Potential Candidates for the Treatment of Type 2 Diabetes mellitus Predicted by 3D QSAR Pharmacophore Models, Molecular Docking and de novo Evolution. Molecules, 2019, 24, 2870.	3.8	22
38	Combining LSTM Network Model and Wavelet Transform for Predicting Self-interacting Proteins. Lecture Notes in Computer Science, 2019, , 166-174.	1.3	2
39	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.	4.4	68
40	Precise Prediction of Pathogenic Microorganisms Using 16S rRNA Gene Sequences. Lecture Notes in Computer Science, 2019, , 138-150.	1.3	5
41	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
42	Predicting of Drug-Disease Associations via Sparse Auto-Encoder-Based Rotation Forest. Lecture Notes in Computer Science, 2019, , 369-380.	1.3	4
43	Learning from Deep Representations of Multiple Networks for Predicting Drugâ€“Target Interactions. Lecture Notes in Computer Science, 2019, , 151-161.	1.3	10
44	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
45	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
46	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
47	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
48	A Learning-Based Method for LncRNA-Disease Association Identification Combing Similarity Information and Rotation Forest. IScience, 2019, 19, 786-795.	4.1	70
49	Drug-Target Interaction Prediction Based on Drug Fingerprint Information and Protein Sequence. Molecules, 2019, 24, 2999.	3.8	20
50	CGMDA: An Approach to Predict and Validate MicroRNA-Disease Associations by Utilizing Chaos Game Representation and LightGBM. IEEE Access, 2019, 7, 133314-133323.	4.2	27
51	An Efficient Attribute-Based Encryption Scheme With Policy Update and File Update in Cloud Computing. IEEE Transactions on Industrial Informatics, 2019, 15, 6500-6509.	11.3	65
52	Predicting Drug-Disease Associations via Using Gaussian Interaction Profile and Kernel-Based Autoencoder. BioMed Research International, 2019, 2019, 1-11.	1.9	28
53	Predicting lncRNA-miRNA Interaction via Graph Convolution Auto-Encoder. Frontiers in Genetics, 2019, 10, 758.	2.3	41
54	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.	5.1	123

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55	Sequence-based Prediction of Protein-Protein Interactions Using Gray Wolf Optimizerâ€“Based Relevance Vector Machine. Evolutionary Bioinformatics, 2019, 15, 117693431984452.	1.2	15
56	In Silico Prediction of Small Molecule-miRNA Associations Based on the HeteSim Algorithm. Molecular Therapy - Nucleic Acids, 2019, 14, 274-286.	5.1	54
57	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.	3.2	111
58	Improved Prediction of Protein-Protein Interactions Using Descriptors Derived From PSSM via Gray Level Co-Occurrence Matrix. IEEE Access, 2019, 7, 49456-49465.	4.2	11
59	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
60	Global Vectors Representation of Protein Sequences and Its Application for Predicting Self-Interacting Proteins with Multi-Grained Cascade Forest Model. Genes, 2019, 10, 924.	2.4	10
61	Predicting drugâ^'disease associations via sigmoid kernel-based convolutional neural networks. Journal of Translational Medicine, 2019, 17, 382.	4.4	33
62	Using discriminative vector machine model with 2DPCA to predict interactions among proteins. BMC Bioinformatics, 2019, 20, 694.	2.6	7
63	Identification of self-interacting proteins by integrating random projection classifier and finite impulse response filter. BMC Genomics, 2019, 20, 928.	2.8	4
64	Construction and Analysis of Molecular Association Network by Combining Behavior Representation and Node Attributes. Frontiers in Genetics, 2019, 10, 1106.	2.3	11
65	An Efficient Ensemble Learning Approach for Predicting Protein-Protein Interactions by Integrating Protein Primary Sequence and Evolutionary Information. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 809-817.	3.0	29
66	MicroRNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2019, 20, 515-539.	6.5	507
67	Plant disease leaf image segmentation based on superpixel clustering and EM algorithm. Neural Computing and Applications, 2019, 31, 1225-1232.	5.6	86
68	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
69	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
70	BNPMDA: Bipartite Network Projection for MiRNAâ€“Disease Association prediction. Bioinformatics, 2018, 34, 3178-3186.	4.1	307
71	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
72	Incorporation of Efficient Second-Order Solvers Into Latent Factor Models for Accurate Prediction of Missing QoS Data. IEEE Transactions on Cybernetics, 2018, 48, 1216-1228.	9.5	207

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73	An improved efficient rotation forest algorithm to predict the interactions among proteins. Soft Computing, 2018, 22, 3373-3381.	3.6	34
74	HEMD: a highly efficient random forest-based malware detection framework for Android. Neural Computing and Applications, 2018, 30, 3353-3361.	5.6	47
75	DroidDet: Effective and robust detection of android malware using static analysis along with rotation forest model. Neurocomputing, 2018, 272, 638-646.	5.9	146
76	Constructing prediction models from expression profiles for large scale lncRNAâ€“miRNA interaction profiling. Bioinformatics, 2018, 34, 812-819.	4.1	91
77	DRMDA: deep representationsâ€based miRNAâ€“disease association prediction. Journal of Cellular and Molecular Medicine, 2018, 22, 472-485.	3.6	75
78	A Computational-Based Method for Predicting Drugâ€“Target Interactions by Using Stacked Autoencoder Deep Neural Network. Journal of Computational Biology, 2018, 25, 361-373.	1.6	140
79	Plant diseased leaf segmentation and recognition by fusion of superpixel, K-means and PHOG. Optik, 2018, 157, 866-872.	2.9	200
80	Learning Latent Patterns in Molecular Data for Explainable Drug Side Effects Prediction. , 2018, , .		5
81	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
82	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.	1.4	94
83	Novel Human miRNA-Disease Association Inference Based on Random Forest. Molecular Therapy - Nucleic Acids, 2018, 13, 568-579.	5.1	97
84	A heterogeneous label propagation approach to explore the potential associations between miRNA and disease. Journal of Translational Medicine, 2018, 16, 348.	4.4	41
85	Prediction of protein self-interactions using stacked long short-term memory from protein sequences information. BMC Systems Biology, 2018, 12, 129.	3.0	17
86	FMSM: a novel computational model for predicting potential miRNA biomarkers for various human diseases. BMC Systems Biology, 2018, 12, 121.	3.0	12
87	Novel link prediction for large-scale miRNA-lncRNA interaction network in a bipartite graph. BMC Medical Genomics, 2018, 11, 113.	1.5	34
88	Accurate Prediction of ncRNA-Protein Interactions From the Integration of Sequence and Evolutionary Information. Frontiers in Genetics, 2018, 9, 458.	2.3	29
89	Using Two-dimensional Principal Component Analysis and Rotation Forest for Prediction of Protein-Protein Interactions. Scientific Reports, 2018, 8, 12874.	3.3	27
90	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

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91	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
92	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
93	A Systematic Prediction of Drug-Target Interactions Using Molecular Fingerprints and Protein Sequences. Current Protein and Peptide Science, 2018, 19, 468-478.	1.4	69
94	Discovering an Integrated Network in Heterogeneous Data for Predicting lncRNA-miRNA Interactions. Lecture Notes in Computer Science, 2018, , 539-545.	1.3	8
95	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
96	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
97	A novel approach based on KATZ measure to predict associations of human microbiota with non-infectious diseases. Bioinformatics, 2017, 33, 733-739.	4.1	222
98	Long non-coding RNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2017, 18, bbw060.	6.5	477
99	Identifying Spurious Interactions in the Protein-Protein Interaction Networks Using Local Similarity Preserving Embedding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 345-352.	3.0	38
100	Distributed Winner-Take-All in Dynamic Networks. IEEE Transactions on Automatic Control, 2017, 62, 577-589.	5.7	109
101	Highly Efficient Framework for Predicting Interactions Between Proteins. IEEE Transactions on Cybernetics, 2017, 47, 731-743.	9.5	107
102	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
103	PSPEL: In Silico Prediction of Self-Interacting Proteins from Amino Acids Sequences Using Ensemble Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1165-1172.	3.0	56
104	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.	1.7	50
105	Leaf image based cucumber disease recognition using sparse representation classification. Computers and Electronics in Agriculture, 2017, 134, 135-141.	7.7	195
106	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
107	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.	1.7	17
108	Predicting proteinâ€“protein interactions from protein sequences by a stacked sparse autoencoder deep neural network. Molecular BioSystems, 2017, 13, 1336-1344.	2.9	114

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109	In silico prediction of drug-target interaction networks based on drug chemical structure and protein sequences. Scientific Reports, 2017, 7, 11174.	3.3	62
110	Fusion of superpixel, expectation maximization and PHOG for recognizing cucumber diseases. Computers and Electronics in Agriculture, 2017, 140, 338-347.	7.7	43
111	MCMDA: Matrix completion for MiRNA-disease association prediction. Oncotarget, 2017, 8, 21187-21199.	1.8	189
112	Prediction of Drugâ€“Target Interaction Networks from the Integration of Protein Sequences and Drug Chemical Structures. Molecules, 2017, 22, 1119.	3.8	61
113	Detection of Interactions between Proteins by Using Legendre Moments Descriptor to Extract Discriminatory Information Embedded in PSSM. Molecules, 2017, 22, 1366.	3.8	28
114	PBHMDA: Path-Based Human Microbe-Disease Association Prediction. Frontiers in Microbiology, 2017, 8, 233.	3.5	97
115	Discriminant WSRC for Large-Scale Plant Species Recognition. Computational Intelligence and Neuroscience, 2017, 2017, 1-10.	1.7	3
116	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, .	3.0	60
117	Jaccard distance based weighted sparse representation for coarse-to-fine plant species recognition. PLoS ONE, 2017, 12, e0178317.	2.5	11
118	Prediction of microbeâ€“disease association from the integration of neighbor and graph with collaborative recommendation model. Journal of Translational Medicine, 2017, 15, 209.	4.4	105
119	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
120	PRMDA: personalized recommendation-based MiRNA-disease association prediction. Oncotarget, 2017, 8, 85568-85583.	1.8	32
121	An ensemble approach for large-scale identification of protein-protein interactions using the alignments of multiple sequences. Oncotarget, 2017, 8, 5149-5159.	1.8	40
122	Computational Methods for the Prediction of Drug-Target Interactions from Drug Fingerprints and Protein Sequences by Stacked Auto-Encoder Deep Neural Network. Lecture Notes in Computer Science, 2017, , 46-58.	1.3	12
123	PBMDA: A novel and effective path-based computational model for miRNA-disease association prediction. PLoS Computational Biology, 2017, 13, e1005455.	3.2	387
124	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.	1.8	36
125	EPMDA: an expression-profile based computational model for microRNA-disease association prediction. Oncotarget, 2017, 8, 87033-87043.	1.8	12
126	CIPPN: computational identification of protein pupylation sites by using neural network. Oncotarget, 2017, 8, 108867-108879.	1.8	16

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127	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
128	FMLNCSIM: fuzzy measure-based lncRNA functional similarity calculation model. Oncotarget, 2016, 7, 45948-45958.	1.8	103
129	HGIMDA: Heterogeneous graph inference for miRNA-disease association prediction. Oncotarget, 2016, 7, 65257-65269.	1.8	219
130	Identification of self-interacting proteins by exploring evolutionary information embedded in PSI-BLAST-constructed position specific scoring matrix. Oncotarget, 2016, 7, 82440-82449.	1.8	24
131	Ens-PPI: A Novel Ensemble Classifier for Predicting the Interactions of Proteins Using Autocovariance Transformation from PSSM. BioMed Research International, 2016, 2016, 1-8.	1.9	21
132	IRWRLDA: improved random walk with restart for lncRNA-disease association prediction. Oncotarget, 2016, 7, 57919-57931.	1.8	200
133	Detection of Interactions between Proteins through Rotation Forest and Local Phase Quantization Descriptors. International Journal of Molecular Sciences, 2016, 17, 21.	4.1	51
134	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
135	Highly Accurate Prediction of Protein-Protein Interactions via Incorporating Evolutionary Information and Physicochemical Characteristics. International Journal of Molecular Sciences, 2016, 17, 1396.	4.1	35
136	WBSMDA: Within and Between Score for MiRNA-Disease Association prediction. Scientific Reports, 2016, 6, 21106.	3.3	314
137	Construction of reliable proteinâ€“protein interaction networks using weighted sparse representation based classifier with pseudo substitution matrix representation features. Neurocomputing, 2016, 218, 131-138.	5.9	45
138	Improving proteinâ€“protein interactions prediction accuracy using protein evolutionary information and relevance vector machine model. Protein Science, 2016, 25, 1825-1833.	7.6	31
139	Large-scale prediction of drug-target interactions from deep representations. , 2016, , .		42
140	Robust and accurate prediction of protein self-interactions from amino acids sequence using evolutionary information. Molecular BioSystems, 2016, 12, 3702-3710.	2.9	17
141	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
142	Sequence-based prediction of protein-protein interactions using weighted sparse representation model combined with global encoding. BMC Bioinformatics, 2016, 17, 184.	2.6	125
143	A Nonnegative Latent Factor Model for Large-Scale Sparse Matrices in Recommender Systems via Alternating Direction Method. IEEE Transactions on Neural Networks and Learning Systems, 2016, 27, 579-592.	11.3	270
144	Inverse-Free Extreme Learning Machine With Optimal Information Updating. IEEE Transactions on Cybernetics, 2016, 46, 1229-1241.	9.5	111

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145	Modeling of signaling crosstalk-mediated drug resistance and its implications on drug combination. Oncotarget, 2016, 7, 63995-64006.	1.8	43
146	ILNCSIM: improved lncRNA functional similarity calculation model. Oncotarget, 2016, 7, 25902-25914.	1.8	122
147	A Highly Efficient Approach to Protein Interactome Mapping Based on Collaborative Filtering Framework. Scientific Reports, 2015, 5, 7702.	3.3	72
148	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
149	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
150	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
151	Improving network topology-based protein interactome mapping via collaborative filtering. Knowledge-Based Systems, 2015, 90, 23-32.	7.1	52
152	An Efficient Second-Order Approach to Factorize Sparse Matrices in Recommender Systems. IEEE Transactions on Industrial Informatics, 2015, 11, 946-956.	11.3	100
153	Prediction of Proteinâ€“Protein Interactions with Clustered Amino Acids and Weighted Sparse Representation. International Journal of Molecular Sciences, 2015, 16, 10855-10869.	4.1	26
154	Detection of Protein-Protein Interactions from Amino Acid Sequences Using a Rotation Forest Model with a Novel PR-LPQ Descriptor. Lecture Notes in Computer Science, 2015, , 713-720.	1.3	37
155	Predicting Protein-Protein Interactions from Amino Acid Sequences Using SaE-ELM Combined with Continuous Wavelet Descriptor and PseAA Composition. Lecture Notes in Computer Science, 2015, , 634-645.	1.3	2
156	Large-Scale Protein-Protein Interactions Detection by Integrating Big Biosensing Data with Computational Model. BioMed Research International, 2014, 2014, 1-9.	1.9	51
157	Using Chou's amphiphilic Pseudo-Amino Acid Composition and Extreme Learning Machine for prediction of Protein-protein interactions. , 2014, , .		5
158	A MapReduce based parallel SVM for large-scale predicting proteinâ€“protein interactions. Neurocomputing, 2014, 145, 37-43.	5.9	109
159	Predicting dynamic deformation of retaining structure by LSSVR-based time series method. Neurocomputing, 2014, 137, 165-172.	5.9	44
160	Orthogonal locally discriminant spline embedding for plant leaf recognition. Computer Vision and Image Understanding, 2014, 119, 116-126.	4.7	20
161	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
162	Identifying Spurious Interactions in the Protein-Protein Interaction Networks Using Local Similarity Preserving Embedding. Lecture Notes in Computer Science, 2014, , 138-148.	1.3	3

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163	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
164	Increasing the reliability of proteinâ€“protein interaction networks via non-convex semantic embedding. Neurocomputing, 2013, 121, 99-107.	5.9	51
165	Increasing reliability of protein interactome by fast manifold embedding. Pattern Recognition Letters, 2013, 34, 372-379.	4.2	28
166	t-LSE: A Novel Robust Geometric Approach for Modeling Protein-Protein Interaction Networks. PLoS ONE, 2013, 8, e58368.	2.5	81
167	A SVM-Based System for Predicting Protein-Protein Interactions Using a Novel Representation of Protein Sequences. Lecture Notes in Computer Science, 2013, , 629-637.	1.3	14
168	Research on Signaling Pathways Reconstruction by Integrating High Content RNAi Screening and Functional Gene Network. Lecture Notes in Computer Science, 2013, , 1-10.	1.3	1
169	Advances in the compression of high-throughput DNA sequencing data. Shenzhen Daxue Xuebao (Ligong Ban)/Journal of Shenzhen University Science and Engineering, 2013, 30, 409-415.	0.2	0
170	A novel method to predict protein-protein interactions based on the information of protein sequence. , 2012, , .		7
171	Assessing and predicting protein interactions by combining manifold embedding with multiple information integration. BMC Bioinformatics, 2012, 13, S3.	2.6	53
172	A Novel Approach to Modelling Protein-Protein Interaction Networks. Lecture Notes in Computer Science, 2012, , 49-57.	1.3	3
173	Prediction of β-Hairpins in Proteins Using Physicochemical Properties and Structure Information. Protein and Peptide Letters, 2010, 17, 1123-1128.	0.9	11
174	Improved Method for Predicting π-Turns in Proteins Using a Two-Stage Classifier. Protein and Peptide Letters, 2010, 17, 1117-1122.	0.9	11
175	A semi-supervised learning approach to predict synthetic genetic interactions by combining functional and topological properties of functional gene network. BMC Bioinformatics, 2010, 11, 343.	2.6	88
176	Using manifold embedding for assessing and predicting protein interactions from high-throughput experimental data. Bioinformatics, 2010, 26, 2744-2751.	4.1	209
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