Zhu-Hong You

List of Publications by Year in Descending Order

182 papers	7,029 citations	46 h-index	78 g-index
190 ext. papers	9,082 ext. citations	4.4 avg, IF	6.68 L-index

#	Paper	IF	Citations
182	SAWRPI: A Stacking Ensemble Framework With Adaptive Weight for Predicting ncRNA-Protein Interactions Using Sequence Information.. *Frontiers in Genetics*, **2022**, 13, 839540	4.5	0
181	A learning-based method to predict LncRNA-disease associations by combining CNN and ELM.. *BMC Bioinformatics*, **2022**, 22, 622	3.6	
180	Predicting Protein-Protein Interactions via Random Ferns with Evolutionary Matrix Representation.. *Computational and Mathematical Methods in Medicine*, **2022**, 2022, 7191684	2.8	
179	A Novel Ensemble Learning-Based Computational Method to Predict Protein-Protein Interactions from Protein Primary Sequences. *Biology*, **2022**, 11, 775	4.9	0
178	BioChemDDI: Predicting DrugDrug Interactions by Fusing Biochemical and Structural Information through a Self-Attention Mechanism. *Biology*, **2022**, 11, 758	4.9	1
177	Learning from low-rank multimodal representations for predicting disease-drug associations. *BMC Medical Informatics and Decision Making*, **2021**, 21, 308	3.6	1
176	Self-Interacting Proteins Prediction from PSSM Based on Evolutionary Information. *Scientific Programming*, **2021**, 2021, 1-10	1.4	0
175	SEDMDroid: An Enhanced Stacking Ensemble Framework for Android Malware Detection. *IEEE Transactions on Network Science and Engineering*, **2021**, 8, 984-994	4.9	20
174	Efficient framework for predicting MiRNA-disease associations based on improved hybrid collaborative filtering. *BMC Medical Informatics and Decision Making*, **2021**, 21, 254	3.6	3
173	FWHT-RF: A Novel Computational Approach to Predict Plant Protein-Protein Interactions via an Ensemble Learning Method. *Scientific Programming*, **2021**, 2021, 1-11	1.4	2
172	LDGRNMF: LncRNA-disease associations prediction based on graph regularized non-negative matrix factorization. *Neurocomputing*, **2021**, 424, 236-245	5.4	23
171	A Novel Network-Based Algorithm for Predicting Protein-Protein Interactions Using Gene Ontology. *Frontiers in Microbiology*, **2021**, 12, 735329	5.7	3
170	Graph representation learning in bioinformatics: trends, methods and applications. *Briefings in Bioinformatics*, **2021**,	13.4	6
169	SANE: A sequence combined attentive network embedding model for COVID-19 drug repositioning. *Applied Soft Computing Journal*, **2021**, 111, 107831	7.5	2
168	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*, **2021**,	13.4	5
167	HINGRL: predicting drug-disease associations with graph representation learning on heterogeneous information networks. *Briefings in Bioinformatics*, **2021**,	13.4	6
166	FCGCNMDA: predicting miRNA-disease associations by applying fully connected graph convolutional networks. *Molecular Genetics and Genomics*, **2020**, 295, 1197-1209	3.1	12

165	RPI-SE: a stacking ensemble learning framework for ncRNA-protein interactions prediction using sequence information. *BMC Bioinformatics*, **2020**, 21, 60	3.6	22
164	Graph convolution for predicting associations between miRNA and drug resistance. *Bioinformatics*, **2020**, 36, 851-858	7.2	12
163	Identification of Autistic Risk Genes Using Developmental Brain Gene Expression Data. *Lecture Notes in Computer Science*, **2020**, 326-338	0.9	
162	LNRLMI: Linear neighbour representation for predicting lncRNA-miRNA interactions. *Journal of Cellular and Molecular Medicine*, **2020**, 24, 79-87	5.6	18
161	Privacy-Preserving Global Structural Balance Computation in Signed Networks. *IEEE Transactions on Computational Social Systems*, **2020**, 7, 164-177	4.5	2
160	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	6.8	14
159	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	10.7	12
158	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	10.7	34
157	A survey of current trends in computational predictions of protein-protein interactions. *Frontiers of Computer Science*, **2020**, 14, 1	2.2	11
156	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	1
155	MIPDH: A Novel Computational Model for Predicting microRNA-mRNA Interactions by DeepWalk on a Heterogeneous Network. *ACS Omega*, **2020**, 5, 17022-17032	3.9	11
154	Ensemble Learning Prediction of Drug-Target Interactions Using GIST Descriptor Extracted from PSSM-Based Evolutionary Information. *BioMed Research International*, **2020**, 2020, 4516250	3	1
153	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	26
152	An Efficient Attribute-Based Encryption Scheme With Policy Update and File Update in Cloud Computing. *IEEE Transactions on Industrial Informatics*, **2019**, 15, 6500-6509	11.9	33
151	Predicting Drug-Disease Associations via Using Gaussian Interaction Profile and Kernel-Based Autoencoder. *BioMed Research International*, **2019**, 2019, 2426958	3	14
150	Predicting lncRNA-miRNA Interaction Graph Convolution Auto-Encoder. *Frontiers in Genetics*, **2019**, 10, 758	4.5	20
149	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	10.7	71
148	Sequence-based Prediction of Protein-Protein Interactions Using Gray Wolf Optimizer-Based Relevance Vector Machine. *Evolutionary Bioinformatics*, **2019**, 15, 1176934319844522	1.9	10

147	In Silico Prediction of Small Molecule-miRNA Associations Based on the HeteSim Algorithm. *Molecular Therapy - Nucleic Acids*, **2019**, 14, 274-286	10.7	34
146	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	5	73
145	. *IEEE Access*, **2019**, 7, 49456-49465	3.5	6
144	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,	6.3	20
143	Protein-Protein Interactions Prediction via Multimodal Deep Polynomial Network and Regularized Extreme Learning Machine. *IEEE Journal of Biomedical and Health Informatics*, **2019**, 23, 1290-1303	7.2	19
142	Discovery of Novel DPP-IV Inhibitors as Potential Candidates for the Treatment of Type 2 Predicted by 3D QSAR Pharmacophore Models, Molecular Docking and Evolution. *Molecules*, **2019**, 24,	4.8	12
141	Combining LSTM Network Model and Wavelet Transform for Predicting Self-interacting Proteins. *Lecture Notes in Computer Science*, **2019**, 166-174	0.9	1
140	MLMDA: a machine learning approach to predict and validate MicroRNA-disease associations by integrating of heterogenous information sources. *Journal of Translational Medicine*, **2019**, 17, 260	8.5	41
139	Precise Prediction of Pathogenic Microorganisms Using 16S rRNA Gene Sequences. *Lecture Notes in Computer Science*, **2019**, 138-150	0.9	2
138	Combining Evolutionary Information and Sparse Bayesian Probability Model to Accurately Predict Self-interacting Proteins. *Lecture Notes in Computer Science*, **2019**, 460-467	0.9	1
137	Predicting of Drug-Disease Associations via Sparse Auto-Encoder-Based Rotation Forest. *Lecture Notes in Computer Science*, **2019**, 369-380	0.9	3
136	Learning from Deep Representations of Multiple Networks for Predicting Drug□arget Interactions. *Lecture Notes in Computer Science*, **2019**, 151-161	0.9	6
135	Combining High Speed ELM with a CNN Feature Encoding to Predict LncRNA-Disease Associations. *Lecture Notes in Computer Science*, **2019**, 406-417	0.9	3
134	MISSIM: Improved miRNA-Disease Association Prediction Model Based on Chaos Game Representation and Broad Learning System. *Lecture Notes in Computer Science*, **2019**, 392-398	0.9	10
133	An Ensemble Classifier to Predict Protein-Protein Interactions by Combining PSSM-based Evolutionary Information with Local Binary Pattern Model. *International Journal of Molecular Sciences*, **2019**, 20,	6.3	14
132	In Silico Identification of Anticancer Peptides with Stacking Heterogeneous Ensemble Learning Model and Sequence Information. *Lecture Notes in Computer Science*, **2019**, 313-323	0.9	1
131	A Learning-Based Method for LncRNA-Disease Association Identification Combing Similarity Information and Rotation Forest. *ISCience*, **2019**, 19, 786-795	6.1	44
130	Drug-Target Interaction Prediction Based on Drug Fingerprint Information and Protein Sequence. *Molecules*, **2019**, 24,	4.8	8

129	CGMDA: An Approach to Predict and Validate MicroRNA-Disease Associations by Utilizing Chaos Game Representation and LightGBM. *IEEE Access*, **2019**, 7, 133314-133323	3.5	22
128	An Efficient LightGBM Model to Predict Protein Self-interacting Using Chebyshev Moments and Bi-gram. *Lecture Notes in Computer Science*, **2019**, 453-459	0.9	1
127	LRMDA: Using Logistic Regression and Random Walk with Restart for MiRNA-Disease Association Prediction. *Lecture Notes in Computer Science*, **2019**, 283-293	0.9	1
126	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	0.9	1
125	Global Vectors Representation of Protein Sequences and Its Application for Predicting Self-Interacting Proteins with Multi-Grained Cascade Forest Model. *Genes*, **2019**, 10,	4.2	5
124	Predicting drug-disease associations via sigmoid kernel-based convolutional neural networks. *Journal of Translational Medicine*, **2019**, 17, 382	8.5	11
123	Using discriminative vector machine model with 2DPCA to predict interactions among proteins. *BMC Bioinformatics*, **2019**, 20, 694	3.6	7
122	Identification of self-interacting proteins by integrating random projection classifier and finite impulse response filter. *BMC Genomics*, **2019**, 20, 928	4.5	1
121	Construction and Analysis of Molecular Association Network by Combining Behavior Representation and Node Attributes. *Frontiers in Genetics*, **2019**, 10, 1106	4.5	8
120	MicroRNAs and complex diseases: from experimental results to computational models. *Briefings in Bioinformatics*, **2019**, 20, 515-539	13.4	296
119	Plant disease leaf image segmentation based on superpixel clustering and EM algorithm. *Neural Computing and Applications*, **2019**, 31, 1225-1232	4.8	39
118	BNPMDA: Bipartite Network Projection for MiRNA-Disease Association prediction. *Bioinformatics*, **2018**, 34, 3178-3186	7.2	204
117	A Deep Learning Framework for Robust and Accurate Prediction of ncRNA-Protein Interactions Using Evolutionary Information. *Molecular Therapy - Nucleic Acids*, **2018**, 11, 337-344	10.7	87
116	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	10.2	135
115	An improved efficient rotation forest algorithm to predict the interactions among proteins. *Soft Computing*, **2018**, 22, 3373-3381	3.5	27
114	HEMD: a highly efficient random forest-based malware detection framework for Android. *Neural Computing and Applications*, **2018**, 30, 3353-3361	4.8	28
113	DroidDet: Effective and robust detection of android malware using static analysis along with rotation forest model. *Neurocomputing*, **2018**, 272, 638-646	5.4	92
112	Constructing prediction models from expression profiles for large scale lncRNA-miRNA interaction profiling. *Bioinformatics*, **2018**, 34, 812-819	7.2	66

111	DRMDA: deep representations-based miRNA-disease association prediction. *Journal of Cellular and Molecular Medicine*, **2018**, 22, 472-485	5.6	58
110	A Computational-Based Method for Predicting Drug-Target Interactions by Using Stacked Autoencoder Deep Neural Network. *Journal of Computational Biology*, **2018**, 25, 361-373	1.7	85
109	Improving Prediction of Self-interacting Proteins Using Stacked Sparse Auto-Encoder with PSSM profiles. *International Journal of Biological Sciences*, **2018**, 14, 983-991	11.2	14
108	An Ensemble Classifier with Random Projection for Predicting Protein–Protein Interactions Using Sequence and Evolutionary Information. *Applied Sciences (Switzerland)*, **2018**, 8, 89	2.6	15
107	PCLPred: A Bioinformatics Method for Predicting Protein-Protein Interactions by Combining Relevance Vector Machine Model with Low-Rank Matrix Approximation. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	21
106	A Systematic Prediction of Drug-Target Interactions Using Molecular Fingerprints and Protein Sequences. *Current Protein and Peptide Science*, **2018**, 19, 468-478	2.8	50
105	Using Weighted Extreme Learning Machine Combined with Scale-Invariant Feature Transform to Predict Protein-Protein Interactions from Protein Evolutionary Information. *Lecture Notes in Computer Science*, **2018**, 527-532	0.9	3
104	Discovering an Integrated Network in Heterogeneous Data for Predicting lncRNA-miRNA Interactions. *Lecture Notes in Computer Science*, **2018**, 539-545	0.9	4
103	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	0.9	8
102	Efficient Framework for Predicting ncRNA-Protein Interactions Based on Sequence Information by Deep Learning. *Lecture Notes in Computer Science*, **2018**, 337-344	0.9	3
101	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*, **2018**,	3	20
100	Plant diseased leaf segmentation and recognition by fusion of superpixel, K-means and PHOG. *Optik*, **2018**, 157, 866-872	2.5	120
99	Learning Latent Patterns in Molecular Data for Explainable Drug Side Effects Prediction **2018**,		2
98	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	15
97	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	2.8	71
96	Novel Human miRNA-Disease Association Inference Based on Random Forest. *Molecular Therapy - Nucleic Acids*, **2018**, 13, 568-579	10.7	63
95	A heterogeneous label propagation approach to explore the potential associations between miRNA and disease. *Journal of Translational Medicine*, **2018**, 16, 348	8.5	30
94	Prediction of protein self-interactions using stacked long short-term memory from protein sequences information. *BMC Systems Biology*, **2018**, 12, 129	3.5	13

93	FMSM: a novel computational model for predicting potential miRNA biomarkers for various human diseases. *BMC Systems Biology*, **2018**, 12, 121	3.5	10
92	Novel link prediction for large-scale miRNA-lncRNA interaction network in a bipartite graph. *BMC Medical Genomics*, **2018**, 11, 113	3.7	26
91	Accurate Prediction of ncRNA-Protein Interactions From the Integration of Sequence and Evolutionary Information. *Frontiers in Genetics*, **2018**, 9, 458	4.5	20
90	Using Two-dimensional Principal Component Analysis and Rotation Forest for Prediction of Protein-Protein Interactions. *Scientific Reports*, **2018**, 8, 12874	4.9	24
89	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	25
88	Distributed Winner-Take-All in Dynamic Networks. *IEEE Transactions on Automatic Control*, **2017**, 62, 577-589	3.9	80
87	Highly Efficient Framework for Predicting Interactions Between Proteins. *IEEE Transactions on Cybernetics*, **2017**, 47, 731-743	10.2	85
86	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	5.4	37
85	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	48
84	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	2.3	41
83	Leaf image based cucumber disease recognition using sparse representation classification. *Computers and Electronics in Agriculture*, **2017**, 134, 135-141	6.5	112
82	A novel computational model based on super-disease and miRNA for potential miRNA-disease association prediction. *Molecular BioSystems*, **2017**, 13, 1202-1212		37
81	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	2.3	15
80	Predicting protein-protein interactions from protein sequences by a stacked sparse autoencoder deep neural network. *Molecular BioSystems*, **2017**, 13, 1336-1344		86
79	Discriminant WSRC for Large-Scale Plant Species Recognition. *Computational Intelligence and Neuroscience*, **2017**, 2017, 9581292	3	3
78	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,	5	34
77	Jaccard distance based weighted sparse representation for coarse-to-fine plant species recognition. *PLoS ONE*, **2017**, 12, e0178317	3.7	7
76	Prediction of microbe-disease association from the integration of neighbor and graph with collaborative recommendation model. *Journal of Translational Medicine*, **2017**, 15, 209	8.5	50

75	PCVMZM: Using the Probabilistic Classification Vector Machines Model Combined with a Zernike Moments Descriptor to Predict Protein-Protein Interactions from Protein Sequences. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	51
74	PRMDA: personalized recommendation-based MiRNA-disease association prediction. *Oncotarget*, **2017**, 8, 85568-85583	3.3	28
73	An ensemble approach for large-scale identification of protein- protein interactions using the alignments of multiple sequences. *Oncotarget*, **2017**, 8, 5149-5159	3.3	32
72	Long non-coding RNAs and complex diseases: from experimental results to computational models. *Briefings in Bioinformatics*, **2017**, 18, 558-576	13.4	329
71	In silico prediction of drug-target interaction networks based on drug chemical structure and protein sequences. *Scientific Reports*, **2017**, 7, 11174	4.9	46
70	Fusion of superpixel, expectation maximization and PHOG for recognizing cucumber diseases. *Computers and Electronics in Agriculture*, **2017**, 140, 338-347	6.5	32
69	MCMDA: Matrix completion for MiRNA-disease association prediction. *Oncotarget*, **2017**, 8, 21187-21199	3.3	144
68	Prediction of Drug-Target Interaction Networks from the Integration of Protein Sequences and Drug Chemical Structures. *Molecules*, **2017**, 22,	4.8	45
67	Detection of Interactions between Proteins by Using Legendre Moments Descriptor to Extract Discriminatory Information Embedded in PSSM. *Molecules*, **2017**, 22,	4.8	25
66	PBHMDA: Path-Based Human Microbe-Disease Association Prediction. *Frontiers in Microbiology*, **2017**, 8, 233	5.7	59
65	PBMDA: A novel and effective path-based computational model for miRNA-disease association prediction. *PLoS Computational Biology*, **2017**, 13, e1005455	5	263
64	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	3.3	33
63	EPMDA: an expression-profile based computational model for microRNA-disease association prediction. *Oncotarget*, **2017**, 8, 87033-87043	3.3	9
62	CIPPN: computational identification of protein pupylation sites by using neural network. *Oncotarget*, **2017**, 8, 108867-108879	3.3	13
61	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	0.9	11
60	A novel approach based on KATZ measure to predict associations of human microbiota with non-infectious diseases. *Bioinformatics*, **2017**, 33, 733-739	7.2	78
59	Inverse-Free Extreme Learning Machine With Optimal Information Updating. *IEEE Transactions on Cybernetics*, **2016**, 46, 1229-41	10.2	92
58	Construction of reliable protein–protein interaction networks using weighted sparse representation based classifier with pseudo substitution matrix representation features. *Neurocomputing*, **2016**, 218, 131-138	5.4	36

57	Improving protein-protein interactions prediction accuracy using protein evolutionary information and relevance vector machine model. *Protein Science*, **2016**, 25, 1825-33	6.3	25
56	Large-scale prediction of drug-target interactions from deep representations **2016**,		21
55	Robust and accurate prediction of protein self-interactions from amino acids sequence using evolutionary information. *Molecular BioSystems*, **2016**, 12, 3702-3710		16
54	Improved protein-protein interactions prediction via weighted sparse representation model combining continuous wavelet descriptor and PseAA composition. *BMC Systems Biology*, **2016**, 10, 120	3.5	23
53	Sequence-based prediction of protein-protein interactions using weighted sparse representation model combined with global encoding. *BMC Bioinformatics*, **2016**, 17, 184	3.6	94
52	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, 579-92	10.3	194
51	Modeling of signaling crosstalk-mediated drug resistance and its implications on drug combination. *Oncotarget*, **2016**, 7, 63995-64006	3.3	32
50	ILNCSIM: improved lncRNA functional similarity calculation model. *Oncotarget*, **2016**, 7, 25902-14	3.3	104
49	Using the Relevance Vector Machine Model Combined with Local Phase Quantization to Predict Protein-Protein Interactions from Protein Sequences. *BioMed Research International*, **2016**, 2016, 4783801	3	16
48	FMLNCSIM: fuzzy measure-based lncRNA functional similarity calculation model. *Oncotarget*, **2016**, 7, 45948-45958	3.3	90
47	HGIMDA: Heterogeneous graph inference for miRNA-disease association prediction. *Oncotarget*, **2016**, 7, 65257-65269	3.3	178
46	Identification of self-interacting proteins by exploring evolutionary information embedded in PSI-BLAST-constructed position specific scoring matrix. *Oncotarget*, **2016**, 7, 82440-82449	3.3	20
45	Ens-PPI: A Novel Ensemble Classifier for Predicting the Interactions of Proteins Using Autocovariance Transformation from PSSM. *BioMed Research International*, **2016**, 2016, 4563524	3	18
44	IRWRLDA: improved random walk with restart for lncRNA-disease association prediction. *Oncotarget*, **2016**, 7, 57919-57931	3.3	142
43	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,	6.3	13
42	Highly Accurate Prediction of Protein-Protein Interactions via Incorporating Evolutionary Information and Physicochemical Characteristics. *International Journal of Molecular Sciences*, **2016**, 17,	6.3	30
41	WBSMDA: Within and Between Score for MiRNA-Disease Association prediction. *Scientific Reports*, **2016**, 6, 21106	4.9	238
40	. *IEEE Transactions on Industrial Informatics*, **2015**, 11, 946-956	11.9	74

39	Prediction of protein-protein interactions with clustered amino acids and weighted sparse representation. *International Journal of Molecular Sciences*, **2015**, 16, 10855-69	6.3	22
38	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	0.9	21
37	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	0.9	2
36	A highly efficient approach to protein interactome mapping based on collaborative filtering framework. *Scientific Reports*, **2015**, 5, 7702	4.9	52
35	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	3.7	96
34	Detecting protein-protein interactions with a novel matrix-based protein sequence representation and support vector machines. *BioMed Research International*, **2015**, 2015, 867516	3	29
33	Using Weighted Sparse Representation Model Combined with Discrete Cosine Transformation to Predict Protein-Protein Interactions from Protein Sequence. *BioMed Research International*, **2015**, 2015, 902198	3	63
32	Improving network topology-based protein interactome mapping via collaborative filtering. *Knowledge-Based Systems*, **2015**, 90, 23-32	7.3	36
31	Detection of Interactions between Proteins through Rotation Forest and Local Phase Quantization Descriptors. *International Journal of Molecular Sciences*, **2015**, 17,	6.3	40
30	Using Chou's amphiphilic Pseudo-Amino Acid Composition and Extreme Learning Machine for prediction of Protein-protein interactions **2014**,		2
29	A MapReduce based parallel SVM for large-scale predicting protein–protein interactions. *Neurocomputing*, **2014**, 145, 37-43	5.4	84
28	Predicting dynamic deformation of retaining structure by LSSVR-based time series method. *Neurocomputing*, **2014**, 137, 165-172	5.4	30
27	Orthogonal locally discriminant spline embedding for plant leaf recognition. *Computer Vision and Image Understanding*, **2014**, 119, 116-126	4.3	19
26	Prediction of protein-protein interactions from amino acid sequences using a novel multi-scale continuous and discontinuous feature set. *BMC Bioinformatics*, **2014**, 15 Suppl 15, S9	3.6	89
25	Large-scale protein-protein interactions detection by integrating big biosensing data with computational model. *BioMed Research International*, **2014**, 2014, 598129	3	36
24	Identifying Spurious Interactions in the Protein-Protein Interaction Networks Using Local Similarity Preserving Embedding. *Lecture Notes in Computer Science*, **2014**, 138-148	0.9	3
23	Prediction of protein-protein interactions from amino acid sequences with ensemble extreme learning machines and principal component analysis. *BMC Bioinformatics*, **2013**, 14 Suppl 8, S10	3.6	180
22	Increasing the reliability of protein–protein interaction networks via non-convex semantic embedding. *Neurocomputing*, **2013**, 121, 99-107	5.4	44

21	Increasing reliability of protein interactome by fast manifold embedding. *Pattern Recognition Letters*, **2013**, 34, 372-379	4.7	27
20	t-LSE: a novel robust geometric approach for modeling protein-protein interaction networks. *PLoS ONE*, **2013**, 8, e58368	3.7	70
19	A SVM-Based System for Predicting Protein-Protein Interactions Using a Novel Representation of Protein Sequences. *Lecture Notes in Computer Science*, **2013**, 629-637	0.9	11
18	Research on Signaling Pathways Reconstruction by Integrating High Content RNAi Screening and Functional Gene Network. *Lecture Notes in Computer Science*, **2013**, 1-10	0.9	1
17	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	1.3	
16	Assessing and predicting protein interactions by combining manifold embedding with multiple information integration. *BMC Bioinformatics*, **2012**, 13 Suppl 7, S3	3.6	46
15	A novel method to predict protein-protein interactions based on the information of protein sequence **2012**,		5
14	A Novel Approach to Modelling Protein-Protein Interaction Networks. *Lecture Notes in Computer Science*, **2012**, 49-57	0.9	2
13	Using manifold embedding for assessing and predicting protein interactions from high-throughput experimental data. *Bioinformatics*, **2010**, 26, 2744-51	7.2	173
12	Prediction of beta-hairpins in proteins using physicochemical properties and structure information. *Protein and Peptide Letters*, **2010**, 17, 1123-8	1.9	9
11	Improved method for predicting phi-turns in proteins using a two-stage classifier. *Protein and Peptide Letters*, **2010**, 17, 1117-22	1.9	10
10	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	3.6	76
9	Increasing Reliability of Protein Interactome by Combining Heterogeneous Data Sources with Weighted Network Topological Metrics. *Lecture Notes in Computer Science*, **2010**, 657-663	0.9	6
8	Comparison of DNA Truncated Barcodes and Full-Barcodes for Species Identification. *Lecture Notes in Computer Science*, **2010**, 108-114	0.9	4
7	Integration of Genomic and Proteomic Data to Predict Synthetic Genetic Interactions Using Semi-supervised Learning. *Lecture Notes in Computer Science*, **2009**, 635-644	0.9	1
6	A Novel Hybrid Method of Gene Selection and Its Application on Tumor Classification. *Lecture Notes in Computer Science*, **2008**, 1055-1068	0.9	5
5	A Localization Error Estimation Method Based on Maximum Likelihood for Wireless Sensor Networks **2007**,		1
4	A Localization Algorithm nin Wireless Sensor Networks Using a Mobile Beacon Node **2007**,		7

3	Environment-Map-free Robot Navigation Based on Wireless Sensor Networks **2007**,	5
2	SP-NN: A novel neural network approach for path planning **2007**,	1
1	Data fusion based on RBF and nonparametric estimation for localization in Wireless Sensor Networks **2007**,	1