

Min Wu

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

93
papers

2,104
citations

21
h-index

44
g-index

111
ext. papers

2,995
ext. citations

4.5
avg, IF

5.57
L-index

#	Paper	IF	Citations
93	A core-attachment based method to detect protein complexes in PPI networks. <i>BMC Bioinformatics</i> , 2009 , 10, 169	3.6	242
92	Computational approaches for detecting protein complexes from protein interaction networks: a survey. <i>BMC Genomics</i> , 2010 , 11 Suppl 1, S3	4.5	227
91	Neighborhood Regularized Logistic Matrix Factorization for Drug-Target Interaction Prediction. <i>PLoS Computational Biology</i> , 2016 , 12, e1004760	5	190
90	Drug-Target Interaction Prediction with Graph Regularized Matrix Factorization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 646-656	3	141
89	An overview of state-of-the-art partial discharge analysis techniques for condition monitoring. <i>IEEE Electrical Insulation Magazine</i> , 2015 , 31, 22-35	2.1	117
88	Computational prediction of drug-target interactions using chemogenomic approaches: an empirical survey. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1337-1357	13.4	101
87	Machine Remaining Useful Life Prediction via an Attention-Based Deep Learning Approach. <i>IEEE Transactions on Industrial Electronics</i> , 2021 , 68, 2521-2531	8.9	86
86	Inferring gene-phenotype associations via global protein complex network propagation. <i>PLoS ONE</i> , 2011 , 6, e21502	3.7	62
85	Drug-target interaction prediction via class imbalance-aware ensemble learning. <i>BMC Bioinformatics</i> , 2016 , 17, 509	3.6	60
84	Drug-target interaction prediction using ensemble learning and dimensionality reduction. <i>Methods</i> , 2017 , 129, 81-88	4.6	57
83	Detecting temporal protein complexes from dynamic protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2014 , 15, 335	3.6	44
82	Semantic proximity search on graphs with metagraph-based learning 2016 ,		40
81	An Attention-Based Deep Learning Approach for Sleep Stage Classification With Single-Channel EEG. <i>IEEE Transactions on Neural Systems and Rehabilitation Engineering</i> , 2021 , 29, 809-818	4.8	39
80	Smartphone Sensor-Based Human Activity Recognition Using Feature Fusion and Maximum Full a Posteriori. <i>IEEE Transactions on Instrumentation and Measurement</i> , 2020 , 69, 3992-4001	5.2	36
79	Repeat Buyer Prediction for E-Commerce 2016 ,		35
78	Predicting human microbe-drug associations via graph convolutional network with conditional random field. <i>Bioinformatics</i> , 2020 , 36, 4918-4927	7.2	31
77	Construction of co-complex score matrix for protein complex prediction from AP-MS data. <i>Bioinformatics</i> , 2011 , 27, i159-66	7.2	30

76	A graph regularized generalized matrix factorization model for predicting links in biomedical bipartite networks. <i>Bioinformatics</i> , 2020 , 36, 3474-3481	7.2	27
75	Contrastive Adversarial Domain Adaptation for Machine Remaining Useful Life Prediction. <i>IEEE Transactions on Industrial Informatics</i> , 2021 , 17, 5239-5249	11.9	24
74	CtIP silencing as a novel mechanism of tamoxifen resistance in breast cancer. <i>Molecular Cancer Research</i> , 2007 , 5, 1285-95	6.6	23
73	Degradation-Aware Remaining Useful Life Prediction With LSTM Autoencoder. <i>IEEE Transactions on Instrumentation and Measurement</i> , 2021 , 70, 1-10	5.2	21
72	Adaptive Cost-Sensitive Online Classification. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2019 , 31, 214-228	4.2	20
71	Discovery of protein complexes with core-attachment structures from Tandem Affinity Purification (TAP) data. <i>Journal of Computational Biology</i> , 2012 , 19, 1027-42	1.7	20
70	Predicting essential genes and synthetic lethality via influence propagation in signaling pathways of cancer cell fates. <i>Journal of Bioinformatics and Computational Biology</i> , 2015 , 13, 1541002	1	19
69	Identifying protein complexes from heterogeneous biological data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 2023-33	4.2	18
68	Computational Prediction of Drug-Target Interactions via Ensemble Learning. <i>Methods in Molecular Biology</i> , 2019 , 1903, 239-254	1.4	18
67	Dual-dropout graph convolutional network for predicting synthetic lethality in human cancers. <i>Bioinformatics</i> , 2020 , 36, 4458-4465	7.2	17
66	In silico prediction of synthetic lethality by meta-analysis of genetic interactions, functions, and pathways in yeast and human cancer. <i>Cancer Informatics</i> , 2014 , 13, 71-80	2.4	17
65	Integrating node embeddings and biological annotations for genes to predict disease-gene associations. <i>BMC Systems Biology</i> , 2018 , 12, 138	3.5	16
64	A two-layer integration framework for protein complex detection. <i>BMC Bioinformatics</i> , 2016 , 17, 100	3.6	15
63	Syn-lethality: an integrative knowledge base of synthetic lethality towards discovery of selective anticancer therapies. <i>BioMed Research International</i> , 2014 , 2014, 196034	3	15
62	A joint classification-regression method for multi-stage remaining useful life prediction. <i>Journal of Manufacturing Systems</i> , 2021 , 58, 109-119	9.1	15
61	Disease gene classification with metagraph representations. <i>Methods</i> , 2017 , 131, 83-92	4.6	13
60	Benchmarking human protein complexes to investigate drug-related systems and evaluate predicted protein complexes. <i>PLoS ONE</i> , 2013 , 8, e53197	3.7	13
59	SLMF: Predicting Synthetic Lethality in Human Cancers via Logistic Matrix Factorization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 748-757	3	12

58	Node-based learning of differential networks from multi-platform gene expression data. <i>Methods</i> , 2017 , 129, 41-49	4.6	11
57	PLW: Probabilistic Local Walks for detecting protein complexes from protein interaction networks. <i>BMC Genomics</i> , 2013 , 14 Suppl 5, S15	4.5	11
56	Integrating diverse biological and computational sources for reliable protein-protein interactions. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 7, S8	3.6	11
55	Learning User Dependencies for Recommendation 2017 ,		11
54	Adversarial Multiple-Target Domain Adaptation for Fault Classification. <i>IEEE Transactions on Instrumentation and Measurement</i> , 2021 , 70, 1-11	5.2	11
53	Protein Complex Detection via Effective Integration of Base Clustering Solutions and Co-Complex Affinity Scores. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 733-739	3	10
52	An Attention Based CNN-LSTM Approach for Sleep-Wake Detection With Heterogeneous Sensors. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , 25, 3270-3277	7.2	10
51	KDnet-RUL: A Knowledge Distillation Framework to Compress Deep Neural Networks for Machine Remaining Useful Life Prediction. <i>IEEE Transactions on Industrial Electronics</i> , 2021 , 1-1	8.9	9
50	Ensembling graph attention networks for human microbe-drug association prediction. <i>Bioinformatics</i> , 2020 , 36, i779-i786	7.2	8
49	Modeling perceived stress via HRV and accelerometer sensor streams. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2015 , 2015, 1625-8	0.9	7
48	An Attention-Based Deep Sequential GRU Model for Sensor Drift Compensation. <i>IEEE Sensors Journal</i> , 2021 , 21, 7908-7917	4	7
47	A Novel Real-Time Deep Learning Approach for Indoor Localization Based on RF Environment Identification 2020 , 4, 1-4		6
46	LDsplit: screening for cis-regulatory motifs stimulating meiotic recombination hotspots by analysis of DNA sequence polymorphisms. <i>BMC Bioinformatics</i> , 2014 , 15, 48	3.6	6
45	Epigenetic functions enriched in transcription factors binding to mouse recombination hotspots. <i>Proteome Science</i> , 2012 , 10 Suppl 1, S11	2.6	6
44	Recent advances in network-based methods for disease gene prediction. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	6
43	Adversarial Transfer Learning for Machine Remaining Useful Life Prediction 2020 ,		6
42	Predicting synthetic lethal interactions in human cancers using graph regularized self-representative matrix factorization. <i>BMC Bioinformatics</i> , 2019 , 20, 657	3.6	6
41	Graph contextualized attention network for predicting synthetic lethality in human cancers. <i>Bioinformatics</i> , 2021 ,	7.2	6

40	Attention-based sequence to sequence model for machine remaining useful life prediction. <i>Neurocomputing</i> , 2021 , 466, 58-68	5.4	6
39	A Novel Ensemble Deep Learning Approach for Sleep-Wake Detection Using Heart Rate Variability and Acceleration. <i>IEEE Transactions on Emerging Topics in Computational Intelligence</i> , 2020 , 1-10	4.1	5
38	Metagraph-Based Learning on Heterogeneous Graphs. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2021 , 33, 154-168	4.2	5
37	Characterising Alzheimer's Disease with EEG-based Energy Landscape Analysis. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , PP,	7.2	5
36	mg2vec: Learning Relationship-Preserving Heterogeneous Graph Representations via Metagraph Embedding. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2020 , 1-1	4.2	4
35	Cost-Sensitive Online Classification with Adaptive Regularization and Its Applications 2015 ,		4
34	Meta-analysis of Genomic and Proteomic Features to Predict Synthetic Lethality of Yeast and Human Cancer 2013 ,		4
33	Deep Learning for Building Occupancy Estimation Using Environmental Sensors. <i>Studies in Computational Intelligence</i> , 2020 , 335-357	0.8	4
32	Automatic detection of retinopathy with optical coherence tomography images via a semi-supervised deep learning method. <i>Biomedical Optics Express</i> , 2021 , 12, 2684-2702	3.5	4
31	KG4SL: knowledge graph neural network for synthetic lethality prediction in human cancers. <i>Bioinformatics</i> , 2021 , 37, i418-i425	7.2	4
30	Contextualized Graph Attention Network for Recommendation with Item Knowledge Graph. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2021 , 1-1	4.2	4
29	Prediction of Synthetic Lethal Interactions in Human Cancers Using Multi-View Graph Auto-Encoder. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , 25, 4041-4051	7.2	4
28	Online Collaborative Filtering with Implicit Feedback. <i>Lecture Notes in Computer Science</i> , 2019 , 433-448	0.9	3
27	A Deep Learning Approach for Sleep-Wake Detection from HRV and Accelerometer Data 2019 ,		3
26	2011 ,		3
25	Disease Gene Classification with Metagraph Representations. <i>Methods in Molecular Biology</i> , 2018 , 1807, 211-224	1.4	3
24	Bi-LSTM based Two-Stream Network for Machine Remaining Useful Life Prediction. <i>IEEE Transactions on Instrumentation and Measurement</i> , 2022 , 1-1	5.2	3
23	Integration of genomic and epigenomic features to predict meiotic recombination hotspots in human and mouse 2012 ,		2

22	Deep learning with long short-term memory networks for classification of dementia related travel patterns. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference, 2020, 2020, 5563-5566</i>	0.9	2
21	Matrix factorization for biomedical link prediction and scRNA-seq data imputation: an empirical survey. <i>Briefings in Bioinformatics, 2021,</i>	13.4	2
20	Adaptive Grid-Based k-median Clustering of Streaming Data with Accuracy Guarantee. <i>Lecture Notes in Computer Science, 2015, 75-91</i>	0.9	2
19	Cross-domain retinopathy classification with optical coherence tomography images via a novel deep domain adaptation method. <i>Journal of Biophotonics, 2021, 14, e202100096</i>	3.1	2
18	Mahalanobis Distance Based Adversarial Network for Anomaly Detection 2020,		1
17	LDSplitDB: a database for studies of meiotic recombination hotspots in MHC using human genomic data. <i>BMC Medical Genomics, 2018, 11, 27</i>	3.7	1
16	Data-driven prediction of cancer cell fates with a nonlinear model of signaling pathways 2014,		1
15	NetPipe 2012,		1
14	Multi-feature Fused Bidirectional Long Short-term Memory for Remaining Useful Life Prediction 2021,		1
13	Multi-View Collaborative Network Embedding. <i>ACM Transactions on Knowledge Discovery From Data, 2021, 15, 1-18</i>	4	1
12	Pre-training Graph Neural Networks for Link Prediction in Biomedical Networks.. <i>Bioinformatics, 2022,</i>	7.2	1
11	Significance of activation functions in developing an online classifier for semiconductor defect detection. <i>Knowledge-Based Systems, 2022, 108818</i>	7.3	1
10	Heterogeneous graph attention networks for drug virus association prediction. <i>Methods, 2021, 198, 11-116</i>	11.6	0
9	Conditional Contrastive Domain Generalization for Fault Diagnosis. <i>IEEE Transactions on Instrumentation and Measurement, 2022, 71, 1-12</i>	5.2	0
8	Finding trans-regulatory genes and protein complexes modulating meiotic recombination hotspots of human, mouse and yeast. <i>BMC Systems Biology, 2014, 8, 107</i>	3.5	
7	The Algorithm of Abstract Extraction Based on Semantics. <i>Applied Mechanics and Materials, 2013, 303-306, 1506-1509</i>	0.3	
6	Design and Implementation of College English Online Courseware Based on the Method of Goal-Directed Interaction Design. <i>Applied Mechanics and Materials, 2013, 380-384, 2058-2062</i>	0.3	
5	Feature selection and domain adaptation for cross-machine product quality prediction. <i>Journal of Intelligent Manufacturing, 1</i>	6.7	

4 Matrix Factorization for Drug-Target Interaction Prediction **2017**, 83-106

3 Design and Implementation of Multimedia Online Courseware Based on XML/XSLT and JavaScript. *Communications in Computer and Information Science*, **2011**, 456-462 0.3

2 Power-Law Modeling of Cancer Cell Fates Driven by Signaling Data to Reveal Drug Effects. *PLoS ONE*, **2016**, 11, e0165049 3.7

1 Predicting Synthetic Lethality in Human Cancers via Multi-Graph Ensemble Neural Network. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference*, **2021**, 2021, 1731-1734 0.9