

Fang-Xiang Wu

List of Publications by Citations

Source: <https://exaly.com/author-pdf/4594811/fang-xiang-wu-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

375
papers

6,394
citations

40
h-index

65
g-index

429
ext. papers

8,640
ext. citations

4.1
avg, IF

6.71
L-index

#	Paper	IF	Citations
375	CytoNCA: a cytoscape plugin for centrality analysis and evaluation of protein interaction networks. <i>BioSystems</i> , 2015 , 127, 67-72	1.9	485
374	Patient geometry-driven information retrieval for IMRT treatment plan quality control. <i>Medical Physics</i> , 2009 , 36, 5497-505	4.4	206
373	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. <i>Bioinformatics</i> , 2016 , 32, 2664-71	7.2	190
372	Recurrent neural network for non-smooth convex optimization problems with application to the identification of genetic regulatory networks. <i>IEEE Transactions on Neural Networks</i> , 2011 , 22, 714-26		159
371	A review on machine learning principles for multi-view biological data integration. <i>Briefings in Bioinformatics</i> , 2018 , 19, 325-340	13.4	159
370	A survey of MRI-based brain tumor segmentation methods. <i>Tsinghua Science and Technology</i> , 2014 , 19, 578-595	3.4	158
369	Prediction of lncRNA-disease associations based on inductive matrix completion. <i>Bioinformatics</i> , 2018 , 34, 3357-3364	7.2	134
368	CircR2Disease: a manually curated database for experimentally supported circular RNAs associated with various diseases. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	110
367	Iteration method for predicting essential proteins based on orthology and protein-protein interaction networks. <i>BMC Systems Biology</i> , 2012 , 6, 87	3.5	105
366	Identifying protein complexes and functional modules--from static PPI networks to dynamic PPI networks. <i>Briefings in Bioinformatics</i> , 2014 , 15, 177-94	13.4	104
365	Classification of Alzheimer's Disease Using Whole Brain Hierarchical Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 624-632	3	80
364	Predicting MicroRNA-Disease Associations Based on Improved MicroRNA and Disease Similarities. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 1774-1782	3	79
363	LDAP: a web server for lncRNA-disease association prediction. <i>Bioinformatics</i> , 2017 , 33, 458-460	7.2	72
362	ClusterViz: A Cytoscape APP for Cluster Analysis of Biological Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 815-22	3	70
361	Detecting Protein Complexes Based on Uncertain Graph Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014 , 11, 486-97	3	67
360	Dynamic protein interaction network construction and applications. <i>Proteomics</i> , 2014 , 14, 338-52	4.8	65
359	A survey on U-shaped networks in medical image segmentations. <i>Neurocomputing</i> , 2020 , 409, 244-258	5.4	64

358	Predicting drug-target interaction using positive-unlabeled learning. <i>Neurocomputing</i> , 2016 , 206, 50-57	5.4	63
357	United Complex Centrality for Identification of Essential Proteins from PPI Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 370-380	3	61
356	A Topology Potential-Based Method for Identifying Essential Proteins from PPI Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 372-83	3	59
355	UDoNC: An Algorithm for Identifying Essential Proteins Based on Protein Domains and Protein-Protein Interaction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 276-88	3	57
354	Prediction of CircRNA-Disease Associations Using KATZ Model Based on Heterogeneous Networks. <i>International Journal of Biological Sciences</i> , 2018 , 14, 1950-1959	11.2	57
353	Sparse representation for classification of tumors using gene expression data. <i>Journal of Biomedicine and Biotechnology</i> , 2009 , 2009, 403689		53
352	DWNN-RLS: regularized least squares method for predicting circRNA-disease associations. <i>BMC Bioinformatics</i> , 2018 , 19, 520	3.6	53
351	Computational approaches to predicting essential proteins: a survey. <i>Proteomics - Clinical Applications</i> , 2013 , 7, 181-92	3.1	50
350	Identifying essential proteins from active PPI networks constructed with dynamic gene expression. <i>BMC Genomics</i> , 2015 , 16 Suppl 3, S1	4.5	50
349	Protein complex identification through Markov clustering with firefly algorithm on dynamic protein-protein interaction networks. <i>Information Sciences</i> , 2016 , 329, 303-316	7.7	49
348	Prediction of essential proteins based on overlapping essential modules. <i>IEEE Transactions on Nanobioscience</i> , 2014 , 13, 415-24	3.4	49
347	Computational approaches for prioritizing candidate disease genes based on PPI networks. <i>Tsinghua Science and Technology</i> , 2015 , 20, 500-512	3.4	48
346	Control performance improvement of a parallel robot via the design for control approach. <i>Mechatronics</i> , 2004 , 14, 947-964	3	48
345	PWCDA: Path Weighted Method for Predicting circRNA-Disease Associations. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	48
344	Complex Brain Network Analysis and Its Applications to Brain Disorders: A Survey. <i>Complexity</i> , 2017 , 2017, 1-27	1.6	46
343	Biomedical data and computational models for drug repositioning: a comprehensive review. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1604-1619	13.4	45
342	Predicting essential proteins based on subcellular localization, orthology and PPI networks. <i>BMC Bioinformatics</i> , 2016 , 17 Suppl 8, 279	3.6	45
341	SinNLRR: a robust subspace clustering method for cell type detection by non-negative and low-rank representation. <i>Bioinformatics</i> , 2019 , 35, 3642-3650	7.2	44

340	Global and robust stability analysis of genetic regulatory networks with time-varying delays and parameter uncertainties. <i>IEEE Transactions on Biomedical Circuits and Systems</i> , 2011 , 5, 391-8	5.1	44
339	Protein-protein interactions: detection, reliability assessment and applications. <i>Briefings in Bioinformatics</i> , 2017 , 18, 798-819	13.4	43
338	CytoCluster: A Cytoscape Plugin for Cluster Analysis and Visualization of Biological Networks. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	43
337	Protein-protein interaction site prediction through combining local and global features with deep neural networks. <i>Bioinformatics</i> , 2020 , 36, 1114-1120	7.2	42
336	Transittability of complex networks and its applications to regulatory biomolecular networks. <i>Scientific Reports</i> , 2014 , 4, 4819	4.9	40
335	DNRLMF-MDA:Predicting microRNA-Disease Associations Based on Similarities of microRNAs and Diseases. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 233-243	3	38
334	Automated ICD-9 Coding via A Deep Learning Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1193-1202	3	38
333	Delay-independent stability of genetic regulatory networks. <i>IEEE Transactions on Neural Networks</i> , 2011 , 22, 1685-93		37
332	Improving Alzheimer's Disease Classification by Combining Multiple Measures. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 1649-1659	3	36
331	A fast and high performance multiple data integration algorithm for identifying human disease genes. <i>BMC Medical Genomics</i> , 2015 , 8 Suppl 3, S2	3.7	36
330	Rechecking the Centrality-Lethality Rule in the Scope of Protein Subcellular Localization Interaction Networks. <i>PLoS ONE</i> , 2015 , 10, e0130743	3.7	36
329	A Deep Learning Framework for Identifying Essential Proteins by Integrating Multiple Types of Biological Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 296-305	3	35
328	deepDriver: Predicting Cancer Driver Genes Based on Somatic Mutations Using Deep Convolutional Neural Networks. <i>Frontiers in Genetics</i> , 2019 , 10, 13	4.5	34
327	Identifying essential proteins based on sub-network partition and prioritization by integrating subcellular localization information. <i>Journal of Theoretical Biology</i> , 2018 , 447, 65-73	2.3	33
326	Alzheimer's Disease Classification Based on Individual Hierarchical Networks Constructed With 3-D Texture Features. <i>IEEE Transactions on Nanobioscience</i> , 2017 , 16, 428-437	3.4	30
325	Deep convolutional neural network for automatically segmenting acute ischemic stroke lesion in multi-modality MRI. <i>Neural Computing and Applications</i> , 2020 , 32, 6545-6558	4.8	30
324	Classification of Schizophrenia Based on Individual Hierarchical Brain Networks Constructed From Structural MRI Images. <i>IEEE Transactions on Nanobioscience</i> , 2017 , 16, 600-608	3.4	29
323	Identifying Cancer-Specific circRNA-RBP Binding Sites Based on Deep Learning. <i>Molecules</i> , 2019 , 24,	4.8	29

322	Improving protein function prediction using domain and protein complexes in PPI networks. <i>BMC Systems Biology</i> , 2014 , 8, 35	3.5	29
321	Disease Gene Prediction by Integrating PPI Networks, Clinical RNA-Seq Data and OMIM Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 222-232	3	29
320	A fast algorithm for nonnegative matrix factorization and its convergence. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2014 , 25, 1855-63	10.3	28
319	Identifying protein complexes in protein-protein interaction networks by using clique seeds and graph entropy. <i>Proteomics</i> , 2013 , 13, 269-77	4.8	28
318	Network output controllability-based method for drug target identification. <i>IEEE Transactions on Nanobioscience</i> , 2015 , 14, 184-91	3.4	27
317	Integrating Omic Data with a Multiplex Network-based Approach for the Identification of Cancer Subtypes. <i>IEEE Transactions on Nanobioscience</i> , 2016 , 15, 335-342	3.4	27
316	DeepDSC: A Deep Learning Method to Predict Drug Sensitivity of Cancer Cell Lines. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 575-582	3	27
315	Enhancing the prediction of disease-gene associations with multimodal deep learning. <i>Bioinformatics</i> , 2019 , 35, 3735-3742	7.2	26
314	Identifying disease genes by integrating multiple data sources. <i>BMC Medical Genomics</i> , 2014 , 7 Suppl 2, S2	3.7	26
313	Stability and Bifurcation of Ring-Structured Genetic Regulatory Networks With Time Delays. <i>IEEE Transactions on Circuits and Systems I: Regular Papers</i> , 2012 , 59, 1312-1320	3.9	26
312	Genetic weighted k-means algorithm for clustering large-scale gene expression data. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 6, S12	3.6	26
311	Dynamic model-based clustering for time-course gene expression data. <i>Journal of Bioinformatics and Computational Biology</i> , 2005 , 3, 821-36	1	26
310	Control principles for complex biological networks. <i>Briefings in Bioinformatics</i> , 2019 , 20, 2253-2266	13.4	26
309	Diagnosis of Autism Spectrum Disorder Based on Eigenvalues of Brain Networks. <i>IEEE Access</i> , 2019 , 7, 128474-128486	3.5	25
308	BOSS: a novel scaffolding algorithm based on an optimized scaffold graph. <i>Bioinformatics</i> , 2017 , 33, 169-176	1.7	25
307	Identification of hierarchical and overlapping functional modules in PPI networks. <i>IEEE Transactions on Nanobioscience</i> , 2012 , 11, 386-93	3.4	25
306	Inference of biological S-system using the separable estimation method and the genetic algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 955-65	3	25
305	BiXGBoost: a scalable, flexible boosting-based method for reconstructing gene regulatory networks. <i>Bioinformatics</i> , 2019 , 35, 1893-1900	7.2	25

304	Attention convolutional neural network for accurate segmentation and quantification of lesions in ischemic stroke disease. <i>Medical Image Analysis</i> , 2020 , 65, 101791	15.4	24
303	Essential protein discovery based on a combination of modularity and conservatism. <i>Methods</i> , 2016 , 110, 54-63	4.6	23
302	Disease gene identification by using graph kernels and Markov random fields. <i>Science China Life Sciences</i> , 2014 , 57, 1054-63	8.5	23
301	Construction of Refined Protein Interaction Network for Predicting Essential Proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1386-1397	3	23
300	Enhancing the feature representation of multi-modal MRI data by combining multi-view information for MCI classification. <i>Neurocomputing</i> , 2020 , 400, 322-332	5.4	23
299	A New Method for Predicting Protein Functions From Dynamic Weighted Interactome Networks. <i>IEEE Transactions on Nanobioscience</i> , 2016 , 15, 131-9	3.4	22
298	STATE-SPACE MODEL WITH TIME DELAYS FOR GENE REGULATORY NETWORKS. <i>Journal of Biological Systems</i> , 2004 , 12, 483-500	1.6	22
297	EPGA: de novo assembly using the distributions of reads and insert size. <i>Bioinformatics</i> , 2015 , 31, 825-337.2		21
296	Prediction of disease genes using tissue-specified gene-gene network. <i>BMC Systems Biology</i> , 2014 , 8 Suppl 3, S3	3.5	21
295	SVM-RFE based feature selection for tandem mass spectrum quality assessment. <i>International Journal of Data Mining and Bioinformatics</i> , 2011 , 5, 73-88	0.5	21
294	DELAY-INDEPENDENT STABILITY OF GENETIC REGULATORY NETWORKS WITH TIME DELAYS. <i>International Journal of Modeling, Simulation, and Scientific Computing</i> , 2009 , 12, 3-19	0.8	21
293	Multi-Receptive-Field CNN for Semantic Segmentation of Medical Images. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020 , 24, 3215-3225	7.2	21
292	A reliable neighbor-based method for identifying essential proteins by integrating gene expressions, orthology, and subcellular localization information. <i>Tsinghua Science and Technology</i> , 2016 , 21, 668-677	3.4	21
291	Automatic ICD code assignment of Chinese clinical notes based on multilayer attention BiRNN. <i>Journal of Biomedical Informatics</i> , 2019 , 91, 103114	10.2	21
290	Efficient multi-kernel DCNN with pixel dropout for stroke MRI segmentation. <i>Neurocomputing</i> , 2019 , 350, 117-127	5.4	20
289	SDLDA: lncRNA-disease association prediction based on singular value decomposition and deep learning. <i>Methods</i> , 2020 , 179, 73-80	4.6	20
288	A novel approach to denoising ion trap tandem mass spectra. <i>Proteome Science</i> , 2009 , 7, 9	2.6	20
287	Detecting protein complexes from DPINs by density based clustering with Pigeon-Inspired Optimization Algorithm. <i>Science China Information Sciences</i> , 2016 , 59, 1	3.4	20

286	Overlap matrix completion for predicting drug-associated indications. <i>PLoS Computational Biology</i> , 2019 , 15, e1007541	5	20
285	Current challenges and solutions of de novo assembly. <i>Quantitative Biology</i> , 2019 , 7, 90-109	3.9	19
284	DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization. <i>Bioinformatics</i> , 2018 , 34, 1597-1599	7.2	19
283	Discovering essential proteins based on PPI network and protein complex. <i>International Journal of Data Mining and Bioinformatics</i> , 2015 , 12, 24-43	0.5	19
282	Optimally-connected hidden markov models for predicting MHC-binding peptides. <i>Journal of Bioinformatics and Computational Biology</i> , 2006 , 4, 959-80	1	19
281	A group LASSO-based method for robustly inferring gene regulatory networks from multiple time-course datasets. <i>BMC Systems Biology</i> , 2014 , 8 Suppl 3, S1	3.5	18
280	Identifying protein complexes based on multiple topological structures in PPI networks. <i>IEEE Transactions on Nanobioscience</i> , 2013 , 12, 165-72	3.4	18
279	Identifying dynamic protein complexes based on gene expression profiles and PPI networks. <i>BioMed Research International</i> , 2014 , 2014, 375262	3	18
278	Computational Drug Repositioning with Random Walk on a Heterogeneous Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1890-1900	3	18
277	Prioritization of orphan disease-causing genes using topological feature and GO similarity between proteins in interaction networks. <i>Science China Life Sciences</i> , 2014 , 57, 1064-71	8.5	17
276	Detecting protein complexes from active protein interaction networks constructed with dynamic gene expression profiles. <i>Proteome Science</i> , 2013 , 11, S20	2.6	17
275	Prioritizing Disease Genes by Using Search Engine Algorithm. <i>Current Bioinformatics</i> , 2016 , 11, 195-202	4.7	17
274	Variational graph auto-encoders for miRNA-disease association prediction. <i>Methods</i> , 2021 , 192, 25-34	4.6	17
273	BRWMDA:Predicting Microbe-Disease Associations Based on Similarities and Bi-Random Walk on Disease and Microbe Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 1595-1604	3	16
272	Schizophrenia Identification Using Multi-View Graph Measures of Functional Brain Networks. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 479	5.8	16
271	Constrained target controllability of complex networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2017 , 2017, 063402	1.9	16
270	RT-PSM, a real-time program for peptide-spectrum matching with statistical significance. <i>Rapid Communications in Mass Spectrometry</i> , 2006 , 20, 1199-208	2.2	16
269	Controllability and Its Applications to Biological Networks. <i>Journal of Computer Science and Technology</i> , 2019 , 34, 16-34	1.7	15

268	Identifying Individual-Cancer-Related Genes by Rebalancing the Training Samples. <i>IEEE Transactions on Nanobioscience</i> , 2016 , 15, 309-315	3.4	15
267	Quality assessment of peptide tandem mass spectra. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 6, S13	3.6	15
266	Analysis of Single-Cell RNA-seq Data by Clustering Approaches. <i>Current Bioinformatics</i> , 2019 , 14, 314-322	4.7	15
265	Identification of Protein Complexes by Using a Spatial and Temporal Active Protein Interaction Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 817-827	3	15
264	Constructing Disease Similarity Networks Based on Disease Module Theory. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 906-915	3	15
263	PECC: Correcting contigs based on paired-end read distribution. <i>Computational Biology and Chemistry</i> , 2017 , 69, 178-184	3.6	14
262	DMFLDA: A Deep Learning Framework for Predicting lncRNA-Disease Associations. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 2353-2363	3	14
261	Minimum steering node set of complex networks and its applications to biomolecular networks. <i>IET Systems Biology</i> , 2016 , 10, 116-23	1.4	14
260	Artificial Fish Swarm Optimization Based Method to Identify Essential Proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 495-505	3	14
259	De novo assembly methods for next generation sequencing data. <i>Tsinghua Science and Technology</i> , 2013 , 18, 500-514	3.4	14
258	Applications of graph theory in protein structure identification. <i>Proteome Science</i> , 2011 , 9 Suppl 1, S17	2.6	14
257	DeepEP: a deep learning framework for identifying essential proteins. <i>BMC Bioinformatics</i> , 2019 , 20, 506	3.6	14
256	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. <i>BMC Systems Biology</i> , 2018 , 12, 105	3.5	14
255	Identification of protein complexes from multi-relationship protein interaction networks. <i>Human Genomics</i> , 2016 , 10 Suppl 2, 17	6.8	13
254	Sprites: detection of deletions from sequencing data by re-aligning split reads. <i>Bioinformatics</i> , 2016 , 32, 1788-96	7.2	13
253	Improved flower pollination algorithm for identifying essential proteins. <i>BMC Systems Biology</i> , 2018 , 12, 46	3.5	13
252	SDTRLs: Predicting Drug-Target Interactions for Complex Diseases Based on Chemical Substructures. <i>Complexity</i> , 2017 , 2017, 1-10	1.6	13
251	Robust and global delay-dependent stability for genetic regulatory networks with parameter uncertainties. <i>IEEE Transactions on Nanobioscience</i> , 2012 , 11, 251-8	3.4	13

250	AIMAFE: Autism spectrum disorder identification with multi-atlas deep feature representation and ensemble learning. <i>Journal of Neuroscience Methods</i> , 2020 , 343, 108840	3	13
249	Improving de novo Assembly Based on Read Classification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 177-188	3	13
248	Diagnosis of Autism Spectrum Disorder Based on Functional Brain Networks with Deep Learning. <i>Journal of Computational Biology</i> , 2021 , 28, 146-165	1.7	13
247	Topology potential based seed-growth method to identify protein complexes on dynamic PPI data. <i>Information Sciences</i> , 2018 , 425, 140-153	7.7	12
246	Prediction of disease-related genes based on weighted tissue-specific networks by using DNA methylation. <i>BMC Medical Genomics</i> , 2014 , 7 Suppl 2, S4	3.7	12
245	Mining, modeling, and evaluation of subnetworks from large biomolecular networks and its comparison study. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2009 , 13, 184-94		12
244	Predicting novel CircRNA-disease associations based on random walk and logistic regression model. <i>Computational Biology and Chemistry</i> , 2020 , 87, 107287	3.6	12
243	Deep convolutional neural network for accurate segmentation and quantification of white matter hyperintensities. <i>Neurocomputing</i> , 2020 , 384, 231-242	5.4	12
242	DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels. <i>BMC Bioinformatics</i> , 2019 , 20, 538	3.6	12
241	MCHMDA: Predicting Microbe-Disease Associations Based on Similarities and Low-Rank Matrix Completion. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 611-620	3	12
240	Biomolecular Network Controllability With Drug Binding Information. <i>IEEE Transactions on Nanobioscience</i> , 2017 , 16, 326-332	3.4	11
239	C-DEVA: Detection, evaluation, visualization and annotation of clusters from biological networks. <i>BioSystems</i> , 2016 , 150, 78-86	1.9	11
238	Charge state determination of peptide tandem mass spectra using support vector machine (SVM). <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2010 , 14, 552-8		11
237	Inference of Gene Regulatory Networks and its Validation. <i>Current Bioinformatics</i> , 2007 , 2, 139-144	4.7	11
236	Control of hybrid Machines with 2-DOF for trajectory tracking problems. <i>IEEE Transactions on Control Systems Technology</i> , 2005 , 13, 338-342	4.8	11
235	MGT-SM: A Method for Constructing Cellular Signal Transduction Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 417-424	3	11
234	Deep Matrix Factorization Improves Prediction of Human CircRNA-Disease Associations. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , 25, 891-899	7.2	11
233	A Hybrid Clustering Algorithm for Identifying Cell Types from Single-Cell RNA-Seq Data. <i>Genes</i> , 2019 , 10,	4.2	10

232	Predicting Human lncRNA-Disease Associations Based on Geometric Matrix Completion. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2020 , 24, 2420-2429	7.2	10
231	NetEPD: A network-based essential protein discovery platform. <i>Tsinghua Science and Technology</i> , 2020 , 25, 542-552	3.4	10
230	Predicting Protein Complexes in Weighted Dynamic PPI Networks Based on ICSC. <i>Complexity</i> , 2017 , 2017, 1-11	1.6	10
229	Symmetry compression method for discovering network motifs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 1776-89	3	10
228	Gene Regulatory Network modelling: a state-space approach. <i>International Journal of Data Mining and Bioinformatics</i> , 2008 , 2, 1-14	0.5	10
227	An Ensemble Method to Reconstruct Gene Regulatory Networks Based on Multivariate Adaptive Regression Splines. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 347-354	3.4	10
226	MMHGE: detecting mild cognitive impairment based on multi-atlas multi-view hybrid graph convolutional networks and ensemble learning. <i>Cluster Computing</i> , 2021 , 24, 103-113	2.1	10
225	A novel method of gene regulatory network structure inference from gene knock-out expression data. <i>Tsinghua Science and Technology</i> , 2019 , 24, 446-455	3.4	9
224	ESTIMATION OF CONTROL ENERGY AND CONTROL STRATEGIES FOR COMPLEX NETWORKS. <i>International Journal of Modeling, Simulation, and Scientific Computing</i> , 2015 , 18, 1550018	0.8	9
223	CytoCtrlAnalyser: a Cytoscape app for biomolecular network controllability analysis. <i>Bioinformatics</i> , 2018 , 34, 1428-1430	7.2	9
222	NovoHCD: de novo peptide sequencing from HCD spectra. <i>IEEE Transactions on Nanobioscience</i> , 2014 , 13, 65-72	3.4	9
221	Two recursive least squares parameter estimation algorithms for multirate multiple-input systems by using the auxiliary model. <i>Mathematics and Computers in Simulation</i> , 2012 , 82, 777-789	3.3	9
220	Reverse engineering of gene regulatory networks from biological data. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2012 , 2, 365-385	6.9	9
219	Protein Inference by Assembling Peptides Identified from Tandem Mass Spectra. <i>Current Bioinformatics</i> , 2009 , 4, 226-233	4.7	9
218	Domain control of nonlinear networked systems and applications to complex disease networks. <i>Discrete and Continuous Dynamical Systems - Series B</i> , 2017 , 22, 2169-2206	1.3	9
217	GapReduce: a gap filling algorithm based on partitioned read sets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 ,	3	9
216	MEC: Misassembly Error Correction in contigs based on distribution of paired-end reads and statistics of GC-contents. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 ,	3	9
215	An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 728-738	3	9

214	EPGA2: memory-efficient de novo assembler. <i>Bioinformatics</i> , 2015 , 31, 3988-90	7.2	8
213	Drug-drug similarity measure and its applications. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	8
212	M-matrix-based stability conditions for genetic regulatory networks with time-varying delays and noise perturbations. <i>IET Systems Biology</i> , 2013 , 7, 214-22	1.4	8
211	SCOP: a novel scaffolding algorithm based on contig classification and optimization. <i>Bioinformatics</i> , 2019 , 35, 1142-1150	7.2	8
210	CASNMF: A Converged Algorithm for symmetrical nonnegative matrix factorization. <i>Neurocomputing</i> , 2018 , 275, 2031-2040	5.4	8
209	A data-driven clustering recommendation method for single-cell RNA-sequencing data. <i>Tsinghua Science and Technology</i> , 2021 , 26, 772-789	3.4	8
208	Identifying Disease-Gene Associations With Graph-Regularized Manifold Learning. <i>Frontiers in Genetics</i> , 2019 , 10, 270	4.5	7
207	Protein complex detection based on flower pollination mechanism in multi-relation reconstructed dynamic protein networks. <i>BMC Bioinformatics</i> , 2019 , 20, 131	3.6	7
206	Prioritizing Cancer Genes Based on an Improved Random Walk Method. <i>Frontiers in Genetics</i> , 2020 , 11, 377	4.5	7
205	A Deep Learning Framework for Gene Ontology Annotations With Sequence- and Network-Based Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 2208-2217	3	7
204	iOPTICS-GSO for identifying protein complexes from dynamic PPI networks. <i>BMC Medical Genomics</i> , 2017 , 10, 80	3.7	7
203	Double-layer clustering method to predict protein complexes based on power-law distribution and protein sublocalization. <i>Journal of Theoretical Biology</i> , 2016 , 395, 186-193	2.3	7
202	Targeting TRPV1 on cellular plasticity regulated by Ovol 2 and Zeb 1 in hepatocellular carcinoma. <i>Biomedicine and Pharmacotherapy</i> , 2019 , 118, 109270	7.5	7
201	Detecting conserved protein complexes using a dividing-and-matching algorithm and unequally lenient criteria for network comparison. <i>Algorithms for Molecular Biology</i> , 2015 , 10, 21	1.8	7
200	A logistic regression based algorithm for identifying human disease genes 2014 ,		7
199	Features-based deisotoping method for tandem mass spectra. <i>Advances in Bioinformatics</i> , 2011 , 2011, 210805	5.5	7
198	Using a state-space model and location analysis to infer time-delayed regulatory networks. <i>Eurasip Journal on Bioinformatics and Systems Biology</i> , 2009 , 484601		7
197	Finding Significantly Expressed genes from time-course expression profiles. <i>International Journal of Bioinformatics Research and Applications</i> , 2009 , 5, 50-63	0.9	7

196	miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 1032-1041	3	7
195	A disease inference method based on symptom extraction and bidirectional Long Short Term Memory networks. <i>Methods</i> , 2020 , 173, 75-82	4.6	7
194	Identifying the tissues-of-origin of circulating cell-free DNAs is a promising way in noninvasive diagnostics. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	7
193	High-Risk Prediction of Cardiovascular Diseases via Attention-Based Deep Neural Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 1093-1105	3	7
192	A Novel Drug Repositioning Approach Based on Collaborative Metric Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 463-471	3	7
191	DPCMNE: detecting protein complexes from protein-protein interaction networks via multi-level network embedding. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , PP,	3	7
190	A Deep Learning Framework for Identifying Essential Proteins Based on Protein-Protein Interaction Network and Gene Expression Data 2018 ,		7
189	A Novel Core-Attachment-Based Method to Identify Dynamic Protein Complexes Based on Gene Expression Profiles and PPI Networks. <i>Proteomics</i> , 2019 , 19, e1800129	4.8	6
188	Identification of Essential Proteins Based on Improved HITS Algorithm. <i>Genes</i> , 2019 , 10,	4.2	6
187	Deep belief network-Based Matrix Factorization Model for MicroRNA-Disease Associations Prediction. <i>Evolutionary Bioinformatics</i> , 2020 , 16, 1176934320919707	1.9	6
186	A novel scaffolding algorithm based on contig error correction and path extension. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 ,	3	6
185	Predicting essential proteins from protein-protein interactions using order statistics. <i>Journal of Theoretical Biology</i> , 2019 , 480, 274-283	2.3	6
184	An unsupervised machine learning method for assessing quality of tandem mass spectra. <i>Proteome Science</i> , 2012 , 10 Suppl 1, S12	2.6	6
183	Robust identification method for nonlinear model structures and its application to high-performance aircraft. <i>International Journal of Systems Science</i> , 2013 , 44, 1040-1051	2.3	6
182	Unifying protein inference and peptide identification with feedback to update consistency between peptides. <i>Proteomics</i> , 2013 , 13, 239-47	4.8	6
181	Computational Methods to Predict Protein Functions from Protein-Protein Interaction Networks. <i>Current Protein and Peptide Science</i> , 2017 , 18, 1120-1131	2.8	6
180	A two-step logistic regression algorithm for identifying individual-cancer-related genes 2015 ,		6
179	ABC and IFC: modules detection method for PPI network. <i>BioMed Research International</i> , 2014 , 2014, 968173	3	6

178	Quality assessment of tandem mass spectra using support vector machine (SVM). <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 1, S49	3.6	6
177	Recent Developments in Computational Methods for De Novo Peptide Sequencing from Tandem Mass Spectrometry (MS/MS). <i>Protein and Peptide Letters</i> , 2015 , 22, 983-91	1.9	6
176	Improving circRNA-disease association prediction by sequence and ontology representations with convolutional and recurrent neural networks. <i>Bioinformatics</i> , 2020 ,	7.2	6
175	Autoencoder Based Methods for Diagnosis of Autism Spectrum Disorder. <i>Lecture Notes in Computer Science</i> , 2020 , 39-51	0.9	6
174	MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 220-225	3	6
173	A Gene Rank Based Approach for Single Cell Similarity Assessment and Clustering. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 431-442	3	6
172	MDIPA: a microRNA-drug interaction prediction approach based on non-negative matrix factorization. <i>Bioinformatics</i> , 2020 , 36, 5061-5067	7.2	5
171	Computational Approaches for Transcriptome Assembly Based on Sequencing Technologies. <i>Current Bioinformatics</i> , 2020 , 15, 2-16	4.7	5
170	Characterizing dynamic regulatory programs in mouse lung development and their potential association with tumourigenesis via miRNA-TF-mRNA circuits. <i>BMC Systems Biology</i> , 2013 , 7 Suppl 2, S113-5	3.5	5
169	Properties of sparse penalties on inferring gene regulatory networks from time-course gene expression data. <i>IET Systems Biology</i> , 2015 , 9, 16-24	1.4	5
168	Estimating parameters of S-systems by an auxiliary function guided coordinate descent method. <i>Systems Science and Control Engineering</i> , 2014 , 2, 125-134	2	5
167	State observer design for delayed genetic regulatory networks. <i>Computational and Mathematical Methods in Medicine</i> , 2014 , 2014, 761562	2.8	5
166	Predicting beta-turns in proteins using support vector machines with fractional polynomials. <i>Proteome Science</i> , 2013 , 11, S5	2.6	5
165	Peptide charge state determination of tandem mass spectra from low-resolution collision induced dissociation. <i>Proteome Science</i> , 2011 , 9 Suppl 1, S3	2.6	5
164	Separable Parameter Estimation Method for Nonlinear Biological Systems 2009 ,		5
163	Stability analysis of genetic regulatory networks with multiple time delays. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2007 , 2007, 1387-90		5
162	A Genetic K-means Clustering Algorithm Applied to Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2003 , 520-526	0.9	5
161	Applications of Random Walk Model on Biological Networks. <i>Current Bioinformatics</i> , 2016 , 11, 211-220	4.7	5

160	Deep learning for brain disorder diagnosis based on fMRI images. <i>Neurocomputing</i> , 2020 ,	5.4	5
159	KAICD: A knowledge attention-based deep learning framework for automatic ICD coding. <i>Neurocomputing</i> , 2020 , 469, 376-376	5.4	5
158	ILLIS: predicting virus-receptor interactions based on similarity and semi-supervised learning. <i>BMC Bioinformatics</i> , 2019 , 20, 651	3.6	5
157	Detecting protein complex based on hierarchical compressing network embedding 2019 ,		5
156	Drug-target interaction prediction using multi-head self-attention and graph attention network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , PP,	3	5
155	DeepLncLoc: a deep learning framework for long non-coding RNA subcellular localization prediction based on subsequence embedding. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	5
154	Chinese clinical named entity recognition via multi-head self-attention based BiLSTM-CRF.. <i>Artificial Intelligence in Medicine</i> , 2022 , 127, 102282	7.4	5
153	NovoExD: De novo Peptide Sequencing for ETD/ECD Spectra. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 337-344	3	4
152	Detecting SNP combinations discriminating human populations from HapMap data. <i>IEEE Transactions on Nanobioscience</i> , 2015 , 14, 220-8	3.4	4
151	ALSBMF: Predicting lncRNA-Disease Associations by Alternating Least Squares Based on Matrix Factorization. <i>IEEE Access</i> , 2020 , 8, 26190-26198	3.5	4
150	Predicting drug-drug interactions based on integrated similarity and semi-supervised learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 ,	3	4
149	De novo peptide sequencing using CID and HCD spectra pairs. <i>Proteomics</i> , 2016 , 16, 2615-2624	4.8	4
148	Feature Selection via Swarm Intelligence for Determining Protein Essentiality. <i>Molecules</i> , 2018 , 23,	4.8	4
147	Predicting Gene-Disease Associations with Manifold Learning. <i>Lecture Notes in Computer Science</i> , 2018 , 265-271	0.9	4
146	An improved peptide-spectral matching algorithm through distributed search over multiple cores and multiple CPUs. <i>Proteome Science</i> , 2014 , 12, 18	2.6	4
145	Inference of gene regulatory subnetworks from time course gene expression data. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 9, S3	3.6	4
144	Prioritizing human disease genes by multiple data integration 2013 ,		4
143	Prioritization of candidate genes based on disease similarity and protein proximity in PPI networks 2013 ,		4

142	Predicting drug-target interaction based on sequence and structure information. <i>IFAC-PapersOnLine</i> , 2015 , 48, 12-16	0.7	4
141	Clustering PPI data by combining FA and SHC method. <i>BMC Genomics</i> , 2015 , 16 Suppl 3, S3	4.5	4
140	A Framework of De Novo Peptide Sequencing for Multiple Tandem Mass Spectra. <i>IEEE Transactions on Nanobioscience</i> , 2015 , 14, 478-484	3.4	4
139	Identification of Essential Proteins by Using Complexes and Interaction Network. <i>Lecture Notes in Computer Science</i> , 2014 , 255-265	0.9	4
138	New global stability conditions for genetic regulatory networks with time-varying delays 2012 ,		4
137	A feedback framework for protein inference with peptides identified from tandem mass spectra. <i>Proteome Science</i> , 2012 , 10, 68	2.6	4
136	Identification of gene regulatory networks from time course gene expression data. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2010 , 2010, 795-8	0.9	4
135	An Improved Graph Entropy-based Method for Identifying Protein Complexes 2011 ,		4
134	Quality Assessment of Tandem Mass Spectra by Using a Weighted K-Means. <i>Clinical Proteomics</i> , 2009 , 5, 15-22	5	4
133	Globally delay-independent stability of ring-structured genetic regulatory networks 2011 ,		4
132	Feature Selection for Tandem Mass Spectrum Quality Assessment 2008 ,		4
131	2008 ,		4
130	GATCDA: Predicting circRNA-Disease Associations Based on Graph Attention Network. <i>Cancers</i> , 2021 , 13,	6.6	4
129	Construction of the spatial and temporal active protein interaction network for identifying protein complexes 2016 ,		4
128	A network clustering based feature selection strategy for classifying autism spectrum disorder. <i>BMC Medical Genomics</i> , 2019 , 12, 153	3.7	4
127	LncRNA-disease association prediction through combining linear and non-linear features with matrix factorization and deep learning techniques 2019 ,		4
126	A survey on predicting microbe-disease associations: biological data and computational methods. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	4
125	PESM: predicting the essentiality of miRNAs based on gradient boosting machines and sequences. <i>BMC Bioinformatics</i> , 2020 , 21, 111	3.6	3

124	Ensemble disease gene prediction by clinical sample-based networks. <i>BMC Bioinformatics</i> , 2020 , 21, 79	3.6	3
123	Evaluation of Pathway Activation for a Single Sample Toward Inflammatory Bowel Disease Classification. <i>Frontiers in Genetics</i> , 2019 , 10, 1401	4.5	3
122	FUNMarker: Fusion Network-Based Method to Identify Prognostic and Heterogeneous Breast Cancer Biomarkers. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 2483-2491	3.4	3
121	MultiGuideScan: a multi-processing tool for designing CRISPR guide RNA libraries. <i>Bioinformatics</i> , 2020 , 36, 920-921	7.2	3
120	Peptide identification based on fuzzy classification and clustering. <i>Proteome Science</i> , 2013 , 11, S10	2.6	3
119	Predicting Eturns in protein using kernel logistic regression. <i>BioMed Research International</i> , 2013 , 2013, 870372	3	3
118	Stability and bifurcation analysis of models for zebrafish somitogenesis. <i>IEEE Transactions on Nanobioscience</i> , 2011 , 10, 239-47	3.4	3
117	Nonlinear model-based method for clustering periodically expressed genes. <i>Scientific World Journal, The</i> , 2011 , 11, 2051-61	2.2	3
116	Statistical Analysis of Mascot Peptide Identification with Active Logistic Regression. <i>International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering</i> , 2010 ,		3
115	Estimation of parameters in rational reaction rates of molecular biological systems via weighted least squares. <i>International Journal of Systems Science</i> , 2010 , 41, 73-80	2.3	3
114	An adaptive approach to denoising tandem mass spectra 2010 ,		3
113	Mining and state-space modeling and verification of sub-networks from large-scale biomolecular networks. <i>BMC Bioinformatics</i> , 2007 , 8, 324	3.6	3
112	Estimation of parameters in the linear-fractional models. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2007 , 2007, 1086-9		3
111	Inferring gene regulatory networks with time delays using a genetic algorithm. <i>IET Systems Biology</i> , 2005 , 152, 67-74		3
110	2006 ,		3
109	A Review of Drug Repositioning Based Chemical-induced Cell Line Expression Data. <i>Current Medicinal Chemistry</i> , 2020 , 27, 5340-5350	4.3	3
108	Predicting drug-drug interactions by graph convolutional network with multi-kernel. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	3
107	Matrix Decomposition Methods in Bioinformatics. <i>Current Bioinformatics</i> , 2013 , 8, 259-266	4.7	3

106	Diagnosis of ASD from rs-fMRI Images Based on Brain Dynamic Networks. <i>Lecture Notes in Computer Science</i> , 2020 , 166-177	0.9	3
105	NovoGMET: De Novo Peptide Sequencing Using Graphs with Multiple Edge Types (GMET) for ETD/ECD Spectra. <i>Lecture Notes in Computer Science</i> , 2014 , 200-211	0.9	3
104	Identifying protein complexes in dynamic protein-protein interaction networks based on Cuckoo Search algorithm 2016 ,		3
103	Finding Community Modules of Brain Networks Based on PSO with Uniform Design. <i>BioMed Research International</i> , 2019 , 2019, 4979582	3	3
102	Predicting miRNA-Disease Associations Based on Multi-View Variational Graph Auto-Encoder with Matrix Factorization. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , PP,	7.2	3
101	Disease Inference with Symptom Extraction and Bidirectional Recurrent Neural Network 2018 ,		3
100	Human Protein Complex Signatures for Drug Repositioning 2019 ,		2
99	IDNDDI: An Integrated Drug Similarity Network Method for Predicting Drug-Drug Interactions. <i>Lecture Notes in Computer Science</i> , 2019 , 89-99	0.9	2
98	MAC: Merging Assemblies by Using Adjacency Algebraic Model and Classification. <i>Frontiers in Genetics</i> , 2019 , 10, 1396	4.5	2
97	VALiBS: a visual aligner for bisulfite sequences. <i>BMC Bioinformatics</i> , 2017 , 18, 410	3.6	2
96	Predicting Disease Genes from Clinical Single Sample-Based PPI Networks. <i>Lecture Notes in Computer Science</i> , 2018 , 247-258	0.9	2
95	EPGA-SC : A Framework for de novo Assembly of Single-Cell Sequencing Reads. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 1492-1503	3	2
94	2013 ,		2
93	Protein Inference from the Integration of Tandem MS Data and Interactome Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 1399-1409	3	2
92	MEC: Misassembly error correction in contigs using a combination of paired-end reads and GC-contents 2017 ,		2
91	NovoPair: De novo peptide sequencing for tandem mass spectra pair 2014 ,		2
90	Not AU protein complexes exhibit dense structures in <i>S. cerevisiae</i> PPI network 2012 ,		2
89	Alternating weighted least squares parameter estimation for biological S-systems 2012 ,		2

88	Parallelizing Peptide-Spectrum scoring using modern graphics processing units 2011 ,		2
87	An adaptive approach to denoising tandem mass spectra. <i>Proteomics</i> , 2011 , 11, 3773-8	4.8	2
86	Iterative Linear Least Squares Method of Parameter Estimation for Linear-Fractional Models of Molecular Biological Systems. <i>International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering</i> , 2010 ,		2
85	Structure identification and parameter estimation of biological s-systems 2010 ,		2
84	Inferring gene regulatory networks from multiple time course gene expression datasets 2011 ,		2
83	Estimating parameters in the caspase-activated apoptosis system. <i>International Journal of Biomedical Engineering and Technology</i> , 2010 , 4, 338	1.3	2
82	Determination of the minimum number of microarray experiments for discovery of gene expression patterns. <i>BMC Bioinformatics</i> , 2006 , 7 Suppl 4, S13	3.6	2
81	A semi-supervised autoencoder for autism disease diagnosis. <i>Neurocomputing</i> , 2022 , 483, 140-147	5.4	2
80	An integrated brain-specific network identifies genes associated with neuropathologic and clinical traits of Alzheimer's disease.. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	2
79	Using Deep Neural Network to Predict Drug Sensitivity of Cancer Cell Lines. <i>Lecture Notes in Computer Science</i> , 2018 , 223-226	0.9	2
78	Identification of Prognostic and Heterogeneous Breast Cancer Biomarkers Based on Fusion Network and Multiple Scoring Strategies. <i>Lecture Notes in Computer Science</i> , 2019 , 529-534	0.9	2
77	RepAHR: an improved approach for de novo repeat identification by assembly of the high-frequency reads. <i>BMC Bioinformatics</i> , 2020 , 21, 463	3.6	2
76	Identifying gene signatures for cancer drug repositioning based on sample clustering. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , PP,	3	2
75	Identifying cell types from single-cell data based on similarities and dissimilarities between cells. <i>BMC Bioinformatics</i> , 2021 , 22, 255	3.6	2
74	Identifying disease genes from PPI networks weighted by gene expression under different conditions 2016 ,		2
73	The MSS of complex networks with centrality based preference and its application to biomolecular networks 2016 ,		2
72	Predicting microRNA-environmental factor interactions based on bi-random walk and multi-label learning 2016 ,		2
71	A Global Similarity Learning for Clustering of Single-Cell RNA-Seq Data 2019 ,		2

70	CSA: a web service for the complete process of CHIP-Seq analysis. <i>BMC Bioinformatics</i> , 2019 , 20, 515	3.6	2
69	Proteoform characterization based on top-down mass spectrometry. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1729-1750	13.4	2
68	SSRE: Cell Type Detection Based on Sparse Subspace Representation and Similarity Enhancement. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 , 19, 282-291	6.5	2
67	Identification of Tumor Tissue of Origin with RNA-Seq Data and Using Gradient Boosting Strategy. <i>BioMed Research International</i> , 2021 , 2021, 6653793	3	2
66	Biomolecular Networks for Complex Diseases. <i>Complexity</i> , 2018 , 2018, 1-3	1.6	2
65	MDAPlatform: A Component-based Platform for Constructing and Assessing miRNA-disease Association Prediction Methods. <i>Current Bioinformatics</i> , 2021 , 16, 710-721	4.7	2
64	Machine learning based liver disease diagnosis: A systematic review. <i>Neurocomputing</i> , 2021 , 468, 492-493	3.4	2
63	Diagnosis of autism spectrum disorder with convolutional autoencoder and structural MRI images 2021 , 23-38		2
62	M-Matrix-Based State Observer Design for Genetic Regulatory Networks With Mixed Delays. <i>IEEE Transactions on Circuits and Systems II: Express Briefs</i> , 2018 , 65, 1054-1058	3.5	1
61	Detecting protein complexes from DPINs by OPTICS based on particle swarm optimization 2016 ,		1
60	Discovering biological patterns from short time-series gene expression profiles with integrating PPI data. <i>Neurocomputing</i> , 2014 , 145, 3-13	5.4	1
59	PPI modules detection method through ABC-IFC algorithm 2013 ,		1
58	Robust inference of gene regulatory networks from multiple microarray datasets 2013 ,		1
57	Nonlinear-model-based analysis methods for time-course gene expression data. <i>Scientific World Journal, The</i> , 2014 , 2014, 313747	2.2	1
56	A dividing-and-matching algorithm to detect conserved protein complexes via local network alignment 2013 ,		1
55	Estimating parameters in genetic regulatory networks with SUM logic. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2011 , 2011, 1371-4	0.9	1
54	Speed improvements of peptide-spectrum matching using single-instruction multiple-data instructions. <i>Proteomics</i> , 2011 , 11, 3779-85	4.8	1
53	Parameter estimation method for improper fractional models and its application to molecular biological systems. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2010 , 2010, 1477-80	0.9	1

52	Alternating Constraint Least Squares Parameter Estimation for S-System Models of Biological Networks. <i>International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010,</i>		1
51	Improve Accuracy of Peptide Identification with Consistency between Peptides 2011,		1
50	Model based clustering for tandem mass spectrum quality assessment. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference, 2009,</i> 2009, 6747-50	0.9	1
49	Parameter estimation in rational models of molecular biological systems. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference, 2009,</i> 2009, 3263-6	0.9	1
48	A fuzzy cluster-based algorithm for peptide identification 2012,		1
47	Subspace pursuit for gene profile classification 2009,		1
46	Dynamic-model-based method for selecting significantly expressed genes from time-course expression profiles. <i>IEEE Transactions on Information Technology in Biomedicine, 2010,</i> 14, 16-22		1
45	A genetic algorithm for inferring time delays in gene regulatory networks		1
44			1
43	RMS-UNet: Residual multi-scale UNet for liver and lesion segmentation.. <i>Artificial Intelligence in Medicine, 2022,</i> 124, 102231	7.4	1
42	Significance Analysis of Time-Course Gene Expression Profiles 2007, 13-24		1
41	A review of drug repositioning based chemical-induced cell line expression data. <i>Current Medicinal Chemistry, 2019,</i> 26,	4.3	1
40	Finding Community of Brain Networks Based on Neighbor Index and DPSO with Dynamic Crossover. <i>Current Bioinformatics, 2020,</i> 15, 287-299	4.7	1
39	MiRNA-Disease Associations Prediction Based on Negative Sample Selection and Multi-layer Perceptron. <i>Lecture Notes in Computer Science, 2020,</i> 178-188	0.9	1
38	Drug Target Identification Based on Structural Output Controllability of Complex Networks. <i>Lecture Notes in Computer Science, 2014,</i> 188-199	0.9	1
37	LSSL: A Novel Scaffolding Method Based on Path Extension. <i>Lecture Notes in Computer Science, 2017,</i> 428-438	0.9	1
36	Relating Diseases Based on Disease Module Theory. <i>Lecture Notes in Computer Science, 2017,</i> 24-33	0.9	1
35	MADA: a web service for analysing DNA methylation array data. <i>BMC Bioinformatics, 2020,</i> 21, 403	3.6	1

34	Mining the plasma-proteome associated genes in patients with gastro-esophageal cancers for biomarker discovery. <i>Scientific Reports</i> , 2021 , 11, 7590	4.9	1
33	Parallel computing for genome sequence processing. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	1
32	Prediction of Target-Drug Therapy by Identifying Gene Mutations in Lung Cancer With Histopathological Stained Image and Deep Learning Techniques. <i>Frontiers in Oncology</i> , 2021 , 11, 642945 ^{5:3}		1
31	Essential Protein Prediction Based on node2vec and XGBoost. <i>Journal of Computational Biology</i> , 2021 , 28, 687-700	1.7	1
30	de novo repeat detection based on the third generation sequencing reads 2019 ,		1
29	Classification of Schizophrenia by Iterative Random Forest Feature Selection Based on DNA Methylation Array Data 2019 ,		1
28	Drug and disease similarity calculation platform for drug repositioning 2019 ,		1
27	DualRank: multiplex network-based dual ranking for heterogeneous complex disease analysis 2019 ,		1
26	D3GRN: a data driven dynamic network construction method to infer gene regulatory networks. <i>BMC Genomics</i> , 2019 , 20, 929	4.5	1
25	IsoResolve: predicting splice isoform functions by integrating gene and isoform-level features with domain adaptation. <i>Bioinformatics</i> , 2021 , 37, 522-530	7.2	1
24	An ensemble hybrid feature selection method for neuropsychiatric disorder classification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , PP,	3	1
23	A dual ranking algorithm based on the multiplex network for heterogeneous complex disease analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , PP,	3	1
22	A sensitive repeat identification framework based on short and long reads. <i>Nucleic Acids Research</i> , 2021 , 49, e100	20.1	1
21	NetAUC: A network-based multi-biomarker identification method by AUC optimization. <i>Methods</i> , 2021 , 198, 56-56	4.6	1
20	A dynamic predictor selection algorithm for predicting stock market movement. <i>Expert Systems With Applications</i> , 2021 , 186, 115836	7.8	1
19	Improved Spectral Clustering Method for Identifying Cell Types from Single-Cell Data. <i>Lecture Notes in Computer Science</i> , 2019 , 177-189	0.9	0
18	Complexity analysis and parameter estimation of dynamic metabolic systems. <i>Computational and Mathematical Methods in Medicine</i> , 2013 , 2013, 698341	2.8	0
17	Prognosticating Outcome in Pancreatic Head Cancer With the use of a Machine Learning Algorithm. <i>Technology in Cancer Research and Treatment</i> , 2021 , 20, 15330338211050767	2.7	0

16	Human Protein Complex-Based Drug Signatures for Personalized Cancer Medicine. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , 25, 4079-4088	7.2	o
15	Predicting Protein Functions Based on Dynamic Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2015 , 390-401	0.9	o
14	Predicting disease-associated genes: Computational methods, databases, and evaluations. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2021 , 11, e1383	6.9	o
13	Machine learning approaches for predicting biomolecule-disease associations. <i>Briefings in Functional Genomics</i> , 2021 , 20, 273-287	4.9	o
12	scASK: A Novel Ensemble Framework for Classifying Cell Types Based on Single-cell RNA-seq Data. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021 , 25, 3230-3239	7.2	o
11	PBMarsNet: A Multivariate Adaptive Regression Splines Based Method to Reconstruct Gene Regulatory Networks. <i>Lecture Notes in Computer Science</i> , 2018 , 38-48	0.9	
10	SPOC: Identification of Drug Targets in Biological Networks via Set Preference Output Control. <i>Lecture Notes in Computer Science</i> , 2020 , 26-37	0.9	
9	Sprites2: Detection of Deletions Based on an Accurate Alignment Strategy. <i>Lecture Notes in Computer Science</i> , 2018 , 139-150	0.9	
8	Assigning probabilities to Mascot peptide identification using logistic regression. <i>Advances in Experimental Medicine and Biology</i> , 2010 , 680, 229-36	3.6	
7	Construction of Uncertain Protein-Protein Interaction Networks and Its Applications. <i>Lecture Notes in Computer Science</i> , 2013 , 286-297	0.9	
6	Searching SNP Combinations Related to Evolutionary Information of Human Populations on HapMap Data. <i>Lecture Notes in Computer Science</i> , 2014 , 278-288	0.9	
5	Deletion Detection Method Using the Distribution of Insert Size and a Precise Alignment Strategy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , 18, 1070-1081	3	
4	Overlap matrix completion for predicting drug-associated indications 2019 , 15, e1007541		
3	Overlap matrix completion for predicting drug-associated indications 2019 , 15, e1007541		
2	Overlap matrix completion for predicting drug-associated indications 2019 , 15, e1007541		
1	Overlap matrix completion for predicting drug-associated indications 2019 , 15, e1007541		