

Fang-Xiang Wu

List of Publications by Year in Descending Order

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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.

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	RMS-UNet: Residual multi-scale UNet for liver and lesion segmentation.. <i>Artificial Intelligence in Medicine</i> , 2022 , 124, 102231	7.4	1
374	A semi-supervised autoencoder for autism disease diagnosis. <i>Neurocomputing</i> , 2022 , 483, 140-147	5.4	2
373	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
372	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
371	Drug-drug similarity measure and its applications. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	8
370	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	3.491	3
369	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
368	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
367	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
366	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
365	Predicting drug-drug interactions by graph convolutional network with multi-kernel. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	3
364	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
363	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	0
362	Biomedical data and computational models for drug repositioning: a comprehensive review. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1604-1619	13.4	45
361	Variational graph auto-encoders for miRNA-disease association prediction. <i>Methods</i> , 2021 , 192, 25-34	4.6	17
360	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
359	Parallel computing for genome sequence processing. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	1

358	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, 642945-53	5.3	1
357	Identifying cell types from single-cell data based on similarities and dissimilarities between cells. <i>BMC Bioinformatics</i> , 2021 , 22, 255	3.6	2
356	GATCDA: Predicting circRNA-Disease Associations Based on Graph Attention Network. <i>Cancers</i> , 2021 , 13,	6.6	4
355	Essential Protein Prediction Based on node2vec and XGBoost. <i>Journal of Computational Biology</i> , 2021 , 28, 687-700	1.7	1
354	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
353	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
352	Proteoform characterization based on top-down mass spectrometry. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1729-1750	13.4	2
351	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
350	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
349	A survey on predicting microbe-disease associations: biological data and computational methods. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	4
348	Predicting disease-associated genes: Computational methods, databases, and evaluations. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2021 , 11, e1383	6.9	0
347	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
346	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
345	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
344	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
343	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
342	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	
341	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

340	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
339	An ensemble hybrid feature selection method for neuropsychiatric disorder classification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , PP,	3	1
338	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
337	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
336	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
335	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
334	Machine learning approaches for predicting biomolecule-disease associations. <i>Briefings in Functional Genomics</i> , 2021 , 20, 273-287	4.9	0
333	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
332	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
331	A sensitive repeat identification framework based on short and long reads. <i>Nucleic Acids Research</i> , 2021 , 49, e100	20.1	1
330	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
329	NetAUC: A network-based multi-biomarker identification method by AUC optimization. <i>Methods</i> , 2021 , 198, 56-56	4.6	1
328	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	0
327	Machine learning based liver disease diagnosis: A systematic review. <i>Neurocomputing</i> , 2021 , 468, 492-493	3.4	2
326	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
325	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
324	A dynamic predictor selection algorithm for predicting stock market movement. <i>Expert Systems With Applications</i> , 2021 , 186, 115836	7.8	1
323	Diagnosis of autism spectrum disorder with convolutional autoencoder and structural MRI images 2021 , 23-38		2

322	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
321	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
320	Prioritizing Cancer Genes Based on an Improved Random Walk Method. <i>Frontiers in Genetics</i> , 2020 , 11, 377	4.5	7
319	SDLDA: lncRNA-disease association prediction based on singular value decomposition and deep learning. <i>Methods</i> , 2020 , 179, 73-80	4.6	20
318	Deep belief network-Based Matrix Factorization Model for MicroRNA-Disease Associations Prediction. <i>Evolutionary Bioinformatics</i> , 2020 , 16, 1176934320919707	1.9	6
317	MDIPA: a microRNA-drug interaction prediction approach based on non-negative matrix factorization. <i>Bioinformatics</i> , 2020 , 36, 5061-5067	7.2	5
316	A survey on U-shaped networks in medical image segmentations. <i>Neurocomputing</i> , 2020 , 409, 244-258	5.4	64
315	PESM: predicting the essentiality of miRNAs based on gradient boosting machines and sequences. <i>BMC Bioinformatics</i> , 2020 , 21, 111	3.6	3
314	Ensemble disease gene prediction by clinical sample-based networks. <i>BMC Bioinformatics</i> , 2020 , 21, 79	3.6	3
313	Computational Approaches for Transcriptome Assembly Based on Sequencing Technologies. <i>Current Bioinformatics</i> , 2020 , 15, 2-16	4.7	5
312	ALSBMF: Predicting lncRNA-Disease Associations by Alternating Least Squares Based on Matrix Factorization. <i>IEEE Access</i> , 2020 , 8, 26190-26198	3.5	4
311	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
310	NetEPD: A network-based essential protein discovery platform. <i>Tsinghua Science and Technology</i> , 2020 , 25, 542-552	3.4	10
309	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
308	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
307	MultiGuideScan: a multi-processing tool for designing CRISPR guide RNA libraries. <i>Bioinformatics</i> , 2020 , 36, 920-921	7.2	3
306	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	
305	A Review of Drug Repositioning Based Chemical-induced Cell Line Expression Data. <i>Current Medicinal Chemistry</i> , 2020 , 27, 5340-5350	4.3	3

304	Finding Community of Brain Networks Based on Neighbor Index and DPSO with Dynamic Crossover. <i>Current Bioinformatics</i> , 2020 , 15, 287-299	4.7	1
303	Improving circRNA-disease association prediction by sequence and ontology representations with convolutional and recurrent neural networks. <i>Bioinformatics</i> , 2020 ,	7.2	6
302	Autoencoder Based Methods for Diagnosis of Autism Spectrum Disorder. <i>Lecture Notes in Computer Science</i> , 2020 , 39-51	0.9	6
301	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
300	MiRNA-Disease Associations Prediction Based on Negative Sample Selection and Multi-layer Perceptron. <i>Lecture Notes in Computer Science</i> , 2020 , 178-188	0.9	1
299	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
298	Deep convolutional neural network for accurate segmentation and quantification of white matter hyperintensities. <i>Neurocomputing</i> , 2020 , 384, 231-242	5.4	12
297	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
296	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
295	Deep learning for brain disorder diagnosis based on fMRI images. <i>Neurocomputing</i> , 2020 ,	5.4	5
294	MADA: a web service for analysing DNA methylation array data. <i>BMC Bioinformatics</i> , 2020 , 21, 403	3.6	1
293	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
292	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
291	KAICD: A knowledge attention-based deep learning framework for automatic ICD coding. <i>Neurocomputing</i> , 2020 , 469, 376-376	5.4	5
290	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
289	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
288	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
287	miRTRS: A Recommendation Algorithm for Predicting miRNA Targets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 1032-1041	3	7

286	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
285	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
284	Improving de novo Assembly Based on Read Classification. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 177-188	3	13
283	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
282	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
281	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
280	Diagnosis of Autism Spectrum Disorder Based on Eigenvalues of Brain Networks. <i>IEEE Access</i> , 2019 , 7, 128474-128486	3.5	25
279	Human Protein Complex Signatures for Drug Repositioning 2019 ,		2
278	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
277	Controllability and Its Applications to Biological Networks. <i>Journal of Computer Science and Technology</i> , 2019 , 34, 16-34	1.7	15
276	A Hybrid Clustering Algorithm for Identifying Cell Types from Single-Cell RNA-Seq Data. <i>Genes</i> , 2019 , 10,	4.2	10
275	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
274	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
273	Current challenges and solutions of de novo assembly. <i>Quantitative Biology</i> , 2019 , 7, 90-109	3.9	19
272	Identifying Disease-Gene Associations With Graph-Regularized Manifold Learning. <i>Frontiers in Genetics</i> , 2019 , 10, 270	4.5	7
271	Efficient multi-kernel DCNN with pixel dropout for stroke MRI segmentation. <i>Neurocomputing</i> , 2019 , 350, 117-127	5.4	20
270	Identification of Essential Proteins Based on Improved HITS Algorithm. <i>Genes</i> , 2019 , 10,	4.2	6
269	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

268	Enhancing the prediction of disease-gene associations with multimodal deep learning. <i>Bioinformatics</i> , 2019 , 35, 3735-3742	7.2	26
267	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
266	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
265	Evaluation of Pathway Activation for a Single Sample Toward Inflammatory Bowel Disease Classification. <i>Frontiers in Genetics</i> , 2019 , 10, 1401	4.5	3
264	MAC: Merging Assemblies by Using Adjacency Algebraic Model and Classification. <i>Frontiers in Genetics</i> , 2019 , 10, 1396	4.5	2
263	Schizophrenia Identification Using Multi-View Graph Measures of Functional Brain Networks. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 479	5.8	16
262	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
261	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
260	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
259	Predicting essential proteins from protein-protein interactions using order statistics. <i>Journal of Theoretical Biology</i> , 2019 , 480, 274-283	2.3	6
258	Identifying Cancer-Specific circRNA-RBP Binding Sites Based on Deep Learning. <i>Molecules</i> , 2019 , 24,	4.8	29
257	A review of drug repositioning based chemical-induced cell line expression data. <i>Current Medicinal Chemistry</i> , 2019 , 26,	4.3	1
256	Analysis of Single-Cell RNA-seq Data by Clustering Approaches. <i>Current Bioinformatics</i> , 2019 , 14, 314-322	4.7	15
255	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
254	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
253	de novo repeat detection based on the third generation sequencing reads 2019 ,		1
252	Classification of Schizophrenia by Iterative Random Forest Feature Selection Based on DNA Methylation Array Data 2019 ,		1
251	IILLS: predicting virus-receptor interactions based on similarity and semi-supervised learning. <i>BMC Bioinformatics</i> , 2019 , 20, 651	3.6	5

250	A network clustering based feature selection strategy for classifying autism spectrum disorder. <i>BMC Medical Genomics</i> , 2019 , 12, 153	3.7	4
249	A Global Similarity Learning for Clustering of Single-Cell RNA-Seq Data 2019 ,		2
248	LncRNA-disease association prediction through combining linear and non-linear features with matrix factorization and deep learning techniques 2019 ,		4
247	Detecting protein complex based on hierarchical compressing network embedding 2019 ,		5
246	Drug and disease similarity calculation platform for drug repositioning 2019 ,		1
245	DualRank: multiplex network-based dual ranking for heterogeneous complex disease analysis 2019 ,		1
244	D3GRN: a data driven dynamic network construction method to infer gene regulatory networks. <i>BMC Genomics</i> , 2019 , 20, 929	4.5	1
243	Finding Community Modules of Brain Networks Based on PSO with Uniform Design. <i>BioMed Research International</i> , 2019 , 2019, 4979582	3	3
242	CSA: a web service for the complete process of CHIP-Seq analysis. <i>BMC Bioinformatics</i> , 2019 , 20, 515	3.6	2
241	DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels. <i>BMC Bioinformatics</i> , 2019 , 20, 538	3.6	12
240	Overlap matrix completion for predicting drug-associated indications. <i>PLoS Computational Biology</i> , 2019 , 15, e1007541	5	20
239	DeepEP: a deep learning framework for identifying essential proteins. <i>BMC Bioinformatics</i> , 2019 , 20, 506	3.6	14
238	SCOP: a novel scaffolding algorithm based on contig classification and optimization. <i>Bioinformatics</i> , 2019 , 35, 1142-1150	7.2	8
237	BiXGBoost: a scalable, flexible boosting-based method for reconstructing gene regulatory networks. <i>Bioinformatics</i> , 2019 , 35, 1893-1900	7.2	25
236	Control principles for complex biological networks. <i>Briefings in Bioinformatics</i> , 2019 , 20, 2253-2266	13.4	26
235	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
234	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
233	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

232	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
231	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
230	Overlap matrix completion for predicting drug-associated indications 2019 , 15, e1007541		
229	Overlap matrix completion for predicting drug-associated indications 2019 , 15, e1007541		
228	Overlap matrix completion for predicting drug-associated indications 2019 , 15, e1007541		
227	Overlap matrix completion for predicting drug-associated indications 2019 , 15, e1007541		
226	CytoCtrlAnalyser: a Cytoscape app for biomolecular network controllability analysis. <i>Bioinformatics</i> , 2018 , 34, 1428-1430	7.2	9
225	DyNetViewer: a Cytoscape app for dynamic network construction, analysis and visualization. <i>Bioinformatics</i> , 2018 , 34, 1597-1599	7.2	19
224	Prediction of lncRNA-disease associations based on inductive matrix completion. <i>Bioinformatics</i> , 2018 , 34, 3357-3364	7.2	134
223	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
222	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
221	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
220	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
219	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
218	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
217	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	
216	Feature Selection via Swarm Intelligence for Determining Protein Essentiality. <i>Molecules</i> , 2018 , 23,	4.8	4
215	Predicting Gene-Disease Associations with Manifold Learning. <i>Lecture Notes in Computer Science</i> , 2018 , 265-271	0.9	4

214	Improved flower pollination algorithm for identifying essential proteins. <i>BMC Systems Biology</i> , 2018 , 12, 46	3.5	13
213	Predicting Disease Genes from Clinical Single Sample-Based PPI Networks. <i>Lecture Notes in Computer Science</i> , 2018 , 247-258	0.9	2
212	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
211	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
210	Sprites2: Detection of Deletions Based on an Accurate Alignment Strategy. <i>Lecture Notes in Computer Science</i> , 2018 , 139-150	0.9	
209	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
208	A review on machine learning principles for multi-view biological data integration. <i>Briefings in Bioinformatics</i> , 2018 , 19, 325-340	13.4	159
207	GapReduce: a gap filling algorithm based on partitioned read sets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 ,	3	9
206	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
205	CASNMF: A Converged Algorithm for symmetrical nonnegative matrix factorization. <i>Neurocomputing</i> , 2018 , 275, 2031-2040	5.4	8
204	A Deep Learning Framework for Identifying Essential Proteins Based on Protein-Protein Interaction Network and Gene Expression Data 2018 ,		7
203	Disease Inference with Symptom Extraction and Bidirectional Recurrent Neural Network 2018 ,		3
202	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
201	An interpretable boosting model to predict side effects of analgesics for osteoarthritis. <i>BMC Systems Biology</i> , 2018 , 12, 105	3.5	14
200	DWNN-RLS: regularized least squares method for predicting circRNA-disease associations. <i>BMC Bioinformatics</i> , 2018 , 19, 520	3.6	53
199	PWCDA: Path Weighted Method for Predicting circRNA-Disease Associations. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	48
198	Biomolecular Networks for Complex Diseases. <i>Complexity</i> , 2018 , 2018, 1-3	1.6	2
197	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

196	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
195	PECC: Correcting contigs based on paired-end read distribution. <i>Computational Biology and Chemistry</i> , 2017 , 69, 178-184	3.6	14
194	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
193	Biomolecular Network Controllability With Drug Binding Information. <i>IEEE Transactions on Nanobioscience</i> , 2017 , 16, 326-332	3.4	11
192	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
191	Predicting Protein Complexes in Weighted Dynamic PPI Networks Based on ICSC. <i>Complexity</i> , 2017 , 2017, 1-11	1.6	10
190	VALiBS: a visual aligner for bisulfite sequences. <i>BMC Bioinformatics</i> , 2017 , 18, 410	3.6	2
189	iOPTICS-GSO for identifying protein complexes from dynamic PPI networks. <i>BMC Medical Genomics</i> , 2017 , 10, 80	3.7	7
188	Protein-protein interactions: detection, reliability assessment and applications. <i>Briefings in Bioinformatics</i> , 2017 , 18, 798-819	13.4	43
187	LDAP: a web server for lncRNA-disease association prediction. <i>Bioinformatics</i> , 2017 , 33, 458-460	7.2	72
186	Constrained target controllability of complex networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2017 , 2017, 063402	1.9	16
185	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
184	BOSS: a novel scaffolding algorithm based on an optimized scaffold graph. <i>Bioinformatics</i> , 2017 , 33, 169-176	17.6	25
183	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
182	MEC: Misassembly error correction in contigs using a combination of paired-end reads and GC-contents 2017 ,		2
181	CytoCluster: A Cytoscape Plugin for Cluster Analysis and Visualization of Biological Networks. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	43
180	SDTRLS: Predicting Drug-Target Interactions for Complex Diseases Based on Chemical Substructures. <i>Complexity</i> , 2017 , 2017, 1-10	1.6	13
179	Complex Brain Network Analysis and Its Applications to Brain Disorders: A Survey. <i>Complexity</i> , 2017 , 2017, 1-27	1.6	46

178	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
177	LSLS: A Novel Scaffolding Method Based on Path Extension. <i>Lecture Notes in Computer Science</i> , 2017 , 428-438	0.9	1
176	Relating Diseases Based on Disease Module Theory. <i>Lecture Notes in Computer Science</i> , 2017 , 24-33	0.9	1
175	C-DEVA: Detection, evaluation, visualization and annotation of clusters from biological networks. <i>BioSystems</i> , 2016 , 150, 78-86	1.9	11
174	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
173	De novo peptide sequencing using CID and HCD spectra pairs. <i>Proteomics</i> , 2016 , 16, 2615-2624	4.8	4
172	Essential protein discovery based on a combination of modularity and conservatism. <i>Methods</i> , 2016 , 110, 54-63	4.6	23
171	Detecting protein complexes from DPINs by OPTICS based on particle swarm optimization 2016 ,		1
170	Identification of protein complexes from multi-relationship protein interaction networks. <i>Human Genomics</i> , 2016 , 10 Suppl 2, 17	6.8	13
169	Identifying Individual-Cancer-Related Genes by Rebalancing the Training Samples. <i>IEEE Transactions on Nanobioscience</i> , 2016 , 15, 309-315	3.4	15
168	Predicting drug-target interaction using positive-unlabeled learning. <i>Neurocomputing</i> , 2016 , 206, 50-57	5.4	63
167	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
166	Sprites: detection of deletions from sequencing data by re-aligning split reads. <i>Bioinformatics</i> , 2016 , 32, 1788-96	7.2	13
165	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
164	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
163	Prioritizing Disease Genes by Using Search Engine Algorithm. <i>Current Bioinformatics</i> , 2016 , 11, 195-202	4.7	17
162	Applications of Random Walk Model on Biological Networks. <i>Current Bioinformatics</i> , 2016 , 11, 211-220	4.7	5
161	Construction of the spatial and temporal active protein interaction network for identifying protein complexes 2016 ,		4

160	Identifying protein complexes in dynamic protein-protein interaction networks based on Cuckoo Search algorithm 2016 ,		3
159	Identifying disease genes from PPI networks weighted by gene expression under different conditions 2016 ,		2
158	Predicting essential proteins based on subcellular localization, orthology and PPI networks. <i>BMC Bioinformatics</i> , 2016 , 17 Suppl 8, 279	3.6	45
157	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
156	The MSS of complex networks with centrality based preference and its application to biomolecular networks 2016 ,		2
155	Predicting microRNA-environmental factor interactions based on bi-random walk and multi-label learning 2016 ,		2
154	Drug repositioning based on comprehensive similarity measures and Bi-Random walk algorithm. <i>Bioinformatics</i> , 2016 , 32, 2664-71	7.2	190
153	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
152	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
151	Network output controllability-based method for drug target identification. <i>IEEE Transactions on Nanobioscience</i> , 2015 , 14, 184-91	3.4	27
150	Detecting SNP combinations discriminating human populations from HapMap data. <i>IEEE Transactions on Nanobioscience</i> , 2015 , 14, 220-8	3.4	4
149	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
148	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
147	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
146	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
145	EPGA2: memory-efficient de novo assembler. <i>Bioinformatics</i> , 2015 , 31, 3988-90	7.2	8
144	CytoNCA: a cytoscape plugin for centrality analysis and evaluation of protein interaction networks. <i>BioSystems</i> , 2015 , 127, 67-72	1.9	485
143	EPGA: de novo assembly using the distributions of reads and insert size. <i>Bioinformatics</i> , 2015 , 31, 825-337.2		21

142	Computational approaches for prioritizing candidate disease genes based on PPI networks. <i>Tsinghua Science and Technology</i> , 2015 , 20, 500-512	3.4	48
141	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
140	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
139	Predicting drug-target interaction based on sequence and structure information. <i>IFAC-PapersOnLine</i> , 2015 , 48, 12-16	0.7	4
138	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
137	Identifying essential proteins from active PPI networks constructed with dynamic gene expression. <i>BMC Genomics</i> , 2015 , 16 Suppl 3, S1	4.5	50
136	Clustering PPI data by combining FA and SHC method. <i>BMC Genomics</i> , 2015 , 16 Suppl 3, S3	4.5	4
135	Rechecking the Centrality-Lethality Rule in the Scope of Protein Subcellular Localization Interaction Networks. <i>PLoS ONE</i> , 2015 , 10, e0130743	3.7	36
134	A two-step logistic regression algorithm for identifying individual-cancer-related genes 2015 ,		6
133	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
132	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
131	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
130	Predicting Protein Functions Based on Dynamic Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2015 , 390-401	0.9	0
129	Detecting Protein Complexes Based on Uncertain Graph Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014 , 11, 486-97	3	67
128	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
127	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
126	Dynamic protein interaction network construction and applications. <i>Proteomics</i> , 2014 , 14, 338-52	4.8	65
125	Discovering biological patterns from short time-series gene expression profiles with integrating PPI data. <i>Neurocomputing</i> , 2014 , 145, 3-13	5.4	1

124	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
123	Improving protein function prediction using domain and protein complexes in PPI networks. <i>BMC Systems Biology</i> , 2014 , 8, 35	3.5	29
122	NovoHCD: de novo peptide sequencing from HCD spectra. <i>IEEE Transactions on Nanobioscience</i> , 2014 , 13, 65-72	3.4	9
121	Prediction of disease genes using tissue-specified gene-gene network. <i>BMC Systems Biology</i> , 2014 , 8 Suppl 3, S3	3.5	21
120	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
119	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
118	Identifying disease genes by integrating multiple data sources. <i>BMC Medical Genomics</i> , 2014 , 7 Suppl 2, S2	3.7	26
117	Transittability of complex networks and its applications to regulatory biomolecular networks. <i>Scientific Reports</i> , 2014 , 4, 4819	4.9	40
116	Identifying dynamic protein complexes based on gene expression profiles and PPI networks. <i>BioMed Research International</i> , 2014 , 2014, 375262	3	18
115	Nonlinear-model-based analysis methods for time-course gene expression data. <i>Scientific World Journal, The</i> , 2014 , 2014, 313747	2.2	1
114	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
113	A logistic regression based algorithm for identifying human disease genes 2014 ,		7
112	Prediction of essential proteins based on overlapping essential modules. <i>IEEE Transactions on Nanobioscience</i> , 2014 , 13, 415-24	3.4	49
111	Identification of Essential Proteins by Using Complexes and Interaction Network. <i>Lecture Notes in Computer Science</i> , 2014 , 255-265	0.9	4
110	ABC and IFC: modules detection method for PPI network. <i>BioMed Research International</i> , 2014 , 2014, 968173	3	6
109	State observer design for delayed genetic regulatory networks. <i>Computational and Mathematical Methods in Medicine</i> , 2014 , 2014, 761562	2.8	5
108	A survey of MRI-based brain tumor segmentation methods. <i>Tsinghua Science and Technology</i> , 2014 , 19, 578-595	3.4	158
107	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

106	Disease gene identification by using graph kernels and Markov random fields. <i>Science China Life Sciences</i> , 2014 , 57, 1054-63	8.5	23
105	NovoPair: De novo peptide sequencing for tandem mass spectra pair 2014 ,		2
104	Drug Target Identification Based on Structural Output Controllability of Complex Networks. <i>Lecture Notes in Computer Science</i> , 2014 , 188-199	0.9	1
103	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
102	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	
101	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
100	PPI modules detection method through ABC-IFC algorithm 2013 ,		1
99	Characterizing dynamic regulatory programs in mouse lung development and their potential association with tumorigenesis via miRNA-TF-mRNA circuits. <i>BMC Systems Biology</i> , 2013 , 7 Suppl 2, S113-5		5
98	Identifying protein complexes based on multiple topological structures in PPI networks. <i>IEEE Transactions on Nanobioscience</i> , 2013 , 12, 165-72	3.4	18
97	De novo assembly methods for next generation sequencing data. <i>Tsinghua Science and Technology</i> , 2013 , 18, 500-514	3.4	14
96	Robust inference of gene regulatory networks from multiple microarray datasets 2013 ,		1
95	Prioritizing human disease genes by multiple data integration 2013 ,		4
94	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
93	2013 ,		2
92	Prioritization of candidate genes based on disease similarity and protein proximity in PPI networks 2013 ,		4
91	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
90	Unifying protein inference and peptide identification with feedback to update consistency between peptides. <i>Proteomics</i> , 2013 , 13, 239-47	4.8	6
89	Computational approaches to predicting essential proteins: a survey. <i>Proteomics - Clinical Applications</i> , 2013 , 7, 181-92	3.1	50

88	Predicting beta-turns in proteins using support vector machines with fractional polynomials. <i>Proteome Science</i> , 2013 , 11, S5	2.6	5
87	Peptide identification based on fuzzy classification and clustering. <i>Proteome Science</i> , 2013 , 11, S10	2.6	3
86	Detecting protein complexes from active protein interaction networks constructed with dynamic gene expression profiles. <i>Proteome Science</i> , 2013 , 11, S20	2.6	17
85	Predicting turns in protein using kernel logistic regression. <i>BioMed Research International</i> , 2013 , 2013, 870372	3	3
84	A dividing-and-matching algorithm to detect conserved protein complexes via local network alignment 2013 ,		1
83	Complexity analysis and parameter estimation of dynamic metabolic systems. <i>Computational and Mathematical Methods in Medicine</i> , 2013 , 2013, 698341	2.8	0
82	Matrix Decomposition Methods in Bioinformatics. <i>Current Bioinformatics</i> , 2013 , 8, 259-266	4.7	3
81	Construction of Uncertain Protein-Protein Interaction Networks and Its Applications. <i>Lecture Notes in Computer Science</i> , 2013 , 286-297	0.9	
80	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
79	Inference of gene regulatory subnetworks from time course gene expression data. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 9, S3	3.6	4
78	An unsupervised machine learning method for assessing quality of tandem mass spectra. <i>Proteome Science</i> , 2012 , 10 Suppl 1, S12	2.6	6
77	Not AU protein complexes exhibit dense structures in <i>S. cerevisiae</i> PPI network 2012 ,		2
76	Identification of hierarchical and overlapping functional modules in PPI networks. <i>IEEE Transactions on Nanobioscience</i> , 2012 , 11, 386-93	3.4	25
75	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
74	Alternating weighted least squares parameter estimation for biological S-systems 2012 ,		2
73	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
72	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
71	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

70	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
69	New global stability conditions for genetic regulatory networks with time-varying delays 2012 ,		4
68	Symmetry compression method for discovering network motifs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012 , 9, 1776-89	3	10
67	A feedback framework for protein inference with peptides identified from tandem mass spectra. <i>Proteome Science</i> , 2012 , 10, 68	2.6	4
66	A fuzzy cluster-based algorithm for peptide identification 2012 ,		1
65	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
64	Parallelizing Peptide-Spectrum scoring using modern graphics processing units 2011 ,		2
63	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
62	Stability and bifurcation analysis of models for zebrafish somitogenesis. <i>IEEE Transactions on Nanobioscience</i> , 2011 , 10, 239-47	3.4	3
61	Delay-independent stability of genetic regulatory networks. <i>IEEE Transactions on Neural Networks</i> , 2011 , 22, 1685-93		37
60	Nonlinear model-based method for clustering periodically expressed genes. <i>Scientific World Journal, The</i> , 2011 , 11, 2051-61	2.2	3
59	Features-based deisotoping method for tandem mass spectra. <i>Advances in Bioinformatics</i> , 2011 , 2011, 210805	5.5	7
58	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
57	Applications of graph theory in protein structure identification. <i>Proteome Science</i> , 2011 , 9 Suppl 1, S17	2.6	14
56	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
55	An adaptive approach to denoising tandem mass spectra. <i>Proteomics</i> , 2011 , 11, 3773-8	4.8	2
54	Speed improvements of peptide-spectrum matching using single-instruction multiple-data instructions. <i>Proteomics</i> , 2011 , 11, 3779-85	4.8	1
53	Improve Accuracy of Peptide Identification with Consistency between Peptides 2011 ,		1

52	Inferring gene regulatory networks from multiple time course gene expression datasets 2011 ,		2
51	An Improved Graph Entropy-based Method for Identifying Protein Complexes 2011 ,		4
50	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
49	Globally delay-independent stability of ring-structured genetic regulatory networks 2011 ,		4
48	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 ,	0.9	1
47	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> ,		2
46	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
45	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</i> , 2010 ,		1
44	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
43	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
42	Structure identification and parameter estimation of biological s-systems 2010 ,		2
41	An adaptive approach to denoising tandem mass spectra 2010 ,		3
40	Estimating parameters in the caspase-activated apoptosis system. <i>International Journal of Biomedical Engineering and Technology</i> , 2010 , 4, 338	1.3	2
39	Dynamic-model-based method for selecting significantly expressed genes from time-course expression profiles. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2010 , 14, 16-22		1
38	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
37	Assigning probabilities to Mascot peptide identification using logistic regression. <i>Advances in Experimental Medicine and Biology</i> , 2010 , 680, 229-36	3.6	
36	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</i> , 2009 , 2009, 6747-50	0.9	1
35	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</i> , 2009 , 2009, 3263-6	0.9	1

34	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
33	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
32	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
31	Protein Inference by Assembling Peptides Identified from Tandem Mass Spectra. <i>Current Bioinformatics</i> , 2009 , 4, 226-233	4.7	9
30	Sparse representation for classification of tumors using gene expression data. <i>Journal of Biomedicine and Biotechnology</i> , 2009 , 2009, 403689		53
29	Patient geometry-driven information retrieval for IMRT treatment plan quality control. <i>Medical Physics</i> , 2009 , 36, 5497-505	4.4	206
28	Quality assessment of tandem mass spectra using support vector machine (SVM). <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 1, S49	3.6	6
27	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
26	Quality Assessment of Tandem Mass Spectra by Using a Weighted K-Means. <i>Clinical Proteomics</i> , 2009 , 5, 15-22	5	4
25	A novel approach to denoising ion trap tandem mass spectra. <i>Proteome Science</i> , 2009 , 7, 9	2.6	20
24	Subspace pursuit for gene profile classification 2009 ,		1
23	Separable Parameter Estimation Method for Nonlinear Biological Systems 2009 ,		5
22	Genetic weighted k-means algorithm for clustering large-scale gene expression data. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 6, S12	3.6	26
21	Quality assessment of peptide tandem mass spectra. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 6, S13	3.6	15
20	Feature Selection for Tandem Mass Spectrum Quality Assessment 2008 ,		4
19	2008 ,		4
18	Gene Regulatory Network modelling: a state-space approach. <i>International Journal of Data Mining and Bioinformatics</i> , 2008 , 2, 1-14	0.5	10
17	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

16	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
15	Inference of Gene Regulatory Networks and its Validation. <i>Current Bioinformatics</i> , 2007 , 2, 139-144	4.7	11
14	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
13	Significance Analysis of Time-Course Gene Expression Profiles 2007 , 13-24		1
12	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
11	Optimally-connected hidden markov models for predicting MHC-binding peptides. <i>Journal of Bioinformatics and Computational Biology</i> , 2006 , 4, 959-80	1	19
10	2006 ,		3
9	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
8	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
7	Inferring gene regulatory networks with time delays using a genetic algorithm. <i>IET Systems Biology</i> , 2005 , 152, 67-74		3
6	Dynamic model-based clustering for time-course gene expression data. <i>Journal of Bioinformatics and Computational Biology</i> , 2005 , 3, 821-36	1	26
5	Control performance improvement of a parallel robot via the design for control approach. <i>Mechatronics</i> , 2004 , 14, 947-964	3	48
4	STATE-SPACE MODEL WITH TIME DELAYS FOR GENE REGULATORY NETWORKS. <i>Journal of Biological Systems</i> , 2004 , 12, 483-500	1.6	22
3	A Genetic K-means Clustering Algorithm Applied to Gene Expression Data. <i>Lecture Notes in Computer Science</i> , 2003 , 520-526	0.9	5
2	A genetic algorithm for inferring time delays in gene regulatory networks		1
1			1