MINT, the molecular interaction database: 2009 update

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Citation Report

#	Article	IF	CITATIONS
1	Stoichiometric protein complex formation and overâ€expression using the prokaryotic native operon structure. FEBS Letters, 2010, 584, 669-674.	1.3	26
2	The FEBS Letters SDA corpus: A collection of protein interaction articles with high quality annotations for the BioCreative II.5 online challenge and the text mining community. FEBS Letters, 2010, 584, 4129-4130.	1.3	8
3	Curating the innate immunity interactome. BMC Systems Biology, 2010, 4, 117.	3.0	68
4	A domain level interaction network of amyloid precursor protein and $\hat{A^2}$ of Alzheimer's disease. Proteomics, 2010, 10, 2377-2395.	1.3	41
6	DynaMod: dynamic functional modularity analysis. Nucleic Acids Research, 2010, 38, W103-W108.	6.5	7
7	Efficient Extraction of Protein-Protein Interactions from Full-Text Articles. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 481-494.	1.9	28
8	An Overview of BioCreative II.5. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 385-399.	1.9	83
9	The GeneMANIA prediction server: biological network integration for gene prioritization and predicting gene function. Nucleic Acids Research, 2010, 38, W214-W220.	6.5	3,436
10	A Computational Approach to Analyze the Mechanism of Action of the Kinase Inhibitor Bafetinib. PLoS Computational Biology, 2010, 6, e1001001.	1.5	23
11	Protein–Protein Interactions Essentials: Key Concepts to Building and Analyzing Interactome Networks. PLoS Computational Biology, 2010, 6, e1000807.	1.5	496
12	iRefWeb: interactive analysis of consolidated protein interaction data and their supporting evidence. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq023-baq023.	1.4	194
14	Mining molecular interactions from scientific literature using cloud computing. , 2010, , .		2
15	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. Nucleic Acids Research, 2011, 39, D561-D568.	6.5	3,014
16	Evolution of biological interaction networks: from models to real data. Genome Biology, 2011, 12, 235.	13.9	37
17	A predicted protein–protein interaction network of the filamentous fungus Neurospora crassa. Molecular BioSystems, 2011, 7, 2278.	2.9	29
18	Using Coevolution to Predict Protein–Protein Interactions. Methods in Molecular Biology, 2011, 781, 237-256.	0.4	21
19	Structural and functional protein network analyses predict novel signaling functions for rhodopsin. Molecular Systems Biology, 2011, 7, 551.	3.2	33
20	Insights into Eukaryotic Interacting Protein Evolution. , 2011, , 51-70.		2

#	Article	IF	CITATIONS
21	MatrixDB, the extracellular matrix interaction database. Nucleic Acids Research, 2011, 39, D235-D240.	6.5	117
22	Omics-Based Molecular Target and Biomarker Identification. Methods in Molecular Biology, 2011, 719, 547-571.	0.4	42
23	PRIN: a predicted rice interactome network. BMC Bioinformatics, 2011, 12, 161.	1.2	157
24	RefNetBuilder: a platform for construction of integrated reference gene regulatory networks from expressed sequence tags. BMC Bioinformatics, 2011, 12, S20.	1.2	5
25	Displaying Chemical Information on a Biological Network Using Cytoscape. Methods in Molecular Biology, 2011, 781, 363-376.	0.4	7
26	Reactome: a database of reactions, pathways and biological processes. Nucleic Acids Research, 2011, 39, D691-D697.	6.5	1,391
27	Systematic Approaches towards the Development of Host-Directed Antiviral Therapeutics. International Journal of Molecular Sciences, 2011, 12, 4027-4052.	1.8	79
28	Production of protein complexes via co-expression. Protein Expression and Purification, 2011, 75, 1-14.	0.6	51
29	Targeting Protein–Protein Interactions and Fragment-Based Drug Discovery. Topics in Current Chemistry, 2011, 317, 145-179.	4.0	88
30	Data Integration in Bioinformatics: Current Efforts and Challenges. , 0, , .		18
31	The Prediction and Analysis of Inter- and Intra-Species Protein-Protein Interaction. , 2011, , .		1
32	Systems-Biology Approaches to Discover Anti-Viral Effectors of the Human Innate Immune Response. Viruses, 2011, 3, 1112-1130.	1.5	9
33	Discovering Networks of Perturbed Biological Processes in Hepatocyte Cultures. PLoS ONE, 2011, 6, e15247.	1.1	10
34	Targeting Protein-Protein Interactions for Parasite Control. PLoS ONE, 2011, 6, e18381.	1.1	31
35	Simplified Method to Predict Mutual Interactions of Human Transcription Factors Based on Their Primary Structure. PLoS ONE, 2011, 6, e21887.	1.1	8
36	Prediction of Body Fluids where Proteins are Secreted into Based on Protein Interaction Network. PLoS ONE, 2011, 6, e22989.	1.1	40
37	Immunogenomics and systems biology of vaccines. Immunological Reviews, 2011, 239, 197-208.	2.8	65
38	HCVpro: Hepatitis C virus protein interaction database. Infection, Genetics and Evolution, 2011, 11, 1971-1977.	1.0	76

#	ARTICLE	IF	Citations
39	Three-dimensional modeling of protein interactions and complexes is going †omics. Current Opinion in Structural Biology, 2011, 21, 200-208.	2.6	86
40	iRefR: an R package to manipulate the iRefIndex consolidated protein interaction database. BMC Bioinformatics, 2011, 12, 455.	1.2	65
41	PPI_SVM: Prediction of protein-protein interactions using machine learning, domain-domain affinities and frequency tables. Cellular and Molecular Biology Letters, 2011, 16, 264-78.	2.7	63
42	A Heuristic Algorithm for Detecting Intercellular Interactions. , 2011, , .		O
43	Human Protein Reference Database and Human Proteinpedia as Discovery Resources for Molecular Biotechnology, Molecular Biotechnology, 2011, 48, 87-95.	1.3	87
44	Prioritizing cancer-related genes with aberrant methylation based on a weighted protein-protein interaction network. BMC Systems Biology, 2011, 5, 158.	3.0	20
45	Network analysis of microRNAs and their regulation in human ovarian cancer. BMC Systems Biology, 2011, 5, 183.	3.0	21
46	Predictive integration of gene functional similarity and co-expression defines treatment response of endothelial progenitor cells. BMC Systems Biology, 2011, 5, 46.	3.0	7
47	Proteomic patterns of cervical cancer cell lines, a network perspective. BMC Systems Biology, 2011, 5, 96.	3.0	52
48	Information encoded in a network of inflammation proteins predicts clinical outcome after myocardial infarction. BMC Medical Genomics, 2011, 4, 59.	0.7	22
49	Transcriptional landscape of bone marrow-derived very small embryonic-like stem cells during hypoxia. Respiratory Research, 2011, 12, 63.	1.4	12
50	MINE: Module Identification in Networks. BMC Bioinformatics, 2011, 12, 192.	1.2	87
51	Bio::Homology::InterologWalk - A Perl module to build putative protein-protein interaction networks through interolog mapping. BMC Bioinformatics, 2011, 12, 289.	1.2	16
52	GPS-Prot: A web-based visualization platform for integrating host-pathogen interaction data. BMC Bioinformatics, 2011, 12, 298.	1.2	73
53	Dynamic programming re-ranking for PPI interactor and pair extraction in full-text articles. BMC Bioinformatics, 2011, 12, 60.	1.2	4
54	Integrating multiple protein-protein interaction networks to prioritize disease genes: a Bayesian regression approach. BMC Bioinformatics, 2011, 12, S11.	1.2	36
55	Constructing a robust protein-protein interaction network by integrating multiple public databases. BMC Bioinformatics, 2011, 12, S7.	1.2	24
56	The Protein-Protein Interaction tasks of BioCreative III: classification/ranking of articles and linking bio-ontology concepts to full text. BMC Bioinformatics, 2011, 12, S3.	1.2	121

#	ARTICLE	IF	CITATIONS
57	Benchmarking of the 2010 BioCreative Challenge III text-mining competition by the BioGRID and MINT interaction databases. BMC Bioinformatics, 2011, 12, S8.	1.2	11
58	Classifying protein-protein interaction articles using word and syntactic features. BMC Bioinformatics, 2011, 12, S9.	1.2	27
59	Identification of dysfunctional modules and disease genes in congenital heart disease by a network-based approach. BMC Genomics, 2011, 12, 592.	1.2	46
60	Prioritizing disease candidate genes by a gene interconnectedness-based approach. BMC Genomics, 2011, 12, S25.	1.2	33
61	A computational tool for identifying minimotifs in protein–protein interactions and improving the accuracy of minimotif predictions. Proteins: Structure, Function and Bioinformatics, 2011, 79, 153-164.	1.5	10
62	Path lengths in protein–protein interaction networks and biological complexity. Proteomics, 2011, 11, 1857-1867.	1.3	30
63	Reactome pathway analysis to enrich biological discovery in proteomics data sets. Proteomics, 2011, 11, 3598-3613.	1.3	89
64	Detecting protein complexes and functional modules from protein interaction networks: A graph entropy approach. Proteomics, 2011, 11, 3835-3844.	1.3	42
65	Systems biology and the future of medicine. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 619-627.	6.6	239
66	Leveraging external knowledge on molecular interactions in classification methods for risk prediction of patients. Biometrical Journal, 2011, 53, 190-201.	0.6	18
67	Experimental and computational approaches for the study of calmodulin interactions. Phytochemistry, 2011, 72, 1007-1019.	1.4	45
68	Modeling Metabolic Networks for Mammalian Cell Systems: General Considerations, Modeling Strategies, and Available Tools., 2011, 127, 71-108.		9
69	BioTRON., 2011,,.		0
70	The role of indirect connections in gene networks in predicting function. Bioinformatics, 2011, 27, 1860-1866.	1.8	71
71	Systems Biology of Apoptosis and Survival: Implications for Drug Development. Current Pharmaceutical Design, 2011, 17, 190-203.	0.9	8
72	KUPS: constructing datasets of interacting and non-interacting protein pairs with associated attributions. Nucleic Acids Research, 2011, 39, D750-D754.	6.5	32
73	HitPredict: a database of quality assessed protein–protein interactions in nine species. Nucleic Acids Research, 2011, 39, D744-D749.	6.5	111
74	DAnCER: Disease-Annotated Chromatin Epigenetics Resource. Nucleic Acids Research, 2011, 39, D889-D894.	6.5	19

#	Article	IF	CITATIONS
75	Prediction of human protein–protein interaction by a mixed Bayesian model and its application to exploring underlying cancer-related pathway crosstalk. Journal of the Royal Society Interface, 2011, 8, 555-567.	1.5	16
76	DroID 2011: a comprehensive, integrated resource for protein, transcription factor, RNA and gene interactions for Drosophila. Nucleic Acids Research, 2011, 39, D736-D743.	6.5	180
77	A novel network-based method for measuring the functional relationship between gene sets. Bioinformatics, 2011, 27, 1521-1528.	1.8	19
78	TcoF-DB: dragon database for human transcription co-factors and transcription factor interacting proteins. Nucleic Acids Research, 2011, 39, D106-D110.	6.5	61
79	Challenges in integrating Escherichia coli molecular biology data. Briefings in Bioinformatics, 2011, 12, 91-103.	3.2	4
80	Drug-target network in myocardial infarction reveals multiple side effects of unrelated drugs. Scientific Reports, $2011,1,52.$	1.6	71
81	Interactome mapping suggests new mechanistic details underlying Alzheimer's disease. Genome Research, 2011, 21, 364-376.	2.4	121
82	SPIKE: a database of highly curated human signaling pathways. Nucleic Acids Research, 2011, 39, D793-D799.	6.5	74
83	BioGRID REST Service, BiogridPlugin2 and BioGRID WebGraph: new tools for access to interaction data at BioGRID. Bioinformatics, 2011, 27, 1043-1044.	1.8	26
84	Proteomic and Functional Genomic Landscape of Receptor Tyrosine Kinase and Ras to Extracellular Signal–Regulated Kinase Signaling. Science Signaling, 2011, 4, rs10.	1.6	87
85	Identification of New Substrates of the Protein-tyrosine Phosphatase PTP1B by Bayesian Integration of Proteome Evidence. Journal of Biological Chemistry, 2011, 286, 4173-4185.	1.6	41
86	ppiTrim: constructing non-redundant and up-to-date interactomes. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar036.	1.4	12
87	An Integrated Approach to Elucidate the Intra-Viral and Viral-Cellular Protein Interaction Networks of a Gamma-Herpesvirus. PLoS Pathogens, 2011, 7, e1002297.	2.1	37
88	Pathway Commons, a web resource for biological pathway data. Nucleic Acids Research, 2011, 39, D685-D690.	6.5	980
89	TRIP Database: a manually curated database of protein–protein interactions for mammalian TRP channels. Nucleic Acids Research, 2011, 39, D356-D361.	6.5	26
90	Tissue-specific subnetworks and characteristics of publicly available human protein interaction databases. Bioinformatics, 2011, 27, 2414-2421.	1.8	46
91	Recovering Protein-Protein and Domain-Domain Interactions from Aggregation of IP-MS Proteomics of Coregulator Complexes. PLoS Computational Biology, 2011, 7, e1002319.	1.5	16
92	Visualization and Biochemical Analyses of the Emerging Mammalian 14-3-3-Phosphoproteome. Molecular and Cellular Proteomics, 2011, 10, M110.005751.	2.5	63

#	Article	IF	Citations
93	Modeling of multi domain contribution to protein interaction. , 2011, , .		0
94	ConsensusPathDB: toward a more complete picture of cell biology. Nucleic Acids Research, 2011, 39, D712-D717.	6.5	537
95	Phospho.ELM: a database of phosphorylation sites-update 2011. Nucleic Acids Research, 2011, 39, D261-D267.	6.5	562
96	MINT, the molecular interaction database: 2012 update. Nucleic Acids Research, 2012, 40, D857-D861.	6.5	917
97	PINA v2.0: mining interactome modules. Nucleic Acids Research, 2012, 40, D862-D865.	6.5	321
98	Drug Target Prediction Based on the Herbs Components: The Study on the Multitargets Pharmacological Mechanism of Qishenkeli Acting on the Coronary Heart Disease. Evidence-based Complementary and Alternative Medicine, 2012, 2012, 1-10.	0.5	73
99	Experimental evaluation of topological-based fitness functions to detect complexes in PPI networks. , 2012, , .		13
100	How to link ontologies and protein-protein interactions to literature: text-mining approaches and the BioCreative experience. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas017-bas017.	1.4	27
101	Minimotif Miner 3.0: database expansion and significantly improved reduction of false-positive predictions from consensus sequences. Nucleic Acids Research, 2012, 40, D252-D260.	6.5	52
103	BioContext: an integrated text mining system for large-scale extraction and contextualization of biomolecular events. Bioinformatics, 2012, 28, 2154-2161.	1.8	45
104	Viral Perturbations of Host Networks Reflect Disease Etiology. PLoS Computational Biology, 2012, 8, e1002531.	1.5	102
105	"Guilt by Association―ls the Exception Rather Than the Rule in Gene Networks. PLoS Computational Biology, 2012, 8, e1002444.	1.5	183
106	Holding Our Breath: The Emerging and Anticipated Roles of microRNA in Pulmonary Hypertension. Pulmonary Circulation, 2012, 2, 278-290.	0.8	53
107	Tissue-Specific Functional Networks for Prioritizing Phenotype and Disease Genes. PLoS Computational Biology, 2012, 8, e1002694.	1.5	137
108	NetAligner-a network alignment server to compare complexes, pathways and whole interactomes. Nucleic Acids Research, 2012, 40, W157-W161.	6.5	46
109	Interactome–transcriptome integration for predicting distant metastasis in breast cancer. Bioinformatics, 2012, 28, 672-678.	1.8	22
110	Discovering the hidden sub-network component in a ranked list of genes or proteins derived from genomic experiments. Nucleic Acids Research, 2012, 40, e158-e158.	6.5	22
111	neXtProt: a knowledge platform for human proteins. Nucleic Acids Research, 2012, 40, D76-D83.	6.5	167

#	Article	IF	Citations
112	Network of Cancer Genes (NCG 3.0): integration and analysis of genetic and network properties of cancer genes. Nucleic Acids Research, 2012, 40, D978-D983.	6.5	38
113	MoNetFamily: a web server to infer homologous modules and module–module interaction networks in vertebrates. Nucleic Acids Research, 2012, 40, W263-W270.	6.5	15
114	Nematode.net update 2011: addition of data sets and tools featuring next-generation sequencing data. Nucleic Acids Research, 2012, 40, D720-D728.	6.5	40
115	Dissecting the Gene Network of Dietary Restriction to Identify Evolutionarily Conserved Pathways and New Functional Genes. PLoS Genetics, 2012, 8, e1002834.	1.5	58
116	Three-dimensional reconstruction of protein networks provides insight into human genetic disease. Nature Biotechnology, 2012, 30, 159-164.	9.4	378
117	A Computational Model for Predicting Protein Interactions Based on Multidomain Collaboration. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1081-1090.	1.9	15
118	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	9.0	500
119	The IntAct molecular interaction database in 2012. Nucleic Acids Research, 2012, 40, D841-D846.	6.5	962
120	The Role of Structural Disorder in the Rewiring of Protein Interactions through Evolution. Molecular and Cellular Proteomics, 2012, 11, M111.014969-1-M111.014969-8.	2.5	67
121	Extending Signaling Pathways with Protein–Interaction Networks. Application to Apoptosis. OMICS A Journal of Integrative Biology, 2012, 16, 245-256.	1.0	5
122	A comprehensive manually curated protein–protein interaction database for the Death Domain superfamily. Nucleic Acids Research, 2012, 40, D331-D336.	6.5	38
123	Involvement of microRNA families in cancer. Nucleic Acids Research, 2012, 40, 8219-8226.	6.5	18
124	BioCreative-2012 Virtual Issue. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas049-bas049.	1.4	19
125	SCPC: a method to structurally compare protein complexes. Bioinformatics, 2012, 28, 324-330.	1.8	9
126	Literature mining of host–pathogen interactions: comparing feature-based supervised learning and language-based approaches. Bioinformatics, 2012, 28, 867-875.	1.8	31
127	IPAVS: Integrated Pathway Resources, Analysis and Visualization System. Nucleic Acids Research, 2012, 40, D803-D808.	6.5	20
128	Identification of Pharmacological Targets in Amyotrophic Lateral Sclerosis Through Genomic Analysis of Deregulated Genes and Pathways. Current Genomics, 2012, 13, 321-333.	0.7	11
129	In Silico Search for Drug Targets of Natural Compounds. Current Pharmaceutical Biotechnology, 2012, 13, 1632-1639.	0.9	5

#	Article	IF	CITATIONS
130	Largeâ€scale mapping of human protein interactome using structural complexes. EMBO Reports, 2012, 13, 266-271.	2.0	43
132	TranscriptomeBrowser 3.0: introducing a new compendium of molecular interactions and a new visualization tool for the study of gene regulatory networks. BMC Bioinformatics, 2012, 13, 19.	1.2	30
133	A Census of Human Soluble Protein Complexes. Cell, 2012, 150, 1068-1081.	13.5	781
134	Network-based characterization of drug-regulated genes, drug targets, and toxicity. Methods, 2012, 57, 499-507.	1.9	88
135	DEFOG: discrete enrichment of functionally organized genes. Integrative Biology (United Kingdom), 2012, 4, 795.	0.6	3
136	ANAP: An Integrated Knowledge Base for Arabidopsis Protein Interaction Network Analysis   Â. Plant Physiology, 2012, 158, 1523-1533.	2.3	31
137	Promiscuous domains: facilitating stability of the yeast protein–protein interaction network. Molecular BioSystems, 2012, 8, 766-771.	2.9	10
138	Robust segmentation of biomedical figures for image-based document retrieval. , 2012, , .		6
139	Neighbor communities in drug combination networks characterize synergistic effect. Molecular BioSystems, 2012, 8, 3185.	2.9	29
140	Negative protein–protein interaction datasets derived from large-scale two-hybrid experiments. Methods, 2012, 58, 343-348.	1.9	38
141	Bioinformatic Challenges in Targeted Proteomics. Journal of Proteome Research, 2012, 11, 4393-4402.	1.8	20
142	A Strategy Based on Protein–Protein Interface Motifs May Help in Identifying Drug Off-Targets. Journal of Chemical Information and Modeling, 2012, 52, 2273-2286.	2.5	30
143	Reconstructing Models from Proteomics Data. , 2012, , 23-80.		0
144	Understanding cancer mechanisms through network dynamics. Briefings in Functional Genomics, 2012, 11, 543-560.	1.3	35
145	Genes2FANs: connecting genes through functional association networks. BMC Bioinformatics, 2012, 13, 156.	1.2	28
146	atBioNet– an integrated network analysis tool for genomics and biomarker discovery. BMC Genomics, 2012, 13, 325.	1.2	33
147	GWIDD: a comprehensive resource for genome-wide structural modeling of protein-protein interactions. Human Genomics, 2012, 6, 7.	1.4	17
148	Rational drug repositioning guided by an integrated pharmacological network of protein, disease and drug. BMC Systems Biology, 2012, 6, 80.	3.0	75

#	Article	IF	CITATIONS
149	A predicted protein interactome for rice. Rice, 2012, 5, 15.	1.7	49
150	A Coclustering Approach for Mining Large Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 717-730.	1.9	29
151	Integrated Inference and Analysis of Regulatory Networks from Multi-Level Measurements. Methods in Cell Biology, 2012, 110, 19-56.	0.5	17
152	Challenges ahead in signal transduction: MAPK as an example. Current Opinion in Biotechnology, 2012, 23, 305-314.	3.3	39
153	Quantitative phosphoproteomics to characterize signaling networks. Seminars in Cell and Developmental Biology, 2012, 23, 863-871.	2.3	58
154	Protein Interactions: Mapping Interactome Networks to Support Drug Target Discovery and Selection. Methods in Molecular Biology, 2012, 910, 279-296.	0.4	13
155	Searching for Hif1- $\hat{l}\pm$ interacting proteins in renal cell carcinoma. Clinical and Translational Oncology, 2012, 14, 698-708.	1.2	13
156	Quantitative Dynamics of Phosphoproteome: The Devil Is in the Details. Analytical Chemistry, 2012, 84, 8431-8436.	3.2	2
157	Multi-scale modeling of gene regulatory networks via integration of temporal and topological biological data., 2012, 2012, 1242-5.		0
158	Discovering pathway cross-talks based on functional relations between pathways. BMC Genomics, 2012, 13, S25.	1.2	13
159	Revealing functionally coherent subsets using a spectral clustering and an information integration approach. BMC Systems Biology, 2012, 6, S7.	3.0	2
160	A simple knowledge-based mining method for exploring hidden key molecules in a human biomolecular network. BMC Systems Biology, 2012, 6, 124.	3.0	1
161	Context-Specific Protein Network Miner – An Online System for Exploring Context-Specific Protein Interaction Networks from the Literature. PLoS ONE, 2012, 7, e34480.	1.1	18
162	A Topology-Based Metric for Measuring Term Similarity in the Gene Ontology. Advances in Bioinformatics, 2012, 2012, 1-17.	5.7	44
163	Infection Strategies of Bacterial and Viral Pathogens through Pathogen–Human Protein–Protein Interactions. Frontiers in Microbiology, 2012, 3, 46.	1.5	63
164	GeNet: A Graph-Based Genetic Programming Framework for the Reverse Engineering of Gene Regulatory Networks. Lecture Notes in Computer Science, 2012, , 97-109.	1.0	2
165	Protein-Protein Interactions and Disease. , 0, , .		1
166	Molecular interaction databases. Proteomics, 2012, 12, 1656-1662.	1.3	72

#	ARTICLE	IF	CITATIONS
167	Computational and informatics strategies for identification of specific protein interaction partners in affinity purification mass spectrometry experiments. Proteomics, 2012, 12, 1639-1655.	1.3	84
168	Analyzing Protein–Protein Interaction Networks. Journal of Proteome Research, 2012, 11, 2014-2031.	1.8	145
169	Coordination of the transcriptome and metabolome by the circadian clock. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5541-5546.	3.3	353
170	Combinatorial drug therapy for cancer in the post-genomic era. Nature Biotechnology, 2012, 30, 679-692.	9.4	883
171	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	6.0	1,095
172	Topology of functional networks predicts physical binding of proteins. Bioinformatics, 2012, 28, 2137-2145.	1.8	5
173	The protein interaction network mediated by human SH3 domains. Biotechnology Advances, 2012, 30, 4-15.	6.0	49
174	Constructing structural networks of signaling pathways on the proteome scale. Current Opinion in Structural Biology, 2012, 22, 367-377.	2.6	61
175	Identification of potential host proteins for influenza A virus based on topological and biological characteristics by proteome-wide network approach. Journal of Proteomics, 2012, 75, 2500-2513.	1.2	10
176	Prediction and characterization of protein-protein interaction networks in swine. Proteome Science, 2012, 10, 2.	0.7	33
177	Accuracy improvement in protein complex prediction from protein interaction networks by refining cluster overlaps. Proteome Science, 2012, 10, S3.	0.7	5
178	Protein-protein interaction sites are hot spots for disease-associated nonsynonymous SNPs. Human Mutation, 2012, 33, 359-363.	1.1	149
179	Integrated analysis of recurrent properties of cancer genes to identify novel drivers. Genome Biology, 2013, 14, R52.	13.9	33
180	The 3rd DBCLS BioHackathon: improving life science data integration with Semantic Web technologies. Journal of Biomedical Semantics, 2013, 4, 6.	0.9	26
181	Complex regulation of autophagy in cancer – Integrated approaches to discover the networks that hold a double-edged sword. Seminars in Cancer Biology, 2013, 23, 252-261.	4.3	83
182	A survey of protein interaction data and multigenic inherited disorders. BMC Bioinformatics, 2013, 14, 47.	1.2	4
183	Predicting PDZ domain mediated protein interactions from structure. BMC Bioinformatics, 2013, 14, 27.	1.2	32
184	NeuroDNet - an open source platform for constructing and analyzing neurodegenerative disease networks. BMC Neuroscience, 2013, 14, 3.	0.8	30

#	Article	IF	Citations
185	Identification of ovarian cancer associated genes using an integrated approach in a Boolean framework. BMC Systems Biology, 2013, 7, 12.	3.0	15
186	PainNetworks: A web-based resource for the visualisation of pain-related genes in the context of their network associations. Pain, 2013, 154, 2586e1-2586e12.	2.0	50
187	Teaching the bioinformatics of signaling networks: an integrated approach to facilitate multi-disciplinary learning. Briefings in Bioinformatics, 2013, 14, 618-632.	3.2	15
188	Protein Interaction Network of the Mammalian Hippo Pathway Reveals Mechanisms of Kinase-Phosphatase Interactions. Science Signaling, 2013, 6, rs15.	1.6	411
189	Network cluster analysis of protein–protein interaction network identified biomarker for early onset colorectal cancer. Molecular Biology Reports, 2013, 40, 6561-6568.	1.0	29
190	Effect of Alternative Splicing on the Degree Centrality of Nodes in Protein–Protein Interaction Networks of ⟨i⟩Homo sapiens⟨i⟩. Journal of Proteome Research, 2013, 12, 1980-1988.	1.8	12
191	A framework for biomedical figure segmentation towards image-based document retrieval. BMC Systems Biology, 2013, 7, S8.	3.0	16
192	Prediction of protein interaction types based on sequence and network features. BMC Systems Biology, 2013, 7, S5.	3.0	5
193	Towards a detailed atlas of protein–protein interactions. Current Opinion in Structural Biology, 2013, 23, 929-940.	2.6	92
194	Global versus Local Hubs in Human Protein–Protein Interaction Network. Journal of Proteome Research, 2013, 12, 5436-5446.	1.8	24
195	Interactome3D: adding structural details to protein networks. Nature Methods, 2013, 10, 47-53.	9.0	449
196	Human protein–protein interaction prediction by a novel sequence-based co-evolution method: co-evolutionary divergence. Bioinformatics, 2013, 29, 92-98.	1.8	32
197	Human diseases through the lens of network biology. Trends in Genetics, 2013, 29, 150-159.	2.9	182
198	Semantically assessing the reliability of protein interactions. Mathematical Biosciences, 2013, 245, 226-234.	0.9	2
199	iBIG: An Integrative Network Tool for Supporting Human Disease Mechanism Studies. Genomics, Proteomics and Bioinformatics, 2013, 11, 166-171.	3.0	7
200	PRASA: An integrated web server that analyzes protein interaction types. Gene, 2013, 518, 78-83.	1.0	1
201	The SH2 Domain Interaction Landscape. Cell Reports, 2013, 3, 1293-1305.	2.9	110
202	Identification of Small Exonic CNV from Whole-Exome Sequence Data and Application to Autism Spectrum Disorder. American Journal of Human Genetics, 2013, 93, 607-619.	2.6	136

#	Article	IF	CITATIONS
203	Finding the targets of a drug by integration of gene expression data with a protein interaction network. Molecular BioSystems, 2013, 9, 1676.	2.9	59
204	$\hat{l}^21$ - and $\hat{l}\pm v$ -class integrins cooperate to regulate myosinÂll during rigidity sensing of fibronectin-based microenvironments. Nature Cell Biology, 2013, 15, 625-636.	4.6	386
205	Visualization and Analysis of Biological Networks. Methods in Molecular Biology, 2013, 1021, 63-88.	0.4	21
206	Assessment of high-confidence protein–protein interactome in yeast. Computational Biology and Chemistry, 2013, 45, 1-8.	1.1	12
207	M-Finder: Uncovering functionally associated proteins from interactome data integrated with GO annotations. Proteome Science, 2013, 11, S3.	0.7	34
208	Probabilistic Biological Network Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 109-121.	1.9	26
209	The TissueNet database of human tissue protein–protein interactions. Nucleic Acids Research, 2013, 41, D841-D844.	6.5	54
210	An integrated approach to identify causal network modules of complex diseases with application to colorectal cancer. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 659-667.	2.2	58
211	An Image-Text Approach for Extracting Experimental Evidence of Protein-Protein Interactions in the Biomedical Literature. , 2013, , .		1
212	Reachability analysis in large probabilistic biological networks. , 2013, , .		0
213	ResponseNet2.0: revealing signaling and regulatory pathways connecting your proteins and genesâ€"now with human data. Nucleic Acids Research, 2013, 41, W198-W203.	6.5	25
214	A Systems Biology-Based Investigation into the Pharmacological Mechanisms of Wu Tou Tang Acting on Rheumatoid Arthritis by Integrating Network Analysis. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-12.	0.5	25
215	Global assessment of network inference algorithms based on available literature of gene/protein interactions. Turkish Journal of Biology, 2013, 37, 547-555.	2.1	14
216	Systems biology of cancer biomarker detection. Cancer Biomarkers, 2013, 13, 201-213.	0.8	15
217	Vitexicarpin Acts as a Novel Angiogenesis Inhibitor and Its Target Network. Evidence-based Complementary and Alternative Medicine, 2013, 2013, 1-13.	0.5	19
218	Linking Proteomic and Transcriptional Data through the Interactome and Epigenome Reveals a Map of Oncogene-induced Signaling. PLoS Computational Biology, 2013, 9, e1002887.	1.5	48
219	A context-sensitive framework for the analysis of human signalling pathways in molecular interaction networks. Bioinformatics, 2013, 29, i210-i216.	1.8	8
220	Target Essentiality and Centrality Characterize Drug Side Effects. PLoS Computational Biology, 2013, 9, e1003119.	1.5	49

#	Article	IF	CITATIONS
221	Proteome-wide Prediction of Self-interacting Proteins Based on Multiple Properties. Molecular and Cellular Proteomics, 2013, 12, 1689-1700.	2.5	31
222	Popular Computational Methods to Assess Multiprotein Complexes Derived From Label-Free Affinity Purification and Mass Spectrometry (AP-MS) Experiments. Molecular and Cellular Proteomics, 2013, 12, 1-13.	2.5	46
223	Cross-Species Protein Interactome Mapping Reveals Species-Specific Wiring of Stress Response Pathways. Science Signaling, 2013, 6, ra38.	1.6	47
224	Protein-Protein Interactions Inferred from Domain-Domain Interactions in Genogroup II Genotype 4 Norovirus Sequences. International Journal of Genomics, 2013, 2013, 1-7.	0.8	0
225	Trinucleotide Repeats: A Structural Perspective. Frontiers in Neurology, 2013, 4, 76.	1.1	49
226	Molecular interaction networks for the analysis of human disease: Utility, limitations, and considerations. Proteomics, 2013, 13, 3393-3405.	1.3	17
227	Network-based Analysis of Genome Wide Association Data Provides Novel Candidate Genes for Lipid and Lipoprotein Traits. Molecular and Cellular Proteomics, 2013, 12, 3398-3408.	2.5	28
229	Protein–protein interaction networks studies and importance of 3D structure knowledge. Expert Review of Proteomics, 2013, 10, 511-520.	1.3	17
230	Assembling cell context-specific gene sets: a case in cardiomyopathy. Journal of Integrative Bioinformatics, 2013, 10, 46-61.	1.0	2
231	Identification of New Protein Interactions between Dengue Fever Virus and Its Hosts, Human and Mosquito. PLoS ONE, 2013, 8, e53535.	1.1	118
232	Inferring Potential microRNA-microRNA Associations Based on Targeting Propensity and Connectivity in the Context of Protein Interaction Network. PLoS ONE, 2013, 8, e69719.	1.1	22
233	Protein-protein interaction network and significant gene analysis of osteoporosis. Genetics and Molecular Research, 2013, 12, 4751-4759.	0.3	3
234	A Systems Biology-Based Approach to Uncovering the Molecular Mechanisms Underlying the Effects of Dragon's Blood Tablet in Colitis, Involving the Integration of Chemical Analysis, ADME Prediction, and Network Pharmacology. PLoS ONE, 2014, 9, e101432.	1.1	39
235	Protein Interaction Networks Reveal Novel Autism Risk Genes within GWAS Statistical Noise. PLoS ONE, 2014, 9, e112399.	1.1	14
236	Network Pharmacology Strategies Toward Multi-Target Anticancer Therapies: From Computational Models to Experimental Design Principles. Current Pharmaceutical Design, 2014, 20, 23-36.	0.9	115
237	Hope for GWAS: Relevant Risk Genes Uncovered from GWAS Statistical Noise. International Journal of Molecular Sciences, 2014, 15, 17601-17621.	1.8	2
238	Effects of destrin pathway mutations on the gene expression profile. Genetics and Molecular Research, 2014, 13, 2628-2637.	0.3	0
239	BEAMS: backbone extraction and merge strategy for the global many-to-many alignment of multiple PPI networks. Bioinformatics, 2014, 30, 531-539.	1.8	63

#	Article	IF	CITATIONS
240	Comprehensive analysis of microRNA-regulated protein interaction network reveals the tumor suppressive role of microRNA-149 in human hepatocellular carcinoma via targeting AKT-mTOR pathway. Molecular Cancer, 2014, 13, 253.	7.9	85
241	Comparative Analysis of Human Tissue Interactomes Reveals Factors Leading to Tissue-Specific Manifestation of Hereditary Diseases. PLoS Computational Biology, 2014, 10, e1003632.	1.5	70
242	Network-based association of hypoxia-responsive genes with cardiovascular diseases. New Journal of Physics, 2014, 16, 105014.	1.2	14
243	Large scale analysis of signal reachability. Bioinformatics, 2014, 30, i96-i104.	1.8	6
244	Integrating omics into the cardiac differentiation of human pluripotent stem cells. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2014, 6, 311-328.	6.6	4
245	Integrating the interactome and the transcriptome of Drosophila. BMC Bioinformatics, 2014, 15, 177.	1.2	4
246	NCG 4.0: the network of cancer genes in the era of massive mutational screenings of cancer genomes. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau015.	1.4	50
247	Molecular signatures of antibody responses derived from a systems biology study of five human vaccines. Nature Immunology, 2014, 15, 195-204.	7.0	672
248	Intercellular network structure and regulatory motifs in the human hematopoietic system. Molecular Systems Biology, 2014, 10, 741.	3.2	57
249	MCentridFS: a tool for identifying module biomarkers for multi-phenotypes from high-throughput data. Molecular BioSystems, 2014, 10, 2870-2875.	2.9	12
250	Network Biology in Medicine and Beyond. Circulation: Cardiovascular Genetics, 2014, 7, 536-547.	5.1	45
251	Data, Databases, Data Format, Database Search, Data Retrieval Systems, and Genome Browsers. , 2014, , 77-131.		0
252	Analysis and identification of essential genes in humans using topological properties and biological information. Gene, 2014, 551, 138-151.	1.0	22
253	Choosing appropriate models for protein–protein interaction networks: a comparison study. Briefings in Bioinformatics, 2014, 15, 823-838.	3.2	15
254	Identification of Functional Modules by Integration of Multiple Data Sources Using a Bayesian Network Classifier. Circulation: Cardiovascular Genetics, 2014, 7, 206-217.	5.1	5
255	Modeling dynamic functional relationship networks and application to <i>ex vivo</i> human erythroid differentiation. Bioinformatics, 2014, 30, 3325-3333.	1.8	10
256	Identification of AKT kinases as unfavorable prognostic factors for hepatocellular carcinoma by a combination of expression profile, interaction network analysis and clinical validation. Molecular BioSystems, 2014, 10, 215-222.	2.9	17
257	Presence and utility of intrinsically disordered regions in kinases. Molecular BioSystems, 2014, 10, 2876-2888.	2.9	26

#	Article	IF	CITATIONS
258	Analysis and identification of toxin targets by topological properties in protein–protein interaction network. Journal of Theoretical Biology, 2014, 349, 82-91.	0.8	16
259	Protein–protein interactions and genetic diseases: The interactome. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 1971-1980.	1.8	105
260	Systems Medicine: from molecular features and models to the clinic in COPD. Journal of Translational Medicine, 2014, 12, S4.	1.8	23
261	Prediction of disease-related genes based on weighted tissue-specific networks by using DNA methylation. BMC Medical Genomics, 2014, 7, S4.	0.7	14
262	BioCreative-IV virtual issue. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau039-bau039.	1.4	43
263	Integrative analysis of human protein, function and disease networks. Scientific Reports, 2015, 5, 14344.	1.6	32
264	Module organization and variance in protein-protein interaction networks. Scientific Reports, 2015, 5, 9386.	1.6	30
265	Counting motifs in probabilistic biological networks. , 2015, , .		11
266	Signal reachability facilitates characterization of probabilistic signaling networks. BMC Bioinformatics, 2015, 16, S6.	1.2	2
267	PrOnto database: GO term functional dissimilarity inferred from biological data. Frontiers in Genetics, 2015, 6, 200.	1.1	8
268	Reconstructing Genome-Wide Protein–Protein Interaction Networks Using Multiple Strategies with Homologous Mapping. PLoS ONE, 2015, 10, e0116347.	1.1	8
269	The neXtProt knowledgebase on human proteins: current status. Nucleic Acids Research, 2015, 43, D764-D770.	6.5	94
270	Deciphering the pharmacological mechanism of the Chinese formula Huanglian-Jie-Du decoction in the treatment of ischemic stroke using a systems biology-based strategy. Acta Pharmacologica Sinica, 2015, 36, 724-733.	2.8	36
271	A systematic investigation based on microRNA-mediated gene regulatory network reveals that dysregulation of microRNA-19a/Cyclin D1 axis confers an oncogenic potential and a worse prognosis in human hepatocellular carcinoma. RNA Biology, 2015, 12, 643-657.	1.5	33
272	Merging and scoring molecular interactions utilising existing community standards: tools, use-cases and a case study. Database: the Journal of Biological Databases and Curation, 2015, 2015, bau131-bau131.	1.4	53
273	Extreme multifunctional proteins identified from a human protein interaction network. Nature Communications, 2015, 6, 7412.	5.8	101
274	Ferret: a sentence-based literature scanning system. BMC Bioinformatics, 2015, 16, 198.	1.2	2
275	Sphingosine kinase 2 is a chikungunya virus host factor co-localized with the viral replication complex. Emerging Microbes and Infections, 2015, 4, 1-9.	3.0	44

#	Article	IF	CITATIONS
276	Reachability Analysis in Probabilistic Biological Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 53-66.	1.9	6
277	HPIminer: A text mining system for building and visualizing human protein interaction networks and pathways. Journal of Biomedical Informatics, 2015, 54, 121-131.	2.5	18
278	Uncovering disease-disease relationships through the incomplete interactome. Science, 2015, 347, 1257601.	6.0	1,219
279	Systematic Identification of Molecular Links between Core and Candidate Genes in Breast Cancer. Journal of Molecular Biology, 2015, 427, 1436-1450.	2.0	24
280	A Systems Biology Perspective on the Molecular Mechanisms Underlying the Therapeutic Effects of Buyang Huanwu Decoction on Ischemic Stroke. Rejuvenation Research, 2015, 18, 313-325.	0.9	31
281	A DiseAse MOdule Detection (DIAMOnD) Algorithm Derived from a Systematic Analysis of Connectivity Patterns of Disease Proteins in the Human Interactome. PLoS Computational Biology, 2015, 11, e1004120.	1.5	310
282	Tree Kernel-based Protein-Protein Interaction Extraction Considering both Modal Verb Phrases and Appositive Dependency Features. , 2015, , .		3
283	Genes Caught In Flagranti: Integrating Renal Transcriptional Profiles With Genotypes and Phenotypes. Seminars in Nephrology, 2015, 35, 237-244.	0.6	1
284	Efficient Prediction of Progesterone Receptor Interactome Using a Support Vector Machine Model. International Journal of Molecular Sciences, 2015, 16, 4774-4785.	1.8	2
285	Arabidopsis thaliana: A Model for Plant Research. , 2015, , 1-26.		5
286	Uncovering pharmacological mechanisms of Wu-tou decoction acting on rheumatoid arthritis through systems approaches: drug-target prediction, network analysis and experimental validation. Scientific Reports, 2015, 5, 9463.	1.6	91
287	Accurate multiple network alignment through context-sensitive random walk. BMC Systems Biology, 2015, 9, S7.	3.0	18
288	Extracting high confidence protein interactions from affinity purification data: At the crossroads. Journal of Proteomics, 2015, 118, 63-80.	1.2	30
289	Biological Databases for Human Research. Genomics, Proteomics and Bioinformatics, 2015, 13, 55-63.	3.0	84
290	Protocols and Methods for the in Silico Reconstruction of the Origin and Evolution of Metabolic Pathways. Springer Briefs in Molecular Science, 2015, , 67-75.	0.1	0
291	Biological pathways and networks implicated in psychiatric disorders. Current Opinion in Behavioral Sciences, 2015, 2, 58-68.	2.0	21
292	Network-based proteomic approaches reveal the neurodegenerative, neuroprotective and pain-related mechanisms involved after retrograde axonal damage. Scientific Reports, 2015, 5, 9185.	1.6	29
293	NetRanker: A network-based gene ranking tool using protein-protein interaction and gene expression data. Biochip Journal, 2015, 9, 313-321.	2.5	4

#	Article	IF	CITATIONS
294	Prediction of host - pathogen protein interactions between Mycobacterium tuberculosis and Homo sapiens using sequence motifs. BMC Bioinformatics, 2015, 16, 100.	1.2	51
295	Searching for repetitions in biological networks: methods, resources and tools. Briefings in Bioinformatics, 2015, 16, 118-136.	3.2	24
296	A systems biology-based investigation into the therapeutic effects of Gansui Banxia Tang on reversing the imbalanced network of hepatocellular carcinoma. Scientific Reports, 2014, 4, 4154.	1.6	52
297	Regulatory consequences of neuronal ELAV-like protein binding to coding and non-coding RNAs in human brain. ELife, 2016, 5, .	2.8	128
298	Biomolecular Relationships Discovered from Biological Labyrinth and Lost in Ocean of Literature: Community Efforts Can Rescue Until Automated Artificial Intelligence Takes Over. Frontiers in Genetics, 2016, 7, 46.	1.1	1
299	Quantitative Determination of Flexible Pharmacological Mechanisms Based On Topological Variation in Mice Anti-Ischemic Modular Networks. PLoS ONE, 2016, 11, e0158379.	1.1	8
300	Revealing the Effects of the Herbal Pair of <i>Euphorbia kansui</i> and <i>Glycyrrhiza</i> on Hepatocellular Carcinoma Ascites with Integrating Network Target Analysis and Experimental Validation. International Journal of Biological Sciences, 2016, 12, 594-606.	2.6	32
301	Unstable Communities in Network Ensembles. , 2016, , .		1
302	Network pharmacology-based identification of key pharmacological pathways of Yin–Huang–Qing–Fei capsule acting on chronic bronchitis. International Journal of COPD, 2017, Volume 12, 85-94.	0.9	80
303	Mining biomedical images towards valuable information retrieval in biomedical and life sciences. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw118.	1.4	19
304	Propagation on Molecular Interaction Networks: Prediction of Effective Drug Combinations and Biomarkers in Cancer Treatment. Current Pharmaceutical Design, 2016, 22, 1-1.	0.9	2
305	Counting independent motifs in probabilistic networks. , 2016, , .		2
306	Network Pharmacology-based Approaches Capture Essence of Chinese Herbal Medicines. Chinese Herbal Medicines, 2016, 8, 107-116.	1.2	61
307	Integration of multiple biological features yields high confidence human protein interactome. Journal of Theoretical Biology, 2016, 403, 85-96.	0.8	25
308	Multi-omics landscapes of colorectal cancer subtypes discriminated by an individualized prognostic signature for 5-fluorouracil-based chemotherapy. Oncogenesis, 2016, 5, e242-e242.	2.1	17
309	Improving extraction of protein $\hat{a} \in \hat{\ }$ Protein interaction datasets from KUPS using hashing approach. , 2016, , .		0
310	Improving drug safety: From adverse drug reaction knowledge discovery to clinical implementation. Methods, 2016, 110, 14-25.	1.9	32
311	Translational Biomedical Informatics. Advances in Experimental Medicine and Biology, 2016, , .	0.8	1

#	ARTICLE	IF	Citations
312	Network-Based Biomedical Data Analysis. Advances in Experimental Medicine and Biology, 2016, 939, 309-332.	0.8	8
313	Entropy-based divergent and convergent modular pattern reveals additive and synergistic anticerebral ischemia mechanisms. Experimental Biology and Medicine, 2016, 241, 2063-2074.	1.1	12
314	Endophenotype Network Models: Common Core of Complex Diseases. Scientific Reports, 2016, 6, 27414.	1.6	72
315	Network-based in silico drug efficacy screening. Nature Communications, 2016, 7, 10331.	5.8	394
316	Systematic analysis of the molecular mechanism underlying atherosclerosis using a text mining approach. Human Genomics, 2016, 10, 14.	1.4	12
317	Effective comparative analysis of protein-protein interaction networks by measuring the steady-state network flow using a Markov model. BMC Bioinformatics, 2016, 17, 395.	1.2	14
318	Cellular compartmentation of energy metabolism: creatine kinase microcompartments and recruitment of B-type creatine kinase to specific subcellular sites. Amino Acids, 2016, 48, 1751-1774.	1,2	76
319	Guizhi-Shaoyao-Zhimu decoction attenuates rheumatoid arthritis partially by reversing inflammation-immune system imbalance. Journal of Translational Medicine, 2016, 14, 165.	1.8	49
320	Comparative analysis of housekeeping and tissue-selective genes in human based on network topologies and biological properties. Molecular Genetics and Genomics, 2016, 291, 1227-1241.	1.0	8
321	Identification of key active constituents of Buchang Naoxintong capsules with therapeutic effects against ischemic stroke by using an integrative pharmacology-based approach. Molecular BioSystems, 2016, 12, 233-245.	2.9	50
322	Algorithms for modeling global and context-specific functional relationship networks. Briefings in Bioinformatics, 2016, 17, 686-695.	3.2	3
323	A Computational Network Biology Approach to Uncover Novel Genes Related to Alzheimer's Disease. Methods in Molecular Biology, 2016, 1303, 435-446.	0.4	4
325	Both Intrinsic Substrate Preference and Network Context Contribute to Substrate Selection of Classical Tyrosine Phosphatases. Journal of Biological Chemistry, 2017, 292, 4942-4952.	1.6	8
326	Integrating Heterogeneous Datasets for Cancer Module Identification. Methods in Molecular Biology, 2017, 1526, 119-137.	0.4	2
327	CanProVar 2.0: An Updated Database of Human Cancer Proteome Variation. Journal of Proteome Research, 2017, 16, 421-432.	1.8	36
328	From protein-protein interactions to protein co-expression networks: a new perspective to evaluate large-scale proteomic data. Eurasip Journal on Bioinformatics and Systems Biology, 2017, 2017, 6.	1.4	81
329	The effect of Bu Zhong Yi Qi decoction on simulated weightlessness-induced muscle atrophy and its mechanisms. Molecular Medicine Reports, 2017, 16, 5165-5174.	1.1	14
330	Protein complexes, big data, machine learning and integrative proteomics: lessons learned over a decade of systematic analysis of protein interaction networks. Expert Review of Proteomics, 2017, 14, 845-855.	1.3	19

#	ARTICLE	IF	CITATIONS
331	Plant Bioinformatics: Next Generation Sequencing Approaches. , 2017, , 1-106.		1
332	An Integrative Approach for Identifying Network Biomarkers of Breast Cancer Subtypes Using Genomic, Interactomic, and Transcriptomic Data. Journal of Computational Biology, 2017, 24, 756-766.	0.8	7
333	Effect of Protein Repetitiveness on Protein–Protein Interaction Prediction Results Using Support Vector Machines. Journal of Computational Biology, 2017, 24, 183-192.	0.8	0
334	Molecular property diagnostic suite (MPDS): Development of disease-specific open source web portals for drug discovery. SAR and QSAR in Environmental Research, 2017, 28, 913-926.	1.0	11
335	Extraction of protein-protein interactions using natural language processing based pattern matching. , 2017, , .		4
336	Network Biomarkers Constructed from Gene Expression and Protein-Protein Interaction Data for Accurate Prediction of Leukemia. Journal of Cancer, 2017, 8, 278-286.	1.2	15
337	ANKRD54 preferentially selects Bruton's Tyrosine Kinase (BTK) from a Human Src-Homology 3 (SH3) domain library. PLoS ONE, 2017, 12, e0174909.	1.1	2
338	Integrated systems biology analysis of KSHV latent infection reveals viral induction and reliance on peroxisome mediated lipid metabolism. PLoS Pathogens, 2017, 13, e1006256.	2.1	53
339	A network pharmacology-based strategy deciphers the underlying molecular mechanisms of Qixuehe Capsule in the treatment of menstrual disorders. Chinese Medicine, 2017, 12, 23.	1.6	36
340	DECIPHERING THE ACTION MECHANISM OF INDONESIA HERBAL DECOCTION IN THE TREATMENT OF TYPE II DIABETES USING A NETWORK PHARMACOLOGY APPROACH. International Journal of Pharmacy and Pharmaceutical Sciences, 2017, 9, 243.	0.3	2
341	A homologous mapping method for three-dimensional reconstruction of protein networks reveals disease-associated mutations. BMC Systems Biology, 2018, 12, 13.	3.0	1
342	The DifferentialNet database of differential protein–protein interactions in human tissues. Nucleic Acids Research, 2018, 46, D522-D526.	6.5	71
343	Main active constituent identification in Guanxinjing capsule, a traditional Chinese medicine, for the treatment of coronary heart disease complicated with depression. Acta Pharmacologica Sinica, 2018, 39, 975-987.	2.8	24
344	Neoteric advancement in TB drugs and an overview on the anti-tubercular role of peptides through computational approaches. Microbial Pathogenesis, 2018, 114, 80-89.	1.3	18
345	Discerning molecular interactions: A comprehensive review on biomolecular interaction databases and network analysis tools. Gene, 2018, 642, 84-94.	1.0	117
346	Network spectra for drug-target identification in complex diseases: new guns against old foes. Applied Network Science, 2018, 3, 51.	0.8	10
347	Shortest path counting in probabilistic biological networks. BMC Bioinformatics, 2018, 19, 465.	1.2	14
348	Prediction of Novel Drugs and Diseases for Hepatocellular Carcinoma Based on Multi-Source Simulated Annealing Based Random Walk. Journal of Medical Systems, 2018, 42, 188.	2.2	2

#	Article	IF	CITATIONS
349	Underutilised and Neglected Crops: Next Generation Sequencing Approaches for Crop Improvement and Better Food Security. , 2018, , 287-380.		3
350	Human Interactomics: Comparative Analysis of Different Protein Interaction Resources and Construction of a Cancer Protein–Drug Bipartite Network. Advances in Protein Chemistry and Structural Biology, 2018, 111, 263-282.	1.0	10
351	Automatic extraction of protein-protein interactions using grammatical relationship graph. BMC Medical Informatics and Decision Making, 2018, 18, 42.	1.5	23
352	Proximal Pathway Enrichment Analysis for Targeting Comorbid Diseases via Network Endopharmacology. Pharmaceuticals, 2018, 11, 61.	1.7	32
353	ProMotE: an efficient algorithm for counting independent motifs in uncertain network topologies. BMC Bioinformatics, 2018, 19, 242.	1.2	4
354	A Parametric Targetability Evaluation Approach for Vitiligo Proteome Extracted through Integration of Gene Ontologies and Protein Interaction Topologies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1830-1842.	1.9	8
355	Protein–Protein Interaction Databases. , 2019, , 849-855.		2
356	Protein–Protein Interaction Databases. , 2019, , 988-996.		3
357	UNIPred-Web: a web tool for the integration and visualization of biomolecular networks for protein function prediction. BMC Bioinformatics, 2019, 20, 422.	1.2	9
358	Membrane protein-regulated networks across human cancers. Nature Communications, 2019, 10, 3131.	5.8	67
359	Quantitative proteomic analysis of sperm in unexplained recurrent pregnancy loss. Reproductive Biology and Endocrinology, 2019, 17, 52.	1.4	17
360	ResponseNet v.3: revealing signaling and regulatory pathways connecting your proteins and genes across human tissues. Nucleic Acids Research, 2019, 47, W242-W247.	6.5	11
361	Molecular mechanisms involved in drug-induced liver injury caused by urate-lowering Chinese herbs: A network pharmacology study and biology experiments. PLoS ONE, 2019, 14, e0216948.	1.1	20
362	A Comprehensive Drosophila melanogaster Transcription Factor Interactome. Cell Reports, 2019, 27, 955-970.e7.	2.9	66
363	Combining network topology with transcriptomic data for identifying radiosensitive gene signatures. Journal of Computational Methods in Sciences and Engineering, 2019, 19, 565-579.	0.1	0
364	Network-principled deep generative models for designing drug combinations as graph sets. Bioinformatics, 2020, 36, i445-i454.	1.8	24
365	Identification of a Two-Gene (PML-EPB41) Signature With Independent Prognostic Value in Osteosarcoma. Frontiers in Oncology, 2019, 9, 1578.	1.3	8
366	Differential network analysis of multiple human tissue interactomes highlights tissue-selective processes and genetic disorder genes. Bioinformatics, 2020, 36, 2821-2828.	1.8	28

#	Article	IF	CITATIONS
367	Using the MINT Database to Search Protein Interactions. Current Protocols in Bioinformatics, 2020, 69, e93.	25.8	13
368	Machine learning approaches and databases for prediction of drug–target interaction: a survey paper. Briefings in Bioinformatics, 2021, 22, 247-269.	3.2	217
369	Molecular Dynamics Simulation of Biomolecular Interactions. , 2021, , 182-189.		9
370	Human gene expression profiling identifies key therapeutic targets in tuberculosis infection: A systematic network meta-analysis. Infection, Genetics and Evolution, 2021, 87, 104649.	1.0	10
372	Navigating the Global Protein–Protein Interaction Landscape Using iRefWeb. Methods in Molecular Biology, 2021, 2199, 191-207.	0.4	2
373	Prediction, Analysis, Visualization, and Storage of Protein–Protein Interactions Using Computational Approaches. , 2021, , 265-346.		1
374	LncTx: A network-based method to repurpose drugs acting on the survival-related lncRNAs in lung cancer. Computational and Structural Biotechnology Journal, 2021, 19, 3990-4002.	1.9	5
375	Integrating 3D structural information into systems biology. Journal of Biological Chemistry, 2021, 296, 100562.	1.6	18
376	A New Family of Similarity Measures for Scoring Confidence of Protein Interactions Using Gene Ontology. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 19-30.	1.9	3
377	Genome analyses of 174 strains of Mycobacterium tuberculosis provide insight into the evolution of drug resistance and reveal potential drug targets. Microbial Genomics, 2021, 7, .	1.0	5
378	Systems biology and bioinformatics approaches in leishmaniasis., 2021,, 509-548.		6
379	Immune Signatures and Systems Biology of Vaccines. , 2011, , 141-167.		2
380	Protein-Protein Interaction Databases. Methods in Molecular Biology, 2015, 1278, 39-56.	0.4	43
381	Automated Extraction and Visualization of Protein–Protein Interaction Networks and Beyond: A Text-Mining Protocol. Methods in Molecular Biology, 2020, 2074, 13-34.	0.4	8
382	Identifying Gene Interaction Networks. Methods in Molecular Biology, 2012, 850, 483-494.	0.4	14
383	Navigating the Global Protein–Protein Interaction Landscape Using iRefWeb. Methods in Molecular Biology, 2014, 1091, 315-331.	0.4	19
384	Reverse Engineering Transcriptional Gene Networks. Methods in Molecular Biology, 2014, 1101, 179-196.	0.4	3
385	Detection of Driver Protein Complexes in Breast Cancer Metastasis by Large-Scale Transcriptome–Interactome Integration. Methods in Molecular Biology, 2014, 1101, 67-85.	0.4	1

#	Article	IF	Citations
386	A Review on Protein-Protein Interaction Network Databases. Springer Proceedings in Mathematics and Statistics, 2014, , 511-519.	0.1	2
387	Sensitivity Analysis of Granularity Levels in Complex Biological Networks. Communications in Computer and Information Science, 2017, , 167-188.	0.4	1
388	Complex Detection in Protein-Protein Interaction Networks: A Compact Overview for Researchers and Practitioners. Lecture Notes in Computer Science, 2012, , 211-223.	1.0	15
389	Integration of Biomolecular Interaction Data in a Genomic and Proteomic Data Warehouse to Support Biomedical Knowledge Discovery. Lecture Notes in Computer Science, 2012, , 112-126.	1.0	10
390	Systems Biology and Integrated Computational Methods for Cancer-Associated Mutation Analysis. , 2020, , 335-362.		3
391	MiRNA-BD: an evidence-based bioinformatics model and software tool for microRNA biomarker discovery. RNA Biology, 2018, 15, 1093-1105.	1.5	31
395	A systems immunology approach identifies the collective impact of 5 miRs in Th2 inflammation. JCI Insight, 2018, 3, .	2.3	10
396	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	7
397	GASOLINE: a Cytoscape app for multiple local alignment of PPI networks. F1000Research, 2014, 3, 140.	0.8	10
398	A Dynamic View of Domain-Motif Interactions. PLoS Computational Biology, 2012, 8, e1002341.	1.5	48
399	Improved Microarray-Based Decision Support with Graph Encoded Interactome Data. PLoS ONE, 2010, 5, e10225.	1.1	6
400	HIPPIE: Integrating Protein Interaction Networks with Experiment Based Quality Scores. PLoS ONE, 2012, 7, e31826.	1.1	297
401	Network Compression as a Quality Measure for Protein Interaction Networks. PLoS ONE, 2012, 7, e35729.	1.1	15
402	CDA: Combinatorial Drug Discovery Using Transcriptional Response Modules. PLoS ONE, 2012, 7, e42573.	1.1	57
403	Cancer Missense Mutations Alter Binding Properties of Proteins and Their Interaction Networks. PLoS ONE, 2013, 8, e66273.	1.1	102
404	Genes Dysregulated to Different Extent or Oppositely in Estrogen Receptor-Positive and Estrogen Receptor-Negative Breast Cancers. PLoS ONE, 2013, 8, e70017.	1.1	10
405	Identification of GRB2 and GAB1 Coexpression as an Unfavorable Prognostic Factor for Hepatocellular Carcinoma by a Combination of Expression Profile and Network Analysis. PLoS ONE, 2013, 8, e85170.	1,1	60
406	GASOLINE: a Greedy And Stochastic algorithm for Optimal Local multiple alignment of Interaction NEtworks. PLoS ONE, 2014, 9, e98750.	1.1	28

#	Article	IF	CITATIONS
407	Systematic Analysis of the Molecular Mechanism Underlying Decidualization Using a Text Mining Approach. PLoS ONE, 2015, 10, e0134585.	1.1	15
408	H-RACS: a handy tool to rank anti-cancer synergistic drugs. Aging, 2020, 12, 21504-21517.	1.4	12
409	inFRank: a ranking-based identification of influential genes in biological networks. Oncotarget, 2017, 8, 43810-43821.	0.8	5
410	An Overview of Computational Life Science Databases & Exchange Formats of Relevance to Chemical Biology Research. Combinatorial Chemistry and High Throughput Screening, 2013, 16, 189-198.	0.6	13
411	Computational Prediction of Protein–Protein Interaction Networks: Algorithms and Resources. Current Genomics, 2013, 14, 397-414.	0.7	119
412	Predicting False Positives of Protein-Protein Interaction Data by Semantic Similarity Measures <sup>§</sup> . Current Bioinformatics, 2013, 8, 339-346.	0.7	19
413	Hypoxamirs in Pulmonary Hypertension: Breathing New Life into Pulmonary Vascular Research. Cardiovascular Diagnosis and Therapy, 2012, 2, 200-212.	0.7	21
414	Constructing human phenome-interactome networks for the prioritization of candidate genes. Statistics and Its Interface, 2012, 5, 137-148.	0.2	6
415	Net2Align: An Algorithm For Pairwise Global Alignment of Biological Networks. Bioinformation, 2016, 12, 408-411.	0.2	3
416	Context-enriched interactome powered by proteomics helps the identification of novel regulators of macrophage activation. ELife, $2018, 7, .$	2.8	11
417	Network-based analysis of differentially expressed genes in cerebrospinal fluid (CSF) and blood reveals new candidate genes for multiple sclerosis. PeerJ, 2016, 4, e2775.	0.9	52
418	Increasing the precision of orthology-based complex prediction through network alignment. PeerJ, 2014, 2, e413.	0.9	1
419	Convolutional neural network for human cancer types prediction by integrating protein interaction networks and omics data. Scientific Reports, 2021, 11, 20691.	1.6	8
420	Knowledge-Driven, Data-Assisted Integrative Pathway Analytics. , 2011, , 225-247.		0
421	Disease Gene Prioritization. , 0, , .		0
422	High Throughput Affinity Purification and Mass Spectrometry to Determine Protein Complex Interactions., 2012,, 139-159.		0
423	Analysis of Labeled Quantitative Mass Spectrometry Proteomics Data., 2012,, 79-91.		0
424	The effect of destrin mutations pathways on the gene expression profile. African Journal of Microbiology Research, 2012, 6, .	0.4	0

#	Article	IF	Citations
425	BioCreative II.5 and the FEBS Letters Experiment on Structured Digital Abstracts., 2013, , 101-106.		0
426	Human Genome Network Platform: A Resource for TFRN Analysis. Methods in Molecular Biology, 2014, 1164, 147-162.	0.4	O
427	Path Finding in Biological Networks. , 2014, , 289-309.		0
429	Building a Hierarchical Organization of Protein Complexes Out of Protein Association Data. PLoS ONE, 2014, 9, e100098.	1.1	0
432	Predicting disease genes for complex diseases using random watcher-walker., 2020,,.		0
433	MICA enhances sensitivity to cisplatin in patients with extensive small cell lung cancer via downregulation of ABCG2. Oncology Letters, 2020, 20, 1143-1152.	0.8	1
435	Network-based protein-protein interaction prediction method maps perturbations of cancer interactome. PLoS Genetics, 2021, 17, e1009869.	1.5	13
436	Knowledge-Driven, Data-Assisted Integrative Pathway Analytics. , 0, , 173-194.		O
437	Expression profile of mitrogen-activated protein kinase (MAPK) signaling genes in the skeletal muscle & liver of rat with type 2 diabetes: role in disease pathology. Indian Journal of Medical Research, 2014, 140, 744-55.	0.4	1
439	TissueNexus: a database of human tissue functional gene networks built with a large compendium of curated RNA-seq data. Nucleic Acids Research, 2022, 50, D710-D718.	6.5	11
440	An Integrative Network Approach to Identify Common Genes for the Therapeutics in Tuberculosis and Its Overlapping Non-Communicable Diseases. Frontiers in Pharmacology, 2021, 12, 770762.	1.6	11
441	Using ortholog information from multiple species to predict barley protein-protein interaction network. Plant Gene, 2022, , 100355.	1.4	1
442	埪ªŽç½'络和埪å›å·®å¼,表达信æ•̄的癌症致病基å›é¢"测. Scientia Sinica Vitae, 2022, , .	0.1	0
448	Assembling cell context-specific gene sets: a case in cardiomyopathy. Journal of Integrative Bioinformatics, 2013, 10, 234.	1.0	2
450	A review of bioinformatics tools and web servers in different microarray platforms used in cancer research. Advances in Protein Chemistry and Structural Biology, 2022, , 85-164.	1.0	15
451	Prediction of Adverse Drug Reaction Linked to Protein Targets Using Network-Based Information and Machine Learning. Frontiers in Bioinformatics, 0, 2, .	1.0	6
453	TCM Analysis Data Resources, Web Services and Visualizations. Translational Bioinformatics, 2022, , 99-110.	0.0	0
454	Alzheimer's disease: insights from a network medicine perspective. Scientific Reports, 2022, 12, .	1.6	2

#	Article	IF	CITATIONS
455	Building a knowledge graph to enable precision medicine. Scientific Data, 2023, 10, .	2.4	51
456	Pathogen-driven cancers from a structural perspective: Targeting host-pathogen protein-protein interactions. Frontiers in Oncology, 0, $13$ , .	1.3	0