

MINT, the molecular interaction database: 2012 update

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Citation Report

#	ARTICLE	IF	CITATIONS
1	CombFunc: predicting protein function using heterogeneous data sources. <i>Nucleic Acids Research</i> , 2012, 40, W466-W470.	6.5	63
2	IntScore: a web tool for confidence scoring of biological interactions. <i>Nucleic Acids Research</i> , 2012, 40, W140-W146.	6.5	51
3	IMP: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. <i>Nucleic Acids Research</i> , 2012, 40, W484-W490.	6.5	105
4	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. <i>Nucleic Acids Research</i> , 2012, 41, D808-D815.	6.5	3,816
5	BIPS: BIANA Interolog Prediction Server. A tool for protein-protein interaction inference. <i>Nucleic Acids Research</i> , 2012, 40, W147-W151.	6.5	57
6	The disease and gene annotations (DGA): an annotation resource for human disease. <i>Nucleic Acids Research</i> , 2012, 41, D553-D560.	6.5	53
7	Managing biological complexity across orthologs with a visual knowledgebase of documented biomolecular interactions. <i>Scientific Reports</i> , 2012, 2, 1011.	1.6	6
8	NEXT-GENERATION ANALYSIS OF CATARACTS: DETERMINING KNOWLEDGE DRIVEN GENE-GENE INTERACTIONS USING BIOFILTER, AND GENE-ENVIRONMENT INTERACTIONS USING THE PHENX TOOLKIT. , 2012, , .		9
9	Text-mining solutions for biomedical research: enabling integrative biology. <i>Nature Reviews Genetics</i> , 2012, 13, 829-839.	7.7	194
10	Computational analysis of interactomes: Current and future perspectives for bioinformatics approaches to model the host-pathogen interaction space. <i>Methods</i> , 2012, 57, 508-518.	1.9	49
11	Global human tissue profiling and protein network analysis reveals distinct levels of transcriptional germline-specificity and identifies target genes for male infertility. <i>Human Reproduction</i> , 2012, 27, 3233-3248.	0.4	82
12	Effects of protein interaction data integration, representation and reliability on the use of network properties for drug target prediction. <i>BMC Bioinformatics</i> , 2012, 13, 294.	1.2	24
13	Methods for visual mining of genomic and proteomic data atlases. <i>BMC Bioinformatics</i> , 2012, 13, 58.	1.2	8
14	Protein stickiness, rather than number of functional protein-protein interactions, predicts expression noise and plasticity in yeast. <i>BMC Systems Biology</i> , 2012, 6, 128.	3.0	20
15	HINT: High-quality protein interactomes and their applications in understanding human disease. <i>BMC Systems Biology</i> , 2012, 6, 92.	3.0	366
16	Using ProHits to Store, Annotate, and Analyze Affinity Purification-Mass Spectrometry (AP-MS) Data. <i>Current Protocols in Bioinformatics</i> , 2012, 39, Unit8.16.	25.8	19
17	Understanding Cancer Progression Using Protein Interaction Networks. , 2012, , 167-195.		1
18	Supervised maximum-likelihood weighting of composite protein networks for complex prediction. <i>BMC Systems Biology</i> , 2012, 6, S13.	3.0	36

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19	A Network Synthesis Model for Generating Protein Interaction Network Families. <i>PLoS ONE</i> , 2012, 7, e41474.	1.1	34
20	Identification of Novel Cholesteatoma-Related Gene Expression Signatures Using Full-Genome Microarrays. <i>PLoS ONE</i> , 2012, 7, e52718.	1.1	38
21	Interactome mapping for analysis of complex phenotypes: Insights from benchmarking binary interaction assays. <i>Proteomics</i> , 2012, 12, 1499-1518.	1.3	52
22	STOP using just GO: a multi-ontology hypothesis generation tool for high throughput experimentation. <i>BMC Bioinformatics</i> , 2013, 14, 53.	1.2	17
23	Interfacing cellular networks of <i>S. cerevisiae</i> and <i>E. coli</i> : Connecting dynamic and genetic information. <i>BMC Genomics</i> , 2013, 14, 324.	1.2	27
24	BioBin: a bioinformatics tool for automating the binning of rare variants using publicly available biological knowledge. <i>BMC Medical Genomics</i> , 2013, 6, S6.	0.7	55
25	Databases as instruments for analysis of large-scale data sets of interactions between molecular biological objects. <i>Biology Bulletin</i> , 2013, 40, 233-242.	0.1	2
26	ROCK: a resource for integrative breast cancer data analysis. <i>Breast Cancer Research and Treatment</i> , 2013, 139, 907-921.	1.1	30
27	A Nutrigenomic Framework to Identify Time-Resolving Responses of Hepatic Genes in Diet-Induced Obese Mice. <i>Molecules and Cells</i> , 2013, 36, 25-38.	1.0	6
28	mentha: a resource for browsing integrated protein-interaction networks. <i>Nature Methods</i> , 2013, 10, 690-691.	9.0	291
29	Functional site plasticity in domain superfamilies. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 874-889.	1.1	31
30	Traditional Chinese medicine network pharmacology: theory, methodology and application. <i>Chinese Journal of Natural Medicines</i> , 2013, 11, 110-120.	0.7	800
31	IntApop: A web service for predicting apoptotic protein interactions in humans. <i>BioSystems</i> , 2013, 114, 238-244.	0.9	4
32	High-resolution network biology: connecting sequence with function. <i>Nature Reviews Genetics</i> , 2013, 14, 865-879.	7.7	92
33	OntoPIN: An ontology-annotated PPI database. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2013, 5, 187-195.	2.2	1
34	Widespread Aggregation and Neurodegenerative Diseases Are Associated with Supersaturated Proteins. <i>Cell Reports</i> , 2013, 5, 781-790.	2.9	245
35	Reconstruction of the experimentally supported human protein interactome: what can we learn?. <i>BMC Systems Biology</i> , 2013, 7, 96.	3.0	28
36	Structure-based protein-protein interaction networks and drug design. <i>Quantitative Biology</i> , 2013, 1, 183-191.	0.3	7

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37	Towards a detailed atlas of proteinâ€protein interactions. <i>Current Opinion in Structural Biology</i> , 2013, 23, 929-940.	2.6	92
38	A Role for Proteinâ€Protein Interaction Networks in the Identification and Characterization of Potential Biomarkers. , 2013, , 333-347.		3
39	Systems biology of pathogenâ€host interaction: Networks of proteinâ€protein interaction within pathogens and pathogenâ€human interactions in the postâ€genomic era. <i>Biotechnology Journal</i> , 2013, 8, 85-96.	1.8	39
40	Interactome3D: adding structural details to protein networks. <i>Nature Methods</i> , 2013, 10, 47-53.	9.0	449
41	From Top-Down to Bottom-Up: Computational Modeling Approaches for Cellular Redoxin Networks. <i>Antioxidants and Redox Signaling</i> , 2013, 18, 2075-2086.	2.5	39
42	HuPho: the human phosphatase portal. <i>FEBS Journal</i> , 2013, 280, 379-387.	2.2	55
43	Plant Protein Interactomes. <i>Annual Review of Plant Biology</i> , 2013, 64, 161-187.	8.6	135
44	Network approaches to drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2013, 8, 7-20.	2.5	40
45	The SH2 Domain Interaction Landscape. <i>Cell Reports</i> , 2013, 3, 1293-1305.	2.9	110
46	An effective, practical and low computational cost framework for the integration of heterogeneous data to predict functional associations between proteins by means of Artificial Neural Networks. <i>Neurocomputing</i> , 2013, 121, 64-78.	3.5	3
47	Structure and dynamics of molecular networks: A novel paradigm of drug discovery. , 2013, 138, 333-408.		779
48	Structure-Based Target Druggability Assessment. <i>Methods in Molecular Biology</i> , 2013, 986, 141-164.	0.4	15
49	Social networks to biological networks: systems biology of <i>Mycobacterium tuberculosis</i> . <i>Molecular BioSystems</i> , 2013, 9, 1584.	2.9	5
50	PPlevo : Proteinâ€protein interaction prediction from PSSM based evolutionary information. <i>Genomics</i> , 2013, 102, 237-242.	1.3	131
51	Practical Use of BiNoM: A Biological Network Manager Software. <i>Methods in Molecular Biology</i> , 2013, 1021, 127-146.	0.4	7
52	Selective Targeting Capability Acquired with a Protein Corona Adsorbed on the Surface of 1,2-Dioleoyl-3-trimethylammonium Propane/DNA Nanoparticles. <i>ACS Applied Materials & Interfaces</i> , 2013, 5, 13171-13179.	4.0	150
53	DBATE: database of alternative transcripts expression. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat050.	1.4	11
54	PCorralâ€interactive mining of protein interactions from MEDLINE. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat030.	1.4	13

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55	Evidence classification of high-throughput protocols and confidence integration in RegulonDB. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas059.	1.4	23
56	Adding Protein Context to the Human Protein-Protein Interaction Network to Reveal Meaningful Interactions. PLoS Computational Biology, 2013, 9, e1002860.	1.5	70
57	Protein Complex-Based Analysis Framework for High-Throughput Data Sets. Science Signaling, 2013, 6, rs5.	1.6	110
58	INstruct: a database of high-quality 3D structurally resolved protein interactome networks. Bioinformatics, 2013, 29, 1577-1579.	1.8	129
59	Capturing cooperative interactions with the PSI-MI format. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat066.	1.4	10
60	Evolutionary Rate Heterogeneity of Core and Attachment Proteins in Yeast Protein Complexes. Genome Biology and Evolution, 2013, 5, 1366-1375.	1.1	11
61	Low Frequency Variants, Collapsed Based on Biological Knowledge, Uncover Complexity of Population Stratification in 1000 Genomes Project Data. PLoS Genetics, 2013, 9, e1003959.	1.5	35
62	Functional Knowledge Transfer for High-accuracy Prediction of Under-studied Biological Processes. PLoS Computational Biology, 2013, 9, e1002957.	1.5	62
63	SpermatogenesisOnline 1.0: a resource for spermatogenesis based on manual literature curation and genome-wide data mining. Nucleic Acids Research, 2013, 41, D1055-D1062.	6.5	35
64	Human Monogenic Disease Genes Have Frequently Functionally Redundant Paralogs. PLoS Computational Biology, 2013, 9, e1003073.	1.5	49
65	GeneMANIA Prediction Server 2013 Update. Nucleic Acids Research, 2013, 41, W115-W122.	6.5	343
66	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
67	SpliceAid-F: a database of human splicing factors and their RNA-binding sites. Nucleic Acids Research, 2013, 41, D125-D131.	6.5	148
68	ValidNESs: a database of validated leucine-rich nuclear export signals. Nucleic Acids Research, 2013, 41, D338-D343.	6.5	75
69	The human gene connectome as a map of short cuts for morbid allele discovery. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5558-5563.	3.3	79
70	Optimization criteria and biological process enrichment in homologous multiprotein modules. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10872-10877.	3.3	5
71	A graph kernel approach for alignment-free domain-peptide interaction prediction with an application to human SH3 domains. Bioinformatics, 2013, 29, i335-i343.	1.8	15
72	Review of Biological Network Data and Its Applications. Genomics and Informatics, 2013, 11, 200.	0.4	79

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73	Molecular interaction networks for the analysis of human disease: Utility, limitations, and considerations. <i>Proteomics</i> , 2013, 13, 3393-3405.	1.3	17
74	Genomic analyses with biofilter 2.0: knowledge driven filtering, annotation, and model development. <i>BioData Mining</i> , 2013, 6, 25.	2.2	50
75	The Impact of Computer Science in Molecular Medicine: Enabling High- Throughput Research. <i>Current Topics in Medicinal Chemistry</i> , 2013, 13, 526-575.	1.0	13
76	The Evolutionary Dynamics of Protein-Protein Interaction Networks Inferred from the Reconstruction of Ancient Networks. <i>PLoS ONE</i> , 2013, 8, e58134.	1.1	47
77	Identification of Gene Expression Changes from Colitis to CRC in the Mouse CAC Model. <i>PLoS ONE</i> , 2014, 9, e95347.	1.1	22
78	An Integrative Omics Strategy to Assess the Germ Cell Secretome and to Decipher Sertoli-Germ Cell Crosstalk in the Mammalian Testis. <i>PLoS ONE</i> , 2014, 9, e104418.	1.1	18
79	RRHGE: A Novel Approach to Classify the Estrogen Receptor Based Breast Cancer Subtypes. <i>Scientific World Journal</i> , The, 2014, 2014, 1-13.	0.8	3
80	Toward a systems-level understanding of gene regulatory, protein interaction, and metabolic networks in cyanobacteria. <i>Frontiers in Genetics</i> , 2014, 5, 191.	1.1	19
81	Use of Bioinformatics Tools in Different Spheres of Life Sciences. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2014, 05, .	0.5	16
82	Mining the Dark Matter of the Cancer Proteome for Novel Biomarkers. <i>Current Cancer Therapy Reviews</i> , 2014, 9, 265-277.	0.2	9
83	Epsteinâ€Barr virus encoded micro<sc>RNA</sc>'s target <sc>SUMO</sc>â€regulated cellular functions. <i>FEBS Journal</i> , 2014, 281, 4935-4950.	2.2	15
84	Identifying candidate genes for discrimination of ulcerative colitis and Crohnâ€™s disease. <i>Molecular Biology Reports</i> , 2014, 41, 6349-6355.	1.0	7
85	Characterization of age signatures of DNA methylation in normal and cancer tissues from multiple studies. <i>BMC Genomics</i> , 2014, 15, 997.	1.2	20
86	A random set scoring model for prioritization of disease candidate genes using protein complexes and data-mining of GeneRIF, OMIM and PubMed records. <i>BMC Bioinformatics</i> , 2014, 15, 315.	1.2	9
87	Reconstruction of metabolic pathways by combining probabilistic graphical model-based and knowledge-based methods. <i>BMC Proceedings</i> , 2014, 8, S5.	1.8	12
88	VarWalker: Personalized Mutation Network Analysis of Putative Cancer Genes from Next-Generation Sequencing Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003460.	1.5	96
89	Linear Motif-Mediated Interactions Have Contributed to the Evolution of Modularity in Complex Protein Interaction Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003881.	1.5	16
90	Lynx web services for annotations and systems analysis of multi-gene disorders. <i>Nucleic Acids Research</i> , 2014, 42, W473-W477.	6.5	5

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91	The Domain Landscape of Virus-Host Interactomes. <i>BioMed Research International</i> , 2014, 2014, 1-13.	0.9	30
92	Integration Strategy Is a Key Step in Network-Based Analysis and Dramatically Affects Network Topological Properties and Inferring Outcomes. <i>BioMed Research International</i> , 2014, 2014, 1-13.	0.9	5
93	Network-Based Disease Gene Prioritization by Hitting Time Analysis. , 2014, , .		0
94	Using biological networks to improve our understanding of infectious diseases. <i>Computational and Structural Biotechnology Journal</i> , 2014, 11, 1-10.	1.9	43
95	A Second-generation Proteinâ€“Protein Interaction Network of <i>Helicobacter pylori</i> . <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1318-1329.	2.5	55
96	From workstations to workbenches: Towards predicting physicochemically viable proteinâ€“protein interactions across a host and a pathogen. <i>IUBMB Life</i> , 2014, 66, 759-774.	1.5	10
97	Drugâ€“Like Proteinâ€“Protein Interaction Modulators: Challenges and Opportunities for Drug Discovery and Chemical Biology. <i>Molecular Informatics</i> , 2014, 33, 414-437.	1.4	93
98	The role of the interactome in the maintenance of deleterious variability in human populations. <i>Molecular Systems Biology</i> , 2014, 10, 752.	3.2	28
99	How do biological networks differ from social networks? (an experimental study). , 2014, , .		2
100	Multiview Clustering on PPI Network for Gene Selection and Enrichment from Microarray Data. , 2014, , .		3
101	P3DB 3.0: From plant phosphorylation sites to protein networks. <i>Nucleic Acids Research</i> , 2014, 42, D1206-D1213.	6.5	75
102	New directions for diffusion-based network prediction of protein function: incorporating pathways with confidence. <i>Bioinformatics</i> , 2014, 30, i219-i227.	1.8	108
103	The MIntAct projectâ€“IntAct as a common curation platform for 11 molecular interaction databases. <i>Nucleic Acids Research</i> , 2014, 42, D358-D363.	6.5	1,634
104	PARK2 and proinflammatory/anti-inflammatory cytokine gene interactions contribute to the susceptibility to leprosy: a caseâ€“control study of North Indian population. <i>BMJ Open</i> , 2014, 4, e004239.	0.8	16
105	NetworkAnalyst - integrative approaches for proteinâ€“protein interaction network analysis and visual exploration. <i>Nucleic Acids Research</i> , 2014, 42, W167-W174.	6.5	398
106	Lynx: a database and knowledge extraction engine for integrative medicine. <i>Nucleic Acids Research</i> , 2014, 42, D1007-D1012.	6.5	40
107	Intuitive, but not simple: Including explicit water molecules in proteinâ€“protein docking simulations improves model quality. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 916-932.	1.5	18
108	Proteomics and integrative genomics for unraveling the mysteries of spermatogenesis: The strategies of a team. <i>Journal of Proteomics</i> , 2014, 107, 128-143.	1.2	15

#	ARTICLE	IF	CITATIONS
109	Systems-Level Analysis of Innate Immunity. <i>Annual Review of Immunology</i> , 2014, 32, 547-577.	9.5	53
110	Systematic large-scale study of the inheritance mode of Mendelian disorders provides new insight into human disease. <i>European Journal of Human Genetics</i> , 2014, 22, 1260-1267.	1.4	4
111	Integrating protein-protein interaction networks with phenotypes reveals signs of interactions. <i>Nature Methods</i> , 2014, 11, 94-99.	9.0	130
112	Integrating In Silico Resources to Map a Signaling Network. <i>Methods in Molecular Biology</i> , 2014, 1101, 197-245.	0.4	18
113	A Proteome-Scale Map of the Human Interactome Network. <i>Cell</i> , 2014, 159, 1212-1226.	13.5	1,199
114	Human pharmacogenomic variation of antihypertensive drugs: from population genetics to personalized medicine. <i>Pharmacogenomics</i> , 2014, 15, 157-167.	0.6	14
115	Characterizing of functional human coding RNA editing from evolutionary, structural, and dynamic perspectives. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 3117-3131.	1.5	15
116	Data, Databases, Data Format, Database Search, Data Retrieval Systems, and Genome Browsers. , 2014, , 77-131.		0
117	Exploring mechanisms of human disease through structurally resolved protein interactome networks. <i>Molecular BioSystems</i> , 2014, 10, 9-17.	2.9	27
118	LocFuse: Human protein-protein interaction prediction via classifier fusion using protein localization information. <i>Genomics</i> , 2014, 104, 496-503.	1.3	51
119	Lean Big Data integration in systems biology and systems pharmacology. <i>Trends in Pharmacological Sciences</i> , 2014, 35, 450-460.	4.0	85
120	Functional and genomic context in pathway analysis of GWAS data. <i>Trends in Genetics</i> , 2014, 30, 390-400.	2.9	95
121	Network-based analysis of genotype-phenotype correlations between different inheritance modes. <i>Bioinformatics</i> , 2014, 30, 3223-3231.	1.8	5
122	Prediction and functional analysis of the sweet orange protein-protein interaction network. <i>BMC Plant Biology</i> , 2014, 14, 213.	1.6	30
123	Screening of Protein-Protein and Protein-DNA Interactions Using Microarrays. <i>Advances in Protein Chemistry and Structural Biology</i> , 2014, 95, 231-281.	1.0	6
124	Plant systems biology: insights, advances and challenges. <i>Planta</i> , 2014, 240, 33-54.	1.6	66
125	Screening of Critical Genes in Lung Adenocarcinoma via Network Analysis of Gene Expression Profile. <i>Pathology and Oncology Research</i> , 2014, 20, 853-858.	0.9	12
126	Unraveling human protein interaction networks underlying co-occurrences of diseases and pathological conditions. <i>Journal of Translational Medicine</i> , 2014, 12, 99.	1.8	26

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127	Computational prediction of the human-microbial oral interactome. <i>BMC Systems Biology</i> , 2014, 8, 24.	3.0	33
128	Presence and utility of intrinsically disordered regions in kinases. <i>Molecular BioSystems</i> , 2014, 10, 2876-2888.	2.9	26
129	The Protein 4.1 family: Hub proteins in animals for organizing membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 605-619.	1.4	119
130	Data Standardization and Sharing—The work of the HUPO-PSI. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 82-87.	1.1	22
131	The emerging era of genomic data integration for analyzing splice isoform function. <i>Trends in Genetics</i> , 2014, 30, 340-347.	2.9	82
132	Mass spectrometry—driven phosphoproteomics: patterning the systems biology mosaic. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , 2014, 3, 83-112.	5.9	63
133	Evolution of protein interactions: From interactomes to interfaces. <i>Archives of Biochemistry and Biophysics</i> , 2014, 554, 65-75.	1.4	49
134	Human Dopamine Receptors Interaction Network (DRIN): A systems biology perspective on topology, stability and functionality of the network. <i>Journal of Theoretical Biology</i> , 2014, 357, 169-183.	0.8	7
135	Identification of New Mechanisms of Cellular Response to Chemotherapy by Tracking Changes in Post-Translational Modifications by Ubiquitin and Ubiquitin-Like Proteins. <i>Journal of Proteome Research</i> , 2014, 13, 2478-2494.	1.8	26
136	Biological network extraction from scientific literature: state of the art and challenges. <i>Briefings in Bioinformatics</i> , 2014, 15, 856-877.	3.2	55
137	Protein—protein interactions: switch from classical methods to proteomics and bioinformatics-based approaches. <i>Cellular and Molecular Life Sciences</i> , 2014, 71, 205-228.	2.4	112
138	Detection of type 2 diabetes related modules and genes based on epigenetic networks. <i>BMC Systems Biology</i> , 2014, 8, S5.	3.0	7
139	Discovery of small protein complexes from PPI networks with size-specific supervised weighting. <i>BMC Systems Biology</i> , 2014, 8, S3.	3.0	34
140	Computational approaches for prioritizing candidate disease genes based on PPI networks. <i>Tsinghua Science and Technology</i> , 2015, 20, 500-512.	4.1	64
141	The hierarchical organization of natural protein interaction networks confers self-organization properties on pseudocells. <i>BMC Systems Biology</i> , 2015, 9, S3.	3.0	5
142	Biology—Driven Gene—Gene Interaction Analysis of Age—Related Cataract in the eMERGE Network. <i>Genetic Epidemiology</i> , 2015, 39, 376-384.	0.6	20
143	TRRUST: a reference database of human transcriptional regulatory interactions. <i>Scientific Reports</i> , 2015, 5, 11432.	1.6	339
144	Fundamentals of protein interaction network mapping. <i>Molecular Systems Biology</i> , 2015, 11, 848.	3.2	226

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145	Exploring novel mechanistic insights in Alzheimer's disease by assessing reliability of protein interactions. <i>Scientific Reports</i> , 2015, 5, 13634.	1.6	9
146	Integrated analysis of global proteome, phosphoproteome and glycoproteome enables complementary interpretation of disease-related protein networks. <i>Scientific Reports</i> , 2015, 5, 18189.	1.6	34
147	GeneSense: a new approach for human gene annotation integrated with protein-protein interaction networks. <i>Scientific Reports</i> , 2014, 4, 4474.	1.6	10
148	NERI: network-medicine based integrative approach for disease gene prioritization by relative importance. <i>BMC Bioinformatics</i> , 2015, 16, S9.	1.2	9
149	ANDSystem: an Associative Network Discovery System for automated literature mining in the field of biology. <i>BMC Systems Biology</i> , 2015, 9, S2.	3.0	58
150	Prediction of problematic complexes from PPI networks: sparse, embedded, and small complexes. <i>Biology Direct</i> , 2015, 10, 40.	1.9	23
151	HitPredict version 4: comprehensive reliability scoring of physical protein-protein interactions from more than 100 species. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav117.	1.4	92
152	Dissecting ancestry genomic background in substance dependence genome-wide association studies. <i>Pharmacogenomics</i> , 2015, 16, 1487-1498.	0.6	22
153	Indexing a protein-protein interaction network expedites network alignment. <i>BMC Bioinformatics</i> , 2015, 16, 326.	1.2	8
154	BioDB extractor: customized data extraction system for commonly used bioinformatics databases. <i>BioData Mining</i> , 2015, 8, 31.	2.2	2
155	FR database 1.0: a resource focused on fruit development and ripening. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav002-bav002.	1.4	6
156	SPECTRA: An Integrated Knowledge Base for Comparing Tissue and Tumor-Specific PPI Networks in Human. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 58.	2.0	13
157	Human protein interaction networks across tissues and diseases. <i>Frontiers in Genetics</i> , 2015, 6, 257.	1.1	76
158	Integrated inference and evaluation of host-fungi interaction networks. <i>Frontiers in Microbiology</i> , 2015, 6, 764.	1.5	63
159	Transcriptator: An Automated Computational Pipeline to Annotate Assembled Reads and Identify Non Coding RNA. <i>PLoS ONE</i> , 2015, 10, e0140268.	1.1	14
160	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. <i>PLoS ONE</i> , 2015, 10, e0144176.	1.1	1
161	Forward Individualized Medicine from Personal Genomes to Interactomes. <i>Frontiers in Physiology</i> , 2015, 6, 364.	1.3	15
162	Exploring potential new floral organ morphogenesis genes of <i>Arabidopsis thaliana</i> using systems biology approach. <i>Frontiers in Plant Science</i> , 2015, 6, 829.	1.7	20

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163	Discovering Distinct Functional Modules of Specific Cancer Types Using Protein-Protein Interaction Networks. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	1
164	Improving the Understanding of Pathogenesis of Human Papillomavirus 16 via Mapping Protein-Protein Interaction Network. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	8
165	NOD-Like Receptor Signaling in Cholesteatoma. <i>BioMed Research International</i> , 2015, 2015, 1-9.	0.9	17
166	A computational framework for finding functional modules across multiple biological networks. , 2015, , .		0
167	The complex portal - an encyclopaedia of macromolecular complexes. <i>Nucleic Acids Research</i> , 2015, 43, D479-D484.	6.5	100
168	From the static interactome to dynamic protein complexes: Three challenges. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1571001.	0.3	30
169	A review on computational systems biology of pathogen-host interactions. <i>Frontiers in Microbiology</i> , 2015, 6, 235.	1.5	93
170	Visualization of module alignment discovery. , 2015, , .		0
171	VirusMentha: a new resource for virus-host protein interactions. <i>Nucleic Acids Research</i> , 2015, 43, D588-D592.	6.5	141
172	FNTM: a server for predicting functional networks of tissues in mouse. <i>Nucleic Acids Research</i> , 2015, 43, W182-W187.	6.5	25
173	Comparative Genomics and Evolutionary Modularity of Prokaryotes. <i>Advances in Experimental Medicine and Biology</i> , 2015, 883, 77-96.	0.8	2
174	Network-based method to infer the contributions of proteins to the etiology of drug side effects. <i>Quantitative Biology</i> , 2015, 3, 124-134.	0.3	1
175	CancerNet: a database for decoding multilevel molecular interactions across diverse cancer types. <i>Oncogenesis</i> , 2015, 4, e177-e177.	2.1	31
176	Proteins involved in more domain types tend to be more essential. <i>International Journal of Bioinformatics Research and Applications</i> , 2015, 11, 91.	0.1	3
177	Innate immune response is differentially dysregulated between bipolar disease and schizophrenia. <i>Schizophrenia Research</i> , 2015, 161, 215-221.	1.1	58
178	Yeast Mitochondrial Protein-Protein Interactions Reveal Diverse Complexes and Disease-Relevant Functional Relationships. <i>Journal of Proteome Research</i> , 2015, 14, 1220-1237.	1.8	18
179	Mechismo: predicting the mechanistic impact of mutations and modifications on molecular interactions. <i>Nucleic Acids Research</i> , 2015, 43, e10-e10.	6.5	95
180	A visual review of the interactome of LRRK2: Using deep-curated molecular interaction data to represent biology. <i>Proteomics</i> , 2015, 15, 1390-1404.	1.3	38

#	ARTICLE	IF	CITATIONS
181	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015, 43, D447-D452.	6.5	9,029
182	PathPPI: an integrated dataset of human pathways and protein-protein interactions. <i>Science China Life Sciences</i> , 2015, 58, 579-589.	2.3	9
183	Systematic Identification of Molecular Links between Core and Candidate Genes in Breast Cancer. <i>Journal of Molecular Biology</i> , 2015, 427, 1436-1450.	2.0	24
184	β 2 catenin is central to DUX4-driven network rewiring in facioscapulohumeral muscular dystrophy. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20140797.	1.5	52
185	Genome-wide identification, classification and expression analysis of GHMP genes family in <i>Arabidopsis thaliana</i> . <i>Plant Systematics and Evolution</i> , 2015, 301, 2125-2140.	0.3	8
186	MatrixDB, the extracellular matrix interaction database: updated content, a new navigator and expanded functionalities. <i>Nucleic Acids Research</i> , 2015, 43, D321-D327.	6.5	118
187	Application of Biotechnology and Bioinformatics Tools in Plant-Fungus Interactions. , 2015, , 49-64.		0
188	Inbreeding Affects Gene Expression Differently in Two Self-Incompatible <i>Arabidopsis lyrata</i> Populations with Similar Levels of Inbreeding Depression. <i>Molecular Biology and Evolution</i> , 2015, 32, 2036-2047.	3.5	15
189	The BioPlex Network: A Systematic Exploration of the Human Interactome. <i>Cell</i> , 2015, 162, 425-440.	13.5	1,241
190	Publisher's Note: Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction. <i>Computational Biology and Chemistry</i> , 2015, 58, 104-119.	1.1	4
191	EcoliNet: a database of cofunctional gene network for <i>Escherichia coli</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	31
192	ComPPI: a cellular compartment-specific database for protein-protein interaction network analysis. <i>Nucleic Acids Research</i> , 2015, 43, D485-D493.	6.5	116
193	Ginsenoside Rb1 prevents hypoxia-reoxygenation-induced apoptosis in H9c2 cardiomyocytes via an estrogen receptor-dependent crosstalk among the Akt, JNK, and ERK 1/2 pathways using a label-free quantitative proteomics analysis. <i>RSC Advances</i> , 2015, 5, 26346-26363.	1.7	18
194	Understanding multicellular function and disease with human tissue-specific networks. <i>Nature Genetics</i> , 2015, 47, 569-576.	9.4	738
195	cisPath: an R/Bioconductor package for cloud users for visualization and management of functional protein interaction networks. <i>BMC Systems Biology</i> , 2015, 9, S1.	3.0	12
196	Amyloid precursor protein interaction network in human testis: sentinel proteins for male reproduction. <i>BMC Bioinformatics</i> , 2015, 16, 12.	1.2	32
197	CD4 T-cell transcriptome analysis reveals aberrant regulation of STAT3 and Wnt signaling pathways in rheumatoid arthritis: evidence from a case-control study. <i>Arthritis Research and Therapy</i> , 2015, 17, 76.	1.6	45
198	The integration of sequencing and bioinformatics in metagenomics. <i>Reviews in Environmental Science and Biotechnology</i> , 2015, 14, 357-383.	3.9	13

#	ARTICLE	IF	CITATIONS
199	Mining Association Rules in Graphs Based on Frequent Cohesive Itemsets. Lecture Notes in Computer Science, 2015, , 637-648.	1.0	15
200	NetworkAnalyst for statistical, visual and network-based meta-analysis of gene expression data. Nature Protocols, 2015, 10, 823-844.	5.5	779
201	The human DEPhOsphorylation database DEPOD: a 2015 update. Nucleic Acids Research, 2015, 43, D531-D535.	6.5	65
202	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
203	Comprehensive discovery of DNA motifs in 349 human cells and tissues reveals new features of motifs. Nucleic Acids Research, 2015, 43, 74-83.	6.5	13
204	Recent findings and technological advances in phosphoproteomics for cells and tissues. Expert Review of Proteomics, 2015, 12, 469-487.	1.3	70
205	Integrated web visualizations for protein-protein interaction databases. BMC Bioinformatics, 2015, 16, 195.	1.2	55
206	Identification of shared and unique susceptibility pathways among cancers of the lung, breast, and prostate from genome-wide association studies and tissue-specific protein interactions. Human Molecular Genetics, 2015, 24, 7406-7420.	1.4	17
207	REGULATOR: a database of metazoan transcription factors and maternal factors for developmental studies. BMC Bioinformatics, 2015, 16, 114.	1.2	13
208	IMP 2.0: a multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks. Nucleic Acids Research, 2015, 43, W128-W133.	6.5	60
209	Reprint of "Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction" Computational Biology and Chemistry, 2015, 59, 123-138.	1.1	14
210	Identification of Caveolar Resident Proteins in Ventricular Myocytes Using a Quantitative Proteomic Approach: Dynamic Changes in Caveolar Composition Following Adrenoceptor Activation. Molecular and Cellular Proteomics, 2015, 14, 596-608.	2.5	25
211	DeAnnCNV: a tool for online detection and annotation of copy number variations from whole-exome sequencing data. Nucleic Acids Research, 2015, 43, W289-W294.	6.5	29
212	Computational Phosphorylation Network Reconstruction: Methods and Resources. Methods in Molecular Biology, 2015, 1306, 177-194.	0.4	2
213	Identifying dense subgraphs in protein-protein interaction network for gene selection from microarray data. Network Modeling Analysis in Health Informatics and Bioinformatics, 2015, 4, 1.	1.2	7
214	Identification of putative drug targets for human sperm-egg interaction defect using protein network approach. BMC Systems Biology, 2015, 9, 37.	3.0	5
215	Analysis of Differentially Expressed Genes Associated With Alzheimer's Disease Based on Bioinformatics Methods. American Journal of Alzheimer's Disease and Other Dementias, 2015, 30, 746-751.	0.9	5
216	Bioinformatics approaches for the functional interpretation of protein lists: From ontology term enrichment to network analysis. Proteomics, 2015, 15, 981-996.	1.3	27

#	ARTICLE	IF	CITATIONS
217	Proteinâ€“protein interaction predictions using text mining methods. <i>Methods</i> , 2015, 74, 47-53.	1.9	73
218	Network inference from AP-MS data: computational challenges and solutions. <i>Briefings in Bioinformatics</i> , 2015, 16, 658-674.	3.2	21
219	A Systems-Level Understanding of Cardiovascular Disease through Networks. , 2016, , 59-81.		3
220	PIPINO: A Software Package to Facilitate the Identification of Protein-Protein Interactions from Affinity Purification Mass Spectrometry Data. <i>BioMed Research International</i> , 2016, 2016, 1-13.	0.9	0
221	Prediction and Analysis of the Protein-Protein Interaction Networks for Chickens, Cattle, Dogs, Horses and Rabbits. <i>Current Bioinformatics</i> , 2016, 11, 131-142.	0.7	5
222	In Vivo Analysis of Proteinâ€“Protein Interactions with Bioluminescence Resonance Energy Transfer (BRET): Progress and Prospects. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1704.	1.8	37
223	A Network Pharmacology Approach to Uncover the Pharmacological Mechanism of XuanHuSuo Powder on Osteoarthritis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2016, 2016, 1-10.	0.5	49
224	A Quantitative Approach to Analyzing Genome Reductive Evolution Using Proteinâ€“Protein Interaction Networks: A Case Study of <i>Mycobacterium leprae</i> . <i>Frontiers in Genetics</i> , 2016, 7, 39.	1.1	11
225	Key Immune Events of the Pathomechanisms of Early Cardioembolic Stroke: Multi-Database Mining and Systems Biology Approach. <i>International Journal of Molecular Sciences</i> , 2016, 17, 305.	1.8	4
226	Identification of Toxic Pyrrolizidine Alkaloids and Their Common Hepatotoxicity Mechanism. <i>International Journal of Molecular Sciences</i> , 2016, 17, 318.	1.8	18
227	Reconstruction and Application of Proteinâ€“Protein Interaction Network. <i>International Journal of Molecular Sciences</i> , 2016, 17, 907.	1.8	67
228	Prediction of Proteinâ€“Protein Interactions by Evidence Combining Methods. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1946.	1.8	28
229	Clinical significance of mitofusin-2 and its signaling pathways in hepatocellular carcinoma. <i>World Journal of Surgical Oncology</i> , 2016, 14, 179.	0.8	20
230	WORMHOLE: Novel Least Diverged Ortholog Prediction through Machine Learning. <i>PLoS Computational Biology</i> , 2016, 12, e1005182.	1.5	21
231	DenHunt - A Comprehensive Database of the Intricate Network of Dengue-Human Interactions. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004965.	1.3	23
232	Correlative Gene Expression to Protective Seroconversion in Rift Valley Fever Vaccinates. <i>PLoS ONE</i> , 2016, 11, e0147027.	1.1	8
233	Integrative Analysis of Subcellular Quantitative Proteomics Studies Reveals Functional Cytoskeleton Membraneâ€“Lipid Raft Interactions in Cancer. <i>Journal of Proteome Research</i> , 2016, 15, 3451-3462.	1.8	15
234	Local Action with Global Impact: Highly Similar Infection Patterns of Human Viruses and Bacteriophages. <i>MSystems</i> , 2016, 1, .	1.7	8

#	ARTICLE	IF	CITATIONS
235	Propagation on Molecular Interaction Networks: Prediction of Effective Drug Combinations and Biomarkers in Cancer Treatment. <i>Current Pharmaceutical Design</i> , 2016, 22, 1-1.	0.9	2
236	A Network of Splice Isoforms for the Mouse. <i>Scientific Reports</i> , 2016, 6, 24507.	1.6	17
237	Understanding the roles of intrinsic disorder in subunits of hemoglobin and the disease process of sickle cell anemia. <i>Intrinsically Disordered Proteins</i> , 2016, 4, e1248273.	1.9	8
238	Semi-supervised graph cut algorithm for drug repositioning by integrating drug, disease and genomic associations. , 2016, , .		2
239	Co-expression network analyses identify functional modules associated with development and stress response in <i>Gossypium arboreum</i> . <i>Scientific Reports</i> , 2016, 6, 38436.	1.6	46
240	Gene expression profiles and protein-protein interaction networks in amyotrophic lateral sclerosis patients with C9orf72 mutation. <i>Orphanet Journal of Rare Diseases</i> , 2016, 11, 148.	1.2	38
241	Modern Proteomics – Sample Preparation, Analysis and Practical Applications. <i>Advances in Experimental Medicine and Biology</i> , 2016, , .	0.8	13
242	Bioinformatics Tools for Proteomics Data Interpretation. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 281-341.	0.8	20
243	An Atlas of the Human Kinome Reveals the Mutational Landscape Underlying Dysregulated Phosphorylation Cascades in Cancer. <i>Cancer Research</i> , 2016, 76, 1733-1745.	0.4	20
244	Protein-protein interactions among signaling pathways may become new therapeutic targets in liver cancer (Review). <i>Oncology Reports</i> , 2016, 35, 625-638.	1.2	8
245	Predicting Protein-Protein Interactions from the Molecular to the Proteome Level. <i>Chemical Reviews</i> , 2016, 116, 4884-4909.	23.0	289
246	Integrated interactions database: tissue-specific view of the human and model organism interactomes. <i>Nucleic Acids Research</i> , 2016, 44, D536-D541.	6.5	212
247	PlantPAN 2.0: an update of plant promoter analysis navigator for reconstructing transcriptional regulatory networks in plants. <i>Nucleic Acids Research</i> , 2016, 44, D1154-D1160.	6.5	336
248	Genome-wide inference of protein interaction network and its application to the study of crosstalk in <i>Arabidopsis</i> abscisic acid signaling. <i>Plant Physiology</i> , 2016, 171, pp.00057.2016.	2.3	27
249	A systems biology and proteomics-based approach identifies SRC and VEGFA as biomarkers in risk factor mediated coronary heart disease. <i>Molecular BioSystems</i> , 2016, 12, 2594-2604.	2.9	14
250	Network analysis and cross species comparison of protein-protein interaction networks of human, mouse and rat cytochrome P450 proteins that degrade xenobiotics. <i>Molecular BioSystems</i> , 2016, 12, 2119-2134.	2.9	11
251	The MIntAct Project and Molecular Interaction Databases. <i>Methods in Molecular Biology</i> , 2016, 1415, 55-69.	0.4	16
252	DNA-binding protects p53 from interactions with cofactors involved in transcription-independent functions. <i>Nucleic Acids Research</i> , 2016, 44, glw770.	6.5	40

#	ARTICLE	IF	CITATIONS
253	Markov random field based method to predict side effects. , 2016, , .		2
254	The epichaperome is an integrated chaperome network that facilitates tumour survival. Nature, 2016, 538, 397-401.	13.7	233
255	Discovery of functional module alignment. Neurocomputing, 2016, 206, 19-27.	3.5	1
256	Integrating phenotypic features and tissue-specific information to prioritize disease genes. Science China Information Sciences, 2016, 59, 1.	2.7	0
257	ModuleAlign: module-based global alignment of proteinâ€“protein interaction networks. Bioinformatics, 2016, 32, i658-i664.	1.8	34
258	InteractoMIX: a suite of computational tools to exploit interactomes in biological and clinical research. Biochemical Society Transactions, 2016, 44, 917-924.	1.6	3
259	Small-molecule binding sites to explore proteinâ€“protein interactions in the cancer proteome. Molecular BioSystems, 2016, 12, 3067-3087.	2.9	15
260	Gene Expression Analysis Through Network Biology: Bioinformatics Approaches. Advances in Biochemical Engineering/Biotechnology, 2016, 160, 15-32.	0.6	2
261	Rigid-Docking Approaches to Explore Proteinâ€“Protein Interaction Space. Advances in Biochemical Engineering/Biotechnology, 2016, 160, 33-55.	0.6	5
262	Identification of lncRNA functions in lung cancer based on associated protein-protein interaction modules. Scientific Reports, 2016, 6, 35939.	1.6	18
263	Defining the human sperm microtubulome: an integrated genomics approach<sup><xref ref-type="fn" rid="afn1"></xref></sup>. Biology of Reproduction, 2017, 96, 93-106.	1.2	15
264	Specificity of broad protein interaction surfaces for proteins with multiple binding partners. Biophysics and Physicobiology, 2016, 13, 105-115.	0.5	7
265	PROPER: global protein interaction network alignment through percolation matching. BMC Bioinformatics, 2016, 17, 527.	1.2	22
266	Comparing Alzheimerâ€™s and Parkinsonâ€™s diseases networks using graph communities structure. BMC Systems Biology, 2016, 10, 25.	3.0	28
267	APID interactomes: providing proteome-based interactomes with controlled quality for multiple species and derived networks. Nucleic Acids Research, 2016, 44, W529-W535.	6.5	112
268	Yeast two-hybrid screening identified WDR77 as a novel interacting partner of TSC22D2. Tumor Biology, 2016, 37, 12503-12512.	0.8	30
269	The principle of conformational signaling. Chemical Society Reviews, 2016, 45, 4252-4284.	18.7	46
270	Use of the BioGRID Database for Analysis of Yeast Protein and Genetic Interactions. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot088880.	0.2	23

#	ARTICLE	IF	CITATIONS
271	Lynx: a knowledge base and an analytical workbench for integrative medicine. <i>Nucleic Acids Research</i> , 2016, 44, D882-D887.	6.5	8
272	Integrated Genomic and Network-Based Analyses of Complex Diseases and Human Disease Network. <i>Journal of Genetics and Genomics</i> , 2016, 43, 349-367.	1.7	21
273	Protein-protein interactions in DNA mismatch repair. <i>DNA Repair</i> , 2016, 38, 50-57.	1.3	38
274	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.	0.8	7
275	Network stratification analysis for identifying function-specific network layers. <i>Molecular BioSystems</i> , 2016, 12, 1232-1240.	2.9	1
276	dbPTM 2016: 10-year anniversary of a resource for post-translational modification of proteins. <i>Nucleic Acids Research</i> , 2016, 44, D435-D446.	6.5	154
277	An integrative <i>C. elegans</i> protein-protein interaction network with reliability assessment based on a probabilistic graphical model. <i>Molecular BioSystems</i> , 2016, 12, 85-92.	2.9	12
278	Network-Assisted Disease Classification and Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2016, 1386, 353-374.	0.4	11
279	PPIM: A Protein-Protein Interaction Database for Maize. <i>Plant Physiology</i> , 2016, 170, 618-626.	2.3	85
280	Computational analysis of protein interaction networks for infectious diseases. <i>Briefings in Bioinformatics</i> , 2016, 17, 517-526.	3.2	63
281	Integration of quantitative proteomics data and interaction networks: Identification of dysregulated cellular functions during cancer progression. <i>Methods</i> , 2016, 93, 103-109.	1.9	6
282	An overview of bioinformatics methods for modeling biological pathways in yeast. <i>Briefings in Functional Genomics</i> , 2016, 15, 95-108.	1.3	18
283	SIGNOR: a database of causal relationships between biological entities. <i>Nucleic Acids Research</i> , 2016, 44, D548-D554.	6.5	243
284	Advances in computational approaches for prioritizing driver mutations and significantly mutated genes in cancer genomes. <i>Briefings in Bioinformatics</i> , 2016, 17, 642-656.	3.2	120
285	Acquisition of estrogen independence induces TOB1-related mechanisms supporting breast cancer cell proliferation. <i>Oncogene</i> , 2016, 35, 1643-1656.	2.6	29
286	PCID: A Novel Approach for Predicting Disease Comorbidity by Integrating Multi-Scale Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 678-686.	1.9	24
287	Cancer subtype prediction from a pathway-level perspective by using a support vector machine based on integrated gene expression and protein network. <i>Computer Methods and Programs in Biomedicine</i> , 2017, 141, 27-34.	2.6	15
288	Identifying Candidate Reprogramming Genes in Mouse Induced Pluripotent Stem Cells. <i>Stem Cell Reviews and Reports</i> , 2017, 13, 532-541.	5.6	1

#	ARTICLE	IF	CITATIONS
289	A computational interactome for prioritizing genes associated with complex agronomic traits in rice (<i>Oryza sativa</i>). <i>Plant Journal</i> , 2017, 90, 177-188.	2.8	44
290	Weighted Protein Interaction Network Analysis of Frontotemporal Dementia. <i>Journal of Proteome Research</i> , 2017, 16, 999-1013.	1.8	39
291	Using structural knowledge in the protein data bank to inform the search for potential host-microbe protein interactions in sequence space: application to <i>Mycobacterium tuberculosis</i> . <i>BMC Bioinformatics</i> , 2017, 18, 201.	1.2	14
292	Translational Bioinformatics and Drug Discovery. <i>Translational Medicine Research</i> , 2017, , 29-53.	0.0	1
293	Allosteric regulation of metabolism in cancer: endogenous mechanisms and considerations for drug design. <i>Current Opinion in Biotechnology</i> , 2017, 48, 102-110.	3.3	11
294	In silico polypharmacology of natural products. <i>Briefings in Bioinformatics</i> , 2018, 19, 1153-1171.	3.2	95
296	LncRNAs2Pathways: Identifying the pathways influenced by a set of lncRNAs of interest based on a global network propagation method. <i>Scientific Reports</i> , 2017, 7, 46566.	1.6	24
297	Architecture of the human interactome defines protein communities and disease networks. <i>Nature</i> , 2017, 545, 505-509.	13.7	1,190
298	Computational modeling of protein assemblies. <i>Current Opinion in Structural Biology</i> , 2017, 44, 179-189.	2.6	47
299	vhfRNAi: a web-platform for analysis of host genes involved in viral infections discovered by genome wide RNAi screens. <i>Molecular BioSystems</i> , 2017, 13, 1377-1387.	2.9	3
300	Drug voyager: a computational platform for exploring unintended drug action. <i>BMC Bioinformatics</i> , 2017, 18, 131.	1.2	8
302	Selecting optimal combinations of transcription factors to promote axon regeneration: Why mechanisms matter. <i>Neuroscience Letters</i> , 2017, 652, 64-73.	1.0	28
303	XTalkDB: a database of signaling pathway crosstalk. <i>Nucleic Acids Research</i> , 2017, 45, D432-D439.	6.5	21
304	HIPPIE v2.0: enhancing meaningfulness and reliability of protein-protein interaction networks. <i>Nucleic Acids Research</i> , 2017, 45, D408-D414.	6.5	401
305	Protein-protein interactions can be predicted using coiled coil co-evolution patterns. <i>Journal of Theoretical Biology</i> , 2017, 412, 198-203.	0.8	18
306	A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. <i>Molecular Cell</i> , 2017, 65, 347-360.	4.5	123
307	Exploring Plant Co-Expression and Gene-Gene Interactions with CORNET 3.0. <i>Methods in Molecular Biology</i> , 2017, 1533, 201-212.	0.4	11
308	Proteome Bioinformatics. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	5

#	ARTICLE	IF	CITATIONS
309	Network Tools for the Analysis of Proteomic Data. <i>Methods in Molecular Biology</i> , 2017, 1549, 177-197.	0.4	17
310	iFrag: A Protein-Protein Interface Prediction Server Based on Sequence Fragments. <i>Journal of Molecular Biology</i> , 2017, 429, 382-389.	2.0	33
311	Molecular mechanisms underlying gliomas and glioblastoma pathogenesis revealed by bioinformatics analysis of microarray data. <i>Medical Oncology</i> , 2017, 34, 182.	1.2	44
312	A genome-wide comparison of mesenchymal stem cells derived from human placenta and umbilical cord. <i>Taiwanese Journal of Obstetrics and Gynecology</i> , 2017, 56, 664-671.	0.5	9
313	Proteomics for Drug Discovery. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	4
314	Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. <i>Scientific Reports</i> , 2017, 7, 10480.	1.6	608
315	Characterization of developmental defects in the forebrain resulting from hyperactivated mTOR signaling by integrative analysis of transcriptomic and proteomic data. <i>Scientific Reports</i> , 2017, 7, 2826.	1.6	15
316	Genetic and functional characterization of disease associations explains comorbidity. <i>Scientific Reports</i> , 2017, 7, 6207.	1.6	28
317	Enriching Traditional Protein-protein Interaction Networks with Alternative Conformations of Proteins. <i>Scientific Reports</i> , 2017, 7, 7180.	1.6	15
318	Non-interacting proteins may resemble interacting proteins: prevalence and implications. <i>Scientific Reports</i> , 2017, 7, 40419.	1.6	12
319	Fusion of expression values and protein interaction information using multi-objective optimization for improving gene clustering. <i>Computers in Biology and Medicine</i> , 2017, 89, 31-43.	3.9	23
320	Bioinformatics Resources for Interpreting Proteomics Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2017, 1647, 267-295.	0.4	1
321	The computational prediction of protein assemblies. <i>Current Opinion in Structural Biology</i> , 2017, 46, 170-175.	2.6	4
322	HDNetDB: A Molecular Interaction Database for Network-Oriented Investigations into Huntington's Disease. <i>Scientific Reports</i> , 2017, 7, 5216.	1.6	20
323	Mechanisms of action of sacubitril/valsartan on cardiac remodeling: a systems biology approach. <i>Npj Systems Biology and Applications</i> , 2017, 3, 12.	1.4	96
324	Finding low-conductance sets with dense interactions (FLCD) for better protein complex prediction. <i>BMC Systems Biology</i> , 2017, 11, 22.	3.0	8
325	Intrinsic disorder in proteins involved in amyotrophic lateral sclerosis. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 1297-1318.	2.4	42
326	CD4-gp120 interaction interface - a gateway for HIV-1 infection in human: molecular network, modeling and docking studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 2631-2644.	2.0	5

#	ARTICLE	IF	CITATIONS
327	ccNET: Database of co-expression networks with functional modules for diploid and polyploid <i>Gossypium</i> . <i>Nucleic Acids Research</i> , 2017, 45, D1090-D1099.	6.5	89
328	Protein-protein interaction analysis to identify biomarker networks for endometriosis. <i>Experimental and Therapeutic Medicine</i> , 2017, 14, 4647-4654.	0.8	8
329	A hybrid protein-protein interaction triple extraction method for biomedical literature. , 2017, , .		4
330	Uncovering the relationship and mechanisms of Tartary buckwheat (<i>Fagopyrum tataricum</i>) and Type II diabetes, hypertension, and hyperlipidemia using a network pharmacology approach. <i>PeerJ</i> , 2017, 5, e4042.	0.9	19
331	Simplified Swarm Optimization-Based Function Module Detection in Protein-Protein Interaction Networks. <i>Applied Sciences (Switzerland)</i> , 2017, 7, 412.	1.3	6
332	Protein-Protein Interactions in Virus-Host Systems. <i>Frontiers in Microbiology</i> , 2017, 8, 1557.	1.5	113
333	Drug Target Protein-Protein Interaction Networks: A Systematic Perspective. <i>BioMed Research International</i> , 2017, 2017, 1-13.	0.9	70
334	A Novel Phosphorylation Site-Kinase Network-Based Method for the Accurate Prediction of Kinase-Substrate Relationships. <i>BioMed Research International</i> , 2017, 2017, 1-11.	0.9	9
335	Evaluation of epidermal growth factor receptor signaling effects in gastric cancer cell lines by detailed motility-focused phenotypic characterization linked with molecular analysis. <i>BMC Cancer</i> , 2017, 17, 845.	1.1	16
336	Investigation and identification of functional post-translational modification sites associated with drug binding and protein-protein interactions. <i>BMC Systems Biology</i> , 2017, 11, 132.	3.0	28
337	Predicting drug-disease interactions by semi-supervised graph cut algorithm and three-layer data integration. <i>BMC Medical Genomics</i> , 2017, 10, 79.	0.7	23
338	PCVMZM: Using the Probabilistic Classification Vector Machines Model Combined with a Zernike Moments Descriptor to Predict Protein-Protein Interactions from Protein Sequences. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1029.	1.8	61
339	Functional Analysis of Human Hub Proteins and Their Interactors Involved in the Intrinsic Disorder-Enriched Interactions. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2761.	1.8	85
340	The TissueNet v.2 database: A quantitative view of protein-protein interactions across human tissues. <i>Nucleic Acids Research</i> , 2017, 45, D427-D431.	6.5	55
341	TcoF-DB v2: update of the database of human and mouse transcription co-factors and transcription factor interactions. <i>Nucleic Acids Research</i> , 2017, 45, D145-D150.	6.5	63
342	Comparative Protein Interaction Network Analysis Identifies Shared and Distinct Functions for the Human ROCO Proteins. <i>Proteomics</i> , 2018, 18, e1700444.	1.3	34
343	Brain-specific functional relationship networks inform autism spectrum disorder gene prediction. <i>Translational Psychiatry</i> , 2018, 8, 56.	2.4	61
344	NIPS, a 3D network-integrated predictor of deleterious protein SAPs, and its application in cancer prognosis. <i>Scientific Reports</i> , 2018, 8, 6021.	1.6	1

#	ARTICLE	IF	CITATIONS
345	Gastric cancer biomarkers; A systems biology approach. <i>Biochemistry and Biophysics Reports</i> , 2018, 13, 141-146.	0.7	20
348	Neuregulin 1 discovered as a cleavage target for the HCV NS3/4A protease by a microfluidic membrane protein array. <i>New Biotechnology</i> , 2018, 45, 113-122.	2.4	1
349	Investigating the Network Basis of Negative Genetic Interactions in <i>Saccharomyces cerevisiae</i> with Integrated Biological Networks and Triplet Motif Analysis. <i>Journal of Proteome Research</i> , 2018, 17, 1014-1030.	1.8	4
350	Thermal proximity coaggregation for system-wide profiling of protein complex dynamics in cells. <i>Science</i> , 2018, 359, 1170-1177.	6.0	161
351	Discovering disease-associated genes in weighted protein-protein interaction networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2018, 496, 53-61.	1.2	9
352	Mapping the Polarity Interactome. <i>Journal of Molecular Biology</i> , 2018, 430, 3521-3544.	2.0	12
353	Interactome INSIDER: a structural interactome browser for genomic studies. <i>Nature Methods</i> , 2018, 15, 107-114.	9.0	133
354	The key genes underlying pathophysiology association between the type 2 diabetic and colorectal cancer. <i>Journal of Cellular Physiology</i> , 2018, 233, 8551-8557.	2.0	20
355	Repository corticotrophin injection exerts direct acute effects on human B cell gene expression distinct from the actions of glucocorticoids. <i>Clinical and Experimental Immunology</i> , 2018, 192, 68-81.	1.1	16
356	A review of computational approaches for analysis of hepatitis C virus-mediated liver diseases. <i>Briefings in Functional Genomics</i> , 2018, 17, 428-440.	1.3	3
357	<i>In silico</i> epigenetics of metal exposure and subclinical atherosclerosis in middle aged men: pilot results from the Aragon Workers Health Study. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2018, 373, 20170084.	1.8	18
358	A survey on Protein Protein Interactions (PPI) methods, databases, challenges and future directions. , 2018, , .		3
359	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.	0.8	46
360	Protein complex prediction by date hub removal. <i>Computational Biology and Chemistry</i> , 2018, 74, 407-419.	1.1	3
361	Cholangiocarcinoma-associated genes identified by integrative analysis of gene expression data. <i>Molecular Medicine Reports</i> , 2018, 17, 5744-5753.	1.1	6
362	Adding biological meaning to human protein-protein interactions identified by yeast two-hybrid screenings: A guide through bioinformatics tools. <i>Journal of Proteomics</i> , 2018, 171, 127-140.	1.2	9
363	Computational systems biology approaches for Parkinson's disease. <i>Cell and Tissue Research</i> , 2018, 373, 91-109.	1.5	19
364	Eukaryotic and prokaryotic promoter databases as valuable tools in exploring the regulation of gene transcription: a comprehensive overview. <i>Gene</i> , 2018, 644, 38-48.	1.0	12

#	ARTICLE	IF	CITATIONS
365	THANATOS: an integrative data resource of proteins and post-translational modifications in the regulation of autophagy. <i>Autophagy</i> , 2018, 14, 296-310.	4.3	41
366	Discerning molecular interactions: A comprehensive review on biomolecular interaction databases and network analysis tools. <i>Gene</i> , 2018, 642, 84-94.	1.0	117
367	Predicting Protein Interactions Using a Deep Learning Method-Stacked Sparse Autoencoder Combined with a Probabilistic Classification Vector Machine. <i>Complexity</i> , 2018, 2018, 1-12.	0.9	17
368	United neighborhood closeness centrality and orthology for predicting essential proteins. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 17, 1-1.	1.9	50
370	Influence of lithium in neuron-glia interaction in hippocampal neurons. , 2018, 97, 533-546.	0.0	0
371	A Network Pharmacology Approach to Uncover the Molecular Mechanisms of Herbal Formula Ban-Xia-Xie-Xin-Tang. <i>Evidence-based Complementary and Alternative Medicine</i> , 2018, 2018, 1-22.	0.5	40
372	Interpretation of an individual functional genomics experiment guided by massive public data. <i>Nature Methods</i> , 2018, 15, 1049-1052.	9.0	5
373	Network Pharmacology to Unveil the Biological Basis of Health-Strengthening Herbal Medicine in Cancer Treatment. <i>Cancers</i> , 2018, 10, 461.	1.7	83
374	Modeling and Simulating the Aerobic Carbon Metabolism of a Green Microalga Using Petri Nets and New Concepts of VANESA. <i>Journal of Integrative Bioinformatics</i> , 2018, 15, .	1.0	3
375	Shared genetic and epigenetic mechanisms between chronic periodontitis and oral squamous cell carcinoma. <i>Oral Oncology</i> , 2018, 86, 216-224.	0.8	32
376	Establishment of stably expandable induced myogenic stem cells by four transcription factors. <i>Cell Death and Disease</i> , 2018, 9, 1092.	2.7	22
377	Chromatographic separation strategies for precision mass spectrometry to study protein-protein interactions and protein phosphorylation. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018, 1102-1103, 96-108.	1.2	15
378	Network pharmacology-based strategy to investigate pharmacological mechanisms of Zuojinwan for treatment of gastritis. <i>BMC Complementary and Alternative Medicine</i> , 2018, 18, 292.	3.7	101
379	An integrative tissue-network approach to identify and test human disease genes. <i>Nature Biotechnology</i> , 2018, 36, 1091-1099.	9.4	54
380	Genomic data integration systematically biases interactome mapping. <i>PLoS Computational Biology</i> , 2018, 14, e1006474.	1.5	33
382	Functional signaling and gene regulatory networks between the oocyte and the surrounding cumulus cells. <i>BMC Genomics</i> , 2018, 19, 351.	1.2	49
383	Factors Associated with Heritable Pulmonary Arterial Hypertension Exert Convergent Actions on the miR-130/301-Vascular Matrix Feedback Loop. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2289.	1.8	24
384	Coupling Large-Scale Omics Data for Deciphering Systems Complexity. <i>RNA Technologies</i> , 2018, , 153-172.	0.2	2

#	ARTICLE	IF	CITATIONS
385	Prediction of Novel Drugs and Diseases for Hepatocellular Carcinoma Based on Multi-Source Simulated Annealing Based Random Walk. <i>Journal of Medical Systems</i> , 2018, 42, 188.	2.2	2
386	The UCSC Genome Browser database: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D762-D769.	6.5	476
387	Systems-level analysis of risk genes reveals the modular nature of schizophrenia. <i>Schizophrenia Research</i> , 2018, 201, 261-269.	1.1	20
388	Network-Based Disease Module Discovery by a Novel Seed Connector Algorithm with Pathobiological Implications. <i>Journal of Molecular Biology</i> , 2018, 430, 2939-2950.	2.0	41
389	Two-Hybrid Systems. <i>Methods in Molecular Biology</i> , 2018, , .	0.4	1
390	Analyses of Protein Interaction Networks Using Computational Tools. <i>Methods in Molecular Biology</i> , 2018, 1794, 97-117.	0.4	6
391	Urinary Proteome Analysis Identified Nephrilysin and VCAM as Proteins Involved in Diabetic Nephropathy. <i>Journal of Diabetes Research</i> , 2018, 2018, 1-12.	1.0	24
392	Human Interactomics: Comparative Analysis of Different Protein Interaction Resources and Construction of a Cancer Protein-Drug Bipartite Network. <i>Advances in Protein Chemistry and Structural Biology</i> , 2018, 111, 263-282.	1.0	10
393	UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 631-640.	3.6	341
395	A network-based zoning for parallel whole-cell simulation. <i>Bioinformatics</i> , 2019, 35, 88-94.	1.8	7
396	Computational Methods for Predicting Protein-Protein Interactions Using Various Protein Features. <i>Current Protocols in Protein Science</i> , 2018, 93, e62.	2.8	47
397	Hub Protein Controversy: Taking a Closer Look at Plant Stress Response Hubs. <i>Frontiers in Plant Science</i> , 2018, 9, 694.	1.7	75
398	The Disordered Landscape of the 20S Proteasome Substrates Reveals Tight Association with Phase Separated Granules. <i>Proteomics</i> , 2018, 18, e1800076.	1.3	32
399	An unsupervised machine learning method for discovering patient clusters based on genetic signatures. <i>Journal of Biomedical Informatics</i> , 2018, 85, 30-39.	2.5	71
400	Identification of Shared Molecular Signatures Indicate the Susceptibility of Endometriosis to Multiple Sclerosis. <i>Frontiers in Genetics</i> , 2018, 9, 42.	1.1	16
401	Identification of Central Regulators of Calcium Signaling and ECM-Receptor Interaction Genetically Associated With the Progression and Recurrence of Atrial Fibrillation. <i>Frontiers in Genetics</i> , 2018, 9, 162.	1.1	18
402	In silico approach in reveal traditional medicine plants pharmacological material basis. <i>Chinese Medicine</i> , 2018, 13, 33.	1.6	75
403	Integrating Rio1 activities discloses its nutrient-activated network in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2018, 46, 7586-7611.	6.5	19

#	ARTICLE	IF	CITATIONS
404	Network-based approach to prediction and population-based validation of in silico drug repurposing. Nature Communications, 2018, 9, 2691.	5.8	351
405	Computational Resources for Predicting Protein-Protein Interactions. Advances in Protein Chemistry and Structural Biology, 2018, 110, 251-275.	1.0	11
406	Evolution of In Silico Strategies for Protein-Protein Interaction Drug Discovery. Molecules, 2018, 23, 1963.	1.7	87
407	Brain region-dependent gene networks associated with selective breeding for increased voluntary wheel-running behavior. PLoS ONE, 2018, 13, e0201773.	1.1	13
408	Bioinformatics and genomic databases. Handbook of Clinical Neurology / Edited By P J Vinken and G W Bruyn, 2018, 147, 75-92.	1.0	15
409	Biological Databases. Translational Bioinformatics, 2018, , 303-337.	0.0	0
410	A systematic atlas of chaperome deregulation topologies across the human cancer landscape. PLoS Computational Biology, 2018, 14, e1005890.	1.5	46
411	Text Mining Resources for Bioinformatics. , 2019, , 1083-1092.		0
412	Exploring the functional impact of alternative splicing on human protein isoforms using available annotation sources. Briefings in Bioinformatics, 2019, 20, 1754-1768.	3.2	23
413	Network-Based Analysis for Biological Discovery. , 2019, , 283-291.		4
414	Genome Analysis - Identification of Genes Involved in Host-Pathogen Protein-Protein Interaction Networks. , 2019, , 410-424.		0
415	A survey of computational methods in protein-protein interaction networks. Annals of Operations Research, 2019, 276, 35-87.	2.6	19
416	Differential network analysis and protein-protein interaction study reveals active protein modules in glucocorticoid resistance for infant acute lymphoblastic leukemia. Molecular Medicine, 2019, 25, 36.	1.9	7
417	A genome-wide positioning systems network algorithm for in silico drug repurposing. Nature Communications, 2019, 10, 3476.	5.8	134
418	Protein-Protein Interactions in Candida albicans. Frontiers in Microbiology, 2019, 10, 1792.	1.5	12
419	Identification of important invasion and proliferation related genes in adrenocortical carcinoma. Medical Oncology, 2019, 36, 73.	1.2	19
420	Exploring the Molecular Mechanism of the Drug-Treated Breast Cancer Based on Gene Expression Microarray. Biomolecules, 2019, 9, 282.	1.8	15
421	AraPPINet: An Updated Interactome for the Analysis of Hormone Signaling Crosstalk in Arabidopsis thaliana. Frontiers in Plant Science, 2019, 10, 870.	1.7	12

#	ARTICLE	IF	CITATIONS
422	Proteomics and Non-proteomics Approaches to Study Stable and Transient Protein-Protein Interactions. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1140, 121-142.	0.8	3
423	AppleMDO: A Multi-Dimensional Omics Database for Apple Co-Expression Networks and Chromatin States. <i>Frontiers in Plant Science</i> , 2019, 10, 1333.	1.7	44
424	CSF1R inhibitor JNJ-40346527 attenuates microglial proliferation and neurodegeneration in P301S mice. <i>Brain</i> , 2019, 142, 3243-3264.	3.7	156
425	Comparing progression molecular mechanisms between lung adenocarcinoma and lung squamous cell carcinoma based on genetic and epigenetic networks: big data mining and genome-wide systems identification. <i>Oncotarget</i> , 2019, 10, 3760-3806.	0.8	12
426	Analyzing the regulation of miRNAs on protein-protein interaction network in Hodgkin lymphoma. <i>BMC Bioinformatics</i> , 2019, 20, 449.	1.2	2
427	A Survey of Gene Prioritization Tools for Mendelian and Complex Human Diseases. <i>Journal of Integrative Bioinformatics</i> , 2019, 16, .	1.0	25
428	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. <i>Nature Communications</i> , 2019, 10, 10.	5.8	193
429	A novel approach for disease comorbidity prediction using weighted association rule mining. <i>Journal of Ambient Intelligence and Humanized Computing</i> , 0, , 1.	3.3	15
430	EvoPPI 1.0: a Web Platform for Within- and Between-Species Multiple Interactome Comparisons and Application to Nine PolyQ Proteins Determining Neurodegenerative Diseases. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2019, 11, 45-56.	2.2	10
431	Identification of key modules and hub genes for small-cell lung carcinoma and large-cell neuroendocrine lung carcinoma by weighted gene co-expression network analysis of clinical tissue-proteomes. <i>PLoS ONE</i> , 2019, 14, e0217105.	1.1	24
432	Cardio-oncology: Network-Based Prediction of Cancer Therapy-Induced Cardiotoxicity. <i>Challenges and Advances in Computational Chemistry and Physics</i> , 2019, , 75-97.	0.6	1
433	Opioid-Induced Hyperalgesia Is Associated with Dysregulation of Circadian Rhythm and Adaptive Immune Pathways in the Mouse Trigeminal Ganglia and Nucleus Accumbens. <i>Molecular Neurobiology</i> , 2019, 56, 7929-7949.	1.9	34
434	Identification of Crucial Candidate Genes and Pathways in Glioblastoma Multiform by Bioinformatics Analysis. <i>Biomolecules</i> , 2019, 9, 201.	1.8	33
435	Systematic analysis of genes and diseases using PheWAS-Associated networks. <i>Computers in Biology and Medicine</i> , 2019, 109, 311-321.	3.9	7
436	Identification of LIFR, PIK3R1, and MMP12 as Novel Prognostic Signatures in Gallbladder Cancer Using Network-Based Module Analysis. <i>Frontiers in Oncology</i> , 2019, 9, 325.	1.3	15
437	Downregulated UCHL1 Accelerates Gentamicin-Induced Auditory Cell Death via Autophagy. <i>Molecular Neurobiology</i> , 2019, 56, 7433-7447.	1.9	12
438	Machine-Learning-Based Predictor of Humanâ€“Bacteria Proteinâ€“Protein Interactions by Incorporating Comprehensive Host-Network Properties. <i>Journal of Proteome Research</i> , 2019, 18, 2195-2205.	1.8	39
439	Proteinâ€“Protein Interaction Data, their Quality, and Major Public Databases. , 2019, , 151-192.		0

#	ARTICLE	IF	CITATIONS
440	Analysis of the Signatures of Cancer Stem Cells in Malignant Tumors Using Protein Interactomes and the STRING Database. , 2019, , 593-620.		0
441	An Improved Deep Forest Model for Predicting Self-Interacting Proteins From Protein Sequence Using Wavelet Transformation. <i>Frontiers in Genetics</i> , 2019, 10, 90.	1.1	31
442	PIMKL: Pathway-Induced Multiple Kernel Learning. <i>Npj Systems Biology and Applications</i> , 2019, 5, 8.	1.4	21
443	Context-specific interaction networks from vector representation of words. <i>Nature Machine Intelligence</i> , 2019, 1, 181-190.	8.3	9
444	Mining Featured Biomarkers Linked with Epithelial Ovarian Cancer Based on Bioinformatics. <i>Diagnostics</i> , 2019, 9, 39.	1.3	3
445	Identification of Important Invasion-Related Genes in Non-functional Pituitary Adenomas. <i>Journal of Molecular Neuroscience</i> , 2019, 68, 565-589.	1.1	8
446	Structural and Computational Characterization of Disease-Related Mutations Involved in Protein-Protein Interfaces. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1583.	1.8	17
447	Investigating Common Pathogenic Mechanisms between Homo sapiens and Different Strains of <i>Candida albicans</i> for Drug Design: Systems Biology Approach via Two-Sided NGS Data Identification. <i>Toxins</i> , 2019, 11, 119.	1.5	3
448	The human DEPhOsphorylation Database DEPOD: 2019 update. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	42
449	Hyperparameter Estimation in SVM with GPU Acceleration for Prediction of Protein-Protein Interactions. , 2019, , .		4
450	Leveraging SMOTE in a Two-Layer Model for Prediction of Protein-Protein Interactions. , 2019, , .		3
451	DualRank: multiplex network-based dual ranking for heterogeneous complex disease analysis. , 2019, , .		1
452	Sequence-Derived Markers of Drug Targets and Potentially Druggable Human Proteins. <i>Frontiers in Genetics</i> , 2019, 10, 1075.	1.1	14
453	The underlying pathophysiology association between the Type 2â€diabetic and hepatocellular carcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 10835-10841.	2.0	12
454	PPIExp: A Web-Based Platform for Integration and Visualization of Proteinâ€Protein Interaction Data and Spatiotemporal Proteomics Data. <i>Journal of Proteome Research</i> , 2019, 18, 633-641.	1.8	8
455	IID 2018 update: context-specific physical proteinâ€protein interactions in human, model organisms and domesticated species. <i>Nucleic Acids Research</i> , 2019, 47, D581-D589.	6.5	164
456	Structural disorder in the proteome and interactome of Alkhurma virus (ALKV). <i>Cellular and Molecular Life Sciences</i> , 2019, 76, 577-608.	2.4	17
457	Computational Prediction of Functional MicroRNAâ€mRNA Interactions. <i>Methods in Molecular Biology</i> , 2019, 1912, 175-196.	0.4	21

#	ARTICLE	IF	CITATIONS
458	Molecular subtyping of cancer and nomination of kinase candidates for inhibition with phosphoproteomics: Reanalysis of CPTAC ovarian cancer. <i>EBioMedicine</i> , 2019, 40, 305-317.	2.7	21
459	The epithelial zinc transporter <i>ZIP10</i> epigenetically regulates human epidermal homeostasis by modulating histone acetyltransferase activity. <i>British Journal of Dermatology</i> , 2019, 180, 869-880.	1.4	21
460	Identification of <i>CD28</i> and <i>PTEN</i> as novel prognostic markers for cervical cancer. <i>Journal of Cellular Physiology</i> , 2019, 234, 7004-7011.	2.0	13
461	Multomics analysis on DNA methylation and the expression of both messenger RNA and microRNA in lung adenocarcinoma. <i>Journal of Cellular Physiology</i> , 2019, 234, 7579-7586.	2.0	23
462	Identification of <i>TAF1</i> , <i>HNF4A</i> , and <i>CALM2</i> as potential therapeutic target genes for liver fibrosis. <i>Journal of Cellular Physiology</i> , 2019, 234, 9045-9051.	2.0	24
463	Integrating molecular networks with genetic variant interpretation for precision medicine. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2019, 11, e1443.	6.6	34
464	Prediction of protein-protein interactions between fungus (<i>Magnaporthe grisea</i>) and rice (<i>Oryza</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.2	21
465	GPS: Identification of disease genes by rank aggregation of multi-genomic scoring schemes. <i>Genomics</i> , 2019, 111, 612-618.	1.3	5
466	Classifying protein-protein interaction articles from biomedical literature using many relevant features and context-free grammar. <i>Journal of King Saud University - Computer and Information Sciences</i> , 2020, 32, 553-560.	2.7	1
467	Network-based methods for predicting essential genes or proteins: a survey. <i>Briefings in Bioinformatics</i> , 2020, 21, 566-583.	3.2	90
468	Protein complex prediction: A survey. <i>Genomics</i> , 2020, 112, 174-183.	1.3	38
469	Weighted matrix factorization on multi-relational data for LncRNA-disease association prediction. <i>Methods</i> , 2020, 173, 32-43.	1.9	36
470	Protein-protein interactions of human viruses. <i>Seminars in Cell and Developmental Biology</i> , 2020, 99, 31-39.	2.3	34
471	Protein-Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2020, , .	0.4	3
472	A paradigm shift in medicine: A comprehensive review of network-based approaches. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194416.	0.9	60
473	Identification of TAF1, SAT1, and ARHGEF9 as DNA methylation biomarkers for hepatocellular carcinoma. <i>Journal of Cellular Physiology</i> , 2020, 235, 611-618.	2.0	17
474	A comprehensive review and evaluation of computational methods for identifying protein complexes from protein-protein interaction networks. <i>Briefings in Bioinformatics</i> , 2020, 21, 1531-1548.	3.2	42
475	Infant Respiratory Syncytial Virus Bronchiolitis and Subsequent Risk of Pneumonia, Otitis Media, and Antibiotic Utilization. <i>Clinical Infectious Diseases</i> , 2020, 71, 211-214.	2.9	8

#	ARTICLE	IF	CITATIONS
476	Prediction and targeting of GPCR oligomer interfaces. <i>Progress in Molecular Biology and Translational Science</i> , 2020, 169, 105-149.	0.9	13
477	Identification of common key genes and pathways between type 1 diabetes and multiple sclerosis using transcriptome and interactome analysis. <i>Endocrine</i> , 2020, 68, 81-92.	1.1	21
478	Computational network biology: Data, models, and applications. <i>Physics Reports</i> , 2020, 846, 1-66.	10.3	126
479	The hybrid protein interactome contributes to rice heterosis as epistatic effects. <i>Plant Journal</i> , 2020, 102, 116-128.	2.8	10
480	Extended Human G-Protein Coupled Receptor Network: Cell-Type-Specific Analysis of G-Protein Coupled Receptor Signaling Pathways. <i>Journal of Proteome Research</i> , 2020, 19, 511-524.	1.8	12
481	Analysis of Differentially Expressed Genes in Coronary Artery Disease by Integrated Microarray Analysis. <i>Biomolecules</i> , 2020, 10, 35.	1.8	12
482	Tumor Microenvironment-Associated Immune-Related Genes for the Prognosis of Malignant Pleural Mesothelioma. <i>Frontiers in Oncology</i> , 2020, 10, 544789.	1.3	11
483	Molecular dynamics of the histamine H3 membrane receptor reveals different mechanisms of GPCR signal transduction. <i>Scientific Reports</i> , 2020, 10, 16889.	1.6	4
484	Clinical Validation of a Blood-Based Predictive Test for Stratification of Response to Tumor Necrosis Factor Inhibitor Therapies in Rheumatoid Arthritis Patients. <i>Network and Systems Medicine</i> , 2020, 3, 91-104.	2.7	26
485	UniProt-Related Documents (UniReD): assisting wet lab biologists in their quest on finding novel counterparts in a protein network. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa005.	1.5	8
486	LRRK2 mediates microglial neurotoxicity via NFATc2 in rodent models of synucleinopathies. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	49
487	Structure-based validation can drastically underestimate error rate in proteome-wide cross-linking mass spectrometry studies. <i>Nature Methods</i> , 2020, 17, 985-988.	9.0	23
488	Structure-Guided Design and In-Cell Target Profiling of a Cell-Active Target Engagement Probe for PARP Inhibitors. <i>ACS Chemical Biology</i> , 2020, 15, 325-333.	1.6	18
489	Harnessing endophenotypes and network medicine for Alzheimer's drug repurposing. <i>Medicinal Research Reviews</i> , 2020, 40, 2386-2426.	5.0	61
490	Bioinformatics analyses of significant genes, related pathways, and candidate diagnostic biomarkers and molecular targets in SARS-CoV-2/COVID-19. <i>Gene Reports</i> , 2020, 21, 100956.	0.4	29
491	Neuronal-Glial Interaction in a Triple-Transgenic Mouse Model of Alzheimer's Disease: Gene Ontology and Lithium Pathways. <i>Frontiers in Neuroscience</i> , 2020, 14, 579984.	1.4	7
492	Network-based modeling of drug effects on disease module in systemic sclerosis. <i>Scientific Reports</i> , 2020, 10, 13393.	1.6	9
493	Lasting and Sex-Dependent Impact of Maternal Immune Activation on Molecular Pathways of the Amygdala. <i>Frontiers in Neuroscience</i> , 2020, 14, 774.	1.4	25

#	ARTICLE	IF	CITATIONS
494	Network-based disease gene prioritization based on Protein-Protein Interaction Networks. Network Modeling Analysis in Health Informatics and Bioinformatics, 2020, 9, 1.	1.2	2
495	Complete Topological Mapping of a Cellular Protein Interactome Reveals Bow-Tie Motifs as Ubiquitous Connectors of Protein Complexes. Cell Reports, 2020, 31, 107763.	2.9	4
496	Using Random Forest Model Combined With Gabor Feature to Predict Protein-Protein Interaction From Protein Sequence. Evolutionary Bioinformatics, 2020, 16, 117693432093449.	0.6	9
497	Systems Biology Approaches to Understanding the Human Immune System. Frontiers in Immunology, 2020, 11, 1683.	2.2	23
498	HIME: Mining and Ensembling Heterogeneous Information for Protein-Protein Interactions Prediction. , 2020, , .		0
499	IHP-PING: generating integrated human protein-protein interaction networks on-the-fly. Briefings in Bioinformatics, 2021, 22, .	3.2	7
500	Investigating Core Signaling Pathways of Hepatitis B Virus Pathogenesis for Biomarkers Identification and Drug Discovery via Systems Biology and Deep Learning Method. Biomedicines, 2020, 8, 320.	1.4	5
501	A novel subnetwork representation learning method for uncovering disease-disease relationships. Methods, 2021, 192, 77-84.	1.9	17
502	MasterPATH: network analysis of functional genomics screening data. BMC Genomics, 2020, 21, 632.	1.2	3
503	Using Alias Sampling Strategy Based on Network Embeddings to Detect Protein Complexes. IEEE Access, 2020, 8, 211773-211783.	2.6	0
504	Differential Co-Expression Analyses Allow the Identification of Critical Signalling Pathways Altered during Tumour Transformation and Progression. International Journal of Molecular Sciences, 2020, 21, 9461.	1.8	27
505	Applications and advancements of FT-ICR-MS for interactome studies. Mass Spectrometry Reviews, 2022, 41, 248-261.	2.8	5
506	A massively parallel barcoded sequencing pipeline enables generation of the first ORFeome and interactome map for rice. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11836-11842.	3.3	16
507	APEX2S: A two-layer machine learning model for discovery of host-pathogen protein-protein interactions on cloud-based multiomics data. Concurrency Computation Practice and Experience, 2020, 32, e5846.	1.4	3
508	Integrated omics in Drosophila uncover a circadian kinome. Nature Communications, 2020, 11, 2710.	5.8	23
509	Abiotic-stress tolerance in plants-system biology approach. , 2020, , 577-609.		6
510	PINOT: an intuitive resource for integrating protein-protein interactions. Cell Communication and Signaling, 2020, 18, 92.	2.7	21
511	Dynamic rewiring of the human interactome by interferon signaling. Genome Biology, 2020, 21, 140.	3.8	25

#	ARTICLE	IF	CITATIONS
512	MIPPIE: the mouse integrated protein-protein interaction reference. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	14
513	Multilevel regulation of muscle-specific transcription factor hlh-1 during <i>Caenorhabditis elegans</i> embryogenesis. <i>Development Genes and Evolution</i> , 2020, 230, 265-278.	0.4	3
514	Systematic analysis of ovarian cancer platinum-resistance mechanisms via text mining. <i>Journal of Ovarian Research</i> , 2020, 13, 27.	1.3	14
515	A three-phase method for identifying functionally related protein groups in weighted PPI networks. <i>Computational Biology and Chemistry</i> , 2020, 86, 107246.	1.1	4
516	Selective Neuronal Vulnerability in Alzheimer's Disease: A Network-Based Analysis. <i>Neuron</i> , 2020, 107, 821-835.e12.	3.8	99
517	Computational Systems Analysis on Polycystic Ovarian Syndrome (PCOS). , 2020, , .		2
518	Exploring the Sirtuin Functionality in Ageing Through Human Protein Interaction Networks. <i>SN Computer Science</i> , 2020, 1, 1.	2.3	1
519	JUPPI: A Multi-Level Feature Based Method for PPI Prediction and a Refined Strategy for Performance Assessment. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 531-542.	1.9	4
520	Systematic comparison of the protein-protein interaction databases from a user's perspective. <i>Journal of Biomedical Informatics</i> , 2020, 103, 103380.	2.5	51
521	PlaPPIsite: a comprehensive resource for plant protein-protein interaction sites. <i>BMC Plant Biology</i> , 2020, 20, 61.	1.6	25
522	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.	1.9	10
523	CellPhoneDB: inferring cell-cell communication from combined expression of multi-subunit ligand-receptor complexes. <i>Nature Protocols</i> , 2020, 15, 1484-1506.	5.5	1,768
524	Genome-wide inference of the <i>Camponotus floridanus</i> protein-protein interaction network using homologous mapping and interacting domain profile pairs. <i>Scientific Reports</i> , 2020, 10, 2334.	1.6	9
525	Target identification among known drugs by deep learning from heterogeneous networks. <i>Chemical Science</i> , 2020, 11, 1775-1797.	3.7	193
526	Using Weighted Extreme Learning Machine Combined with Scale-invariant Feature Transform to Predict Protein-Protein Interactions from Protein Evolutionary Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 1-1.	1.9	14
527	Tracking the functional meaning of the human oral-microbiome protein-protein interactions. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020, 121, 199-235.	1.0	7
528	Using the MINT Database to Search Protein Interactions. <i>Current Protocols in Bioinformatics</i> , 2020, 69, e93.	25.8	13
529	MaXLinker: Proteome-wide Cross-link Identifications with High Specificity and Sensitivity. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 554-568.	2.5	38

#	ARTICLE	IF	CITATIONS
530	Bioinformatics for Renal and Urinary Proteomics: Call for Aggrandization. <i>International Journal of Molecular Sciences</i> , 2020, 21, 961.	1.8	9
531	WeiBI (web-based platform): Enriching integrated interaction network with increased coverage and functional proteins from genome-wide experimental OMICS data. <i>Scientific Reports</i> , 2020, 10, 5618.	1.6	3
532	Screening and identification of potential prognostic biomarkers in bladder urothelial carcinoma: Evidence from bioinformatics analysis. <i>Gene Reports</i> , 2020, 20, 100658.	0.4	0
533	Systematic evaluation of machine learning methods for identifying human-“pathogen protein”-protein interactions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	23
534	Ellagic acid and human cancers: a systems pharmacology and docking study to identify principal hub genes and main mechanisms of action. <i>Molecular Diversity</i> , 2021, 25, 333-349.	2.1	11
535	Emerging Methods and Resources for Biological-Interrogation of Neuropsychiatric Polygenic Signal. <i>Biological Psychiatry</i> , 2021, 89, 41-53.	0.7	38
536	Machine learning approaches and databases for prediction of drug-“target interaction: a survey paper. <i>Briefings in Bioinformatics</i> , 2021, 22, 247-269.	3.2	217
537	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. <i>Briefings in Bioinformatics</i> , 2021, 22, 1656-1678.	3.2	66
538	Integrative biomarker detection on high-dimensional gene expression data sets: a survey on prior knowledge approaches. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	12
539	Practical Applications of Computational Biology & Bioinformatics, 14th International Conference (PACBB 2020). <i>Advances in Intelligent Systems and Computing</i> , 2021, , .	0.5	2
540	Predicting disease-associated genes: Computational methods, databases, and evaluations. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2021, 11, e1383.	4.6	4
541	Protein-“protein interaction network: an emerging tool for understanding fish disease in aquaculture. <i>Reviews in Aquaculture</i> , 2021, 13, 156-177.	4.6	14
542	BastionHub: a universal platform for integrating and analyzing substrates secreted by Gram-negative bacteria. <i>Nucleic Acids Research</i> , 2021, 49, D651-D659.	6.5	34
543	The Integrin Interactome. <i>Methods in Molecular Biology</i> , 2021, , .	0.4	0
544	Biological network analysis with deep learning. <i>Briefings in Bioinformatics</i> , 2021, 22, 1515-1530.	3.2	98
545	Computational Analysis of Phosphoproteomics Data in Multi-“Omics Cancer Studies. <i>Proteomics</i> , 2021, 21, e1900312.	1.3	20
546	Computational Prediction of Protein-Protein Interactions in Plants Using Only Sequence Information. <i>Lecture Notes in Computer Science</i> , 2021, , 115-125.	1.0	1
547	Systems Medicine Design based on Systems Biology Approaches and Deep Neural Network for Gastric Cancer. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 3019-3031.	1.9	0

#	ARTICLE	IF	CITATIONS
548	New potential anticancer drug-like compounds for squamous cell lung cancer using transcriptome network analysis. <i>Informatics in Medicine Unlocked</i> , 2021, 24, 100599.	1.9	0
549	Common Network Pharmacology Software. , 2021, , 127-173.		0
550	A network-based deep learning methodology for stratification of tumor mutations. <i>Bioinformatics</i> , 2021, 37, 82-88.	1.8	10
551	Integrative analysis of transcriptomic data for identification of T-cell activation-related mRNA signatures indicative of preterm birth. <i>Scientific Reports</i> , 2021, 11, 2392.	1.6	3
552	HVIDB: a comprehensive database for human-virus protein-protein interactions. <i>Briefings in Bioinformatics</i> , 2021, 22, 832-844.	3.2	48
555	Databases for Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2021, 2361, 229-248.	0.4	6
556	A Dual Ranking Algorithm Based on the Multiplex Network for Heterogeneous Complex Disease Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1993-2002.	1.9	1
557	Getting to know each other: PPIMem, a novel approach for predicting transmembrane protein-protein complexes. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5184-5197.	1.9	5
558	Towards a Shared, Conceptual Model-Based Understanding of Proteins and Their Interactions. <i>IEEE Access</i> , 2021, 9, 73608-73623.	2.6	3
559	Open Science Resources for the Mass Spectrometry-Based Analysis of SARS-CoV-2. <i>Journal of Proteome Research</i> , 2021, 20, 1464-1475.	1.8	11
560	A systems-based method to repurpose marketed therapeutics for antiviral use: a SARS-CoV-2 case study. <i>Life Science Alliance</i> , 2021, 4, e202000904.	1.3	1
563	Human pathways in animal models: possibilities and limitations. <i>Nucleic Acids Research</i> , 2021, 49, 1859-1871.	6.5	35
564	Bioinformatic Analysis of Structure and Function of LIM Domains of Human Zyxin Family Proteins. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2647.	1.8	12
565	A survey on computational models for predicting protein-protein interactions. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	92
567	Identification of IFN-Induced Transmembrane Protein 1 With Prognostic Value in Pancreatic Cancer Using Network Module-Based Analysis. <i>Frontiers in Oncology</i> , 2021, 11, 626883.	1.3	5
568	Network-Based Analysis of Cognitive Impairment and Memory Deficits from Transcriptome Data. <i>Journal of Molecular Neuroscience</i> , 2021, 71, 2415-2428.	1.1	4
571	Identification of the Key Role of NF- κ B Signaling Pathway in the Treatment of Osteoarthritis With Bushen Zhuangjin Decoction, a Verification Based on Network Pharmacology Approach. <i>Frontiers in Pharmacology</i> , 2021, 12, 637273.	1.6	4
572	Predicting Protein-Protein Interactions Using Symmetric Logistic Matrix Factorization. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 1670-1682.	2.5	8

#	ARTICLE	IF	CITATIONS
573	An integrative drug repositioning framework discovered a potential therapeutic agent targeting COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 165.	7.1	89
574	Leveraging proteomics in orphan disease research: pitfalls and potential. <i>Expert Review of Proteomics</i> , 2021, 18, 315-327.	1.3	2
575	Prioritizing Molecular Biomarkers in Asthma and Respiratory Allergy Using Systems Biology. <i>Frontiers in Immunology</i> , 2021, 12, 640791.	2.2	8
577	NIDM: network impulsive dynamics on multiplex biological network for disease-gene prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	19
578	Network-based modeling of herb combinations in traditional Chinese medicine. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	62
579	Lysosome-targeted photodynamic treatment induces primary keratinocyte differentiation. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2021, 218, 112183.	1.7	2
580	Characterization of SNPs in RNF4 and their Implication In Cancer. , 2021, , .		0
581	Integrating protein networks and machine learning for disease stratification in the Hereditary Spastic Paraplegias. <i>IScience</i> , 2021, 24, 102484.	1.9	8
582	KEA3: improved kinase enrichment analysis via data integration. <i>Nucleic Acids Research</i> , 2021, 49, W304-W316.	6.5	55
583	A New Sequential Forward Feature Selection (SFFS) Algorithm for Mining Best Topological and Biological Features to Predict Protein Complexes from Protein-Protein Interaction Networks (PPINs). <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2021, 13, 371-388.	2.2	8
584	FunCoup 5: Functional Association Networks in All Domains of Life, Supporting Directed Links and Tissue-Specificity. <i>Journal of Molecular Biology</i> , 2021, 433, 166835.	2.0	25
585	Elucidation of the Mechanisms and Molecular Targets of Qishen Yiqi Formula for the Treatment of Pulmonary Arterial Hypertension using a Bioinformatics/Network Topology-based Strategy. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2021, 24, 701-715.	0.6	5
586	Drug Repurposing: A Network-based Approach to Amyotrophic Lateral Sclerosis. <i>Neurotherapeutics</i> , 2021, 18, 1678-1691.	2.1	24
587	Identification of Diagnostic Markers for Major Depressive Disorder Using Machine Learning Methods. <i>Frontiers in Neuroscience</i> , 2021, 15, 645998.	1.4	17
589	Network medicine links SARS-CoV-2/COVID-19 infection to brain microvascular injury and neuroinflammation in dementia-like cognitive impairment. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 110.	3.0	108
591	mPPI: a database extension to visualize structural interactome in a one-to-many manner. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	6
592	Proteomics based drug repositioning applied to improve in vitro fertilization implantation: an artificial intelligence model. <i>Systems Biology in Reproductive Medicine</i> , 2021, 67, 281-297.	1.0	1
593	Network-based analysis of virulence factors for uncovering <i>Aeromonas veronii</i> pathogenesis. <i>BMC Microbiology</i> , 2021, 21, 188.	1.3	5

#	ARTICLE	IF	CITATIONS
594	A comprehensive review of integrative pharmacology-based investigation: A paradigm shift in traditional Chinese medicine. <i>Acta Pharmaceutica Sinica B</i> , 2021, 11, 1379-1399.	5.7	61
595	Utilizing image and caption information for biomedical document classification. <i>Bioinformatics</i> , 2021, 37, i468-i476.	1.8	8
596	Enzymes in the Cholesterol Synthesis Pathway: Interactomics in the Cancer Context. <i>Biomedicines</i> , 2021, 9, 895.	1.4	22
597	Applications and analytical tools of cell communication based on ligand-receptor interactions at single cell level. <i>Cell and Bioscience</i> , 2021, 11, 121.	2.1	21
599	Multimodal single-cell omics analysis identifies epithelium-immune cell interactions and immune vulnerability associated with sex differences in COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 292.	7.1	13
600	CFTR Lifecycle Map—A Systems Medicine Model of CFTR Maturation to Predict Possible Active Compound Combinations. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7590.	1.8	6
601	An atlas of protein-protein interactions across mouse tissues. <i>Cell</i> , 2021, 184, 4073-4089.e17.	13.5	59
602	alfaNET: A Database of Alfalfa-Bacterial Stem Blight Protein-Protein Interactions Revealing the Molecular Features of the Disease-causing Bacteria. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8342.	1.8	7
604	Biomolecule and Bioentity Interaction Databases in Systems Biology: A Comprehensive Review. <i>Biomolecules</i> , 2021, 11, 1245.	1.8	17
605	Robust and accurate prediction of protein-protein interactions by exploiting evolutionary information. <i>Scientific Reports</i> , 2021, 11, 16910.	1.6	12
606	Tau Protein Interaction Partners and Their Roles in Alzheimer's Disease and Other Tauopathies. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9207.	1.8	50
607	Drug Discovery of Spinal Muscular Atrophy (SMA) from the Computational Perspective: A Comprehensive Review. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8962.	1.8	6
608	Identifying Protein Complexes With Clear Module Structure Using Pairwise Constraints in Protein Interaction Networks. <i>Frontiers in Genetics</i> , 2021, 12, 664786.	1.1	4
609	Revealing protein-protein interactions at the transcriptome scale by sequencing. <i>Molecular Cell</i> , 2021, 81, 4091-4103.e9.	4.5	28
610	Protein Interaction Network-based Deep Learning Framework for Identifying Disease-Associated Human Proteins. <i>Journal of Molecular Biology</i> , 2021, 433, 167149.	2.0	4
611	The protein-protein interaction network alignment using recurrent neural network. <i>Medical and Biological Engineering and Computing</i> , 2021, 59, 2263-2286.	1.6	3
614	PncsHub: a platform for annotating and analyzing non-classically secreted proteins in Gram-positive bacteria. <i>Nucleic Acids Research</i> , 2021, , .	6.5	4
615	Detecting Rewiring Events in Protein-Protein Interaction Networks Based on Transcriptomic Data. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	1.0	4

#	ARTICLE	IF	CITATIONS
617	Text Mining for Building Biomedical Networks Using Cancer as a Case Study. <i>Biomolecules</i> , 2021, 11, 1430.	1.8	7
618	Alternative Splicing Mechanisms Underlying Opioid-Induced Hyperalgesia. <i>Genes</i> , 2021, 12, 1570.	1.0	7
619	FordNet: Recommending traditional Chinese medicine formula via deep neural network integrating phenotype and molecule. <i>Pharmacological Research</i> , 2021, 173, 105752.	3.1	33
620	Identification of potential and novel target genes in pituitary prolactinoma by bioinformatics analysis. <i>AIMS Neuroscience</i> , 2021, 8, 254-283.	1.0	7
622	Gene Expression Microarray: Technical Fundamentals and Data Analysis. , 2021, , 291-312.		3
623	Pathogen and Host-Pathogen Protein Interactions Provide a Key to Identify Novel Drug Targets. , 2021, , 543-553.		3
624	Analyzing IDPs in Interactomes. <i>Methods in Molecular Biology</i> , 2020, 2141, 895-945.	0.4	24
625	Functional Bioinformatics Analyses of the Matrisome and Integrin Adhesome. <i>Methods in Molecular Biology</i> , 2021, 2217, 285-300.	0.4	8
626	Biological Information Extraction and Co-occurrence Analysis. <i>Methods in Molecular Biology</i> , 2014, 1159, 77-92.	0.4	19
627	Structure-Based Computational Approaches for Small-Molecule Modulation of Protein-Protein Interactions. <i>Methods in Molecular Biology</i> , 2015, 1278, 77-92.	0.4	5
628	Systems Analysis for Interpretation of Phosphoproteomics Data. <i>Methods in Molecular Biology</i> , 2016, 1355, 341-360.	0.4	15
629	Protein Bioinformatics Databases and Resources. <i>Methods in Molecular Biology</i> , 2017, 1558, 3-39.	0.4	154
630	Bioinformatics Analysis of Protein Phosphorylation in Plant Systems Biology Using P3DB. <i>Methods in Molecular Biology</i> , 2017, 1558, 127-138.	0.4	12
631	Informed Use of Proteinâ€“Protein Interaction Data: A Focus on the Integrated Interactions Database (IID). <i>Methods in Molecular Biology</i> , 2020, 2074, 125-134.	0.4	12
632	Generation and Interpretation of Context-Specific Human Proteinâ€“Protein Interaction Networks with HIPPIE. <i>Methods in Molecular Biology</i> , 2020, 2074, 135-144.	0.4	4
633	De Novo Pathway-Based Classification of Breast Cancer Subtypes. <i>Methods in Molecular Biology</i> , 2020, 2074, 201-213.	0.4	2
634	Computational Analysis of Virusâ€“Host Interactomes. <i>Methods in Molecular Biology</i> , 2013, 1064, 115-130.	0.4	3
635	Reverse Engineering Transcriptional Gene Networks. <i>Methods in Molecular Biology</i> , 2014, 1101, 179-196.	0.4	3

#	ARTICLE	IF	CITATIONS
636	Network Based Deciphering of the Mechanism of TCM. , 2014, , 81-96.		1
637	Comparative Genomics Approaches to Identifying Functionally Related Genes. Lecture Notes in Computer Science, 2014, , 1-24.	1.0	2
638	Proteomics Defines Protein Interaction Network of Signaling Pathways. Translational Bioinformatics, 2013, , 17-38.	0.0	1
639	Emerging Technologies for Gene Identification in Rare Diseases. Advances in Predictive, Preventive and Personalised Medicine, 2015, , 33-45.	0.6	1
640	Discovering the genes mediating the interactions between chronic respiratory diseases in the human interactome. Nature Communications, 2020, 11, 811.	5.8	25
641	Identification of cancer driver genes based on nucleotide context. Nature Genetics, 2020, 52, 208-218.	9.4	170
642	Mechanical forces induce an asthma gene signature in healthy airway epithelial cells. Scientific Reports, 2020, 10, 966.	1.6	34
643	<i>In silico</i> prediction of host-pathogen protein interactions in melioidosis pathogen <i>Burkholderia pseudomallei</i> and human reveals novel virulence factors and their targets. Briefings in Bioinformatics, 2021, 22, .	3.2	16
644	The IMEx coronavirus interactome: an evolving map of <i>Coronaviridae</i> host molecular interactions. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	34
645	PINA 3.0: mining cancer interactome. Nucleic Acids Research, 2021, 49, D1351-D1357.	6.5	26
663	MicroRNA-140-5p and SMURF1 regulate pulmonary arterial hypertension. Journal of Clinical Investigation, 2016, 126, 2495-2508.	3.9	119
664	NLPEI: A Novel Self-Interacting Protein Prediction Model Based on Natural Language Processing and Evolutionary Information. Evolutionary Bioinformatics, 2020, 16, 117693432098417.	0.6	3
665	Systems Biology Application to Decipher Mechanisms and Novel Biomarkers in CNS Trauma. , 2015, , 448-461.		12
666	PPI layouts: BioJS components for the display of Protein-Protein Interactions. F1000Research, 2014, 3, 50.	0.8	9
667	A network medicine approach to investigation and population-based validation of disease manifestations and drug repurposing for COVID-19. PLoS Biology, 2020, 18, e3000970.	2.6	139
668	Network-Based Interpretation of Diverse High-Throughput Datasets through the Omics Integrator Software Package. PLoS Computational Biology, 2016, 12, e1004879.	1.5	123
669	Transcriptional Alterations Related to Neuropathology and Clinical Manifestation of Alzheimer's Disease. PLoS ONE, 2012, 7, e48751.	1.1	39
670	Integrating Structure to Protein-Protein Interaction Networks That Drive Metastasis to Brain and Lung in Breast Cancer. PLoS ONE, 2013, 8, e81035.	1.1	38

#	ARTICLE	IF	CITATIONS
671	Expression Profiling of Mitochondrial Voltage-Dependent Anion Channel-1 Associated Genes Predicts Recurrence-Free Survival in Human Carcinomas. PLoS ONE, 2014, 9, e110094.	1.1	28
672	The Identification of Specific Methylation Patterns across Different Cancers. PLoS ONE, 2015, 10, e0120361.	1.1	48
673	Meta-Analysis of Large-Scale Toxicogenomic Data Finds Neuronal Regeneration Related Protein and Cathepsin D to Be Novel Biomarkers of Drug-Induced Toxicity. PLoS ONE, 2015, 10, e0136698.	1.1	16
674	Hepatitis C Virus Protein Interaction Network Analysis Based on Hepatocellular Carcinoma. PLoS ONE, 2016, 11, e0153882.	1.1	9
675	HTS-Net: An integrated regulome-interactome approach for establishing network regulation models in high-throughput screenings. PLoS ONE, 2017, 12, e0185400.	1.1	13
676	Knowledge-based bioinformatics for the study of mammalian oocytes. International Journal of Developmental Biology, 2012, 56, 859-866.	0.3	1
677	Genomic and proteomic data integration for comprehensive biodata search. EMBnet Journal, 2012, 18, 89.	0.2	1
678	Protein Function Easily Investigated by Genomics Data Mining Using the ProteINSIDE Online Tool. Genomics and Computational Biology, 2015, 1, 16.	0.7	12
679	Exploring the interactions of the RAS family in the human protein network and their potential implications in RAS-directed therapies. Oncotarget, 2016, 7, 75810-75826.	0.8	5
680	Genomic expression differences between cutaneous cells from red hair color individuals and black hair color individuals based on bioinformatic analysis. Oncotarget, 2017, 8, 11589-11599.	0.8	5
681	Systematic analysis of molecular mechanisms for HCC metastasis via text mining approach. Oncotarget, 2017, 8, 13909-13916.	0.8	6
682	Rapamycin-induced miR-21 promotes mitochondrial homeostasis and adaptation in mTORC1 activated cells. Oncotarget, 2017, 8, 64714-64727.	0.8	18
683	An Atlas of Protein-Protein Interactions Across Mammalian Tissues. SSRN Electronic Journal, 0, , .	0.4	8
684	Analysis of Protein-Protein Interaction Networks through Computational Approaches. Protein and Peptide Letters, 2020, 27, 265-278.	0.4	5
685	Mapping of Protein-Protein Interactions: Web-Based Resources for Revealing Interactomes. Current Medicinal Chemistry, 2019, 26, 3890-3910.	1.2	11
686	VANESA - a software application for the visualization and analysis of networks in system biology applications. Journal of Integrative Bioinformatics, 2014, 11, 239.	1.0	11
687	Protein â€“ Protein EtkileÄŸimi Tespit YÄŸntemleri, Veri TabanlarÄ± ve Veri GÃ¼venilirliÄŸi. European Journal of Science and Technology, 0, , 722-733.	0.5	2
688	Unfoldomics of prostate cancer: on the abundance and roles of intrinsically disordered proteins in prostate cancer. Asian Journal of Andrology, 2016, 18, 662.	0.8	6

#	ARTICLE	IF	CITATIONS
689	Strategy of systems biology for visualizing the “Black box” of traditional Chinese medicine. World Journal of Traditional Chinese Medicine, 2020, 6, 260.	0.9	8
690	The mechanisms of pei-yuan-tong-nao capsule as a therapeutic agent against cerebrovascular disease. World Journal of Traditional Chinese Medicine, 2020, 6, 331.	0.9	5
691	A Systems Level Comparison of Mycobacterium tuberculosis, Mycobacterium leprae and Mycobacterium smegmatis Based on Functional Interaction Network Analysis. Journal of Bacteriology & Parasitology, 2013, 04, .	0.2	9
692	Genocms - The Content Management System for Genes and Proteins. Journal of Proteomics and Bioinformatics, 2013, 06, .	0.4	1
693	The Software-Landscape in (Prote)Omic Research. Journal of Proteomics and Bioinformatics, 2015, 08, .	0.4	2
694	Novel genes underlying beta cell survival in metabolic stress. Bioinformation, 2013, 9, 37-41.	0.2	14
695	A computational interactome and functional annotation for the human proteome. ELife, 2016, 5, .	2.8	58
696	Human cytomegalovirus interactome analysis identifies degradation hubs, domain associations and viral protein functions. ELife, 2019, 8, .	2.8	84
697	ksrMKL: a novel method for identification of kinase “substrate relationships using multiple kernel learning. PeerJ, 2017, 5, e4182.	0.9	5
698	Hub-Based Reliable Gene Expression Algorithm to Classify ER+ and ER- Breast Cancer Subtypes. International Journal of Bioscience, Biochemistry, Bioinformatics (IJBBB), 2013, , 20-26.	0.2	1
699	Extraction of specific common genetic network of side effect pair, and prediction of side effects for a drug based on PPI network. Journal of the Korea Society of Computer and Information, 2016, 21, 115-123.	0.0	1
700	The IntAct database: efficient access to fine-grained molecular interaction data. Nucleic Acids Research, 2022, 50, D648-D653.	6.5	89
701	Low-density-lipoprotein-receptor-related protein 1 mediates Notch pathway activation. Developmental Cell, 2021, 56, 2902-2919.e8.	3.1	22
702	Computational methods for protein localization prediction. Computational and Structural Biotechnology Journal, 2021, 19, 5834-5844.	1.9	12
703	Metabolic endophenotype associated with right ventricular glucose uptake in pulmonary hypertension. Pulmonary Circulation, 2021, 11, 1-12.	0.8	5
704	Computational repurposing of therapeutic small molecules from cancer to pulmonary hypertension. Science Advances, 2021, 7, eabh3794.	4.7	16
705	GreeningDB: A Database of Host “Pathogen Protein” Protein Interactions and Annotation Features of the Bacteria Causing Huanglongbing HLB Disease. International Journal of Molecular Sciences, 2021, 22, 10897.	1.8	3
706	Network-driven analysis of human “Plasmodium falciparum interactome: processes for malaria drug discovery and extracting in silico targets. Malaria Journal, 2021, 20, 421.	0.8	7

#	ARTICLE	IF	CITATIONS
707	HUPHO: the human phosphatase portal. EMBnet Journal, 2012, 18, 55.	0.2	0
708	USING BIOBIN TO EXPLORE RARE VARIANT POPULATION STRATIFICATION. , 2012, , .		7
709	Network Biomarkers for Diagnosis and Prognosis of Human Prostate Cancer. Translational Bioinformatics, 2013, , 207-220.	0.0	1
710	Chapter 9: Characterization and Prediction of Human Protein-Protein Interactions. Science, Engineering, and Biology Informatics, 2014, , 237-261.	0.1	1
711	The Identification of Differentially Expressed Genes of Human Prolactinoma by Microarray. Cancer Genetics and Epigenetics, 0, , .	0.0	0
712	A Systems Biology Comparison of Ovarian Cancers Implicates Putative Somatic Driver Mutations through Protein-Protein Interaction Models. PLoS ONE, 2016, 11, e0163353.	1.1	5
720	Inference of Gene Regulatory Networks by Topological Prior Information and Data Integration. , 2019, , 265-304.		1
721	Computer aided analysis of disease linked protein networks. Bioinformatics, 2019, 15, 513-522.	0.2	2
723	Transcriptome and Network Dissection of Microsatellite Stable and Highly Instable Colorectal Cancer. Asian Pacific Journal of Cancer Prevention, 2019, 20, 2445-2454.	0.5	1
728	A Network-Based Methodology to Identify Subnetwork Markers for Diagnosis and Prognosis of Colorectal Cancer. Frontiers in Genetics, 2021, 12, 721949.	1.1	12
735	Systems Approach to Pathogenic Mechanism of Type 2 Diabetes and Drug Discovery Design Based on Deep Learning and Drug Design Specifications. International Journal of Molecular Sciences, 2021, 22, 166.	1.8	9
737	Protein-protein interactions at a glance: Protocols for the visualization of biomolecular interactions. Methods in Cell Biology, 2021, 166, 271-307.	0.5	2
738	Modelling Oxidative Stress Pathways. Computational Biology, 2020, , 277-300.	0.1	0
739	Predicting Protein-Protein Interactions from Protein Sequence Using Locality Preserving Projections and Rotation Forest. Lecture Notes in Computer Science, 2020, , 121-131.	1.0	0
740	Review of Computational Method for Protein Complex Identification Based on Dynamic PPI Networks. Computer Science and Application, 2020, 10, 2419-2424.	0.0	0
741	IID 2021: towards context-specific protein interaction analyses by increased coverage, enhanced annotation and enrichment analysis. Nucleic Acids Research, 2022, 50, D640-D647.	6.5	38
742	ConsensusPathDB 2022:Âmolecular interactions update as a resource for network biology. Nucleic Acids Research, 2022, 50, D587-D595.	6.5	32
745	Towards A More Effective Bidirectional LSTM-Based Learning Model for Human-Bacterium Protein-Protein Interactions. Advances in Intelligent Systems and Computing, 2021, , 91-101.	0.5	1

#	ARTICLE	IF	CITATIONS
746	Inference of Gene Regulatory Networks by Topological Prior Information and Data Integration. <i>Advances in Medical Technologies and Clinical Practice Book Series</i> , 0, , 1-51.	0.3	0
750	Construction of Protein Expression Network. <i>Methods in Molecular Biology</i> , 2021, 2189, 119-132.	0.4	1
751	Next-generation analysis of cataracts: determining knowledge driven gene-gene interactions using Biofilter, and gene-environment interactions using the PhenX Toolkit. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013, , 147-58.	0.7	13
752	Using BioBin to explore rare variant population stratification. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2013, , 332-43.	0.7	11
753	Proteomics and bioinformatics analysis of mouse hypothalamic neurogenesis with or without EPHX2 gene deletion. <i>International Journal of Clinical and Experimental Pathology</i> , 2015, 8, 12634-45.	0.5	3
754	Centrality Analysis of Protein-Protein Interaction Networks and Molecular Docking Prioritize Potential Drug-Targets in Type 1 Diabetes. <i>Iranian Journal of Pharmaceutical Research</i> , 2020, 19, 121-134.	0.3	4
755	Systems biology and big data analytics. , 2022, , 425-442.		0
756	In silico Methods for Identification of Potential Therapeutic Targets. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2022, 14, 285-310.	2.2	17
757	Protein-protein interactions: Methods, databases, and applications in virus-host study. <i>World Journal of Virology</i> , 2021, 10, 288-300.	1.3	10
758	Computational Network Pharmacology-Based Strategy to Capture Key Functional Components and Decode the Mechanism of Chai-Hu-Shu-Gan-San in Treating Depression. <i>Frontiers in Pharmacology</i> , 2021, 12, 782060.	1.6	6
759	Network pharmacology to unveil the mechanism of Moluodan in the treatment of chronic atrophic gastritis. <i>Phytomedicine</i> , 2022, 95, 153837.	2.3	73
761	Potential Molecular Mechanisms and Remdesivir Treatment for Acute Respiratory Syndrome Corona Virus 2 Infection/COVID 19 Through RNA Sequencing and Bioinformatics Analysis. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110673.	1.0	2
762	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2022, , .	3.2	1
763	Proteomic Approaches to Understand Plant Response to Abiotic Stresses. , 2021, , 351-383.		2
764	Better Link Prediction for Protein-Protein Interaction Networks. , 2020, , .		6
765	Biomedical data, computational methods and tools for evaluating disease-disease associations. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	12
766	Investigating the Role of Obesity in Prostate Cancer and Identifying Biomarkers for Drug Discovery: Systems Biology and Deep Learning Approaches. <i>Molecules</i> , 2022, 27, 900.	1.7	5
768	Unravelling Mechanisms of Doxorubicin-Induced Toxicity in 3D Human Intestinal Organoids. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1286.	1.8	12

#	ARTICLE	IF	CITATIONS
769	How Far Are We from the Completion of the Human Protein Interactome Reconstruction?. <i>Biomolecules</i> , 2022, 12, 140.	1.8	11
770	Simple But Efficacious Enrichment of Integral Membrane Proteins and Their Interactions for In-Depth Membrane Proteomics. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100206.	2.5	20
771	Plant Reactome and PubChem: The Plant Pathway and (Bio)Chemical Entity Knowledgebases. <i>Methods in Molecular Biology</i> , 2022, 2443, 511-525.	0.4	7
772	The Landscape of Aminoacyl-tRNA Synthetases Involved in Severe Acute Respiratory Syndrome Coronavirus 2 Infection. <i>Frontiers in Physiology</i> , 2021, 12, 818297.	1.3	10
773	Using ortholog information from multiple species to predict barley protein-protein interaction network. <i>Plant Gene</i> , 2022, , 100355.	1.4	1
774	Artificial intelligence approaches to human-microbiome protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2022, 73, 102328.	2.6	13
775	Network Medicine Framework for Identifying Drug Repurposing Opportunities for COVID-19. <i>ArXiv Org</i> , 2020, , .	1.2	4
776	Interactomes: Experimental and In Silico Approaches. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1346, 107-117.	0.8	1
777	Computational Systems Biology of Alfalfa Bacterial Blight Host-Pathogen Interactions: Uncovering the Complex Molecular Networks for Developing Durable Disease Resistant Crop. <i>Frontiers in Plant Science</i> , 2021, 12, 807354.	1.7	8
779	Antifungal activity of an artificial peptide aptamer SNP-D4 against <i>Fusarium oxysporum</i> . <i>PeerJ</i> , 2022, 10, e12756.	0.9	2
780	Deciphering the Host-Pathogen Interactome of the Wheat-Common Bunt System: A Step towards Enhanced Resilience in Next Generation Wheat. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2589.	1.8	7
781	Repurposing Multiple-Molecule Drugs for COVID-19-Associated Acute Respiratory Distress Syndrome and Non-Viral Acute Respiratory Distress Syndrome via a Systems Biology Approach and a DNN-DTI Model Based on Five Drug Design Specifications. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3649.	1.8	5
782	Exploring protein-protein interactions at the proteome level. <i>Structure</i> , 2022, 30, 462-475.	1.6	13
783	Protein interaction network analysis reveals genetic enrichment of immune system genes in frontotemporal dementia. <i>Neurobiology of Aging</i> , 2022, 116, 67-79.	1.5	2
784	Recent advances in predicting protein-protein interactions with the aid of artificial intelligence algorithms. <i>Current Opinion in Structural Biology</i> , 2022, 73, 102344.	2.6	24
785	Interpretation of network-based integration from multi-omics longitudinal data. <i>Nucleic Acids Research</i> , 2022, 50, e27-e27.	6.5	28
788	Comprehensive network medicine-based drug repositioning via integration of therapeutic efficacy and side effects. <i>Npj Systems Biology and Applications</i> , 2022, 8, 12.	1.4	9
789	An atlas of posttranslational modifications on RNA binding proteins. <i>Nucleic Acids Research</i> , 2022, 50, 4329-4339.	6.5	8

#	ARTICLE	IF	CITATIONS
811	Predicting Protein-Protein Interactions via Random Ferns with Evolutionary Matrix Representation. <i>Computational and Mathematical Methods in Medicine</i> , 2022, 2022, 1-11.	0.7	1
813	Identification of Potential Muscle Biomarkers in McArdle Disease: Insights from Muscle Proteome Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4650.	1.8	0
814	Bioinformatics-Based Approaches to Study Virus-Host Interactions During SARS-CoV-2 Infection. <i>Methods in Molecular Biology</i> , 2022, 2452, 197-212.	0.4	1
815	Proteome-wide prediction and analysis of the <i>Cryptosporidium parvum</i> protein-protein interaction network through integrative methods. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2322-2331.	1.9	2
817	ProFuMCell and ProModb: Web services for analyzing interaction-based functionally localized protein modules in a cell. <i>Journal of Molecular Modeling</i> , 2022, 28, .	0.8	0
818	WeCoNET: a host-pathogen interactome database for deciphering crucial molecular networks of wheat-common bunt cross-talk mechanisms. <i>Plant Methods</i> , 2022, 18, .	1.9	6
819	Deep learning frameworks for protein-protein interaction prediction. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3223-3233.	1.9	24
820	Graphical Data Representation and Analytics to Link the Potential Interaction for Lung Cancer Genes. <i>International Journal of Pharmaceutical Research and Allied Sciences</i> , 2022, 11, 62-72.	0.1	2
821	Repurposing Histaminergic Drugs in Multiple Sclerosis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6347.	1.8	5
822	An approach to cellular tropism of SARS-CoV-2 through protein-protein interaction and enrichment analysis. <i>Scientific Reports</i> , 2022, 12, .	1.6	3
824	Network assisted analysis of de novo variants using protein-protein interaction information identified 46 candidate genes for congenital heart disease. <i>PLoS Genetics</i> , 2022, 18, e1010252.	1.5	3
825	Systems Drug Discovery for Diffuse Large B Cell Lymphoma Based on Pathogenic Molecular Mechanism via Big Data Mining and Deep Learning Method. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6732.	1.8	2
827	In vitro ve in silico analizi ile metforminin meme t $\frac{1}{4}$ m $\frac{1}{4}$ h $\frac{1}{4}$ crelerinde protein profili $\frac{1}{4}$ zerindeki etkinli $\frac{1}{4}$ yi. <i>Ege Tıp Dergisi</i> , 0, , 215-224.	0.1	0
828	Deciphering the Crosstalk Mechanisms of Wheat-Stem Rust Pathosystem: Genome-Scale Prediction Unravels Novel Host Targets. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
829	PHILM2Web: A high-throughput database of macromolecular host-pathogen interactions on the Web. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	1
830	Transcriptomic analysis reveals pathophysiological relationship between chronic obstructive pulmonary disease (COPD) and periodontitis. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	8
831	Predicting Protein-Protein Interactions Based on Ensemble Learning-Based Model from Protein Sequence. <i>Biology</i> , 2022, 11, 995.	1.3	1
832	TritiKBdb: A Functional Annotation Resource for Deciphering the Complete Interaction Networks in Wheat-Karnal Bunt Pathosystem. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7455.	1.8	1

#	ARTICLE	IF	CITATIONS
833	Single-cell network biology characterizes cell type gene regulation for drug repurposing and phenotype prediction in Alzheimer's disease. <i>PLoS Computational Biology</i> , 2022, 18, e1010287.	1.5	9
834	Protocol for establishing a protein-protein interaction network using tandem affinity purification followed by mass spectrometry in mammalian cells. <i>STAR Protocols</i> , 2022, 3, 101569.	0.5	6
835	NTD-DR: Nonnegative tensor decomposition for drug repositioning. <i>PLoS ONE</i> , 2022, 17, e0270852.	1.1	3
837	ProteinPrompt: a webserver for predicting protein-protein interactions. <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	3
838	<i>Polypharmacology and Natural Products</i> , 2022, , 625-646.		1
839	<i>Polypharmacology in Drug Design and Discovery</i> —Basis for Rational Design of Multitarget Drugs. , 2022, , 397-533.		1
840	BioAlign: An Accurate Global PPI Network Alignment Algorithm. <i>Evolutionary Bioinformatics</i> , 2022, 18, 117693432211106.	0.6	2
841	TAIGET: A small-molecule target identification and annotation web server. <i>Frontiers in Pharmacology</i> , 0, 13, .	1.6	2
842	RTN2, a new member of circadian clock genes identified by database mining and bioinformatics prediction, is highly expressed in ovarian cancer. <i>Molecular Medicine Reports</i> , 2022, 26, .	1.1	0
843	DGHNE: network enhancement-based method in identifying disease-causing genes through a heterogeneous biomedical network. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	10
844	ADH-PPI: An attention-based deep hybrid model for protein-protein interaction prediction. <i>IScience</i> , 2022, 25, 105169.	1.9	6
845	Phosphoproteomics of extracellular vesicles integrated with multiomics analysis reveals novel kinase networks for lung cancer. <i>Molecular Carcinogenesis</i> , 2022, 61, 1116-1127.	1.3	2
847	TREAT: Therapeutic RNAs exploration inspired by artificial intelligence technology. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5680-5689.	1.9	1
848	A comprehensive SARS-CoV-2-human protein-protein interactome reveals COVID-19 pathobiology and potential host therapeutic targets. <i>Nature Biotechnology</i> , 2023, 41, 128-139.	9.4	61
849	EvoPPI 2: A Web and Local Platform for the Comparison of Protein-Protein Interaction Data from Multiple Sources from the Same and Distinct Species. <i>Lecture Notes in Networks and Systems</i> , 2023, , 101-110.	0.5	1
850	Lipopolysaccharide distinctively alters human microglia transcriptomes to resemble microglia from Alzheimer's disease mouse models. <i>DMM Disease Models and Mechanisms</i> , 2022, 15, .	1.2	7
851	Assessment of DDAH1 and DDAH2 Contributions to Psychiatric Disorders via In Silico Methods. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11902.	1.8	0
852	A network view of human immune system and virus-human interaction. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	0

#	ARTICLE	IF	CITATIONS
853	Identification of Potential Repurposable Drugs in Alzheimer's Disease Exploiting a Bioinformatics Analysis. <i>Journal of Personalized Medicine</i> , 2022, 12, 1731.	1.1	2
854	Revealing the characteristics of ZIKV infection through tissue-specific transcriptome sequencing analysis. <i>BMC Genomics</i> , 2022, 23, .	1.2	2
855	SIGNOR 3.0, the SIGNaling network open resource 3.0: 2022 update. <i>Nucleic Acids Research</i> , 2023, 51, D631-D637.	6.5	38
856	Computational Methods and Deep Learning for Elucidating Protein Interaction Networks. <i>Methods in Molecular Biology</i> , 2023, , 285-323.	0.4	1
858	Systems Drug Design for Muscle Invasive Bladder Cancer and Advanced Bladder Cancer by Genome-Wide Microarray Data and Deep Learning Method with Drug Design Specifications. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13869.	1.8	4
859	Multiple-Molecule Drug Repositioning for Disrupting Progression of SARS-CoV-2 Infection by Utilizing the Systems Biology Method through Host-Pathogen-Interactive Time Profile Data and DNN-Based DTI Model with Drug Design Specifications. <i>Stresses</i> , 2022, 2, 405-436.	1.8	2
860	Integrative network analysis interweaves the missing links in cardiomyopathy disease. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
863	Interpretable deep learning translation of GWAS and multi-omics findings to identify pathobiology and drug repurposing in Alzheimer's disease. <i>Cell Reports</i> , 2022, 41, 111717.	2.9	20
864	konnnect2prot: a web application to explore the protein properties in a functional protein-protein interaction network. <i>Bioinformatics</i> , 2023, 39, .	1.8	1
866	DrugRepo: a novel approach to repurposing drugs based on chemical and genomic features. <i>Scientific Reports</i> , 2022, 12, .	1.6	9
868	Graph embedding and Gaussian mixture variational autoencoder network for end-to-end analysis of single-cell RNA sequencing data. <i>Cell Reports Methods</i> , 2023, 3, 100382.	1.4	21
869	An efficient weighted network centrality approach for exploring mechanisms of action of the Ruellia herbal formula for treating rheumatoid arthritis. <i>Applied Network Science</i> , 2023, 8, .	0.8	1
870	Network pharmacology, a promising approach to reveal the pharmacology mechanism of Chinese medicine formula. <i>Journal of Ethnopharmacology</i> , 2023, 309, 116306.	2.0	89
871	Drug screening and biomarker gene investigation in cancer therapy through the human transcriptional regulatory network. <i>Computational and Structural Biotechnology Journal</i> , 2023, 21, 1557-1572.	1.9	4
872	HuCoPIA: An Atlas of Human vs. SARS-CoV-2 Interactome and the Comparative Analysis with Other Coronaviridae Family Viruses. <i>Viruses</i> , 2023, 15, 492.	1.5	1
873	Normalized L3-based link prediction in protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2023, 24, .	1.2	3
874	On the identification of potential novel therapeutic targets for spinocerebellar ataxia type 1 (SCA1) neurodegenerative disease using EvoPPI3. <i>Journal of Integrative Bioinformatics</i> , 2023, .	1.0	0
876	Deep learning-assisted prediction of protein-protein interactions in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2023, 114, 984-994.	2.8	2

#	ARTICLE	IF	CITATIONS
877	Systems biology tools for the identification of potential drug targets and biological markers effective for cancer therapeutics. , 2023, , 259-292.		0
882	Computational methods in the analysis of viral-host interactions. , 2023, , 285-302.		0
885	Proteomic applications in identifying protein-protein interactions. Advances in Protein Chemistry and Structural Biology, 2024, , 1-48.	1.0	0
897	Network Science and Machine Learning for Precision Nutrition. , 2024, , 367-402.		0