

Biological Network Exploration with Cytoscape 3

Current Protocols in Bioinformatics

47, 8.13.1-24

DOI: [10.1002/0471250953.bi0813s47](https://doi.org/10.1002/0471250953.bi0813s47)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Transcript co-variance with Nestin in two mouse genetic reference populations identifies Lef1 as a novel candidate regulator of neural precursor cell proliferation in the adult hippocampus. <i>Frontiers in Neuroscience</i> , 2014, 8, 418.	1.4	11
2	Fundamentals of protein interaction network mapping. <i>Molecular Systems Biology</i> , 2015, 11, 848.	3.2	226
3	Evolutionary rescue by compensatory mutations is constrained by genomic and environmental backgrounds. <i>Molecular Systems Biology</i> , 2015, 11, 832.	3.2	56
4	iRegulon and cisTarget: Reconstructing Regulatory Networks Using Motif and Track Enrichment. <i>Current Protocols in Bioinformatics</i> , 2015, 52, 2.16.1-2.16.39.	25.8	35
5	High-throughput transcriptomics reveals common and strain-specific responses of human macrophages to infection with <i>Mycobacterium abscessus</i> Smooth and Rough variants. <i>BMC Genomics</i> , 2015, 16, 1046.	1.2	13
6	The Mechanism Research of Qishen Yiqi Formula by Module-Network Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2015, 2015, 1-12.	0.5	3
7	Potential role of lncRNA cyp2c91 protein interactions on diseases of the immune system. <i>Frontiers in Genetics</i> , 2015, 6, 255.	1.1	30
8	Merging and scoring molecular interactions utilising existing community standards: tools, use-cases and a case study. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bau131-bau131.	1.4	53
9	Scoring Large-Scale Affinity Purification Mass Spectrometry Datasets with MiST. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 8.19.1-8.19.16.	25.8	58
10	Temporal Dynamics of Intrahost Molecular Evolution for a Plant RNA Virus. <i>Molecular Biology and Evolution</i> , 2015, 32, 1132-1147.	3.5	33
11	Systems biologic analysis of T regulatory cells genetic pathways in murine primary biliary cirrhosis. <i>Journal of Autoimmunity</i> , 2015, 59, 26-37.	3.0	45
12	Small RNA Transcriptome of the Oral Microbiome during Periodontitis Progression. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6688-6699.	1.4	28
13	Gene pathway development in human epicardial adipose tissue during early life. <i>JCI Insight</i> , 2016, 1, e87460.	2.3	20
14	Significant Modules and Biological Processes between Active Components of <i>Salvia miltiorrhiza</i> Depside Salt and Aspirin. <i>Evidence-based Complementary and Alternative Medicine</i> , 2016, 2016, 1-10.	0.5	2
15	AcsF Catalyzes the ATP-dependent Insertion of Nickel into the Ni ₂ S ₂ [4Fe4S] Cluster of Acetyl-CoA Synthase. <i>Journal of Biological Chemistry</i> , 2016, 291, 18129-18138.	1.6	17
16	Dynamic and modular gene regulatory networks drive the development of gametogenesis. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw056.	3.2	4
17	Identification of miRNAs and their targets involved in the secondary metabolic pathways of <i>Mentha</i> spp.. <i>Computational Biology and Chemistry</i> , 2016, 64, 154-162.	1.1	58
18	Enhancing Multiple Routing Configurations through systematic analysis of topological characteristics. <i>International Journal of Network Management</i> , 2016, 26, 176-198.	1.4	1

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19	MBPpred: Proteome-wide detection of membrane lipid-binding proteins using profile Hidden Markov Models. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 747-754.	1.1	22
20	Transcriptome-wide sequencing provides insights into geocarpy in peanut (<i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2016, 14, 1215-1224.	4.1	30
21	Metabolites involved in glycolysis and amino acid metabolism are altered in short children born small for gestational age. <i>Pediatric Research</i> , 2016, 80, 299-305.	1.1	6
22	Diurnal Regulation of Cellular Processes in the Cyanobacterium <i>Synechocystis</i> sp. Strain PCC 6803: Insights from Transcriptomic, Fluxomic, and Physiological Analyses. <i>MBio</i> , 2016, 7, .	1.8	84
23	High-resolution metabolomics of occupational exposure to trichloroethylene. <i>International Journal of Epidemiology</i> , 2016, 45, 1517-1527.	0.9	87
24	A systems biology-led insight into the role of the proteome in neurodegenerative diseases. <i>Expert Review of Proteomics</i> , 2016, 13, 845-855.	1.3	22
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26	Lifestyle chemistries from phones for individual profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7645-E7654.	3.3	55
27	An expression based REST signature predicts patient survival and therapeutic response for glioblastoma multiforme. <i>Scientific Reports</i> , 2016, 6, 34556.	1.6	14
28	SorghumFDB: sorghum functional genomics database with multidimensional network analysis. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw099.	1.4	47
29	Metabolic Pathways and Networks Associated With Tobacco Use in Military Personnel. <i>Journal of Occupational and Environmental Medicine</i> , 2016, 58, S111-S116.	0.9	28
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31	Protein-glycosaminoglycan interaction networks: Focus on heparan sulfate. <i>Perspectives in Science</i> , 2017, 11, 62-69.	0.6	13
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33	A new genome-mining tool redefines the lasso peptide biosynthetic landscape. <i>Nature Chemical Biology</i> , 2017, 13, 470-478.	3.9	346
34	Fingolimod alters the transcriptome profile of circulating CD4+ cells in multiple sclerosis. <i>Scientific Reports</i> , 2017, 7, 42087.	1.6	37
35	Phosphoproteome analysis reveals a critical role for hedgehog signalling in osteoblast morphological transitions. <i>Bone</i> , 2017, 103, 55-63.	1.4	28
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37	Identification and interaction analysis of key genes and microRNAs in hepatocellular carcinoma by bioinformatics analysis. <i>World Journal of Surgical Oncology</i> , 2017, 15, 63.	0.8	41
38	The pangenome of the genus <i>Clostridium</i> . <i>Environmental Microbiology</i> , 2017, 19, 2588-2603.	1.8	43
39	Systematic classification of the His-Me finger superfamily. <i>Nucleic Acids Research</i> , 2017, 45, 11479-11494.	6.5	22
40	Genome-wide integrative analysis identified SNP-miRNA-mRNA interaction networks in peripheral blood mononuclear cells. <i>Epigenomics</i> , 2017, 9, 1287-1298.	1.0	5
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45	DTNI: a novel toxicogenomics data analysis tool for identifying the molecular mechanisms underlying the adverse effects of toxic compounds. <i>Archives of Toxicology</i> , 2017, 91, 2343-2352.	1.9	16
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47	Gene expression profiling and bioinformatics analysis of hereditary gingival fibromatosis. <i>Biomedical Reports</i> , 2017, 8, 133-137.	0.9	11
48	Proteomic View of the Crosstalk between <i>Lactobacillus mucosae</i> and Intestinal Epithelial Cells in Co-culture Revealed by Q Exactive-Based Quantitative Proteomics. <i>Frontiers in Microbiology</i> , 2017, 8, 2459.	1.5	19
49	Identification of Linkages between EDCs in Personal Care Products and Breast Cancer through Data Integration Combined with Gene Network Analysis. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 1158.	1.2	6
51	Comprehensive list of SUMO targets in <i>Caenorhabditis elegans</i> and its implication for evolutionary conservation of SUMO signaling. <i>Scientific Reports</i> , 2018, 8, 1139.	1.6	18
52	LitPathExplorer: a confidence-based visual text analytics tool for exploring literature-enriched pathway models. <i>Bioinformatics</i> , 2018, 34, 1389-1397.	1.8	4
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55	Gancao-Gansui combination impacts gut microbiota diversity and related metabolic functions. <i>Journal of Ethnopharmacology</i> , 2018, 214, 71-82.	2.0	48

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57	Potential of <i>Oryza officinalis</i> to augment the cold tolerance genetic mechanisms of <i>Oryza sativa</i> by network complementation. <i>Scientific Reports</i> , 2018, 8, 16346.	1.6	32
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60	Bioinformatics analysis of key differentially expressed genes in well and poorly differentiated endometrial carcinoma. <i>Molecular Medicine Reports</i> , 2018, 18, 467-476.	1.1	6
61	A three-long non-coding RNA-expression-based risk score system can better predict both overall and recurrence-free survival in patients with small hepatocellular carcinoma. <i>Aging</i> , 2018, 10, 1627-1639.	1.4	43
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64	Heterologous Hsp90 promotes phenotypic diversity through network evolution. <i>PLoS Biology</i> , 2018, 16, e2006450.	2.6	24
65	Gene's hubs in retinal diseases: A retinal disease network. <i>Heliyon</i> , 2018, 4, e00867.	1.4	7
66	A Six-LncRNA Expression Signature Associated with Prognosis of Colorectal Cancer Patients. <i>Cellular Physiology and Biochemistry</i> , 2018, 50, 1882-1890.	1.1	18
67	Identification of potential genes and pathways for response prediction of neoadjuvant chemoradiotherapy in patients with rectal cancer by systemic biological analysis. <i>Oncology Letters</i> , 2018, 17, 492-501.	0.8	1
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71	Profiles of alternative splicing in colorectal cancer and their clinical significance: A study based on large-scale sequencing data. <i>EBioMedicine</i> , 2018, 36, 183-195.	2.7	123
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73	Molecular investigation to RNA and protein based interaction induced <i>in vivo</i> biocompatibility of phytofabricated AuNP with embryonic zebrafish. <i>Artificial Cells, Nanomedicine and Biotechnology</i> , 2018, 46, 671-684.	1.9	34
74	Impact of worker emigration on HIV epidemics in labour export areas: a molecular epidemiology investigation in Guangyuan, China. <i>Scientific Reports</i> , 2018, 8, 16046.	1.6	16

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75	Risk assessment model constructed by differentially expressed lncRNAs for the prognosis of glioma. <i>Oncology Reports</i> , 2018, 40, 2467-2476.	1.2	6
76	Continuous cropping tobacco caused variance of chemical properties and structure of bacterial network in soils. <i>Land Degradation and Development</i> , 2018, 29, 4106-4120.	1.8	85
77	Differential Expression of Coding and Long Noncoding RNAs in Keratoconus-Affected Corneas. , 2018, 59, 2717.		45
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82	Melittin Constrains the Expression of Identified Key Genes Associated with Bladder Cancer. <i>Journal of Immunology Research</i> , 2018, 2018, 1-16.	0.9	10
83	Wild tomato endosperm transcriptomes reveal common roles of genomic imprinting in both nuclear and cellular endosperm. <i>Plant Journal</i> , 2018, 95, 1084-1101.	2.8	38
84	Expression profile of microRNAs following bone marrow-derived mesenchymal stem cell treatment in lipopolysaccharide-induced acute lung injury. <i>Experimental and Therapeutic Medicine</i> , 2018, 15, 5495-5502.	0.8	20
85	The Synergistic Combination of Everolimus and Paroxetine Exerts Post-ischemic Neuroprotection In Vitro. <i>Cellular and Molecular Neurobiology</i> , 2018, 38, 1383-1397.	1.7	3
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87	Metabolomics Investigation of an Association of Induced Features and Corresponding Fungus during the Co-culture of <i>Trametes versicolor</i> and <i>Ganoderma applanatum</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2647.	1.5	37
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92	Identification and interaction analysis of key genes and microRNAs in atopic dermatitis by bioinformatics analysis. <i>Clinical and Experimental Dermatology</i> , 2019, 44, 257-264.	0.6	23

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93	Co-occurrence of Anaerobes in Human Chronic Wounds. <i>Microbial Ecology</i> , 2019, 77, 808-820.	1.4	40
94	Identification of a key candidate gene's phenotype network mediated by glycyrrhizic acid using pharmacogenomic analysis. <i>Molecular Medicine Reports</i> , 2019, 20, 2657-2666.	1.1	1
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96	Identification of Potential Immune-Related circRNA-miRNA-mRNA Regulatory Network in Intestine of <i>Paralichthys olivaceus</i> During <i>Edwardsiella tarda</i> Infection. <i>Frontiers in Genetics</i> , 2019, 10, 731.	1.1	49
97	Depicting the Core Transcriptome Modulating Multiple Abiotic Stresses Responses in Sesame (<i>Sesamum</i>) Tj ETQq0,0,0 rgBT /Overlock 1	1.8	45
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100	Construction and analysis of degradome-dependent microRNA regulatory networks in soybean. <i>BMC Genomics</i> , 2019, 20, 534.	1.2	12
101	<p>Bioinformatics analysis of molecular genetic targets and key pathways for hepatocellular carcinoma</p>. <i>OncoTargets and Therapy</i> , 2019, Volume 12, 5153-5162.	1.0	18
102	An integrated approach for mining precise RNA-based cervical cancer staging biomarkers. <i>Gene</i> , 2019, 712, 143961.	1.0	24
103	ScCobB2-mediated Lysine Desuccinylation Regulates Protein Biosynthesis and Carbon Metabolism in <i>Streptomyces coelicolor</i> *[S]. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2003-2017.	2.5	16
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105	Identification and Interaction Analysis of Key Genes and MicroRNAs in Systemic Sclerosis by Bioinformatics Approaches. <i>Current Medical Science</i> , 2019, 39, 645-652.	0.7	8
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107	Core regulon of the global anaerobic regulator Anr targets central metabolism functions in <i>Pseudomonas</i> species. <i>Scientific Reports</i> , 2019, 9, 9065.	1.6	22
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109	Potential protein biomarkers for systemic lupus erythematosus determined by bioinformatics analysis. <i>Computational Biology and Chemistry</i> , 2019, 83, 107135.	1.1	14
110	Identification of key candidate genes and molecular pathways in white fat browning: an anti-obesity drug discovery based on computational biology. <i>Human Genomics</i> , 2019, 13, 55.	1.4	8

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112	Transcriptomic and metabolomic profiling provide novel insights into fruit development and flesh coloration in <i>Prunus mira</i> Koehne, a special wild peach species. <i>BMC Plant Biology</i> , 2019, 19, 463.	1.6	45
113	Seasonal Dynamics of Algae-Infecting Viruses and Their Inferred Interactions with Protists. <i>Viruses</i> , 2019, 11, 1043.	1.5	10
114	Exploring the Molecular Mechanism underlying the Stable Purple-Red Leaf Phenotype in <i>Lagerstroemia indica</i> cv. Ebony Embers. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5636.	1.8	23
115	LINC00460 Hypomethylation Promotes Metastasis in Colorectal Carcinoma. <i>Frontiers in Genetics</i> , 2019, 10, 880.	1.1	23
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118	Integrated Analysis of Oncogenic Networks in Colorectal Cancer Identifies <i>GUCA2A</i> as a Molecular Marker. <i>Biochemistry Research International</i> , 2019, 2019, 1-13.	1.5	24
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125	Bladder cancer stage-associated hub genes revealed by WGCNA co-expression network analysis. <i>Hereditas</i> , 2019, 156, 7.	0.5	79
126	A Soluble Metabolon Synthesizes the Isoprenoid Lipid Ubiquinone. <i>Cell Chemical Biology</i> , 2019, 26, 482-492.e7.	2.5	46
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128	Identification of hub genes and therapeutic drugs in esophageal squamous cell carcinoma based on integrated bioinformatics strategy. <i>Cancer Cell International</i> , 2019, 19, 142.	1.8	21

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131	What Changed on the Folliculogenesis in the Process of Mouse Ovarian Aging?. BioMed Research International, 2019, 2019, 1-10.	0.9	5
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138	Bioinformatic Mapping of Radical S-Adenosylmethionine-Dependent Ribosomally Synthesized and Post-Translationally Modified Peptides Identifies New C ¹ , C ² , and C ³ -Linked Thioether-Containing Peptides. Journal of the American Chemical Society, 2019, 141, 8228-8238.	6.6	123
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145	Identification of Novel Interaction Partners of Ets-1: Focus on DNA Repair. Genes, 2019, 10, 206.	1.0	1
146	NetworkAnalyst 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis. Nucleic Acids Research, 2019, 47, W234-W241.	6.5	1,191

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148	Circular RNA circVAPA is up-regulated and exerts oncogenic properties by sponging miR-101 in colorectal cancer. <i>Biomedicine and Pharmacotherapy</i> , 2019, 112, 108611.	2.5	90
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151	Multigenerational metabolic profiling in the Michigan PBB registry. <i>Environmental Research</i> , 2019, 172, 182-193.	3.7	17
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153	A Network Pharmacology Approach for the Identification of Common Mechanisms of Drug-induced Peripheral Neuropathy. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2019, 8, 211-219.	1.3	4
154	TPM2 as a potential predictive biomarker for atherosclerosis. <i>Aging</i> , 2019, 11, 6960-6982.	1.4	44
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702	A study on the anti-osteoporosis mechanism of isopsoralen based on network pharmacology and molecular experiments. <i>Journal of Orthopaedic Surgery and Research</i> , 2023, 18, .	0.9	0
704	<i>Maliibacterium massiliense</i> gen. nov. sp. nov., Isolated from Human Feces and Proposal of <i>Maliibacteriaceae</i> fam. nov.. <i>Current Microbiology</i> , 2023, 80, .	1.0	0
776	Natural Products: Exploring Potential Against SARS CoV2. , 2024, , 441-474.		0