

# The BioGRID interaction database: 2019 update

Nucleic Acids Research

47, D529-D541

DOI: [10.1093/nar/gky1079](https://doi.org/10.1093/nar/gky1079)

Citation Report

#	ARTICLE	IF	CITATIONS
1	New advances in extracting and learning from proteinâ€“protein interactions within unstructured biomedical text data. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 357-369.	2.6	1
2	Protein-Protein Interactions in <i>Candida albicans</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1792.	3.5	12
3	Identification of important invasion and proliferation related genes in adrenocortical carcinoma. <i>Medical Oncology</i> , 2019, 36, 73.	2.5	19
4	Ultra-soft X-ray system for imaging the early cellular responses to X-ray induced DNA damage. <i>Nucleic Acids Research</i> , 2019, 47, e100-e100.	14.5	9
5	Comprehensive in vivo identification of the c-Myc mRNA protein interactome using HyPR-MS. <i>Rna</i> , 2019, 25, 1337-1352.	3.5	15
6	Discovering Innovative Drugs Targeting Both Cancer and Cardiovascular Disease by Shared Proteinâ€“Protein Interaction Network Analyses. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 417-425.	2.0	5
7	Proteomics Approaches for Biomarker and Drug Target Discovery in ALS and FTD. <i>Frontiers in Neuroscience</i> , 2019, 13, 548.	2.8	57
8	A Robust Approach for Identification of Cancer Biomarkers and Candidate Drugs. <i>Medicina (Lithuania)</i> , 2019, 55, 269.	2.0	13
9	Biological Network Approaches and Applications in Rare Disease Studies. <i>Genes</i> , 2019, 10, 797.	2.4	30
10	Characterization of the transient fluorescence wave phenomenon that occurs during H <sub>2</sub> production in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 6321-6336.	4.8	15
11	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2019, 48, D676-D681.	14.5	18
12	Therapeutic target database 2020: enriched resource for facilitating research and early development of targeted therapeutics. <i>Nucleic Acids Research</i> , 2020, 48, D1031-D1041.	14.5	488
13	SIGNOR 2.0, the SIGnaling Network Open Resource 2.0: 2019 update. <i>Nucleic Acids Research</i> , 2020, 48, D504-D510.	14.5	160
14	AppleMDO: A Multi-Dimensional Omics Database for Apple Co-Expression Networks and Chromatin States. <i>Frontiers in Plant Science</i> , 2019, 10, 1333.	3.6	44
15	The English People at War in the Age of Henry VIII, by Steven Gunn. <i>English Historical Review</i> , 2019, , .	0.0	0
16	The Tumor Suppressor SCRIB is a Negative Modulator of the Wnt/ $\beta$ -Catenin Signaling Pathway. <i>Proteomics</i> , 2019, 19, e1800487.	2.2	14
17	DNA Replication Inhibitor Geminin and Retinoic Acid Signaling Participate in Complex Interactions Associated With Pluripotency. <i>Cancer Genomics and Proteomics</i> , 2019, 16, 593-601.	2.0	9
18	Integrated bioinformatics analysis reveals role of the LINC01093/miRâ€“96â€“5p/ZFAND5/NFâ€“ $\kappa$ B signaling axis in hepatocellular carcinoma. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 3853-3860.	1.8	10

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19	ResponseNet v.3: revealing signaling and regulatory pathways connecting your proteins and genes across human tissues. Nucleic Acids Research, 2019, 47, W242-W247.	14.5	11
20	Interaction networks of Weibel-Palade body regulators syntaxin-3 and syntaxin binding protein 5 in endothelial cells. Journal of Proteomics, 2019, 205, 103417.	2.4	6
21	Gene Information eXtension (GIX): effortless retrieval of gene product information on any website. Nature Methods, 2019, 16, 665-666.	19.0	3
22	To Embed or Not: Network Embedding as a Paradigm in Computational Biology. Frontiers in Genetics, 2019, 10, 381.	2.3	123
23	Cell contact and Nf2/Merlin-dependent regulation of TEAD palmitoylation and activity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9877-9882.	7.1	59
24	Mining Featured Biomarkers Linked with Epithelial Ovarian Cancer Based on Bioinformatics. Diagnostics, 2019, 9, 39.	2.6	3
25	RN+: A Novel Biclustering Algorithm for Analysis of Gene Expression Data Using Protein-Protein Interaction Network. Journal of Computational Biology, 2019, 26, 432-441.	1.6	0
26	The Alliance of Genome Resources: Building a Modern Data Ecosystem for Model Organism Databases. Genetics, 2019, 213, 1189-1196.	2.9	41
27	Computational Identification of Metabolites for Pathways Related to Huntington's Disease. , 2019, , .		0
28	Critical nodes reveal peculiar features of human essential genes and protein interactome. , 2019, , .		1
29	Varying Mutational Classes Illuminate Differential Genetic Patterns Between Schizophrenia and Bipolar Disorder. , 2019, , .		0
30	Predicting gene-disease associations from the heterogeneous network using graph embedding. , 2019, , .		21
31	Sequence-Derived Markers of Drug Targets and Potentially Druggable Human Proteins. Frontiers in Genetics, 2019, 10, 1075.	2.3	14
32	A single ChIP-seq dataset is sufficient for comprehensive analysis of motifs co-occurrence with MCOT package. Nucleic Acids Research, 2019, 47, e139-e139.	14.5	28
33	TGFB1-Mediated Gliosis in Multiple Sclerosis Spinal Cords Is Favored by the Regionalized Expression of HOXA5 and the Age-Dependent Decline in Androgen Receptor Ligands. International Journal of Molecular Sciences, 2019, 20, 5934.	4.1	16
34	Human SNORA31 variations impair cortical neuron-intrinsic immunity to HSV-1 and underlie herpes simplex encephalitis. Nature Medicine, 2019, 25, 1873-1884.	30.7	76
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36	Transcription factor regulatory modules provide the molecular mechanisms for functional redundancy observed among transcription factors in yeast. BMC Bioinformatics, 2019, 20, 630.	2.6	8

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37	Common Neurodegeneration-Associated Proteins Are Physiologically Expressed by Human B Lymphocytes and Are Interconnected via the Inflammation/Autophagy-Related Proteins TRAF6 and SQSTM1. <i>Frontiers in Immunology</i> , 2019, 10, 2704.	4.8	13
38	Transcriptome Meta-Analysis Deciphers a Dysregulation in Immune Response-Associated Gene Signatures during Sepsis. <i>Genes</i> , 2019, 10, 1005.	2.4	26
39	Alliance of Genome Resources Portal: unified model organism research platform. <i>Nucleic Acids Research</i> , 2020, 48, D650-D658.	14.5	145
40	A paradigm shift in medicine: A comprehensive review of network-based approaches. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194416.	1.9	60
41	APEX2-mediated proximity labeling resolves protein networks in <i>Saccharomyces Cerevisiae</i> cells. <i>FEBS Journal</i> , 2020, 287, 325-344.	4.7	17
42	Hallmarks of ribosomopathies. <i>Nucleic Acids Research</i> , 2020, 48, 1013-1028.	14.5	122
43	Gene regulatory network inference resources: A practical overview. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194430.	1.9	93
44	The Monarch Initiative in 2019: an integrative data and analytic platform connecting phenotypes to genotypes across species. <i>Nucleic Acids Research</i> , 2020, 48, D704-D715.	14.5	178
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50	Prediction and targeting of GPCR oligomer interfaces. <i>Progress in Molecular Biology and Translational Science</i> , 2020, 169, 105-149.	1.7	13
51	Peroxiredoxin-1 regulates lipid peroxidation in corneal endothelial cells. <i>Redox Biology</i> , 2020, 30, 101417.	9.0	54
52	Reduced Translational Efficiency of Eukaryotic Genes after Duplication Events. <i>Molecular Biology and Evolution</i> , 2020, 37, 1452-1461.	8.9	9
53	MASS SPECTROMETRY IN VIROLOGICAL SCIENCES. <i>Mass Spectrometry Reviews</i> , 2020, 39, 499-522.	5.4	22
54	The Emerging Role of Cytidine Deaminase in Human Diseases: A New Opportunity for Therapy?. <i>Molecular Therapy</i> , 2020, 28, 357-366.	8.2	53

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56	Cross-linking Mass Spectrometry Analysis of the Yeast Nucleus Reveals Extensive Protein-Protein Interactions Not Detected by Systematic Two-Hybrid or Affinity Purification-Mass Spectrometry. Analytical Chemistry, 2020, 92, 1874-1882.	6.5	20
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66	Protein complex prediction in interaction network based on network motif. Computational Biology and Chemistry, 2020, 89, 107399.	2.3	6
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79	Genome-wide and structural analyses of pseudokinases encoded in the genome of <i>Arabidopsis thaliana</i> provide functional insights. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1620-1638.	2.6	9
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109	Robust edge-based biomarker discovery improves prediction of breast cancer metastasis. <i>BMC Bioinformatics</i> , 2020, 21, 359.	2.6	4

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160	Predicted <i>Drosophila</i> Interactome Resource and web tool for functional interpretation of differentially expressed genes. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	8
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