

The BioGRID interaction database: 2019 update

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Citation Report

#	ARTICLE	IF	CITATIONS
1	New advances in extracting and learning from protein-protein interactions within unstructured biomedical text data. <i>Emerging Topics in Life Sciences</i> , 2019, 3, 357-369.	1.1	1
2	Protein-Protein Interactions in <i>Candida albicans</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1792.	1.5	12
3	Identification of important invasion and proliferation related genes in adrenocortical carcinoma. <i>Medical Oncology</i> , 2019, 36, 73.	1.2	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.	6.5	9
5	Comprehensive in vivo identification of the c-Myc mRNA protein interactome using HyPR-MS. <i>Rna</i> , 2019, 25, 1337-1352.	1.6	15
6	Discovering Innovative Drugs Targeting Both Cancer and Cardiovascular Disease by Shared Protein-Protein Interaction Network Analyses. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 417-425.	1.0	5
7	Proteomics Approaches for Biomarker and Drug Target Discovery in ALS and FTD. <i>Frontiers in Neuroscience</i> , 2019, 13, 548.	1.4	57
8	A Robust Approach for Identification of Cancer Biomarkers and Candidate Drugs. <i>Medicina (Lithuania)</i> , 2019, 55, 269.	0.8	13
9	Biological Network Approaches and Applications in Rare Disease Studies. <i>Genes</i> , 2019, 10, 797.	1.0	30
10	Characterization of the transient fluorescence wave phenomenon that occurs during H2 production in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 6321-6336.	2.4	15
11	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2019, 48, D676-D681.	6.5	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.	6.5	488
13	SIGNOR 2.0, the SIGnaling Network Open Resource 2.0: 2019 update. <i>Nucleic Acids Research</i> , 2020, 48, D504-D510.	6.5	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.	1.7	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/ β -Catenin Signaling Pathway. <i>Proteomics</i> , 2019, 19, e1800487.	1.3	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.	1.0	9
18	Integrated bioinformatics analysis reveals role of the LINC01093/miR-96-5p/ZFAND5/NF- κ B signaling axis in hepatocellular carcinoma. <i>Experimental and Therapeutic Medicine</i> , 2019, 18, 3853-3860.	0.8	10

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19	ResponseNet v.3: revealing signaling and regulatory pathways connecting your proteins and genes across human tissues. <i>Nucleic Acids Research</i> , 2019, 47, W242-W247.	6.5	11
20	Interaction networks of Weibel-Palade body regulators syntaxin-3 and syntaxin binding protein 5 in endothelial cells. <i>Journal of Proteomics</i> , 2019, 205, 103417.	1.2	6
21	Gene Information eXtension (GIX): effortless retrieval of gene product information on any website. <i>Nature Methods</i> , 2019, 16, 665-666.	9.0	3
22	To Embed or Not: Network Embedding as a Paradigm in Computational Biology. <i>Frontiers in Genetics</i> , 2019, 10, 381.	1.1	123
23	Cell contact and Nf2/Merlin-dependent regulation of TEAD palmitoylation and activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9877-9882.	3.3	59
24	Mining Featured Biomarkers Linked with Epithelial Ovarian Cancer Based on Bioinformatics. <i>Diagnostics</i> , 2019, 9, 39.	1.3	3
25	RN+: A Novel Biclustering Algorithm for Analysis of Gene Expression Data Using Protein-Protein Interaction Network. <i>Journal of Computational Biology</i> , 2019, 26, 432-441.	0.8	0
26	The Alliance of Genome Resources: Building a Modern Data Ecosystem for Model Organism Databases. <i>Genetics</i> , 2019, 213, 1189-1196.	1.2	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. <i>Frontiers in Genetics</i> , 2019, 10, 1075.	1.1	14
32	A single ChIP-seq dataset is sufficient for comprehensive analysis of motifs co-occurrence with MCOT package. <i>Nucleic Acids Research</i> , 2019, 47, e139-e139.	6.5	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. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5934.	1.8	16
34	Human SNORA31 variations impair cortical neuron-intrinsic immunity to HSV-1 and underlie herpes simplex encephalitis. <i>Nature Medicine</i> , 2019, 25, 1873-1884.	15.2	76
35	Bioinformatics Approaches for Anti-cancer Drug Discovery. <i>Current Drug Targets</i> , 2019, 21, 3-17.	1.0	73
36	Transcription factor regulatory modules provide the molecular mechanisms for functional redundancy observed among transcription factors in yeast. <i>BMC Bioinformatics</i> , 2019, 20, 630.	1.2	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.	2.2	13
38	Transcriptome Meta-Analysis Deciphers a Dysregulation in Immune Response-Associated Gene Signatures during Sepsis. <i>Genes</i> , 2019, 10, 1005.	1.0	26
39	Alliance of Genome Resources Portal: unified model organism research platform. <i>Nucleic Acids Research</i> , 2020, 48, D650-D658.	6.5	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.	0.9	60
41	APEX2-mediated proximity labeling resolves protein networks in <i>Saccharomyces Cerevisiae</i> cells. <i>FEBS Journal</i> , 2020, 287, 325-344.	2.2	17
42	Hallmarks of ribosomopathies. <i>Nucleic Acids Research</i> , 2020, 48, 1013-1028.	6.5	122
43	Gene regulatory network inference resources: A practical overview. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194430.	0.9	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.	6.5	178
45	Plant Regulomics: a data-driven interface for retrieving upstream regulators from plant multi-omics data. <i>Plant Journal</i> , 2020, 101, 237-248.	2.8	75
46	VarSite: Disease variants and protein structure. <i>Protein Science</i> , 2020, 29, 111-119.	3.1	77
47	Data mining for traffic information. <i>Traffic</i> , 2020, 21, 162-168.	1.3	5
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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.	0.9	13
51	Peroxiredoxin-1 regulates lipid peroxidation in corneal endothelial cells. <i>Redox Biology</i> , 2020, 30, 101417.	3.9	54
52	Reduced Translational Efficiency of Eukaryotic Genes after Duplication Events. <i>Molecular Biology and Evolution</i> , 2020, 37, 1452-1461.	3.5	9
53	MASS SPECTROMETRY IN VIROLOGICAL SCIENCES. <i>Mass Spectrometry Reviews</i> , 2020, 39, 499-522.	2.8	22
54	The Emerging Role of Cytidine Deaminase in Human Diseases: A New Opportunity for Therapy?. <i>Molecular Therapy</i> , 2020, 28, 357-366.	3.7	53

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55	Shot-gun proteomics: why thousands of unidentified signals matter. <i>FEMS Yeast Research</i> , 2020, 20, .	1.1	14
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. <i>Analytical Chemistry</i> , 2020, 92, 1874-1882.	3.2	20
57	Sudden unexpected death in asymptomatic infants due to PPA2 variants. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1008.	0.6	17
58	Bioinformatics-assisted, integrated omics studies on medicinal plants. <i>Briefings in Bioinformatics</i> , 2020, 21, 1857-1874.	3.2	26
59	Connecting proteins: shareable tools for reproducible interaction mapping. <i>Biochemistry and Cell Biology</i> , 2020, 98, 309-313.	0.9	0
60	AMPK Interactome Reveals New Function in Non-homologous End Joining DNA Repair. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 467-477.	2.5	11
61	Construction and Characterization of UBC4 Mutants with Single Residues Swapped from UBC5. <i>Cell Biochemistry and Biophysics</i> , 2020, 78, 43-53.	0.9	0
62	Analysis of Differentially Expressed Genes in Coronary Artery Disease by Integrated Microarray Analysis. <i>Biomolecules</i> , 2020, 10, 35.	1.8	12
63	Application of topic models to a compendium of ChIP-Seq datasets uncovers recurrent transcriptional regulatory modules. <i>Bioinformatics</i> , 2020, 36, 2352-2358.	1.8	2
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65	SARS-CoV-2-human protein-protein interaction network. <i>Informatics in Medicine Unlocked</i> , 2020, 20, 100413.	1.9	42
66	Protein complex prediction in interaction network based on network motif. <i>Computational Biology and Chemistry</i> , 2020, 89, 107399.	1.1	6
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69	Predicted functional interactome of <i>Caenorhabditis elegans</i> and a web tool for the functional interpretation of differentially expressed genes. <i>Biology Direct</i> , 2020, 15, 20.	1.9	3
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72	Analytical Guidelines for co-fractionation Mass Spectrometry Obtained through Global Profiling of Gold Standard <i>Saccharomyces cerevisiae</i> Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1876-1895.	2.5	14
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74	Community curation in PomBase: enabling fission yeast experts to provide detailed, standardized, sharable annotation from research publications. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	19
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77	Robustness of plant quantitative disease resistance is provided by a decentralized immune network. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18099-18109.	3.3	34
78	Combining Proximity Labeling and Cross-Linking Mass Spectrometry for Proteomic Dissection of Nuclear Envelope Interactome. Journal of Proteome Research, 2020, 19, 1109-1118.	1.8	15
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.	1.5	9
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85	Inferring the molecular and phenotypic impact of amino acid variants with MutPred2. Nature Communications, 2020, 11, 5918.	5.8	305
86	TRP Channels Regulation of Rho GTPases in Brain Context and Diseases. Frontiers in Cell and Developmental Biology, 2020, 8, 582975.	1.8	8
87	A review of protein-protein interaction network alignment: From pathway comparison to global alignment. Computational and Structural Biotechnology Journal, 2020, 18, 2647-2656.	1.9	17
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96	A ubiquitin ligase mediates target-directed microRNA decay independently of tailing and trimming. <i>Science</i> , 2020, 370, .	6.0	135
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101	Genome-Wide Screens Reveal that Resveratrol Induces Replicative Stress in Human Cells. <i>Molecular Cell</i> , 2020, 79, 846-856.e8.	4.5	18
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111	Roles of Farnesyl-Diphosphate Farnesyltransferase 1 in Tumour and Tumour Microenvironments. Cells, 2020, 9, 2352.	1.8	31
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145	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1330-1341.	1.9	16

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153	Role of Anillin in Tumour: From a Prognostic Biomarker to a Novel Target. <i>Cancers</i> , 2020, 12, 1600.	1.7	28
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