

Resource Summary Report

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Biological General Repository for Interaction Datasets (BioGRID)

RRID:SCR_007393

Type: Tool

Proper Citation

Biological General Repository for Interaction Datasets (BioGRID) (RRID:SCR_007393)

Resource Information

URL: <http://www.thebiogrid.org/>

Proper Citation: Biological General Repository for Interaction Datasets (BioGRID) (RRID:SCR_007393)

Description: Curated protein-protein and genetic interaction repository of raw protein and genetic interactions from major model organism species, with data compiled through comprehensive curation efforts.

Abbreviations: BioGRID

Synonyms: , BioGRID, Biological General Repository for Interaction Datasets

Resource Type: data or information resource, database

Defining Citation: [PMID:23203989](#), [PMID:21071413](#), [PMID:16381927](#), [PMID:12620108](#)

Keywords: budding yeast, fission yeast, protein, gene, protein interaction, genetic interaction, model organism, interaction, dataset, gene annotation, phenotype, orthologous interaction, yeast, cellular interaction network, physical interaction, protein-peptide, protein-rna, protein-protein interaction, genetics, publication, raw protein, genetic interaction, web service, pathway, network, biology, gene mapping, statistics, bio.tools, FASEB list

Funding: NCRR R01 RR024031;
NHGRI HG02223;
Canadian Institutes of Health Research ;
BBSRC ;
NIH Office of the Director R24 OD011194

Availability: Free, Freely available

Resource Name: Biological General Repository for Interaction Datasets (BioGRID)

Resource ID: SCR_007393

Alternate IDs: nif-0000-00432, r3d100010350, OMICS_01901, biotools:the_grid

Alternate URLs: <https://orip.nih.gov/comparative-medicine/programs/genetic-biological-and-information-resources>, https://bio.tools/the_grid, <https://doi.org/10.17616/R34C7G>

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260729T044148+0000

Ratings and Alerts

No rating or validation information has been found for Biological General Repository for Interaction Datasets (BioGRID).

No alerts have been found for Biological General Repository for Interaction Datasets (BioGRID).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2554 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Jin SK, et al. (2026) Deubiquitomic and bioinformatic analyses in cisplatin-treated lung cancer cells. International journal of medical sciences, 23(1), 1.

Rizvi SA, et al. (2026) Scaling Large Language Models for Next-Generation Single-Cell Analysis. bioRxiv : the preprint server for biology.

Yang YF, et al. (2026) Integrative analysis identifies PIGK as an oncogenic glycosylphosphatidylinositol transamidase subunit with prognostic, immunological, and therapeutic relevance in head and neck cancer. International journal of medical sciences, 23(1), 161.

Ding M, et al. (2025) Identification of a Novel Gene ARNT2 for Osteogenic Differentiation of Mesenchymal Stem Cells. Calcified tissue international, 116(1), 100.

Marino GB, et al. (2025) GeneSetCart: assembling, augmenting, combining, visualizing, and analyzing gene sets. GigaScience, 14.

Cigler M, et al. (2025) Orpinolide disrupts a leukemic dependency on cholesterol transport by inhibiting OSBP. Nature chemical biology, 21(2), 193.

- Ozisik O, et al. (2025) A collaborative network analysis for the interpretation of transcriptomics data in Huntington's disease. *Scientific reports*, 15(1), 1412.
- Ho JJ, et al. (2025) The BLM-TOP3A-RMI1-RMI2 proximity map reveals that RAD54L2 suppresses sister chromatid exchanges. *EMBO reports*, 26(5), 1290.
- Liu X, et al. (2025) Establishment of an alternative splicing prognostic risk model and identification of FN1 as a potential biomarker in glioblastoma multiforme. *Scientific reports*, 15(1), 6716.
- Zhou H, et al. (2025) MTHFD2 promotes esophageal squamous cell carcinoma progression via m6A modification-mediated upregulation and modulation of the PEBP1-RAF1 interaction. *International journal of molecular medicine*, 55(5).
- Monti M, et al. (2025) catGRANULE 2.0: accurate predictions of liquid-liquid phase separating proteins at single amino acid resolution. *Genome biology*, 26(1), 33.
- Dipalma A, et al. (2025) Sensitivity analysis on protein-protein interaction networks through deep graph networks. *BMC bioinformatics*, 26(1), 124.
- Frommelt F, et al. (2025) The solute carrier superfamily interactome. *Molecular systems biology*, 21(6), 632.
- Zhang H, et al. (2025) Targeting Senescence with Apigenin Improves Chemotherapeutic Efficacy and Ameliorates Age-Related Conditions in Mice. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(20), e2412950.
- Shalaby KS, et al. (2025) SynDRep: a synergistic partner prediction tool based on knowledge graph for drug repurposing. *Bioinformatics advances*, 5(1), vbaf092.
- Das A, et al. (2025) Generative artificial intelligence, integrative bioinformatics, and single-cell analysis reveal Alzheimer's genetic and immune landscape. *Molecular therapy. Nucleic acids*, 36(2), 102546.
- Zheng R, et al. (2025) MEBOCOST maps metabolite-mediated intercellular communications using single-cell RNA-seq. *Nucleic acids research*, 53(12).
- Senagolage MD, et al. (2025) NAMPT haploinsufficiency is a collateral lethal therapeutic vulnerability in high-risk myeloid malignancies with TP53 inactivation. *Blood neoplasia*, 2(3), 100119.
- Song X, et al. (2025) Development and validation of G2M signature-based prognostic model for stratifying colon cancer prognosis. *Discover oncology*, 16(1), 1516.
- Noh SG, et al. (2025) Co-regulation of Nr1d1 and Ppar α in age-related changes of lipid metabolism and its modulation by calorie restriction. *Aging*, 17(7), 1810.