

# The BioGRID Interaction Database

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**The goal of the Biological General Repository for Interaction Datasets (BioGRID) is to archive and freely disseminate collections of genetic and protein interactions from major model organisms. BioGRID currently contains over 355,000 interactions curated from high-throughput datasets and individual focused studies from over 23,000 publications in the primary literature. Complete coverage of the entire literature for both the budding yeast *Saccharomyces cerevisiae* and the fission yeast *Schizosaccharomyces pombe* has been achieved and efforts to expand curation across multiple species are underway.**

## Displaying Interactions

The new search results display provides a summary of the total number of curated interactions for the gene or protein of interest, as well as the number of physical or genetic interactions for each interactor. The interactions may be filtered according to whether they are low or high throughput. Details are provided for different experiment types including the role of the interactor and experimental throughput. Mousing over icons in the notes column reveals further details including phenotypes, post-translational modifications, quantitative scores, and notes, if applicable. The summary view shown below may be switched to a table view that can be sorted by interactor, experiment type, publication, or throughput, among other options.

**CDC28** *Saccharomyces cerevisiae*

CDK1, SRM5, HSL5, YBR160W

Catalytic subunit of the main cell cycle cyclin-dependent kinase (CDK); alternately associates with G1 cyclins (CLNs) and G2/M cyclins (CLBs) which direct the CDK to specific substrates

GO Process: 13 Terms GO Function: 1 Terms GO Component: 8 Terms

EXTERNAL DATABASE LINKOUTS  
SGD | Entrez Gene | RefSeq | GenBank | UniprotKB | GeneDB | PhosphoGRID

Download 352 Associations For This Protein

Switch View: Summary Sortable Table

Displaying 1 - 300 of 352 total unique interactors

< Previous | 2 | Next >

**CLN2** | YPL256C  
G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends on transcription factor complexes, MBF (Swi6p-Mbp1p) and SBF (Swi6p-Swi4p)

| Experimental Evidence Code | Role             | Publication          | Throughput      | Notes |
|----------------------------|------------------|----------------------|-----------------|-------|
| Affinity Capture-MS        | HIT              | Gavin AC (2002)      | High Throughput | -     |
|                            | BAIT             | Ho Y (2002)          | High Throughput | -     |
|                            | BAIT             | Archambault V (2004) | Low Throughput  | -     |
| Affinity Capture-Western   | HIT              | Gavin AC (2006)      | High Throughput | -     |
|                            | HIT              | Collins SR (2007)    | High Throughput | -     |
|                            | BAIT             | Kito K (2008)        | Low Throughput  | -     |
| Biochemical Activity       | HIT              | Breitkreutz A (2010) | High Throughput | -     |
|                            | HIT              | Ceccarelli E (2001)  | Low Throughput  | -     |
|                            | BAIT             | Peter M (1994)       | Low Throughput  | -     |
| Reconstituted Complex      | BAIT             | Wang H (2004)        | Low Throughput  | -     |
|                            | BAIT             | Deshais RJ (1995)    | Low Throughput  | -     |
|                            | BAIT             | Lim HH (1996)        | Low Throughput  | -     |
| Dosage Rescue              | BAIT             | Miller ME (2005)     | Low Throughput  | -     |
|                            | BAIT             | Kono K (2008)        | Low Throughput  | -     |
|                            | BAIT             | Lanker S (1996)      | Low Throughput  | -     |
| Synthetic Rescue           | HIT              | Lanker S (1996)      | Low Throughput  | -     |
|                            | HIT              | Tyers M (1993)       | Low Throughput  | -     |
|                            | HIT              | Reed SI (1989)       | Low Throughput  | -     |
| Synthetic Rescue           | HIT              | Queraf E (2004)      | Low Throughput  | -     |
|                            | BAIT             | Levine K (1998)      | Low Throughput  | -     |
| BAIT                       | Miller ME (2005) | Low Throughput       | -               |       |

**CLB2** | YPR119W  
B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the transition from G2 to M phase; accumulates during G2 and M, then targeted via a destruction box motif for ubiquitin-mediated degradation by the proteasome

## PhosphoGRID Database

Direct links are provided from BioGRID's Interaction Summary page to various resources including PhosphoGRID, a database of experimentally verified phosphorylation sites curated from the *S. cerevisiae* literature. In this example, phosphorylation sites in the protein sequence of CDC28 are shown in red and protein kinase motifs are highlighted in blue. Details for each phosphorylation site are provided in the table below, or in a pop-up window viewable by mousing over a phosphorylated residue of interest. PhosphoGRID documents over 5000 phosphorylated residues found in 1495 gene products. All curated data in PhosphoGRID are freely available and may be downloaded at [www.phosphogrid.org](http://www.phosphogrid.org).

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**YBR160W / CDC28**

Description: Catalytic subunit of the main cell cycle cyclin-dependent kinase (CDK); alternately associates with G1 cyclins (CLNs) and G2/M cyclins (CLBs) which direct the CDK to specific substrates

Other Aliases: CDK1, SRM5, HSL5

External IDs: S000000364 (sgd),

Protein Sequence Mouse over phosphorylation sites for more details

1 MSGELANYKR LEKVGEGT**YG** VVYKALDLRP GQGQRVVALK KIRLE**SEDEG** VPSTAIRSIS  
61 LKELKDDNI VRLYDIVHSD AHKLYLVFEP LLDLKLRYME GIPKQPLGA DIVKKFMMQL  
121 CKGIAYCHSH RILHRDLKPQ NLLINKDGNL KLGDFGLARA FGVPLR**YTH** EIVTLWYRAP  
181 EVLGGKQYS TGVDTWSIGC IFAEMCNRPK IFSGDSEIDQ IFKIFRVLGT PNEAIWPDIV  
241 YLPDFKPSFP QWRRKDLISQV VPSLDPRGID LLDKLLAYDP INRISARRAA IHPYFQES

Protein Kinase Motifs Mouse over Motifs to highlight region in sequence

46 - 49: Casein Kinase II (CKII, CK-2)

Phosphorylation Sites

| Location | Residue | Evidence   | Condition(s)  | Function(s)                   | Note(s)        |
|----------|---------|--|---|-------------------------------|----------------|
| 19       | Y       | Mass Spec Sequencing Of A Phosphopeptide<br>Phosphopeptide Fingerprint<br>Loss Of 32P Label From Protein With A Mutation | Cell Cycle Regulated - M Phase<br>Cell Cycle Regulated - G2 Phase | Inhibits The Protein Function | [ view notes ] |

## Searching BioGRID

BioGRID may be searched using various protein or gene identifiers, including UniProt and NCBI IDs, as well as keywords and PubMed IDs. Searches may be limited to an organism of interest, or else performed on all 50 organisms including yeast, human, and mouse. In this example, CDC28 is entered as the search term and *S. cerevisiae* is selected as the organism.

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Welcome to the Biological General Repository for Interaction Datasets

Search the BioGRID  
Search by identifiers, keywords, and gene names...

CDC28

Saccharomyces cerevisiae

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AREAS OF INTEREST TO HELP YOU GET STARTED

- Build and Download Interaction Datasets: Create custom interaction datasets by protein or by publication. You can also download our entire dataset in a wide variety of standard formats.
- Link To Us or Submit Interactions: Send us your datasets or link to the BioGRID directly from your own website or database. Full details on how to contribute are available here.
- Online Tools and Resources: We've developed tools that make use of BioGRID data. Check out the list of tools to see if we can help you work with our data.
- View Our Interaction Statistics: Find out how many organisms, proteins, publications, and interactions are available in the current release of the BioGRID.

BIOGRID FUNDING AND PARTNERS

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## New project in conjunction with other databases

BioGRID is initiating a new project to provide high-quality coverage of biological processes of relevance to human disease. Our initial focus is on genes in the Wnt signaling pathway, recently co-curated as part of the Gene Ontology (GO) Consortium Reference Genome project. BioGRID and WormBase curators are curating *C. elegans* physical and genetic interactions using papers annotated with the GO evidence codes IPI (Inferred from Physical Interaction) or IGI (Inferred from Genetic Interaction). BioGRID captures specific information not collected during GO curation, such as specific experimental systems and (for genetic interactions) phenotypes from the Worm Phenotype Ontology, and displays additional notes and details (see figure below). We will soon expand this focused curation into additional organisms. By coordinating our efforts with the GO Consortium and the Linking Animal Models to Human Disease Initiative (LAMHDI) Consortium, we hope to provide a more complete picture of important processes.

**BAR-1** *Caenorhabditis elegans*

C54D1.6

Beta-catenin/Armadillo Related family member (bar-1)

GO Process: 17 Terms GO Function: 3 Terms GO Component: 6 Terms

GENE ONTOLOGY MOLECULAR FUNCTION  
Protein Binding (IP)  
Transcription Coactivator Activity (IDA)  
Transcription Factor Binding (IP)

EXTERNAL DATABASE LINKOUTS  
WormBase | Entrez Gene | RefSeq | GenBank | UniprotKB

Download 180 Associations For This Protein

Switch View: Summary Sortable Table

Displaying 180 [175 filtered] total unique interactors

**POP-1** | W10C8.2  
Posterior Pharynx defect family member (pop-1)

**DAF-16** | R13H8.1  
abnormal DAuer Formation family member (daf-16)

| Experimental Evidence Code | Role | Publication      | Throughput     | Notes |
|----------------------------|------|------------------|----------------|-------|
| Affinity Capture-Western   | BAIT | Essers MA (2005) | Low Throughput | -     |
| Phenotypic Suppression     | HIT  | Essers MA (2005) | Low Throughput | -     |

Additional Notes  
RNAi inhibition of DAF-16 partially suppresses the dauer inducing effects of over-expressing BAR-1

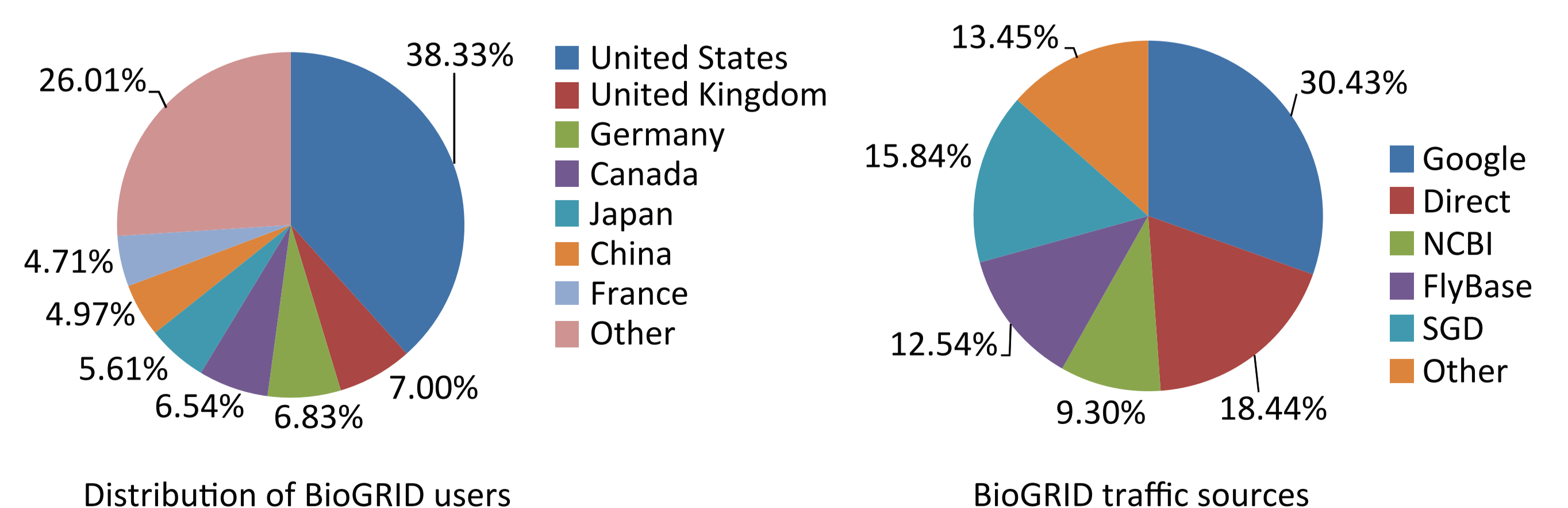
Phenotypes  
dauer constitutive

## BioGRID Database Statistics

The number of interactions ("edges" in the table below) and the number of papers curated in BioGRID has nearly tripled since July 2006. 99% of interactions come from the six model organisms shown, with 68% coming from *S. cerevisiae*.

| Organism                             | Type | July 2006 (2.0.17) |         |        | August 2010 (3.0.67) |         |        |
|--------------------------------------|------|--------------------|---------|--------|----------------------|---------|--------|
|                                      |      | nodes              | edges   | papers | nodes                | edges   | papers |
| <i>A. thaliana</i> (thale cress)     | PI   | 0                  | 0       | 0      | 1,735                | 4,719   | 747    |
|                                      | GI   | 0                  | 0       | 0      | 88                   | 174     | 55     |
| <i>C. elegans</i> (worm)             | PI   | 2,790              | 4,433   | 1      | 2,813                | 4,663   | 12     |
|                                      | GI   | 0                  | 0       | 0      | 1,030                | 2,112   | 5      |
| <i>D. melanogaster</i> (fly)         | PI   | 6,997              | 22,133  | 2      | 7,396                | 24,480  | 167    |
|                                      | GI*  | 1,189              | 10,314  | 1,493  | 982                  | 9,994   | 1,466  |
| <i>H. sapiens</i> (human)            | PI   | 3,380              | 7,238   | 178    | 9,467                | 48,368  | 10,203 |
|                                      | GI   | 0                  | 0       | 0      | 479                  | 463     | 178    |
| <i>S. cerevisiae</i> (budding yeast) | PI   | 5,144              | 49,297  | 3,267  | 5,783                | 90,769  | 5,444  |
|                                      | GI   | 3,352              | 24,636  | 3,796  | 5,357                | 146,081 | 5,606  |
| <i>S. pombe</i> (fission yeast)      | PI   | 0                  | 0       | 0      | 1,441                | 4,019   | 769    |
|                                      | GI   | 0                  | 0       | 0      | 1,340                | 11,527  | 953    |
| All other organisms                  | PI   | 284                | 620     | 73     | 2,288                | 2,985   | 830    |
| Total                                | ALL  | 19,176             | 118,671 | 7818   | 30,665               | 347,966 | 23,451 |

Increase in BioGRID data content, 2006-2010. \* from FlyBase



## References

(1) Breitkreutz BJ, Stark C, Reguly T, Boucher L, Breitkreutz A, Livstone M, Oughtred R, Lackner DH, Bähler J, Wood V, Dolinski K, Tyers M. "The BioGRID Interaction Database: 2008 update." *Nucleic Acids Res.* 2008 Jan;36(Database issue):D637-40.

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All data in BioGRID are freely available and may also be downloaded via:

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