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BINDing molecules

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Abstract

The Biomolecular Interaction Network Database (BIND) was developed to undertake the mammoth task of providing a public database of all known biomolecular interactions.

Content

BIND was developed to undertake the mammoth task of providing a public database of all known biomolecular interactions. A simple search engine enables the user to quickly type in their protein of interest and generate a list of interactions in seconds. These 'Interaction' records describe the binding event between two molecules. The advanced search feature can also return records for 'Molecular Complexes' and 'Pathways', although these are currently limited in number. A Molecular Complex is taken to be a stable aggregate of molecules that function when linked together (the ribosome, for example), and the Molecular Complex record lists the series of Interaction records that are present in the complex. The Pathway record describes a cellular process as a sequential list of Interaction records, and provides associated data such as phenotype. With these expanding levels of interaction data, the claim is that the database can be used to study networks of interactions, generate information for kinetic simulations, and map pathways across taxonomic branches. Indeed, 12 species are currently included in the BIND database (including human, mouse and yeast), and there are a further 96 alternatives currently listed in the submission section. The open submission format, permitting the input of data from any published paper (so long as a Medline Unique Identifier or PubMed Identification Number is available) means that this number will probably expand in future. BIND-related tools include BIND BLAST (for BLASTing against the proteins found in the BIND database) and PreBIND, a tool that searches the scientific literature for possible interactions and then submits *bona fide* interactions to BIND. PreBIND-searches and direct submission of experimental data are the two primary mechanisms of importing new data into BIND. Although BIND currently only accepts protein-protein and protein-nucleic acid interactions, tools are being developed for the site to accept small-molecule data.

Navigation

The site is well structured, using a single navigation bar that is visible on all pages. Each page has a separate URL for bookmarking and is printer-friendly.

Reporter's comments

Timeliness

The curators on the BIND team enter new data continually. Users are also encouraged to enter records into the database via web-based submission forms. BIND was originally designed by researchers at the University of Toronto (a list of key people is available at the site), but has since been passed into the hands of blueprint WORLDWIDE Inc., a non-profit organization specializing in biomolecular data management. To my mind this greatly increases the chances of BIND avoiding 'orphan database' syndrome and instead maturing into a highly useful online tool.

Best feature

The 'visualize interaction' feature in the search results is entertaining - clicking on a protein unleashes a series of connecting boxes identifying all the proteins known (to BIND) to interact with it. The same can be done for each interacting protein, enabling the user to generate a tangled network of protein interactions.

Worst feature

Other than the limited number of interactions currently available, the only negative aspect of the site is a rather undiscerning search engine. For example, a search on 'estrogen receptor' produced 110 records of interaction. The same 110 were displayed when the search was narrowed to 'receptor', whereas there were no records with 'estrogen'.

Wish list

BIND is still in the early stages of development and therefore contains a limited number of interactions (5,843 as of 8 July 2001). Naturally, my wish is that there were more interactions to search. These will hopefully appear in time and the site will stand or fall depending on how many can be incorporated.

Related websites

The 'related databases' page contains links to over 60 interaction and small-molecule databases.

Table of links

The Biomolecular Interaction Network Database (BIND)

References

1. The Biomolecular Interaction Network Database (BIND).