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The Biomolecular Interaction Network Database (BIND)

Status	Past
Competition	II
Sector	Health
Genome Centre	Ontario Genomics Institute
Project Leader	Christopher Hogue

Project Description

Human Genome Project researchers worldwide produce a huge amount of raw information about genes and proteins. This information must be turned into knowledge if it is to be useful for further studies and for practical applications. It must be organized into databases, analyzed in a great many ways and above all made available to researchers everywhere.

In our project, we set up specialized databases used by genomic researchers around the world. The first database, called BIND, contains information for over 200,000 protein and DNA interactions, which are the biological processes that drive living cells and are central to biological and medical research. The second database, called SMID, details over 13 million chemical binding sites on protein molecules; these can be used to identify medical and industrial applications for chemicals that are known to alter proteins involved in biological processes. A third database, called SeqHound, contains the raw information from the Human Genome Project upon which we built BIND and SMID. We screened the information in these databases meticulously to be sure that it has the very high quality necessary for research. We also created a large set of software tools that enable many different kinds of analysis of the information contained in our databases.

Thousands of biomedical researchers all over the world use our databases to discover new connections among genes and proteins that otherwise may have been missed. This reduces the cost and time of research, and leads to a better understanding of how cells work. Using BIND and SMID gives scientists the possibility of designing new drugs for the treatment of many diseases.

Fast Facts

<i>Highlighted outcome:</i>	Creation of databases that contain crucial molecular-interaction data that are used by the worldwide biomedical research community.
<i>Number of research personnel employed by the project:</i>	more than 100
<i>Number of peer reviewed publications published:</i>	20 plus 48 invited presentations; plus hundreds of publications that used the databases
<i>Number of patents in process or obtained:</i>	1
<i>Resources generated:</i>	SeqHound, BIND, SMID databases for public use plus a large set of analytical software
<i>Number of public outreach events held:</i>	30