Integrated Receptor Database

Kotoko Nakata **Takako Igarashi** **Tsuguchika Kaminuma**
nakata@nihs.go.jp taka@nihs.go.jp kaminuma@nihs.go.jp
Division of Chem-Bio Informatics, National Institute of Health Sciences
1-18-1, Kamiyoga, Setagaya-ku, Tokyo 158, Japan

Abstract

A database for receptors on cell membrane has been developed. The system can collect data items such as attributes of proteins from distributed data sources on the Internet. Such sources include internationally standard biological databases such as the updated genetic database of PIR, Swiss Prot, PDB, GenBank, EMBL and GDB. The system provides various viewing tools that effectively displays different types of receptor data; DNA sequences, amino acids sequences, DNA binding sites, ligand binding sites, gene and disease information, and the protein structural information. It can also display three dimensional images using a freeware program RASMOL. DNA binding sites, ligand binding sites and active sites are classified by coloring the sequences. PDB matching sites are classified by italicization. CSNDB (Cell Signaling Networks Database), which is a database for cellular signal transduction of human is also linked in the system. The database may be useful for quick reference for ligand - membrane receptors and signal transduction in the drug design.

1 Introduction

A cell responds to a particular extracellular signaling molecule depends on its having specific proteins, called receptors, that bind the signal molecule. Each receptor recognize an unique ligand or class of ligands, and is realized as the site of action of endogenous regulators whether called transmitters, hormones, growth controllers. As those information regarding the structure of receptors and the site of action on the receptor are highly interesting in biologically, medically and pharmacologically, we collected such information as much as possible. We integrated the database, using a database management system ACEDB and started a service on World Wide Web.

2 Method and System

ACEDB is an object oriented database management system, which has been developed as part of the Caenorhabditis elegans genome research. This database system is a generalized genome database system, and can be used to create new database without the need for any reprogramming or in fact any sophisticated computer skills. Combining some perl programs, the system provides various viewing tools that effectively display different types of receptor data; DNA sequences, amino acids sequences, DNA binding sites, ligand binding sites, gene and disease information, and the protein structural information. It can also display three dimensional structure of molecules using a freeware molecular graphics RASMOL, and the results of secondary structure prediction.

3 Reference

Richard Durbin and Jean Thierry Mieg: (1991-). A C. elegans Database.
Documentation, code and data available from anonymous FTP servers at lirmm.lirmm.fr, cele.mrc-lmb.cam.ac.uk and ncbi.nlm.nih.gov.
Receptor Database: http://impact.nihs.go.jp/RDB.html