Receptor Database (RDB) in 1999

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1 Introduction

Receptor information on structure and function is important base for understanding living systems and diseases, and for designing new drugs. We have developed the Receptor Database (RDB) [1], based on the Internet/World Wide Web (WWW) technology. Further more, the RDB has been extended by combining new items, for instance, TRANSFAC information and the sequence similarity information.

A user can carry out one-stop shopping on receptor data from this site. It is a good 'portal' site of the receptor structure and function among many WWW sites. The system provided a good viewer to represent not only molecular structural data, but also transduction of signals, which are triggered by a ligand binding.

2 Database

The RDB has been developed using an object oriented database management system ACEDB [A Caenorhabditis elegans Database [2]. For the modification of data, PERL programs were integrated in the system. According to the architecture of ACEDB, all information was hierarchically stored in objects, in a structure called a tree. The data structure in RDB was shown in Table 1. The three-dimensional structural image is instanced by the computer commands that call the visualization tool, such as RasMol. The system has a browser interface so that RDB can be accessed via WWW.

Information on receptors was collected from databases, original papers and books [3, 4]. We referred to PIR and Swiss Prot for protein sequences, and PDB for three-dimensional structure, to GenBank for DNA sequences that are translated to the receptor protein, to GDB for gene data, to CSNDB for cellular signal transduction of humans and to TRANSFAC for transcription factors.

In RDB, data are retrieved directly from the sources located on the Internet. The URL for the database can be involved, whatever the original site or the mirror site, as long as the database format is the same, and the contents are frequently updated. As for the secondary structure prediction of receptor protein sequences, the input data for the analytical system was prepared in the RDB, and sent for the remote system 'BCM Search Launcher' [5] on the Internet. While the main species sequence in a group, that is usually human sequence, was previously sent for the BLAST search [6], and the result was converted using MView program [7] for sequence similarity information.

RDB is available through the Internet at URL http://impact.nihs.go.jp/RDB.html

References

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Table 1. Data Structure in RDB.

class	object		label for	detail information
	LG list		(LG Name)	
LG	MG list		(MG Name)	
	Group list		(Group Name)	
MG	Group list		(Group Name)	
Group	MView	(query sequence)	MulSq	Sequence Similarity
	Species list		(Receptor Name)	
Receptor	PIR	Entry Name Accession No. No. of Sequences DNA Binding Region Ligand Binding Region Transmembrane	PIR ref PIR seq St 2D-pred	PIR data Highlighted Functional Regions Secondary Structure Prediction
	Swiss Prot	Entry Name Accession No. No. of Sequences DNA Binding Region Ligand Binding Region Transmembrane	SP ref SP seq St 2D-pred	Swiss Prot data Highlighted Functional Regions Secondary Structure Prediction
	MView	(query sequence)	MulSq	Sequence Similarity
	PDB	Entry Name No. of Sequences Overlap Site with PIR or Swiss Prot	PDB ref St 3D-image	PDB data Three Dimensional Image
	GB	Entry Name Accession No. No. of Sequence	GB ref GB seq	GenBank data DNA sequences
	GDB	Entry Name Symbol Map Position	GDB ref	GDB data
	CSNDB	Entry Name	Signaling	Cell Signaling Networks Data
	TRANSFAC	Entry Name	Transfac	Transfac Data