Receptor Database (RDB) As an Analytical Tool

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1 Introduction

Receptor information on structure and function is an important base for understanding living systems and diseases, and for designing new drugs. Recently, the so-called endocrine disruptors become an important working hypothesis for ecotoxicology researchers. They may mimic the sex hormones estrogen or androgen, binding with the corresponding hormone receptor. The xeno-biotic ligands that bind to the same receptor usually binding to a biotic ligand may not result the same phenomena. We had developed the receptor database (RDB) [1, 2], based on the Internet/World Wide Web (WWW) technology. Since then, new items and new data, especially relating to endocrine disruptors were included in RDB.

2 Method and Results

Flexibility for data updating which sometimes requires even structural change to data, we used an object-oriented database management system ACEDB (A Caenorhabditis elegans Database), instead of relational database. RDB includes the following information;
(a) Functional and structural information of receptor proteins.
  (a-1) Amino acid sequence (PIR, Swiss Prot)
  (a-2) DNA binding site, ligand binding site and transmembrane region
(with highlighted functional region)
  (a-3) Secondary structure prediction
  (a-4) Three-dimensional image (PDB)
  (a-5) Sequence similarity information (BLAST search and MView)
(b) DNA and gene information
  (b-1) DNA sequence (GenBank)
  (b-2) gene data (GDB)
(c) Cell signaling information
  (c-1) Cell signaling networks (CSNDB)
(d) Cellular molecular interaction
  (d-1) Transcription factor information (Transfac) [3]
  (d-2) Transcription regulation information (TRRD) [4]
(e) Interaction of exogenous chemicals and biomolecule
  (e-1) Binding affinity database for endocrine disruptor (BADB) [5]

RDB is available through the Internet at http://impact.nihs.go.jp/RDB.html
A user can carry out one-stop shopping on receptor data from this site. The searching results may be used more detail analysis.

References

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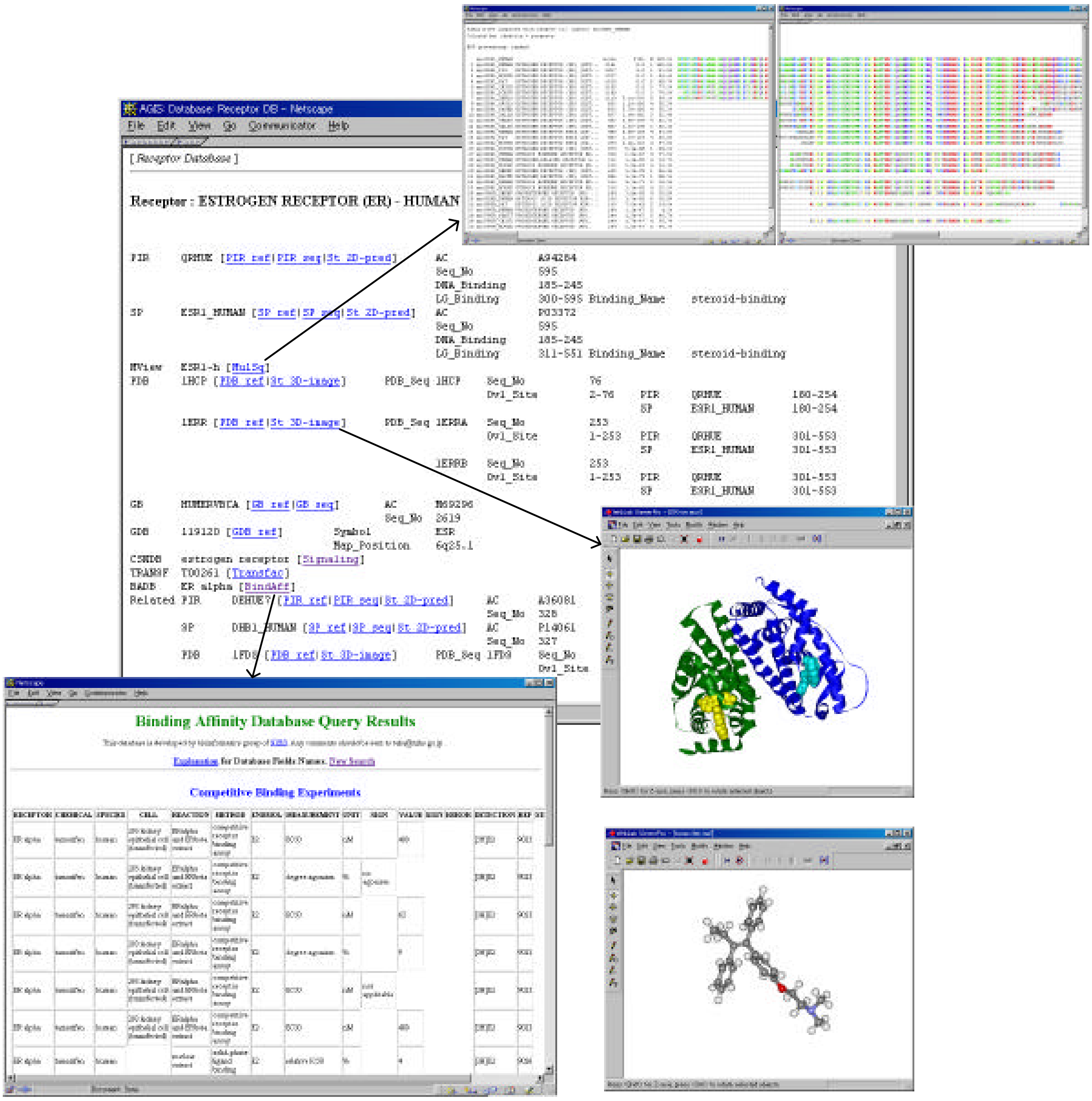
AGIS Database: Receptor DB - Netscape
File Edit View Go Communicator Help
[Receptor Database]
Receptor : ESTROGEN RECEPTOR (ER) - HUMAN
PIR QRHUE [PIR ref|PIR seq|St 2D-pred] AC A94284
Seq_No 595
DNA_Binding 185-245
LG_Binding 300-595 Binding_Name steroid-binding
SP ESR1_HUMAN [SP ref|SP seq|St 2D-pred] AC P03372
Seq_No 595
DNA_Binding 185-245
LG_Binding 311-551 Binding_Name steroid-binding
MView ESR1-h [MulSq]
PDB 1HCP [PDB ref|St 3D-image] PDB_Seq 1HCP Seq_No 76
Ovl_Site 2-76 PIR QRHUE 180-254
SP ESR1_HUMAN 180-254
1ERR [PDB ref|St 3D-image] PDB_Seq 1ERRA Seq_No 253
Ovl_Site 1-253 PIR QRHUE 301-553
SP ESR1_HUMAN 301-553
1ERRB Seq_No 253
Ovl_Site 1-253 PIR QRHUE 301-553
SP ESR1_HUMAN 301-553
GB HUMERVBCA [GB ref|GB seq] AC M69296
Seq_No 2619
GDB 119120 [GDB ref] Symbol ESR
Map_Position 6q25.1
CSNDB estrogen receptor [Signaling]
TRANSF T00261 [Transfac]
BADB ER alpha [BindAff]
Related PIR DEHUE7 [PIR ref|PIR seq|St 2D-pred] AC A36081
Seq_No 328
SP DHB1_HUMAN [SP ref|SP seq|St 2D-pred] AC P14061
Seq_No 327
PDB 1FDS [PDB ref|St 3D-image] PDB_Seq 1FDS Seq_No
Ovl_Site
Binding Affinity Database Query Results
Explanation for Database Fields Names. New Search
Competitive Binding Experiments