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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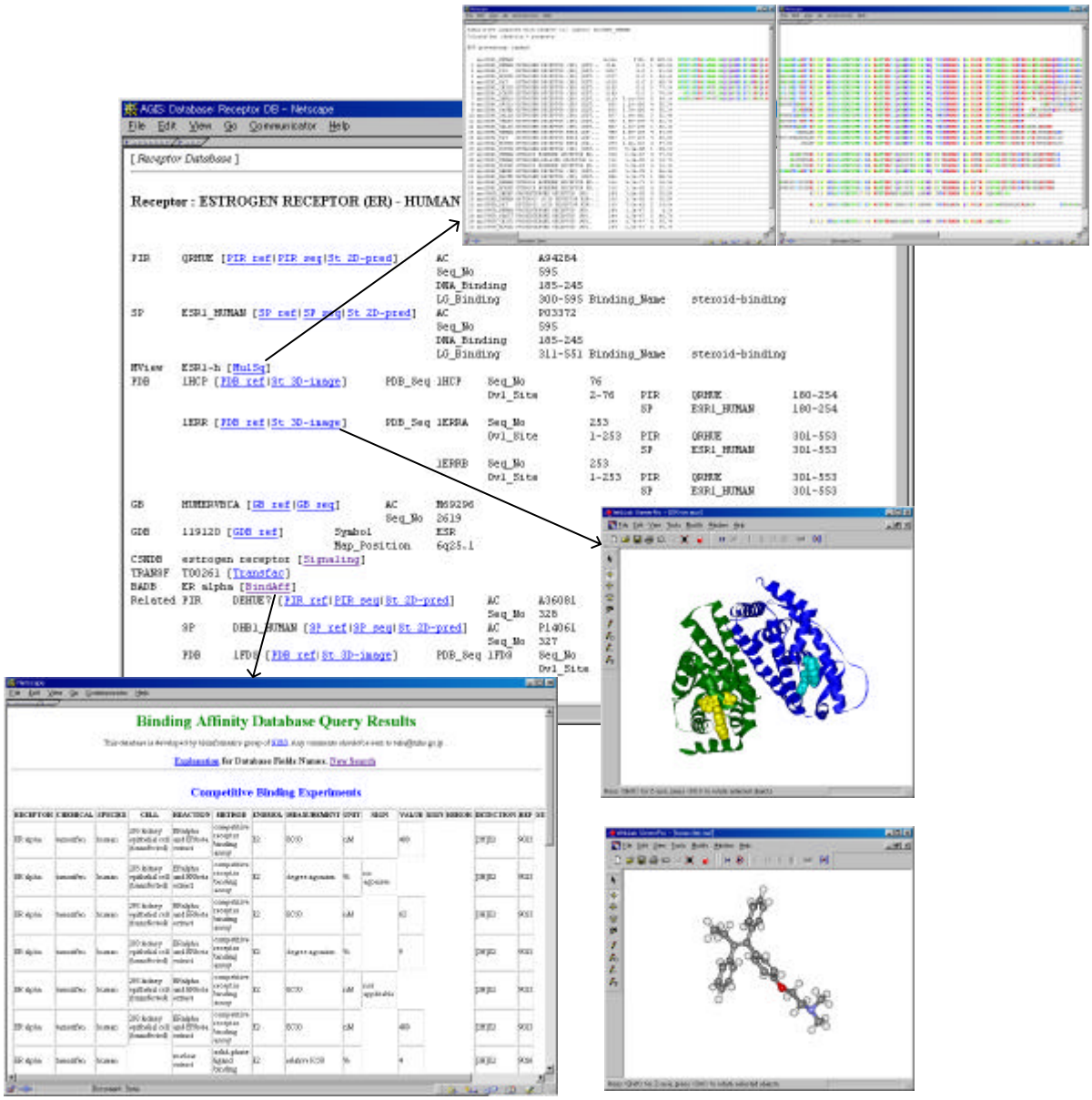
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Binding Affinity Database Query Results
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