

Receptor Database (RDB) As an Analytical Tool

Kotoko Nakata

nakata@nihs.go.jp

Tatsuya Nakano

nakano@nihs.go.jp

Takako Takai

taka@nihs.go.jp

Tsuguchika Kaminuma

kaminuma@nihs.go.jp

Division of Chem-Bio Informatics, National Institute of Health Sciences,
1-18-1, Kamiyoga, Setagaya-ku, Tokyo 158-8501, Japan

Keywords: receptor, internet, binding affinity

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

- [1] Nakata, K., Takai, T. and Kaminuma, T., Development of the receptor database (RDB): application to the endocrine disruptor problem, *Bioinformatics*, 15(7-8):544–552, 1999.
- [2] Nakata, K., Takai, T. and Kaminuma, T., Receptor Database (RDB) in 1999, *Genome Informatics*, 10:278–279, 1999.
- [3] Wingender, E., Chen, X. et al., TRANSFAC: an integrated system for gene expression regulation, *Nucleic Acids Res.*, 28(1):316–319, 2000.
- [4] Kolchanov, N.A., Podkolodnaya et al., Transcription Regulatory Regions Database (TRRD): its status in 2000. *Nucleic Acids Res.*, 28(1):298–301, 2000.
- [5] Kaminuma, T., Takai-Igarashi, T., Nakano, T. and Nakata, K., Modeling of signaling pathways for endocrine disruptors, *BioSystems*, (in press).

Receptor: ESTROGEN RECEPTOR (ER) - HUMAN

FIR QPHUE [FIR_ref|FIR_seq|St_2D-pred] AC A94264
Seq_Mo 595
DNA_Binding 185-245
LQ_Binding 300-595 Binding_Name steroid-binding

SP ESR1_HUMAN [SP_ref|SP_seq|St_2D-pred] AC P03372
Seq_Mo 595
DNA_Binding 185-245
LQ_Binding 311-551 Binding_Name steroid-binding

View ESR1-h [MulSeq]

PDB 1HCP [PDB_ref|St_3D-image] PDB_Seq 1HCP Seq_Mo 76
Dvl_Site 2-76 FIR QPHUE 180-254
SP ESR1_HUMAN 180-254

1EPR [PDB_ref|St_3D-image] PDB_Seq 1EPR Seq_Mo 253
Dvl_Site 1-253 FIR QPHUE 301-553
SP ESR1_HUMAN 301-553

JEPRB Seq_Mo 253
Dvl_Site 1-253 FIR QPHUE 301-553
SP ESR1_HUMAN 301-553

GB MIMR5VICA [GB_ref|GB_seq] AC B69290
Seq_Mo 2619

GB 11912D [GB_ref] Symbol
Map_Position 6q25.1

CNIB estrogen receptor [Signaling]

TPAMSP T00261 [TransFac]

DADE ER_alpha [BindAff]

Related FIR DEHUE7 [FIR_ref|FIR_seq|St_3D-pred] AC A96081
Seq_Mo 328

SP ESR1_HUMAN [SP_ref|SP_seq|St_2D-pred] AC P14061
Seq_Mo 327

PDB 1FD9 [PDB_ref|St_3D-image] PDB_Seq 1FD9 Seq_Mo
Dvl_Site

Binding Affinity Database Query Results

Competitive Binding Experiments

RECEPTOR	CHEMICAL	SPECIES	CELL	REACTION	ASSAY	DRUGS	MEASURE	UNIT	SECT	VALUE	REV	SCORE	EXCISION	REP	DT
ER	spiro	human	hsc27	estrogen	competitive binding	ER	ER	IC50	nM	400	100	100	100	100	100
ER	spiro	human	hsc27	estrogen	competitive binding	ER	ER	agonist	agonism	100	100	100	100	100	100
ER	spiro	human	hsc27	estrogen	competitive binding	ER	ER	IC50	nM	10	100	100	100	100	100
ER	spiro	human	hsc27	estrogen	competitive binding	ER	ER	agonist	agonism	10	100	100	100	100	100
ER	spiro	human	hsc27	estrogen	competitive binding	ER	ER	IC50	nM	100	100	100	100	100	100
ER	spiro	human	hsc27	estrogen	competitive binding	ER	ER	agonist	agonism	100	100	100	100	100	100
ER	spiro	human	hsc27	estrogen	competitive binding	ER	ER	IC50	nM	100	100	100	100	100	100
ER	spiro	human	hsc27	estrogen	competitive binding	ER	ER	agonist	agonism	100	100	100	100	100	100

3D Protein Structure

Ligand Structure