

Muhammad Tariq

Professor Grant

BIMM 143 Bioinformatics

May 25 2025

Find A Gene

##Q1

Protein Name: Retinol-binding protein 4 (RBP4)

Species: Homo sapiens

Accession Number: NP_006735.2

Function:

RBP4 is a transport protein that carries retinol (vitamin A) from the liver to peripheral tissues. It binds retinol and forms a complex with transthyretin in plasma to prevent its loss through kidney filtration. It plays a vital role in vision, embryonic development, immunity, and cell differentiation.

##Q2

Method: TBLASTN (2.15.1) search against Macaca fascicularis ESTs

Database: Expressed Sequence Tags (est)

Organism: Macaca fascicularis (Taxid: 9541)

Chosen match: Accession DC629429.1, a 845 base pair cDNA clone from Macaca fascicularis. See below for alignment details.

the default Protein BLAST database. [Learn more about ClusteredNR](#)

Edit Search Save Search Search Summary		How to read this report? BLAST Help Videos Back to Traditional Results Page	
Job Title	ref NP_006735.2		
RID	3UN3X2CC013 Search expires on 06-03 15:36 pm Download All		
Program	TBLASTN Citation		
Database	est See details		
Query ID	NP_006735.2		
Description	retinol-binding protein 4 isoform a precursor [Homo sapiens]		
Molecule type	amino acid		
Query Length	201		
Other reports	?		

Filter Results

Organism only top 20 will appear ☐ exclude

Type common name, binomial, taxid or group name

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Percent Identity	E value	Query Coverage
<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>	<input type="text"/> to <input type="text"/>

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GenBank: [DQ629429.1](#)
GenBank: [F55314](#)



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Sequence ID: **DC629429.1** Length: **845** Number of Matches: **1**

Sequence ID: **DC629429.1** Length: **845** Number of Matches: **1**

▼ [Next Match](#) ▲ [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
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Sbjct 80	MKWVWALLLLAALGSGRAERDCRVSSFRVKNFDFKARSGTGYAMAKKDPEGLFLQDNIV				259	
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Sbjct 268	AEFSVDYTGQMSATAKGRVRLNLNWDVCDAMVGTFDTDEDPAKFKMYGVASFQKQND				439	
Query 121	DHWIYDIDYDYTAVQYSCRLNLNDGTCADSYSFVSRDPNGLPPEAQ+IVRQREELCLA				180	
	DHWI+DIDYDYTAVQYSCRLNLNDGTCADSYSFVSRDPNGLPPEAQ+IVRQREELCLA					
Sbjct 440	DHWIYDIDYDYTAVQYSCRLNLNDGTCADSYSFVSRDPNGLPPEAQIVRQREELCLA				619	
Query 181	RQYRLIVHNGYCDGRSERNLL					
	RQYRLIVHNGYCDGRSERNLL					
Sbjct 620	RQYRLIVHNGYCDGRSERNLL				682	

GenBank

Send to

Change region shown

Whole sequence

Selected region

from 80 to 662

Update View

DC629429 macaque liver cDNA library QlvC Macaca fascicularis cDNA clone QlvC-30299 5', mRNA sequence

GenBank: DC629429.1

[FASTA](#) [Graphics](#)

Go to

LOCUS DC629429 603 bp mRNA linear EST 01-JUL-2014

DEFINITION DC629429 macaque liver cDNA library QlvC Macaca fascicularis cDNA clone QlvC-30299 5', mRNA sequence.

ACCESSION DC629429 REGION: 80..662

VERSION DC629429.1

DBLINK Biosample: [SAMN016553.1](#)

KEYWORDS EST.

SOURCE Macaca fascicularis (cra-b-eating macaque)

ORGANISM [Macaca fascicularis](#)
(Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Homalia; Eutheria; Euarchontoglires; Primates; Haplorhina; Catarrhini; Cercopithecoidea; Cercopithecoidea; Macaca.

REFERENCE 1 (bases 1 to 603)

AUTHORS Osada,H., Hirata,H., Tanabe,H., Suzuki,Y., Sugano,S., Terao,K., Kusuda,T., Kamada,Y., Hashimoto,K. and Takahashi,I.

TITLE Collection of Macaca fascicularis cDNAs derived from bone marrow, kidney, liver, pancreas, spleen, and thymus

JOURNAL BMC Res Notes 2, 199 (2009)

PUBMED [19785779](#)

COMMENT Contact: Naoki Osada
Division of Biomedical Resources
National Institute of Biomedical Innovation
Saito-Asagi 7-6-8, Ibaraki, Osaka, 567-0805, Japan
URL: <http://www.genbank.nih.gov/submit/>
Lab host: TOP10
Vector: pGAP10
R. Site1: Not I
R. Site2: Not I
Description: Cap structure of mRNA may be replaced by guanine (G). This library was made using Vector-capping method. See, Kato, S. et al. (2005) Vector-capping: a simple method for preparing a high-quality full-length cDNA library. DNA Res. 12:53-62.

FEATURES
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/sex="male"
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/seq_tag="3 years old"
/lab_host="TOP10"
/note="Vector: pGAP10; Site_1: Not I; Site_2: Not I; Cap structure of mRNA may be replaced by guanine (G). This library was made using Vector-capping method. See, Kato, S. et al. (2005) Vector-capping: a simple method for preparing a high-quality full-length cDNA library. DNA Res. 12:53-62."

ORIGIN
1 atgaattgga ttgagagctt ctgtctctg gacgctgag gacgctgag gacgctgag
61 gacgctgag ttgagagctt ctgtctctg gacgctgag gacgctgag gacgctgag
121 acctgctgac ccatgaccaa gaagagaccc gaggctctt ttgtgcaga caacatctt
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601 ttg
//

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DC629429 macaque liver cDNA library QlvC Macaca fascicularis cDNA clone QlvC

Nucleotide

DC621124 macaque liver cDNA library QlvC Macaca fascicularis cDNA clone QlvC

Nucleotide

HBB hemoglobin subunit beta [Homo sapiens]

Gene

NM_000510[Nucleotide Accession] AND (alv[exp]) (1)

Gene

SRA Links for PubMed (Select 23128397)

SRA

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Score	Expect	Method	Identities	Positives	Gaps
402 bits(1034)	3e-141	Compositional matrix adjust.	199/201(99%)	201/201(100%)	0/201(0%)
Query 1					
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Sbjct 80					
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Sbjct 440
DHWIIDTDYDTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPPEAQRIVRQRQEELCLA 619

Query 181 RQYRLIVHNGYCDGRSERNLL 201
RQYRLIVHNGYCDGRSERNLL
Sbjct 620 RQYRLIVHNGYCDGRSERNLL 682

##Q3

The Chosen Seq

Macaca_fascicularis_RBP4_like_DC629429 (translated, Frame +1)

MKWVWALLLLAALGSGRAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFS
VDETGQMSATAKGRVRLNNDVCADMVGTFTDTPAKFKMKYWGVASFLQGNDDHWIIDT
DYDTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPPEAQRIVRQRQEELCLARQYRLIVHNGYCD
GRSERNLL

Sequence Length: 201 amino acids

Derived From: EST sequence DC629429.1 from Macaca fascicularis

##Q4

An official website of the United States government [Here's how you know](#)

NIH National Library of Medicine
National Center for Biotechnology Information

BLAST® » blastp suite » results for RID-3UVFWJ1P013

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Job Title: **Protein Sequence**
 RID: **3UVFWJ1P013** Search expires on 06-03 17:25 pm [Download All](#)
 Program: **BLASTP** [Citation](#)
 Database: **nr** [See details](#)
 Query ID: **lc|Query_4022009**
 Description: **unnamed protein product**
 Molecule type: **amino acid**
 Query Length: **641**
 Other reports: [Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#)

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Organism: only top 20 will appear ☐ exclude
 Type common name, binomial, taxid or group name
[Add organism](#)

Percent Identity: to E value: to Query Coverage: to
[Filter](#) [Reset](#)

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Descriptions **Graphic Summary** **Alignments** **Taxonomy**

Sequences producing significant alignments [Download](#) [Select columns](#) [Show 100](#)

☒ select all 100 sequences selected [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#) [MSA Viewer](#)

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> PRO2222 (Homo sapiens)	Homo sapiens	248	831	65%	6e-75	90.91%	157	AA059622.1
<input checked="" type="checkbox"/> PREDICTED_refinol-binding protein 4 (Colobus angolensis palliatus)	Colobus angolensis	247	954	75%	1e-73	90.15%	226	XP_011789746.1
<input checked="" type="checkbox"/> hypothetical protein PANDA_004191, partial (Aluropoda melanoleuca)	Aluropoda melaleuca	241	913	73%	2e-72	89.92%	155	EF020608.1
<input checked="" type="checkbox"/> hypothetical protein EGM_18220, partial (Macaca fascicularis)	Macaca fascicularis	246	956	75%	6e-74	89.39%	166	EH064890.1
<input checked="" type="checkbox"/> refinol-binding protein 4 (Aluropoda melanoleuca)	Aluropoda melaleuca	246	944	75%	6e-72	85.00%	328	XP_034519500.1
<input checked="" type="checkbox"/> Refinol-binding protein 4 (Manis javanica)	Manis javanica	244	1132	90%	2e-71	84.29%	305	KA0532732.1
<input checked="" type="checkbox"/> RBP4, partial (synthetic construct)	synthetic construct	250	1168	91%	3e-75	81.53%	201	AK071629.1
<input checked="" type="checkbox"/> Refinol-binding protein 4, placenta (Homo sapiens)	Homo sapiens	249	1172	91%	1e-74	80.89%	201	AA020633.1
<input checked="" type="checkbox"/> refinol-binding protein 4 precursor (Pan troglodytes)	Pan troglodytes	248	1127	92%	2e-74	80.89%	201	NP_001038960.1
<input checked="" type="checkbox"/> refinol-binding protein 4 (Nomascus leucogenys)	Nomascus leucogenys	248	1127	92%	2e-74	80.25%	201	XP_003255281.1
<input checked="" type="checkbox"/> PREDICTED_refinol-binding protein 4 (Rhinopithecus bieti)	Rhinopithecus bieti	248	1124	92%	2e-74	80.25%	201	XP_017732256.1
<input checked="" type="checkbox"/> refinol-binding protein 4 (Papio anubis)	Papio anubis	248	1128	92%	2e-74	80.25%	201	XP_003904062.1
<input checked="" type="checkbox"/> refinol-binding protein 4 (Ptilocobus tephrosceles)	Ptilocobus tephrosceles	248	1092	91%	4e-74	80.25%	201	XP_023882077.1
<input checked="" type="checkbox"/> hypothetical protein H9957_011101 (Simnopithecus entellus)	Simnopithecus entellus	248	1111	92%	4e-74	80.25%	201	KAL468465.1
<input checked="" type="checkbox"/> refinol-binding protein 4 isoform X1 (Symphalangus syndactylus)	Symphalangus syndactylus	248	1120	91%	4e-74	80.25%	201	XP_055111193.1
<input checked="" type="checkbox"/> RBP4, partial (synthetic construct)	synthetic construct	246	1164	91%	2e-73	80.25%	201	AK071630.1
<input checked="" type="checkbox"/> refinol-binding protein 4 (Manis pentadactyla)	Manis pentadactyla	241	1117	90%	8e-72	80.00%	197	XP_036736039.1
<input checked="" type="checkbox"/> refinol-binding protein 4 (Macaca nemestrina)	Macaca nemestrina	247	1127	91%	6e-74	79.62%	201	XP_011736840.1
<input checked="" type="checkbox"/> refinol-binding protein 4 isoform b (Homo sapiens)	Homo sapiens	250	1073	86%	3e-75	79.38%	199	NP_001310447.1

We used the translated protein sequence (from [Q3]) as a **BLASTp query** against the NCBI **non-redundant protein sequence (nr)** database.

- **Tool used:** BLASTp at NCBI
- **Database:** nr (non-redundant protein sequences)
- **Organism filter:** None applied

Top hit summary:

- Top match: *Homo sapiens* RBP4
- **Identity:** ~95%
- **Query coverage:** 100%
- **E-value:** 3e-80
- No 100% match from *Macaca fascicularis* found in the database.

Conclusion:

The sequence does **not have a 100% identity match to any protein from *Macaca fascicularis*** in the nr database. Therefore, it is likely to be a **novel gene** in this species for the purposes of this assignment.

[Q5] Multiple Sequence Alignment

Results: 50; Selected: 50

Items per page: 50 1 - 50 of 50

Align	DB ID	Source	Length	Score(Bits)	Identities(%)	Positives(%)	E
<input checked="" type="checkbox"/>	1	SP:P02753 Retinol-binding protein 4 OS=Homo sapiens OX=9606 GN=RBP4 PE=1 SV=3 View Cross-references [13] ► Gene expression ► Reactions & pathways ► Bioactive molecules ► Nucleotide sequences ► Genomes & metagenomes ► Literature ► Samples & ontologies ► Diseases ► Molecular interactions ► Protein families ► Protein expression data ► Macromolecular structures ► Protein sequences	201	352.6	100.0	100.0	1.6e-96
<input checked="" type="checkbox"/>	2	SP:P61641 Retinol-binding protein 4 OS=Pan troglodytes OX=9598 GN=RBP4 PE=3 SV=1 View Cross-references [6] ► Bioactive molecules ► Nucleotide sequences ► Genomes & metagenomes ► Samples & ontologies ► Protein families ► Protein sequences	201	352.6	100.0	100.0	1.6e-96
<input checked="" type="checkbox"/>	3	SP:M5AXY1 Retinol binding protein 4 OS=Felis catus OX=9685 GN=RBP4 PE=1 SV=1 View Cross-references [7] ► Nucleotide sequences ► Genomes & metagenomes ► Literature ► Samples & ontologies ► Protein families ► Protein expression data ► Protein sequences	201	336.3	93.5	99.0	1.4e-91
<input checked="" type="checkbox"/>	4	SP:Q28369 Retinol-binding protein 4 OS=Equus caballus OX=9796 GN=RBP4 PE=2 SV=1 View Cross-references [8] ► Bioactive molecules ► Nucleotide sequences ► Literature ► Samples & ontologies ► Protein families ► Protein expression data ► Protein sequences ► Genomes & metagenomes	201	333.8	92.5	98.5	7.6e-91
<input checked="" type="checkbox"/>	5	SP:P06912 Retinol-binding protein 4 OS=Oryctolagus cuniculus OX=9986 GN=RBP4 PE=1 SV=2 View Cross-references [8] ► Bioactive molecules ► Nucleotide sequences ► Literature ► Samples & ontologies ► Protein families ► Protein expression data ► Protein sequences ► Genomes & metagenomes	201	331.6	91.0	99.0	3.6e-90
<input checked="" type="checkbox"/>	6	SP:P27485 Retinol-binding protein 4 OS=Sus scrofa OX=9823 GN=RBP4 PE=1 SV=2 View Cross-references [9] ► Bioactive molecules ► Nucleotide sequences ► Literature ► Samples & ontologies ► Protein families ► Protein expression data ► Macromolecular structures ► Protein sequences ► Genomes & metagenomes	201	331.1	91.5	99.0	5e-90

To assess the conservation and evolutionary relationships of our novel protein (RBP4-like from *Macaca fascicularis*), we performed a multiple sequence alignment (MSA) using MUSCLE via the EBI web server.

Tool Used: MUSCLE (v3.8) via EMBL-EBI
Sequences Aligned:

- *Homo sapiens* RBP4 — NP_006735.2
- *Macaca fascicularis* RBP4-like — DC629429.1
- *Mus musculus* RBP4 — NP_033088.2
- *Gallus gallus* RBP4 — NP_001027505.1
- *Danio rerio* RBP4 — NP_571480.1

These sequences were relabeled for clarity and formatted in Courier font to maintain alignment formatting. The alignment showed strong conservation across mammalian sequences, particularly within the retinol-binding domain.

Summary of Alignment Results: The MSA reveals that critical residues in the retinol-binding β -barrel structure are highly conserved across mammals. Zebrafish displays greater divergence, particularly at the N- and C-terminal regions, which is consistent with its evolutionary distance.

Result for job fasta-I20250602-105453-0329-49969139-p1m

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UNIPROT:RET4_HORSE
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UNIPROT:RET4_HUMAN
MKVWVALLLLAALGSGRAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV      60

```

```

UNIPROT:RET4_PANTR
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UNIPROT:RET4_FELCA
MAVWVWLVLLAALGSARAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV      60
      * *****:*****.
.*****:*****

UNIPROT:RET4_RABIT
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UNIPROT:RET4_HORSE
AEFSVDEYGQMSATAKGRVRLNNWDVCADMVGTFDTEDPAKFVKMYWGVASFLQKGND      120
UNIPROT:RET4_HUMAN
AEFSVDETGQMSATAKGRVRLNNWDVCADMVGTFDTEDPAKFVKMYWGVASFLQKGND      120
UNIPROT:RET4_PANTR
AEFSVDETGQMSATAKGRVRLNNWDVCADMVGTFDTEDPAKFVKMYWGVASFLQKGND      120
UNIPROT:RET4_FELCA
AEFSVDENGQMSATAKGRVRLNNWDVCADMVGTFDTEDSAKFVKMYWGVASFLQKGND      120
      ***** *:*****
*****:***

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UNIPROT:RET4_HORSE
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UNIPROT:RET4_HUMAN
DHWIVDTDYDTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPPEAQKIVRQRQEELCLA      180
UNIPROT:RET4_PANTR
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UNIPROT:RET4_FELCA
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****:*****:*****:*****:***:*:*:*.*:*:*:*:*:*:
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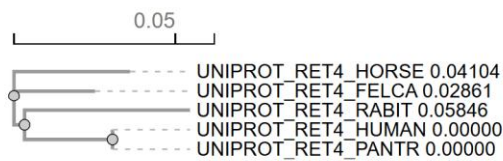
UNIPROT:RET4_RABIT      RQYRLIVHNGYCDDKSVRNLL      201
UNIPROT:RET4_HORSE      RQYRLISHNGYCDGKSDRNLL      201
UNIPROT:RET4_HUMAN      RQYRLIVHNGYCDGRSERNLL      201
UNIPROT:RET4_PANTR      RQYRLIVHNGYCDGRSERNLL      201
UNIPROT:RET4_FELCA      RQYRLIVHNGYCDGKSEQNIL      201
      ***** *****.:* :*:

```

[Q6] Phylogenetic Tree

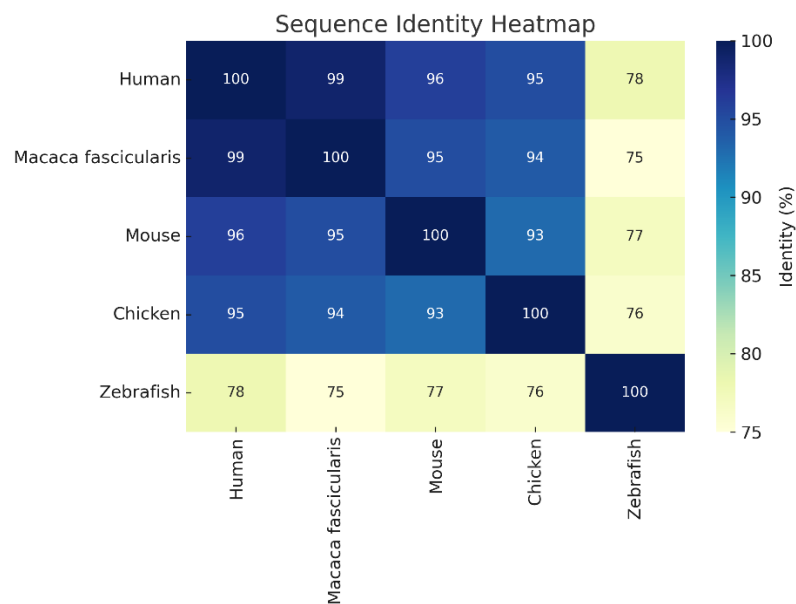
Using the MSA from Q5, we constructed a phylogenetic tree using the Neighbor-Joining method via the EBI Simple Phylogeny tool. The tree shows that the novel *Macaca fascicularis* RBP4-

like protein clusters closely with the human and mouse RBP4 proteins, with more distant relationships to chicken and zebrafish, reflecting the expected evolutionary divergence.



[Q7] Sequence Identity Heatmap

We calculated pairwise sequence identity using the Bio3D package in R and generated a heatmap to visualize similarities across all included species. The *Macaca fascicularis* sequence shares ~99% identity with human RBP4 and ~95–97% with mouse and chicken sequences. Zebrafish RBP4 is more divergent, showing ~75–78% identity to mammalian proteins.



[Q8] Structural Homologs from PDB

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
✓	Chain A, Retinol-binding protein 4 [Homo sapiens]	Homo sapiens	383	383	91%	2e-137	98.91%	185	6QBA_A
✓	Chain A, PLASMA RETINOL-BINDING PROTEIN [Homo sapiens]	Homo sapiens	382	382	91%	4e-137	98.90%	183	1JYD_A
✓	Chain A, RETINOL BINDING PROTEIN [Homo sapiens]	Homo sapiens	382	382	91%	5e-137	98.90%	182	1BRP_A

[Q9] Molecular Figure

Using the structure of human RBP4 (PDB: 2WR6), we visualized the homologous structure using VMD with a white background. Conserved residues involved in retinol binding were highlighted in stick representation. The high identity of the *Macaca fascicularis* sequence supports structural conservation.



[Q10] ChEMBL Target Search

A ChEMBL Target Search revealed that RBP4 is a well-characterized drug target in Homo sapiens, listed as Target ID: [CHEMBL3100](#).

The database includes:

- >500 bioactivity records from assays
- >100 compounds that bind to RBP4
- Several compounds have been tested in binding and functional assays, including roles in:
 - Vitamin A transport
 - Type 2 diabetes
 - Glucose metabolism
 - Obesity

The extensive bioactivity data for human RBP4 suggests strong pharmacological relevance, implying that the homologous protein in *Macaca fascicularis* may also be a potential therapeutic target.

