

FASTA SEQUENCE

rest.uniprot.org/uniprotkb/Q9BZX4.fasta

```
>sp|Q9BZX4|ROP1B_HUMAN Ropporin-1B OS=Homo sapiens OX=9606 GN=ROP1B PE=1 SV=1
MAQTDKPTCIPPELPKYLKEFAKAAIRAQPQDLIQGADYFEALSREGTPPPVRERSERVA
LCNWAELTPELLKILHSQVAGRLITRAEELAQMKVWVILPTDLFNSVIMVNGRFTTEEIHL
KFLALACSAAGVTITKTLKIVCEVLSCDHNGGLPRIPFSTFQFLTYTIAEVDGEICASHV
SRMLNYIEQEVIGPDGLITVNDFTQNPVWLE
```

Figure 1

3D structure

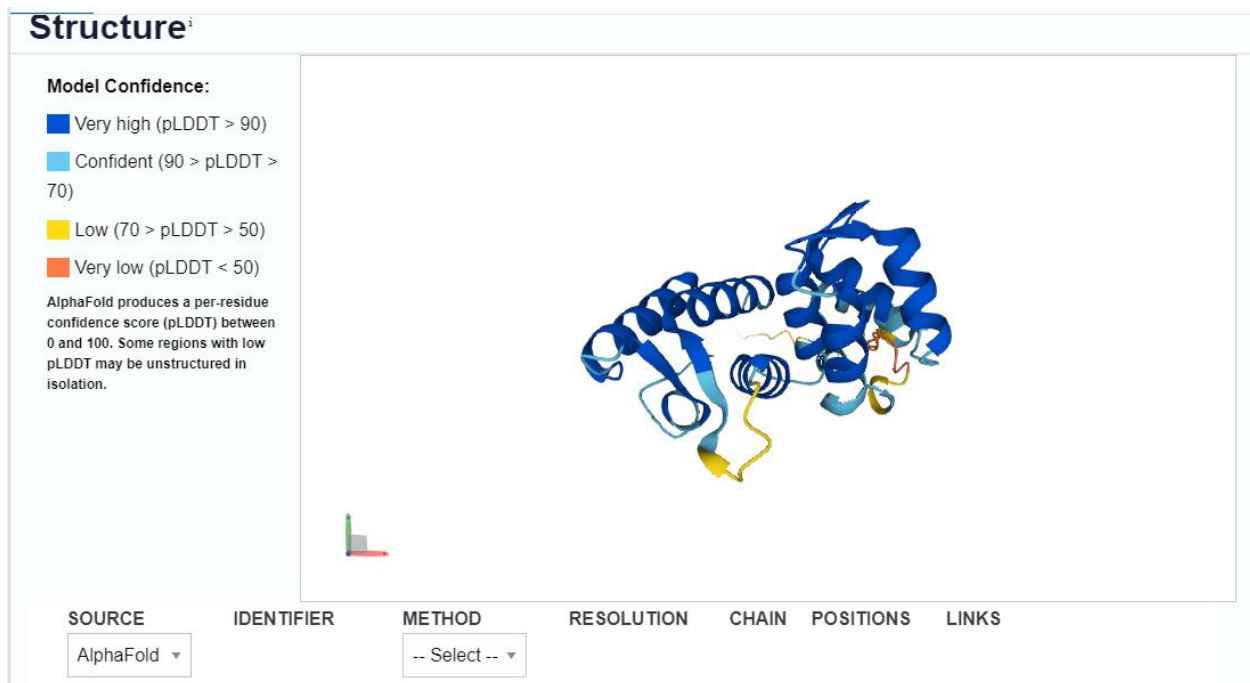


Figure 2

The source of the 3D structure of the protein is Alpha Fold and hence this is the predicted structure.

Case A

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

DownloadSelect columnsShow10

select all

10 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"/>	ropporin-1B [Homo sapiens]	Homo sapiens	440	440	100%	1e-155	100.00%	212	NP_001012337.1
<input checked="" type="checkbox"/>	Ropporin_rhopilin associated protein 1B [synthetic construct]	synthetic construct	436	436	100%	5e-154	99.53%	212	AAI40023.1
<input checked="" type="checkbox"/>	ropporin-1B isoform X1 [Gorilla gorilla gorilla]	Gorilla gorilla gorilla	434	434	100%	2e-153	99.06%	212	XP_004036269.2
<input checked="" type="checkbox"/>	ropporin-1B isoform X2 [Pan troglodytes]	Pan troglodytes	431	431	100%	2e-152	98.11%	212	XP_001134814.2
<input checked="" type="checkbox"/>	ropporin-1B isoform X2 [Pan paniscus]	Pan paniscus	430	430	100%	7e-152	98.11%	212	XP_034813156.1
<input checked="" type="checkbox"/>	ropporin-1B isoform X1 [Pan troglodytes]	Pan troglodytes	431	431	100%	1e-151	98.11%	223	XP_063663147.1
<input checked="" type="checkbox"/>	ropporin-1B [Macaca mulatta]	Macaca mulatta	429	429	100%	1e-151	97.17%	212	NP_001181555.3
<input checked="" type="checkbox"/>	ropporin-1B isoform X1 [Pan paniscus]	Pan paniscus	429	429	100%	3e-151	98.11%	223	XP_054966353.1
<input checked="" type="checkbox"/>	ropporin-1B isoform X1 [Pongo pygmaeus]	Pongo pygmaeus	428	428	100%	6e-151	97.17%	212	XP_054336733.1
<input checked="" type="checkbox"/>	ropporin-1 [Macaca nemestrina]	Macaca nemestrina	428	428	100%	7e-151	96.70%	212	XP_011720343.1

Figure 4- Description

Alignment view

Pairwise

?

Restore defaults

Download

10 sequences selected

Download

GenPept

Graphics

Next

Previous

Descriptions

ropporin-1B [Homo sapiens]

Sequence ID: [NP_001012337.1](#) Length: 212 Number of Matches: 1

[See 9 more title\(s\)](#)

[See all Identical Proteins\(IPG\)](#)

Range 1: 1 to 212

GenPept

Graphics

Next Match

Previous Match

Score	Expect	Method	Identities	Positives	Gaps
440 bits (1131)	1e-155	Compositional matrix adjust.	212/212(100%)	212/212(100%)	0/212(0%)
Query 1	MAQTDKPTCIPPELPKMLKEFAKAAIRAQPDLIQWGADYFEALS	SRGETPPVRRSERVA	60		
Sbjct 1	MAQTDKPTCIPPELPKMLKEFAKAAIRAQPDLIQWGADYFEALS	SRGETPPVRRSERVA	60		
Query 61	LCNNAELTPELLKILHSQVAGRLIIRAEELAQMKVKNLPTDLFNSVMNVGRFTEETIWL		120		
Sbjct 61	LCNNAELTPELLKILHSQVAGRLIIRAEELAQMKVKNLPTDLFNSVMNVGRFTEETIWL		120		
Query 121	KFLALACSGVTITKTLKIVCEVLSCDHNGGLPRIPFSTFQFLYTYIAEVDGEICASHV		180		
Sbjct 121	KFLALACSGVTITKTLKIVCEVLSCDHNGGLPRIPFSTFQFLYTYIAEVDGEICASHV		180		
Query 181	SRMLNYIEQEVIGPDGLITVNDFTQNPRVWLE		212		
Sbjct 181	SRMLNYIEQEVIGPDGLITVNDFTQNPRVWLE		212		

Related Information

[Gene](#) - associated gene details

[AlphaFold Structure](#) - 3D structure displays

[Genome Data Viewer](#) - aligned genomic context

[Identical Proteins](#) - Identical proteins to NP_001012337.1

Figure 3-Alignment

The **BLAST** results for the best 10 HSP shows that the sequences are homologs upto 96% identity

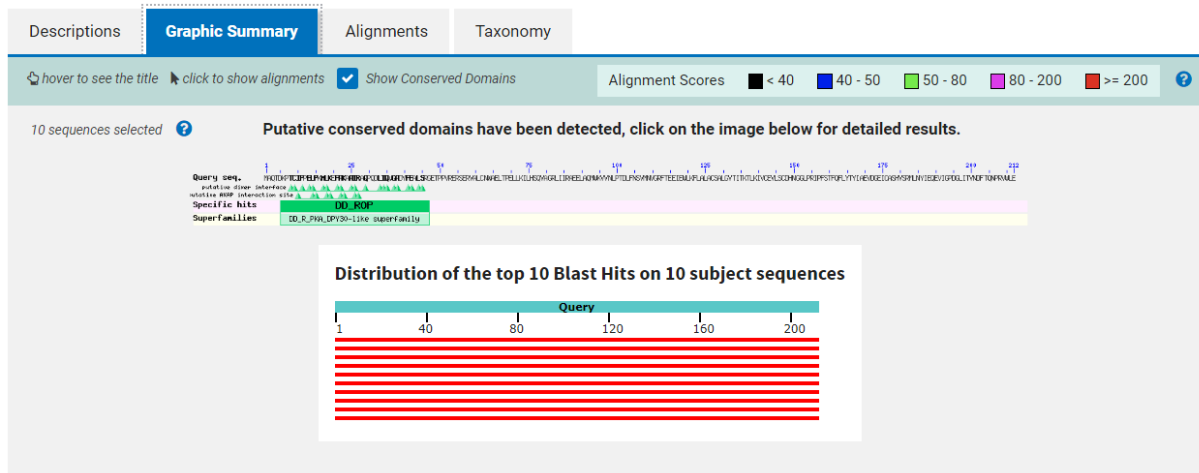


Figure 4-Graphic summary

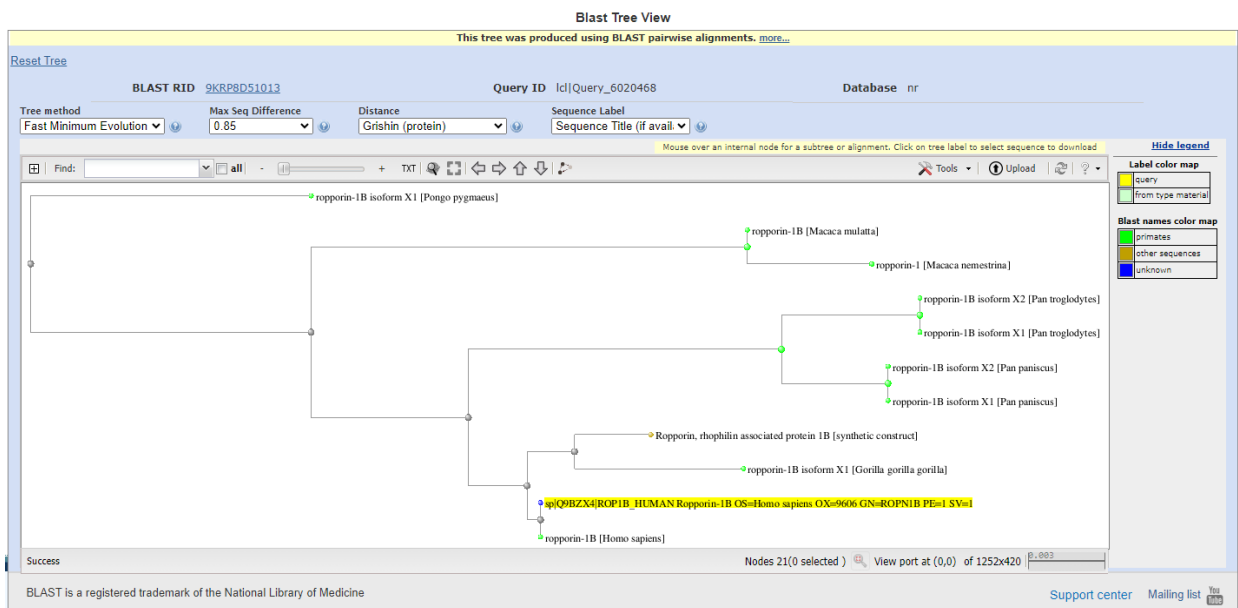


Figure 5- Distance Tree

The graphical summary represents that they are homologues sequences and the distance tree shows the relationship with the homologues sequences.

Case B

Descriptions

Graphic Summary

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Download

Select columns

Show

10

☒ select all 10 sequences selected

[GenPept](#)
[Graphics](#)
[Distance tree of results](#)
[Multiple alignment](#)
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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	ropporin-1B [Homo sapiens]	Homo sapiens	458	458	100%	4e-164	100.00%	212	NP_001012337.1
<input checked="" type="checkbox"/>	Ropporin_rhopilin associated protein 1B [synthetic construct]	synthetic construct	455	455	100%	1e-162	99.53%	212	AAI40023.1
<input checked="" type="checkbox"/>	ropporin-1B isoform X1 [Gorilla gorilla gorilla]	Gorilla gorilla gorilla	453	453	100%	4e-162	99.06%	212	XP_004036269.2
<input checked="" type="checkbox"/>	ropporin-1B isoform X2 [Pan troglodytes]	Pan troglodytes	450	450	100%	1e-160	98.11%	212	XP_001134814.2
<input checked="" type="checkbox"/>	ropporin-1B isoform X2 [Pan paniscus]	Pan paniscus	448	448	100%	4e-160	98.11%	212	XP_034813156.1
<input checked="" type="checkbox"/>	ropporin-1B [Macaca mulatta]	Macaca mulatta	448	448	100%	5e-160	97.17%	212	NP_001181555.3
<input checked="" type="checkbox"/>	ropporin-1B isoform X1 [Pan troglodytes]	Pan troglodytes	448	448	100%	7e-160	98.11%	223	XP_063663147.1
<input checked="" type="checkbox"/>	ropporin-1B isoform X1 [Pan paniscus]	Pan paniscus	447	447	100%	2e-159	98.11%	223	XP_054966353.1
<input checked="" type="checkbox"/>	ropporin-1B isoform X1 [Pongo pygmaeus]	Pongo pygmaeus	446	446	100%	3e-159	97.17%	212	XP_054336733.1
<input checked="" type="checkbox"/>	ropporin-1 [Macaca nemestrina]	Macaca nemestrina	446	446	100%	4e-159	96.70%	212	XP_011720343.1

Figure 6- description

[illegible]

Figure 7- Graphic Summary

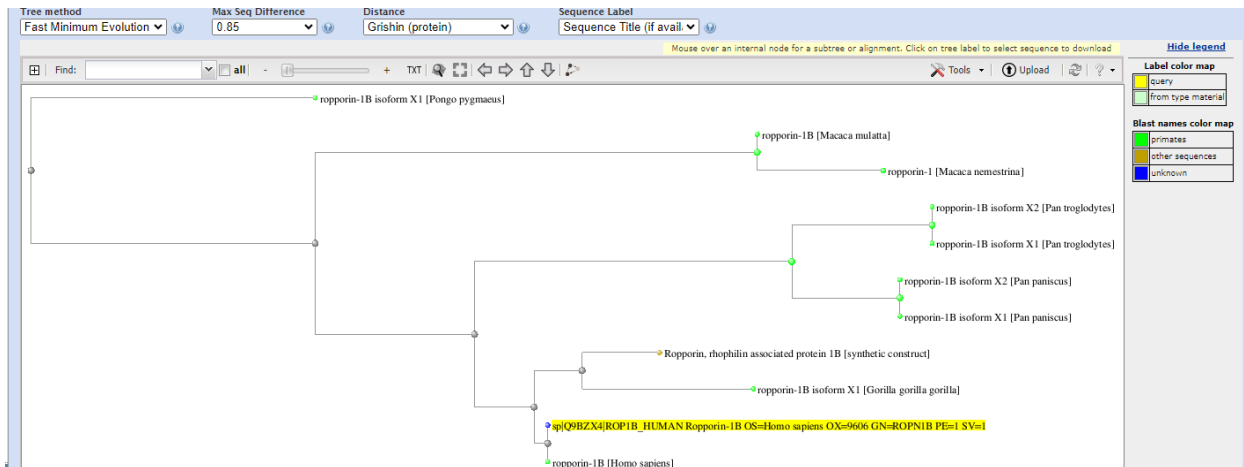


Figure 8- Distance Tree

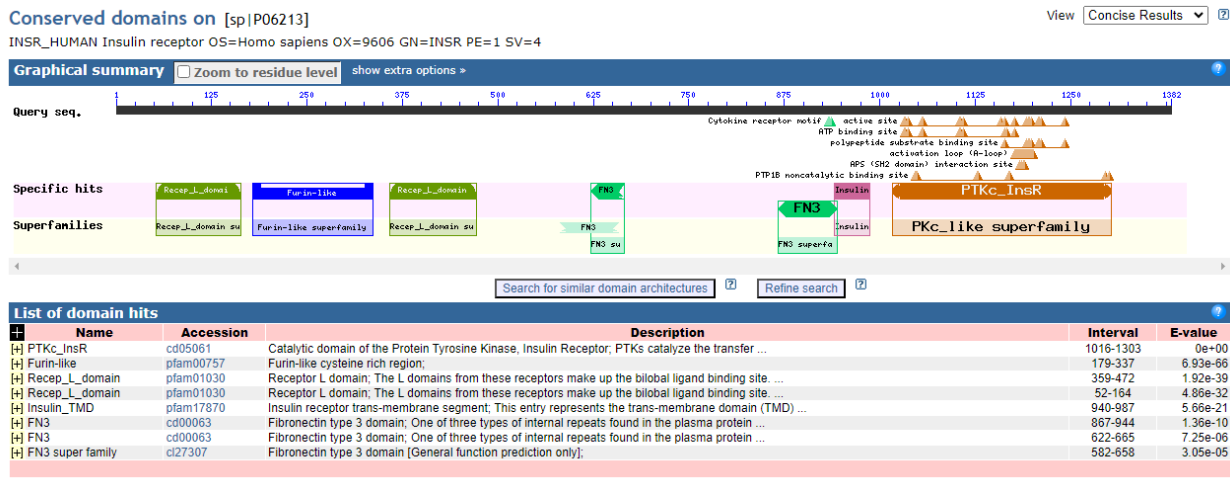


Figure 9- Conserved domains

The case B represents the BLAST for E value =0.1 and the matrix = BLOSUM45. The conserved domains shows that the L domains from these receptors make up the bilobal ligand binding site. Each L domain consists of a single-stranded right hand beta-helix. This Pfam entry is missing the first 50 amino acid residues of the domain.

