

Q1:

Protein Name: RBP4 retinol binding protein 4

Gene ID: 5950 <https://www.ncbi.nlm.nih.gov/gene/5950>

Species: Homo Sapiens (Humans)

Accession Number: NP_006735

Function: It's expressed in the liver, a member of the lipocalin family and works as retinol carrier(vitamin A alcohol) in the blood. It delivers retinol from the liver stores to the peripheral tissues. A deficiency of vitamin A blocks secretion of the binding protein post translationally and results in defective delivery and supply to the epidermal cells.

Q2:

Method: TBLASTN (2.7.1) search in dog, cayote and wolf against ESTs

Database: expressed sequence tags(ESTs)

Organism: dog, coyote, wolf (taxid: 9608)

Translated BLAST: tblastn

blastnblasttblastntblastx

Enter Query Sequence

TBLASTN search translated nucleotide databases using a protein query. [more...](#)

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

NP_006735

Query subrange [?](#)

From

To

Or, upload file

Choose File No file chosen [?](#)

Job Title

NP_006735:retinol-binding protein 4 isoform...

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Database

Expressed sequence tags (est) [?](#)

Organism

Optional

dog, coyote, wolf, fox (taxid:9608) ☐ exclude [Add organism](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

Exclude

Optional

☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Limit to

Optional

☐ Sequences from type material

Entrez Query

Optional

[YouTube](#) [Create custom database](#)

Enter an Entrez query to limit search [?](#)

BLAST

Search database est using Tblastn (search translated nucleotide databases using a protein query)

☐ Show results in a new window

◀ Edit Search

Save Search






Search Summary ▼

🔗 How to read this report?

📺 BLAST Help Videos

↶ Back to Traditional Results Page

📘 Your search is limited to records that include: dog, coyote, wolf, fox (taxid:9608)

Job Title	NP_006735:retinol-binding protein 4		
RID	PBXB034S01N	Search expires on 10-14 04:51 am	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

+ [Add organism](#)

Percent Identity

to

E value

to

Query Coverage

to

Filter

Reset

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download ▼

New Select columns ▼

Show



☒ select all 100 sequences selected

[GenBank](#)

[Graphics](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_61_H02.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 61_H02_mRNA s...	Canis lupus famil...	382	382	100%	3e-136	90.05%	690	GR896676.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_67_D04.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 67_D04_mRNA s...	Canis lupus famil...	380	380	100%	1e-135	89.55%	682	GR898450.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_85_C08.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 85_C08_mRNA s...	Canis lupus famil...	380	380	100%	2e-135	89.55%	727	GR899794.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_73_B05.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 73_B05_mRNA s...	Canis lupus famil...	380	380	100%	3e-135	89.55%	759	GR894423.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_90_C12.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 90_C12_mRNA s...	Canis lupus famil...	380	380	100%	3e-135	89.55%	772	GR899440.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_52_G10.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 52_G10_mRNA s...	Canis lupus famil...	380	380	100%	4e-135	89.55%	788	GR900778.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_57_D08.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 57_D08_mRNA s...	Canis lupus famil...	379	379	100%	8e-135	89.55%	737	GR896818.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_60_F06.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 60_F06_mRNA s...	Canis lupus famil...	378	378	100%	2e-134	89.05%	726	GR900917.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_90_G06.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 90_G06_mRNA s...	Canis lupus famil...	379	379	100%	2e-134	89.55%	824	GR895923.1
<input checked="" type="checkbox"/>	JHU073E01L911 Canine cardiovascular system biased cDNA Canis lupus familiaris cDNA similar to Hs retinol bin...	Canis lupus famil...	380	380	100%	3e-134	89.55%	911	DR104816.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_89_C03.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 89_C03_mRNA s...	Canis lupus famil...	374	374	97%	5e-133	90.26%	665	GR896779.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_76_E12.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 76_E12_mRNA s...	Canis lupus famil...	370	370	97%	7e-132	89.74%	664	GR893934.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_79_A07.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 79_A07_mRNA s...	Canis lupus famil...	369	369	100%	8e-131	87.06%	737	GR896490.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_005_008_K10.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 005_K10_...	Canis lupus famil...	367	367	95%	3e-130	90.10%	671	GR898800.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_82_A06.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 82_A06_mRNA s...	Canis lupus famil...	362	362	91%	2e-128	93.48%	678	GR901864.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_60_D07.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 60_D07_mRNA s...	Canis lupus famil...	360	360	94%	1e-127	89.95%	648	GR894812.1
<input checked="" type="checkbox"/>	DP020002000E11 Canine normalized prcd affected retinal cDNA library Canis lupus familiaris cDNA clone DP020...	Canis lupus famil...	354	354	93%	1e-125	89.84%	595	DT536195.1
<input checked="" type="checkbox"/>	or15c02.y1 Dog eye minus lens and cornea Unnormalized (or) Canis lupus familiaris cDNA clone or15c02 5' mR...	Canis lupus famil...	353	353	93%	3e-125	89.84%	636	DN904904.1
<input checked="" type="checkbox"/>	or14c10.y1 Dog eye minus lens and cornea Unnormalized (or) Canis lupus familiaris cDNA clone or14c10 5' mR...	Canis lupus famil...	352	352	92%	1e-124	89.78%	620	DN904827.1
<input checked="" type="checkbox"/>	or17d05.y1 Dog eye minus lens and cornea Unnormalized (or) Canis lupus familiaris cDNA clone or17d05 5' mR...	Canis lupus famil...	350	350	92%	9e-124	89.73%	631	DN905069.1
<input checked="" type="checkbox"/>	or19f11.y1 Dog eye minus lens and cornea Unnormalized (or) Canis lupus familiaris cDNA clone or19f11 5' mRN...	Canis lupus famil...	346	346	91%	3e-122	89.62%	622	DN905262.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_009_012_M21.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 009_M21_...	Canis lupus famil...	345	345	88%	6e-122	92.66%	600	GR896689.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_89_E05.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 89_E05_mRNA s...	Canis lupus famil...	342	342	84%	3e-120	95.86%	701	GR899097.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_84_E01.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 84_E01_mRNA s...	Canis lupus famil...	342	342	84%	6e-120	95.86%	756	GR900161.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_62_H03.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 62_H03_mRNA s...	Canis lupus famil...	335	335	83%	2e-117	94.61%	715	GR896853.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_009_012_M02.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 009_M02_...	Canis lupus famil...	332	332	85%	7e-117	92.98%	650	GR899818.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_68_G02.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 68_G02_mRNA s...	Canis lupus famil...	330	330	83%	2e-115	93.41%	698	GR893892.1
<input checked="" type="checkbox"/>	CANFLECK_JINDO_LV_70_G04.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 70_G04_mRNA s...	Canis lupus famil...	328	328	87%	3e-115	88.57%	602	GR899279.1

Alignment Scores ■ < 40 ■ 40 - 50 ■ 50 - 80 ■ 80 - 200 ■ >= 200

Distribution of the top 118 Blast Hits on 100 subject sequences



CANFLECK_JINDO_LV_70_G04.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 70_G04, mRNA sequence
Sequence ID: [GR899279.1](#) Length: 602 Number of Matches: 1

Range 1: 76 to 600 [GenBank](#) [Graphics](#) [▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps	Frame
328 bits(840)	3e-115	Compositional matrix adjust.	162/175(93%)	169/175(96%)	0/175(0%)	+1
Query 1	MKWVW	all11a	alGSGRAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV	60		
Sbjct 76	MEWVW	ALELLA	ALGSARAESDCRVSNFQVKKTFDKARFAGTWYAMAKKDPEGLFLQDNIV	255		
Query 61	AEFSV	DETGQ	MSATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND	120		
Sbjct 256	AEFSV	DE G+M	SATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND	435		
Query 121	DHWIV	DTDYD	TYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPPEAQKIVRQRQE	175		
Sbjct 436	DHWI	DTDYD	TYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPEAQKIVRQRQE	600		

The chosen match is accession [GR899279.1](#), with 602 nucleotides in the sequence, and belongs to the *Canis lupus familiaris* species.

CANFLECK_JINDO_LV_70_G04.ab1 Jindo liver cDNA library Canis lupus familiaris cDNA clone 70_G04, mRNA sequence

Sequence ID: [GR899279.1](#) Length: 602 Number of Matches: 1

Range 1: 76 to 600

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
328 bits(840)	3e-115	Compositional matrix adjust.	162/175(93%)	169/175(96%)	0/175(0%)	+1
Query 1	MKWVW	all11a	alGSGRAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV	60		
	M+WVW	AL LLA	ALGS RAE DCRVS+F+VK+ FDKARF+GTWYAMAKKDPEGLFLQDNIV			
Sbjct 76	MEWVW	ALELLA	ALGSARAESDCRVSNFQVKKTFDKARFAGTWYAMAKKDPEGLFLQDNIV	255		
Query 61	AEFSV	DETGQ	MSATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND	120		
	AEFSV	DE G+M	SATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND			
Sbjct 256	AEFSV	DENGR	MSATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND	435		
Query 121	DHWIV	DTDYD	TYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPPEAQKIVRQRQE	175		
	DHWI	+DTDY	DTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLP EAQKIVRQRQE			
Sbjct 436	DHWI	IDTDY	DTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPEAQKIVRQRQE	600		

Q3: The sequence is :

>dog| GR899279.1|C. lupus familiaris liver protein(sequence taken from BLAST result)

MEWVWALELLAALGSARAESDCRVSNFQVKKTFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGRMSAT
AKGRVRLNNWDVCADMVGTFDTEDPAKFKMKYWGVSFLQKGNDDHWIIDTDYDTYAVQYSCRLLNLDGTCA
DSYSFVFSRDPNGLPLEAQKIVRQRQE

Name: Canis lupus familiaris Liver protein

Animalia, Chordata, Mammalia, Carnivora, Canidae, Canis, Lupus, familiaris

Q4:

A BLAST-P search against NR database (see setup in first screen-shot below) yielded a top hit result is to a protein from Canis lupus familiaris.

Since the percent identity is 98.9% less than 100%, it's likely to be a novel protein.

blastnblasttblastntblastx

Standard Protein BLAST

BLASTP programs search protein databases using a protein query. [more...](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

>C. lupus familiaris liver protein(sequence taken from BLAST result)
MEWVWALELLAALGSARAESDCRVSNFQVKKTFDKARFAGTWYAMAKKD
PEGLFLQDNIVAEFSVDENGR
MSATAKGRVRLNNWDVCADMVGTFDTEDPAKFKMKYWGVSFLQKGN

Query subrange [?](#)

From

To

Or, upload file

No file chosen [?](#)

Job Title

C. lupus familiaris liver protein(sequence...
[?](#) Enter a descriptive title for your BLAST search

☐ Align two or more sequences [?](#)

Choose Search Set

Database

Non-redundant protein sequences (nr) [?](#)

Organism

Optional

☐ exclude [Add organism](#)

[?](#) Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude

Optional

☐ Models (XM/XP) ☐ Non-redundant RefSeq proteins (WP) ☐ Uncultured/environmental sample sequences

Program Selection

Algorithm

☐ Quick BLASTP (Accelerated protein-protein BLAST)

☒ blastp (protein-protein BLAST)

☐ PSI-BLAST (Position-Specific Iterated BLAST)

☐ PHI-BLAST (Pattern Hit Initiated BLAST)

☐ DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

[?](#) Choose a BLAST algorithm

BLAST

Search database nr using Blastp (protein-protein BLAST)

☐ Show results in a new window

Job Title	Protein Sequence
RID	PC0DGV701N Search expires on 10-14 05:44 am Download All ▼
Program	BLASTP ? Citation ▼
Database	nr See details ▼
Query ID	Id Query_518795
Description	None
Molecule type	amino acid
Query Length	175
Other reports	Distance tree of results Multiple alignment MSA viewer ?

Filter Results

☐ exclude

Organism only top 20 will appear

[+ Add organism](#)

Percent Identity

to

E value

to

Query Coverage

to

[Filter](#)

[Reset](#)

Descriptions	Graphic Summary	Alignments	Taxonomy
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Sequences producing significant alignments									
Download ▼ New Select columns ▼ Show 100 ▼ ?									
<input checked="" type="checkbox"/> select all 100 sequences selected	GenPept	Graphics	Distance tree of results	Multiple alignment	New MSA Viewer				
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	retinol-binding protein 4 [Canis lupus familiaris]	Canis lupus fami...	360	360	100%	3e-125	98.86%	201	XP_038295882.1
<input checked="" type="checkbox"/>	retinol-binding protein 4 [Canis lupus dingo]	Canis lupus dingo	362	362	100%	8e-125	98.86%	267	XP_025322340.2
<input checked="" type="checkbox"/>	retinol-binding protein 4 [Suricata suricatta]	Suricata suricatta	342	342	100%	4e-118	93.14%	201	XP_029788103.1
<input checked="" type="checkbox"/>	retinol-binding protein 4 [Manis javanica]	Manis javanica	341	341	100%	1e-117	92.00%	197	XP_036871530.1
<input checked="" type="checkbox"/>	Retinol binding protein 4, plasma [Homo sapiens]	Homo sapiens	341	341	100%	1e-117	92.57%	201	AAH20633.1
<input checked="" type="checkbox"/>	PREDICTED: retinol-binding protein 4 isoform X1 [Odobenus rosmarus divergens]	Odobenus rosm...	343	343	100%	1e-117	91.43%	265	XP_004412625.2
<input checked="" type="checkbox"/>	PREDICTED: retinol-binding protein 4 [Mustela putorius furo]	Mustela putorius...	341	341	100%	1e-117	92.00%	201	XP_004749701.1
<input checked="" type="checkbox"/>	retinol-binding protein 4 [Callorhinus ursinus]	Callorhinus ursinus	341	341	100%	1e-117	91.43%	201	XP_025736400.1
<input checked="" type="checkbox"/>	retinol-binding protein 4 [Zalophus californianus]	Zalophus califor...	341	341	100%	2e-117	91.43%	201	XP_027452391.1

This protein seems to be a novel protein as it has 98.9% identity with the top hit.

The e-value is 3×10^{-125}

Alignment view

Pairwise

?

Restore defaults

Download

100 sequences selected

?

Download

GenPept

Graphics

Next

Previous

Descriptions

retinol-binding protein 4 [Canis lupus familiaris]

Sequence ID: XP_038295882.1

Length: 201

Number of Matches: 1

See 3 more title(s)

See all Identical Proteins(IPG)

Range 1: 1 to 175

GenPept

Graphics

Next Match

Previous Match

Score	Expect	Method	Identities	Positives	Gaps
360 bits(924)	3e-125	Compositional matrix adjust.	173/175(99%)	173/175(98%)	0/175(0%)
Query 1	MEWVWALELLAALGSARAE	SDCRVSNFQVKKTFDKARFAGTWYAMAKKDPEGLFLQDNIV	60		
Sbjct 1	MEWVWAL LLAALGSARAE	SDCRVSNFQVKK FDKARFAGTWYAMAKKDPEGLFLQDNIV	60		
Query 61	AEFSVDENGRMSATAKGRVRL	LNNDVCDMVGTFDTEDPAKFKMKYWGVSFLQKGND	120		
Sbjct 61	AEFSVDENGRMSATAKGRVRL	LNNDVCDMVGTFDTEDPAKFKMKYWGVSFLQKGND	120		
Query 121	DHWIIDTDYDTYAVQYSCRL	LNLDGTCADSYSFVFSRDPNGLPLEAQKIVRQRE	175		
Sbjct 121	DHWIIDTDYDTYAVQYSCRL	LNLDGTCADSYSFVFSRDPNGLPLEAQKIVRQRE	175		

Related Information

Gene - associated gene details

Genome Data Viewer - aligned genomic context

Identical Proteins - Identical proteins to XP_038295882.1

Related Information

[Gene](#) - associated gene details
[Genome Data Viewer](#) - aligned genomic context
[Identical Proteins](#) - Identical proteins to XP_038295882.1

Q4's Fasta result:

<https://www.ebi.ac.uk/Tools/services/web/toolresult.ebi?jobId=fasta-l20211104-184820-0908-48368064-p2m>

Q5.

The re-labeled sequences

>Human|NP_006735.2|Homo sapiens|RBP4

MKWVWALLLLAALGSGRAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDETGQMSATAKG
RVRLNNWDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGNDHWDIDTDYDTYAVQYSCRLLNLDGTCA
DSYSFVFSRDPNGLPPEAQKIVRQRQEELCLARQYRLIVHNGYCDGRSERNLL

>dog|GR899279.1|C. lupus familiaris liver protein

MEVWVALELLAALGSARAESDCRVSNFQVKKTFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGRMSAT
AKGRVRLNNWDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGNDHWDIDTDYDTYAVQYSCRLLNLDGTCA
DSYSFVFSRDPNGLPLEAQKIVRQRQE

>Lynx|XP_030190934.1|Lynx canadensis|RBP4

MAVWVALVLLAALGSARAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDENGQMSAT
AKGRVRLNNWDVCADMVGTFDTEDSAKFKMKYWGVASFLQKGNDHWDIDTDYDTYAVQYSCRLLNLDGTCA
DSYSFVFARDPNGLPLDVQKIVRQRQD

>Lesser Egyptian Jerboa|XP_044986072.1|Jaculus jaculus|RBP4

MEWMVALVLLAALGSGRAERDCRVSSFRVKENFDKARFSGTWYAIKKDPEGLFLQDNIIAEFAVDENGHMSAT
AKGRVRLLSNWEVCADMVGTFDTEDPAKFKMKYWGVASFLQKGNDHWDIDTDYDTYALQYSCRLLNLDGTCA
DSYSFVFSRDPNGLPPETRKLVRQRQE

>horses|XP_023498127.1|Equus caballus|RBP4 isoform X1

MEVWVALVLLAALGSARAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDEYQMSAT
AKGRVRLNNWDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGNDHWDIDTDYDTYAVQYSCRLLNLDGTCA
DSYSFVFARDPNGLPPEVQIVRRRQE

>yak|QDZ58630.1|Bos grunniens|RBP4

MEVWVALVLLAAPGSAQAERDCRVSSFRVKENFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGHMSAT
AKGRVRLNNWDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGNDHWDIDTDYETFAVQYSCRLLNLGGTCA
DSYSFVFARDPSGFSPEVQKIVRQRQE

>panther|XP_019300661.1|Panthera pardus|RBP4

MAVWVALVLLAALGSARAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDENGQMSAT

AKGRVRLNNWDVCADMVGTFDTEDSAKFKMKYWGVASFLQKGNDHWIIDTDYDTYAVQYSCRLLNLDGTCA
DSYSFVFARDPNGLPPDVQKIVRQRQD

Alignment: Obtained using MUSCLE (version 3.8) at EBI

EBI MUSCLE results:

```
Jerboa      MEWMWALVLLAALGSGRAERDCRVSSFRVKENFDKARFSGTWYAIKKDPEGLFLQDNII
yak|QDZ58630.1|Bos      MEWVWALVLLAAPGSAQAERDCRVSSFRVKENFDKARFAGTWYAMAKKDPEGLFLQDNIV
dog|GR899279.1|C.      MEWVWALELLAALGSARAESDCRVSNFQVKTFDKARFAGTWYAMAKKDPEGLFLQDNIV
Human|NP_006735.2|Homo  MKVWVALLLLAALGSGRAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV
horses|XP_023498127.1|Equus  MEWVWALVLLAALGSARAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV
Lynx|XP_030190934.1|Lynx  MAWVWALVLLAALGSARAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV
panther|XP_019300661.1|Panthera  MAWVWALVLLAALGSARAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV
* *:*** :*** ** .** *****.*.**:*****:*****:*****:*****:
Jerboa      AEFAVDENGHMSATAKGRVRLLSNWEVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND
yak|QDZ58630.1|Bos      AEFSVDENGHMSATAKGRVRLNNWDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND
dog|GR899279.1|C.      AEFSVDENGRMSATAKGRVRLNNWDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND
Human|NP_006735.2|Homo  AEFSVDETGQMSATAKGRVRLNNWDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND
horses|XP_023498127.1|Equus  AEFSVDEYQGMSATAKGRVRLNNWDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND
Lynx|XP_030190934.1|Lynx  AEFSVDENGQMSATAKGRVRLNNWDVCADMVGTFDTEDSAKFKMKYWGVASFLQKGND
panther|XP_019300661.1|Panthera  AEFSVDENGQMSATAKGRVRLNNWDVCADMVGTFDTEDSAKFKMKYWGVASFLQKGND
***:*** *.*****.**:*****.*****:*****
Jerboa      DHWIIDTDYDTYALQYSCRLLNLDGTCADSYSFVFSRDPNGLPPETRKLVRQRQE
yak|QDZ58630.1|Bos      DHWIIDTDYETFAVQYSCRLLNLGGTCADSYSFVFARDPGSGFSPEVQKIVRQRQE
dog|GR899279.1|C.      DHWIIDTDYDTYAVQYSCRLLNLDGTCADSYSFVFSRDPNGLPLEAQKIVRQRQE
Human|NP_006735.2|Homo  DHWIVDTDYDTYAVQYSCRLLNLDGTCADSYSFVFSRDPNGLPPEAQKIVRQRQE
horses|XP_023498127.1|Equus  DHWIIDTDYDTYAVQYSCRLLNLDGTCADSYSFVFARDPNGFPPEVQRIVRRRQE
Lynx|XP_030190934.1|Lynx  DHWIIDTDYDTYAVQYSCRLLNLDGTCADSYSFVFARDPNGLPLDVQKIVRQRQD
panther|XP_019300661.1|Panthera  DHWIIDTDYDTYAVQYSCRLLNLDGTCADSYSFVFARDPNGLPPDVQKIVRQRQD
****:****.*:*.*****.*****.***.*: . :...:*.**:
```

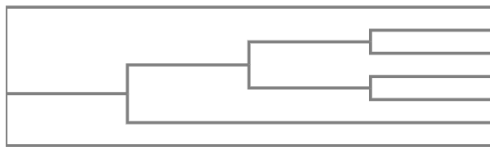
Q6

Used Simple-Phylogeny function of EBI

Phylogenetic Tree

This is a Neighbour-joining tree without distance corrections.

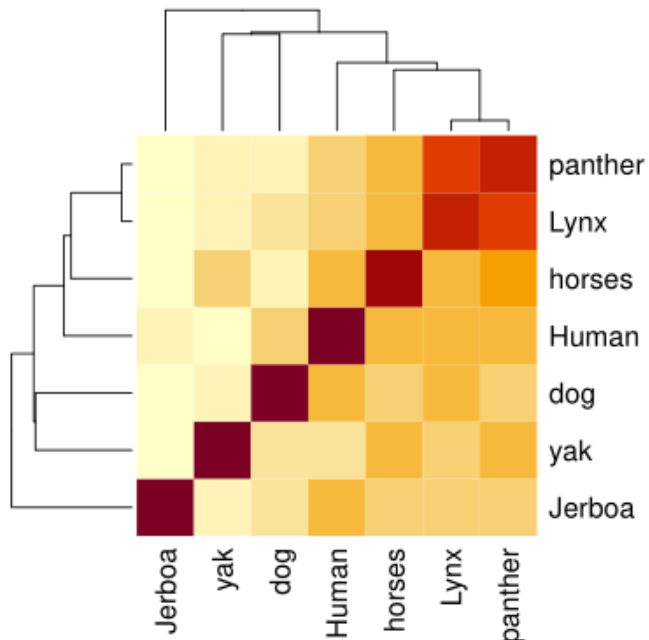
Branch length: ☒ Cladogram ☐ Real



Lesser 0.06179
yak|QDZ58630.1|Bos 0.04857
horses|XP_023498127.1|Equus 0.02571
Lynx|XP_030190934.1|Lynx 0.00457
panther|XP_019300661.1|Panthera 0.00114
dog|GR899279.1|C. 0.04821
Human|NP_006735.2|Homo 0.02393

Q7

Using the heatmap function of R:

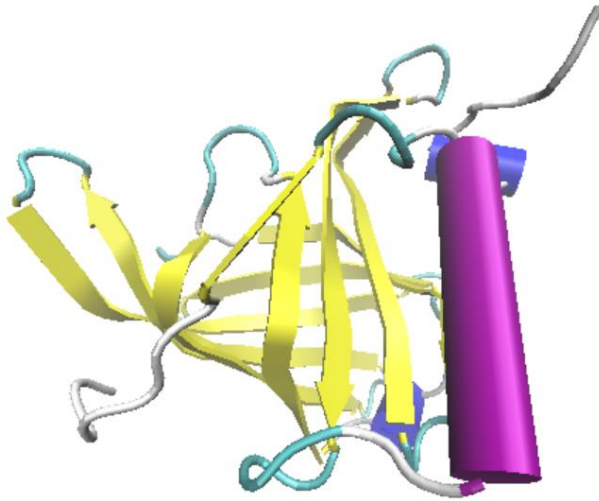


Q8.

ID	Methods	Sources	Resolution	e-value	Identity
1ERB	X-RAY DIFFRACTION	Bos taurus	1.9	8.30e-107	91.083
1IIU	X-RAY DIFFRACTION	Gallus gallus	2.5	1.63e-101	85.714
6QBA	X-RAY DIFFRACTION	Saccharolobus solfataricus	1.8	3.46e-110	93.631

Q9

The human RBP4 structure is very similar to the structure of lupus familiaris liver protein because they have high sequence similarity (>90%).



Human RBP4

Q10

29 assays, including 16 functional assays and 12 binding assays, 1 ADME assay were found,
https://www.ebi.ac.uk/chembl/g/#search_results/targets/query=RBP4

One of the top binding techniques, CHEMBL4304746, is retinol-induced MBP-tagged RBP4, testing for the activity of the RBP4 protein, suggesting that RBP4 antagonists may also have therapeutic utility for the treatment of NAFLD(nonalcoholic fatty liver disease).

Cioffi CL, Racz B, Varadi A, Freeman EE, Conlon MP, Chen P, Zhu L, Kitchen DB, Barnes KD, Martin WH, Pearson PG, Johnson G, Blaner WS, Petrukhin K. Design, Synthesis, and Preclinical Efficacy of Novel Nonretinoid Antagonists of Retinol-Binding Protein 4 in the Mouse Model of Hepatic Steatosis. *J Med Chem* (2019) 62:5470-5500.

10.1021/acs.jmedchem.9b00352