

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 FileNo 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

E value

Query Coverage

to

to

to

Filter

Reset

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

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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	MKWVWl1111aa1GSGRAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV					60
	M+VWVWAL LLAALGS RAE DCRVS+F+VK+ FDKARF+GTWYAMAKKDPEGLFLQDNIV					
Sbjct 76	MEWVWALELLAALGSARAESDCRVSNFQVKKTFDKARFAGTWYAMAKKDPEGLFLQDNIV					255
Query 61	AEFSVDETGQMSATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND					120
	AEFSVDE G+MSATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND					
Sbjct 256	AEFSVDENGRMSATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND					435
Query 121	DHWIVDTDYDTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPPEAQKIVRQRQE					175
	DHWI+DTDYDTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLP EAQKIVRQRQE					
Sbjct 436	DHWIIDTDYDTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPLEAQKIVRQRQE					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	MKWVWl1111aa1GSGRAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV					60
	M+VWVWAL LLAALGS RAE DCRVS+F+VK+ FDKARF+GTWYAMAKKDPEGLFLQDNIV					
Sbjct 76	MEWVWALELLAALGSARAESDCRVSNFQVKKTFDKARFAGTWYAMAKKDPEGLFLQDNIV					255
Query 61	AEFSVDETGQMSATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND					120
	AEFSVDE G+MSATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND					
Sbjct 256	AEFSVDENGRMSATAKGRVRLNNNDVCADMVGTFDTEDPAKFKMKYWGVASFLQKGND					435
Query 121	DHWIVDTDYDTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPPEAQKIVRQRQE					175
	DHWI+DTDYDTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLP EAQKIVRQRQE					
Sbjct 436	DHWIIDTDYDTYAVQYSCRLNLDGTCADSYSFVFSRDPNGLPLEAQKIVRQRQE					600

Q3: The sequence is :

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

```
MEWVWALELLAALGSARAESDCRVSNFQVKKTFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGRMSAT
AKGRVRLNNWVDCADMVGTFDTEDPAKFKMKYWGVSFLQKGNDDHWIIDTDYDTYAVQYSCRLLNLDGTCA
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.

blastn

blastp

blastx

tblastn

tblastx

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
MSATAKGRVRLNNWVDCADMVGTFDTEDPAKFKMKYWGVSFLQKGN

Query subrange [?](#)
From
To

Or, upload file
 No file chosen [?](#)

Job Title

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

☐ Align two or more sequences [?](#)

Choose Search Set

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

Organism
Optional

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

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	PC0DGVM701N Search expires on 10-14 05:44 am Download All ▼
Program	BLASTP ? Citation ▼
Database	nr See details ▼
Query ID	lcl Query_518795
Description	None
Molecule type	amino acid
Query Length	175
Other reports	Distance tree of results Multiple alignment MSA viewer ?

Filter Results

Organism only top 20 will appear ☐ exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity

E value

Query Coverage

to

to

to

Filter

Reset

- Descriptions
- Graphic Summary
- Alignments
- Taxonomy

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 $3 \times 10^{(-125)}$

Alignment view		Pairwise	? Restore defaults	Download ▼
100 sequences selected ?				
<div>Download ▼ GenPept Graphics Next Previous Descriptions</div> <div>retinol-binding protein 4 [Canis lupus familiaris]</div> <div>Sequence ID: XP_038295882.1 Length: 201 Number of Matches: 1</div> <div>See 3 more title(s) ▼ See all Identical Proteins(IPG)</div>				
Range 1: 1 to 175 GenPept Graphics Next Match Previous Match				
Score	Expect	Method	Identities	Positives
360 bits(924)	3e-125	Compositional matrix adjust.	173/175(99%)	173/175(98%)
Gaps				0/175(0%)
Query 1	MEWWALELLAALGSARAESDCRVSNFQVKKTFDKARFAGTWYAMAKKDPEGLFLQDNIV	60		
Sbjct 1	MEWWAL LLAALGSARAESDCRVSNFQVKK FDKARFAGTWYAMAKKDPEGLFLQDNIV	60		
Query 61	AEFSVDENGRMSATAKGRVRLNNWDVCADMGVTFDTEDPAKFKMKYNGVASFLQKGND	120		
Sbjct 61	AEFSVDENGRMSATAKGRVRLNNWDVCADMGVTFDTEDPAKFKMKYNGVASFLQKGND	120		
Query 121	DHWIIDTDYDTYAVQYSCRLNLNLDGTCADSYSFVSRDPNGLPLEAQKIVRQROE	175		
Sbjct 121	DHWIIDTDYDTYAVQYSCRLNLNLDGTCADSYSFVSRDPNGLPLEAQKIVRQROE	175		

Related Information

[Gene](#) - associated gene details

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

[Identical Proteins](#) - Identical proteins to XP_038295882.1