## 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

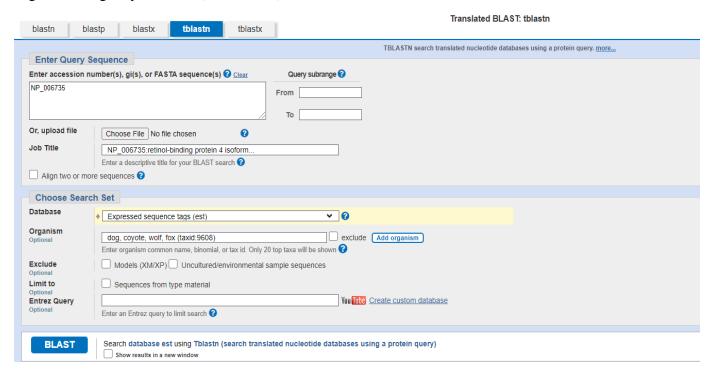
Function: It's expressed in the liver, a member of the lipocalin family and works as retinol carrier(vitamin A alcohol) in the blood. It delivers retinol from the liver stores to the peripheral tissues. A deficiency of vitamin A blocks secretion of the binding protein post translationally and results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

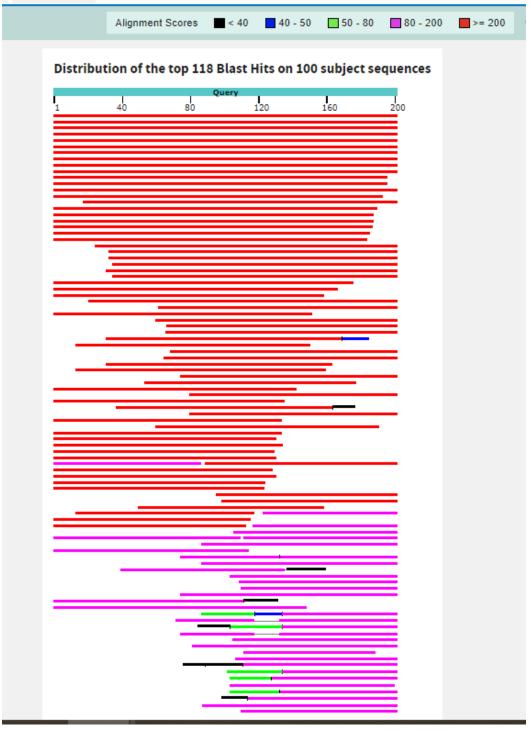
### Q2:

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

Database: expressed sequence tags(ESTs)

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





## 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 Mi												
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	<u>l</u>				NFDKARFSGTWYAN FDKARF+GTWYAN							
Sbjct 7	6				FDKARFAGTWYAM							
Query 6	1				/GTFTDTEDPAKFK /GTFTDTEDPAKFK							
Sbjct 2	56				/GTFTDTEDPAKFK							
Query 1	21				SFVFSRDPNGLPPE SFVFSRDPNGLP E		175					
Sbjct 4	36				FVFSRDPNGLPLE		500					

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	MKWVWallllaalGSGRAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIV 60								
		M+WVWAL	LLAALGS RAE DCRVS+F+VK+ F	-DKARF+GTWYAMA	KKDPEGLFLQDNI	V				
Sbjct	76	MEWVWAL	ELLAALGSARAESDCRVSNFQVKKTF	FDKARFAGTWYAMA	KKDPEGLFLQDNI	V 255				
Query	61	AEFSVDE	TGQMSATAKGRVRLLNNWDVCADMV0	GTFTDTEDPAKFKM	KYWGVASFLQKGNI	D 120				
		AEFSVDE	G+MSATAKGRVRLLNNWDVCADMV0	GTFTDTEDPAKFKM	KYWGVASFLQKGNI	D				
Sbjct	256	AEFSVDE	NGRMSATAKGRVRLLNNWDVCADMVO	GTFTDTEDPAKFKM	KYWGVASFLQKGNI	D 435				
Query	121	DHWIVDT	DYDTYAVQYSCRLLNLDGTCADSYSF	VFSRDPNGLPPEA	QKIVRQRQE 17	5				
		DHWI+DT	DYDTYAVQYSCRLLNLDGTCADSYSF	VFSRDPNGLP EA	QKIVRQRQE					
Sbjct	436	DHWIIDT	DYDTYAVQYSCRLLNLDGTCADSYSF	VFSRDPNGLPLEA	QKIVRQRQE 600	9				

### Q3: The sequence is:

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

MEWVWALELLAALGSARAESDCRVSNFQVKKTFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGRMSAT AKGRVRLLNNWDVCADMVGTFTDTEDPAKFKMKYWGVASFLQKGNDDHWIIDTDYDTYAVQYSCRLLNLDGTCA DSYSFVFSRDPNGLPLEAQKIVRQRQE

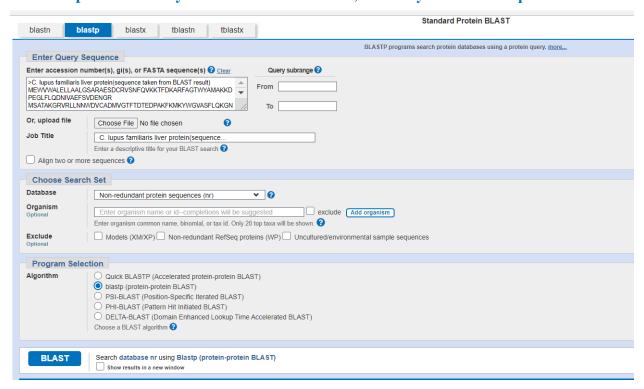
Name: Canis lupus familiaris Liver protein

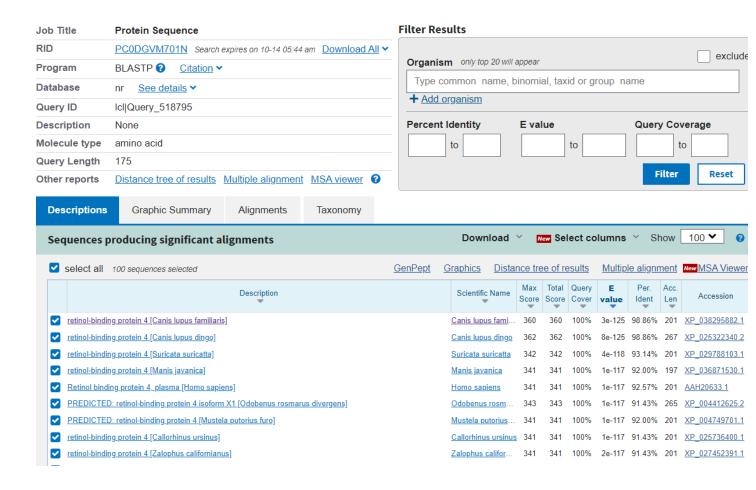
Animalia, Chordata, Mammalia, Carnivora, Canidae, Canis, Lupus, familiaris

### O4:

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.





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



