

Q1
RBP4

retinol binding protein 4

Accession number: KAI6070658.1 (Can't find a reference ID from NIBH, This is from genbank)

Species: Homo Sapiens

Function: The protein belongs to lipocalin family and is the specific carrier for retinol (vitamin A alcohol) in the blood. It will bind to retinol, and deliver retinol from liver to the surrounding tissues.

Q2:

Method: TBLASTN against Chimpanzee EST

Database: Expressed sequence tags

Organism: chimpanzee (taxid:9598)

The screenshot displays the NCBI BLAST search results for the query sequence KAI6070658.1 (RBP4) against the chimpanzee EST database. The search parameters are as follows:

- Query sequence: KAI6070658.1
- Database: Expressed sequence tags (est)
- Organism: chimpanzee (taxid:9598)
- Exclude: Models (XMP), Sequences from type material
- Limit to: Entire query

The BLAST results table shows the following sequences producing significant alignments:

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
12822010_rev_1_804_1_941 Chimpanzee brain library Kios Pan troglodytes cDNA clone 12822010_rev_1_B... Pan troglodytes	Pan troglodytes	53.5	53.5	75%	2e-09	30.49%	689	CB295970.1
12822050_rev_1_A12_1_597 Chimpanzee brain library Kios Pan troglodytes cDNA clone 12822050_rev_1_A... Pan troglodytes	Pan troglodytes	53.5	53.5	75%	2e-09	31.33%	640	CB295968.1
12822027_rev_1_F67_1_963 Chimpanzee brain library Kios Pan troglodytes cDNA clone 12822027_rev_1_F... Pan troglodytes	Pan troglodytes	47.4	47.4	61%	1e-07	31.30%	491	CB295969.1
DC522873 chimpanzee brain cDNA library PRB Pan troglodytes versus cDNA clone PRB3195.5' mRNA sequence	Pan troglodytes	47.0	47.0	62%	3e-07	31.85%	540	DC522873.1

Chosen match: CB295970.1, A 689 base pair clone from chimpanzee brain library Pan troglodytes. See below for more details

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12B22010_rev_1_B04_r_041.ab1 Chimpanzee brain library Koos Pan troglodytes cDNA clone 12B22010_rev_1_B04_r_041.ab1 5', mRNA sequence

Sequence ID: [CB295970.1](#) Length: 689 Number of Matches: 1

Range 1: 138 to 560 [GenBank](#) [Graphics](#)

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
53.5 bits(127)	2e-09	Compositional matrix adjust.	50/164(30%)	77/164(46%)	35/164(21%)	+3
Query 14	GSGRAERDCRVSSFRVKNFDKTLFSGTWYAIKKDPEGLFLQDNIVAEFSVDENGHMSA	73				
Sbjct 138	AEGQAFHLGKCPKPPVQENFDVNKYLGRWYEI-EKIPTTFENGRCIQANYSLMENG----	302				
Query 74	TAKGRVRLLSNWEVCADMV-----GTFTDTEPAKFKMKY-WGAASFQIGIDDHWII	125				
Sbjct 303	----KIKVL-NQELRADGTVNQIEGATPVNLTEPAKLEVKFSWFMPSPYWILATDYENYALVYSCTSI	449				
Query 126	DTDYHTFALQYSC-----RLNFDGTCADSYSPVFARDPNGLTPE	165				
Sbjct 450	ATDYENYALVYSCTSIQLFHVD-----FAMILARNPN-LPPE	560				

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12B22050_rev_1_A12_r_097.ab1 Chimpanzee brain library Koos Pan troglodytes cDNA clone 12B22050_rev_1_A12_r_097.ab1 5', mRNA sequence

12B22010_rev_1_B04_r_041.ab1 Chimpanzee brain library Koos Pan troglodytes cDNA clone 12B22010_rev_1_B04_r_041.ab1 5', mRNA sequence

GenBank: [CB295970.1](#)

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LOCUS	CB295970	689 bp	mRNA	linear	EST 03-FEB-2011
DEFINITION	12B22010_rev_1_B04_r_041.ab1 Chimpanzee brain library Koos Pan troglodytes cDNA clone 12B22010_rev_1_B04_r_041.ab1 5', mRNA sequence.				
ACCESSION	CB295970				
VERSION	CB295970.1				
DBLINK	BioSample: SAMN00172268				
KEYWORDS	EST.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes ; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Pan.				
REFERENCE	1 (bases 1 to 689)				
AUTHORS	Hellmann, I., Zollner, S., Enard, W., Ebersberger, I., Nickel, B. and Paabo, S.				
TITLE	Selection on human genes as revealed by comparisons to chimpanzee cDNA				
JOURNAL	Genome Res. 13 (5), 831-837 (2003)				
PUBMED	12727903				

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12B22010_rev_1_B04_r_041.ab1 Chimpanzee brain library Koc Nucleotide

RBP4 [Marmota monax]

Q3

Chosen sequence:

Using EMBOSS Transeq and identify the reading frame with same AA sequence on the alignment page, we result in the following AA sequence.

> chimpanzee protein

ASQIG*FCIWKLPS*KKRSLQPPSPKMVMLLLFSALAGLFGAAEGQAFHLGKCPKPP
 VQENFDVNKYLGRWYEIEKIPTTFENGRCIQANYSLMENGKIKVLNQELRADGTVNQIE
 G
 EATPVNLTEPAKLEVKFSWFMPSPYWILATDYENYALVYSCTSIQLFHVDFAWILARN

PNLPPETVDSLKNILTSNNIDVKKMTVTDXVNC PKLS*PGXTGRLHPLX

Protein name: APOD isoform 3

ORGANISM [Pan troglodytes](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Pan.

A BLASTP search against NR database (see setup in first screen-shot below) yielded a top hit result is to a protein from Pan Troglodytes

Top result is to a protein from Pan Troglodytes.

Molecule typeamino acid

Query Length229

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	APOD isoform 3 [Pan troglodytes]	Pan troglodytes	407	407	90%	1e-142	96.19%	215	PN124132.1
<input checked="" type="checkbox"/>	apolipoprotein D [Pan troglodytes]	Pan troglodytes	390	390	82%	3e-136	99.47%	189	XP_516965.1
<input checked="" type="checkbox"/>	apolipoprotein D [Pan paniscus]	Pan paniscus	388	388	82%	2e-135	98.94%	189	XP_003807686
<input checked="" type="checkbox"/>	apolipoprotein D [Gorilla gorilla gorilla]	Gorilla gorilla gorilla	385	385	82%	3e-134	97.88%	189	XP_004038293
<input checked="" type="checkbox"/>	apolipoprotein D precursor [Homo sapiens]	Homo sapiens	384	384	82%	1e-133	97.88%	189	NP_001638.1
<input checked="" type="checkbox"/>	apolipoprotein D [synthetic construct]	synthetic construct	384	384	82%	1e-133	97.88%	190	AAX29138.1
<input checked="" type="checkbox"/>	apolipoprotein D [synthetic construct]	synthetic construct	384	384	82%	2e-133	97.88%	190	AAX36879.1
<input checked="" type="checkbox"/>	APOD [synthetic construct]	synthetic construct	382	382	82%	9e-133	97.35%	189	AKI70359.1
<input checked="" type="checkbox"/>	APOD [synthetic construct]	synthetic construct	381	381	82%	1e-132	97.35%	189	AKI70358.1
<input checked="" type="checkbox"/>	apolipoprotein D [Homo sapiens]	Homo sapiens	380	380	90%	8e-132	94.76%	215	KAJ2533078.1
<input checked="" type="checkbox"/>	APOD isoform 3 [Pongo abelii]	Pongo abelii	362	362	90%	2e-124	90.00%	215	PNJ69522.1

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APOD isoform 3, partial [Pan troglodytes]

Sequence ID: [PN124132.1](#) Length: 215 Number of Matches: 1

Range 1: 7 to 215GenPeptGraphics▼Next Match▲Previous Match

Score	Expect	Method	Identities	Positives	Gaps
407 bits(1047)	1e-142	Compositional matrix adjust.	202/210(96%)	202/210(96%)	3/210(1%)
Query 8	CINWKLPS--KKRSLQPPSPKHMVLLLSALAGLFGAAEQAFHLGKCFKPPVQENF				65
CI LPSS	RSLQPPSPKHMVLLLSALAGLFGAAEQAFHLGKCFKPPVQENF				
Sbjct 7	CI-SLPSSCDYSSRSLQPPSPKHMVLLLSALAGLFGAAEQAFHLGKCFKPPVQENF				65
Query 66	DVNKYLGRWYEIEKIPTTFENGRCIQANYSIMENGKIKVLNQELRADGTVNQIEGEATPV				125
DVNKYLGRWYEIEKIPTTFENGRCIQANYSIMENGKIKVLNQELRADGTVNQIEGEATPV					
Sbjct 66	DVNKYLGRWYEIEKIPTTFENGRCIQANYSIMENGKIKVLNQELRADGTVNQIEGEATPV				125
Query 126	NLTEPAKLEVKFSWFMPSAPYWLATDYENYALVYSCTSI IQLFHVDFAWILARNPHLPP				185
NLTEPAKLEVKFSWFMPSAPYWLATDYENYALVYSCTSI IQLFHVDFAWILARNPHLPP					
Sbjct 126	NLTEPAKLEVKFSWFMPSAPYWLATDYENYALVYSCTSI IQLFHVDFAWILARNPHLPP				185
Query 186	ETVDSLKNILTSNNIDVKKMTVTDVNC PK				215
ETVDSLKNILTSNNIDVKKMTVTD VNC PK					
Sbjct 186	ETVDSLKNILTSNNIDVKKMTVTDQVNC PK				215

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