

Project: find-a-Gene BGGN-213: FOUNDATIONS OF BIOINFORMATICS

Xuerui Huang (A91018769)

Q1

Protein Name

Accession

Species

Function known

Q2

Blast Method

Database

Limits applied

Search output list

Alignment of choice

Alignment details (Alignment of choice)

Q3

Protein sequence

Name

Species

Q4

Program run

Result and Top alignment

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Sequence Collection

Multiple sequence alignment by MUSCLE (version 3.8) at EBI

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Sequence clustering pattern

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Heatmap figure with 6 samples

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3 Unique hits info

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Structure Info

Structure figure

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Link to ChEMBL

ChEMBL Info

Binding assay

Project: find-a-Gene BGGN-213: FOUNDATIONS OF BIOINFORMATICS

Xuerui Huang (A91018769)

Q1

Protein Name

retinol-binding protein 4 isoform a precursor (RBP4)

Accession

NP_006735

Species

Homo sapiens

Function known

This protein belongs to the lipocalin family and is the specific carrier for retinol (vitamin A) in the blood. It delivers retinol from the liver stores to the peripheral tissues. Plasma concentration of Retinol Binding Protein 4 (RBP4) in relation to nutritional status and kidney function in older population of PolSeniorStudy

Q2

Blast Method

blastn

blastp

blastx

tblastn

tblastx

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

NP_006735

Clear

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

Nematocera (taxid:7148)

☐ exclude

+

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

Database

Expressed Sequence Tags (est)

Limits applied

Organism: Nematocera (taxid:7148)

Search output list

BLAST Results

ⓘ

Your search is limited to records that include: Nematocera (taxid:7148) > Full Entrez Query

Edit and Resubmit

Save Search Strategies

Formatting options

Download

Job title:

You [How to read this page](#) [Blast report description](#)

[Click here](#) to see the new BLAST results page

NP_006735:retinol-binding protein 4 isoform...

RID

DJ40TZKM014

(Expires on 05-14 14:35 pm)

Query ID

NP_006735.2

Description

retinol-binding protein 4 isoform a precursor [Homo sapiens]

Molecule type

amino acid

Query Length

201

Database Name

est

Description

Database of GenBank+EMBL+DDBJ sequences from EST Divisions

Program

TBLASTN 2.9.0+ > Citation

Other reports:

[Search Summary](#) [Taxonomy reports](#)

Graphic Summary

Distribution of the top 101 Blast Hits on 100 subject sequences

Mouse over to see the title, click to show alignments

Color key for alignment scores

<40

40-50

50-80

80-200

>=200

Query

1

40

80

120

160

200

Descriptions

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

Alignments

Download

GenBank

Graphics

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/>	17000687077725 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 19600449704508 5'. mRNA sequence	53.1	53.1	69%	2e-07	30.56%	BM605887.1
<input type="checkbox"/>	17000687162529 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 19600449701755 5'. mRNA sequence	52.8	52.8	72%	2e-07	28.67%	BM576500.1
<input type="checkbox"/>	PRAG-aad13c09.g1 Sand_fly_EST Normalized Phlebotomus papatasi cDNA 5'. mRNA sequence	50.1	50.1	71%	1e-06	24.16%	FK816124.1
<input type="checkbox"/>	AsAmUn182G12.b Mosquito midgut cDNA Library Anopheles stephensi cDNA 5'. mRNA sequence	50.1	50.1	74%	1e-06	27.63%	EX226080.1
<input type="checkbox"/>	AsAmUn182G12.b1 Mosquito midgut cDNA Library Anopheles stephensi cDNA 5'. mRNA sequence	50.1	50.1	74%	1e-06	27.63%	EX226079.1
<input type="checkbox"/>	NACAB32TR Aedes aegypti infected with Brugia Malayi Aedes aegypti cDNA clone NACAB32. mRNA sequence	47.4	47.4	67%	9e-06	28.17%	DV359978.1
<input type="checkbox"/>	G771P567RN15.T0 Culex pipiens quinquefasciatus Mixed Tissue Control Library Culex quinquefasciatus cDNA. mRNA sequence	47.4	47.4	67%	2e-05	26.95%	EV358039.1
<input type="checkbox"/>	17000687314648 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 19600449699991 5'. mRNA sequence	46.2	46.2	50%	2e-05	30.48%	BM586390.1
<input type="checkbox"/>	G771P567FN15.T0 Culex pipiens quinquefasciatus Mixed Tissue Control Library Culex quinquefasciatus cDNA. mRNA sequence	45.8	45.8	64%	5e-05	26.72%	EV358360.1

Alignment of choice

Chosen match: Accesion BM605887.1, a 679 base pair clone from Anopheles gambiae

Alignment details (Alignment of choice)



score: 53.1

Evalue: 2e-07

Identities: 43/150(29%)
Positives: 74/150(49%)
Gaps: 15/150(10%)
Frame: +1

1 17000687077725 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 19600449704508
5', mRNA sequence
2 Sequence ID: BM605887.1Length: 679Number of Matches: 1
3 Related Information
4 UniGene-clustered expressed sequence tags
5 Range 1: 186 to 590GenBankGraphicsNext MatchPrevious Match
6 Alignment statistics for match #1
7 Score Expect Method Identities Positives Gaps
8 Frame
9 53.1 bits(126) 2e-07 Compositional matrix adjust. 44/144(31%) 71/144(49%)
13/144(9%)
10 +3
11 Query 38 FSGTWYAMAKKDPEGLFLQDNIVAEFSVDETGQMSATAK-GRVRLNNWDVCADMVGTTFT 96
12 ++G WY + + + D +VAE+ +TG S + K G L NN V AD +
13 Sbjct 186 YAGRWYEIKRYEQFYEKDLCVVAEYQ--KTGDNSSISVKNGAFSLANNTRVVADGTAVVS 359
14
15 Query 97 ---DTEDPAKFKMKYWGVASFLQKGNDHWHIVDTDYDTYAVQYSCRLLNLDGTCADSYSF 153
16 DT PAK + ++G + ++W++DTDY ++AV +SC D + +
17 Sbjct 360 YPDDTTHPAKLSVAFFGA----KADRSNYWVLDTDYTSFAVVWSCEPFFRDPSKNVLGFW 527
18
19 Query 154 VFSRDPNGLPPEAQKIVRQRQEEL 177
20 +FSR+P EA V +R +EL
21 Sbjct 528 IFSRNPTFPTDEA---VVKRVDEL 590

 [Download](#) [GenBank](#) [Graphics](#)

17000687077725 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone 19600449704508 5', mRNA sequence						
Sequence ID: BM605887.1 Length: 679 Number of Matches: 1						
Range 1: 186 to 590				 Next Match	 Previous Match	
Score	Expect	Method	Identities	Positives	Gaps	Frame
53.1 bits(126)	2e-07	Compositional matrix adjust.	44/144(31%)	71/144(49%)	13/144(9%)	+3
Query	38	FSGTWYAMAKKDPEGLFLQDNIVAEFSVDETGQMSATAK-GRVRLNNWDVCADMVGTTFT	96			
		++G WY + + + D +VAE+ +TG S + K G L NN V AD +				
Sbjct	186	YAGRWYEIKRYEQFYEKDLCVVAEYQ--KTGDNSSISVKNGAFSLANNTRVVADGTAVVS	359			
Query	97	---DTEDPAKFKMKYWGVASFLQKGNDHWHIVDTDYDTYAVQYSCRLLNLDGTCADSYSF	153			
		DT PAK + ++G + ++W++DTDY ++AV +SC D + +				
Sbjct	360	YPDDTTHPAKLSVAFFGA----KADRSNYWVLDTDYTSFAVVWSCEPFFRDPSKNVLGFW	527			
Query	154	VFSRDPNGLPPEAQKIVRQRQEEL	177			
		+FSR+P EA V +R +EL				
Sbjct	528	IFSRNPTFPTDEA---VVKRVDEL	590			

Q3

Protein sequence

```
1 > A. Apolipoprotein D precursor (sequence taken from BLAST result)
2 YAGRWYEIKRYEQFYEKDLDCVVAEYQKTGDNSISVKNGAFSLANNTRVVADGTAVVSYPDDTTHPAKLSVAFFGAKADRS
  NYWVLDTDYTSFAVVWSCEPFPRDPSKNVLGFWIFSRNPTFPTDEAVVKRVDEL
```

Name

Name: Apolipoprotein D precursor

Species

Anopheles gambiae (African malaria mosquito)

Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;

Pterygota; Neoptera; Holometabola; Diptera;

Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.

Q4

Program run

blastn blastp **blastx** tblastn tblastx

BLASTP programs search

Enter Query Sequence

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

>A. Anopheles gambiae protein (sequence taken from BLAST result)
YAGRWYEIKRYEQFYEKDLDCVVAEYQKTGDNISVKNAGAFSLANNTRVADGTAVVSYPDDTT
HPAKLSVAFFGAKADRSNYWVLDTDYTSFAVVWSCEPFFRDPSKNVLGFWIFSRNPTFPTDEAV
VKRVDEL [G](#)

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 [?](#)

Organism [Optional](#) ☐ exclude

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 [?](#)

Result and Top alignment

Evalue: 2e-78

Per.Identity: 82.96%

The top result is to a protein from Anopheles sinensis, see second screen shot below for alignment details:

Sequences producing significant alignments:

Select: All None Selected:0

Alignments							
	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/>	hypothetical protein ZHAS_00021950 [Anopheles sinensis]	239	239	100%	2e-78	82.96%	KFB53445.1
<input type="checkbox"/>	apolipoprotein D [Anopheles darlingi]	214	214	100%	2e-68	74.81%	ETN60997.1
<input type="checkbox"/>	hypothetical protein RP20_CCG011993 [Aedes albopictus]	152	152	100%	7e-44	53.33%	KXJ75306.1
<input type="checkbox"/>	hypothetical protein RP20_CCG016633 [Aedes albopictus]	151	151	100%	1e-43	53.33%	KXJ73039.1
<input type="checkbox"/>	PREDICTED: apolipoprotein D-like [Aedes albopictus]	150	150	100%	2e-43	54.07%	XP_019565260.1
<input type="checkbox"/>	PREDICTED: apolipoprotein D-like [Aedes albopictus]	150	150	100%	3e-43	54.07%	XP_019931866.1
<input type="checkbox"/>	apolipoprotein D [Aedes aegypti]	147	147	100%	4e-42	51.11%	XP_001660231.2

Alignments

Download

GenPept

Graphics

▼ Next ▲ Previous ▲ Descriptions

hypothetical protein ZHAS_00021950 [Anopheles sinensis]
Sequence ID: [KFB53445.1](#) Length: 200 Number of Matches: 1

Range 1: 42 to 176

GenPept

Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
239 bits(611)	2e-78	Compositional matrix adjust.	112/135(83%)	122/135(90%)	0/135(0%)
Query 1	YAGRWYEIKRYEQFYEKDLDCVVAEYQKTGDNSISVKNGAFSLANNTRVVADGTAVVSYP	60			
Sbjct 42	+AGRWYE KRYEQFYEKDLDC VAEYQ TG N+ISVKG F+ ANNTRVVADGTAV+S+P	101			
Query 61	DOTTHPAKLSVAFFGAKADRSNYWVLDTDYTSFAVWWSCEPFRDPSKNVLGFWIFSRNP	120			
Sbjct 102	DOT+ P KL+VAFFGAK DRSNYWVLDTDYTS+ VV+SCEPF+D SKNVLGFWIFSR P	161			
Query 121	TFPTDEAVVKRVDEL	135			
Sbjct 162	TFPTDEAVVKRVDEL	176			

Download

GenPept

Graphics

▼ Next ▲ Previous ▲ Descriptions

apolipoprotein D [Anopheles darlingi]
Sequence ID: [ETN60997.1](#) Length: 199 Number of Matches: 1

Range 1: 42 to 174

GenPept

Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
214 bits(545)	2e-68	Compositional matrix adjust.	101/135(75%)	111/135(82%)	2/135(1%)
Query 1	YAGRWYEIKRYEQFYEKDLDCVVAEYQKTGDNSISVKNGAFSLANNTRVVADGTAVVSYP	60			
Sbjct 42	Y GRWYEIKRYEQFYEKDLDCVVAEYQPREGGITVANGAFSLANNTRVVGQGVGIISYP	101			
Query 61	DOTTHPAKLSVAFFGAKADRSNYWVLDTDYTSFAVWWSCEPFRDPSKNVLGFWIFSRNP	120			
Sbjct 102	+--AKDGRLSVAFFGAKPDRSNYWVLDTDYTSFAVWWSCEPFTTKRASKNVLGFWIFSRNP	159			
Query 121	TFPTDEAVVKRVDEL	135			
Sbjct 160	TFPTDETTVKHVDEL	174			

Q5

Sequence Collection

Collected in total of 6 sequences with different species

1	>Human_RBP4 gi 30497399 ref NP_006735 retinol-binding protein 4 isoform a precursor [Homo sapiens]
2	MKWVWALLLLAALGSGRAERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFVSDETGQ
3	MSATAKGRVRLNNWDVCADMVGTFDTDPAKFMMKYWGVASFLLQKGNDDHWIVDTDYDTYAVQYSCRL
4	LNLDGTCADSYSFVFSRDPNGLPPEAQKIVRQRQEELCLARQYRLIVHNGYCDGRSERNLL
5	
6	>Apolipoprotein_D_precursor (sequence taken from BLAST result) [Anopheles sinensis]
7	YAGRWYEIKRYEQFYEKDLDCVVAEYQKTGDNSISVKNGAFSLANNTRVVADGTAVVSYPDDTTHPAKLS
8	VAFFGAKADRSNYWVLDTDYTSFAVWWSCEPFRDPSKNVLGFWIFSRNPFTPTDEAVVKRVDEL
9	
10	>Riverine_mosquito gi 20920257 Accession ETN60997 apolipoprotein D [Anopheles darling
11	MHSSLLAIVLLATVAATVTGLLTDSACPEGVKVKQNFSLKDYVGRWYEIKRYEQFYEKDLDCVVAEYQPR
12	EEGGITVANGAFSLANNTRVVVGQGVGIISYPEAKDGKLSVAFFGAKPDRSNYWVLDTDYTSYAVVFSCEP
13	YYKDASKNVLGFWIFSRQPTFPTDETTVKHVQELVKQYGDSEKFEITNQSDERCPRSYV
14	
15	>Southern_house_mosquito Accession XP_001866789.1 apolipoprotein D [Culex quinquefasciatus]
16	MYKSPQVFAAALLVLGLSSAVVYGVYDRPCRTEISVVQNFCLDRYLGKWEYLQRYEQPFQTKVDCTTAN
17	YGLLDSATVSVRNSAFSLINGTSSEAIGTAVLSFPEQEIVQAKLNVSFFGAPNDRSNYWVIDTDYENFAI


```

18 VWSCEPLPQDQSSEGFWFLSRERKFTDDKDANERAFGAIRKYIDQSEIRFTNQADERCPDF
19
20 >Atlantic_salmon Accession|XP_014045104.1|PREDICTED: apolipoprotein D-like [Salmo
    salar]
21 MQALHVLSTLLSILTANAQTLRPGKCPQPPVQANFDAARYLGKWEIKKLPVVFQKGECTTATYSLESP
22 GVVGVNLNRELLADNTVSVITGYAKAKDPSEPAKLEVTFEFDSPPGNYWVLSTDYEGHSSVVSCTDILGTF
23 HADFAWILSRESTLSEEKLEELYNVFTSNGIDIDGMTVTNQSQELCADMPLWA
24
25 >Chicken Accession|NP_990569.1|retinol-binding protein 4 precursor [Gallus
    gallus]
26 MAYTWRALLLLALAF LGSSMAERDCRVSSFKVKENFDKNRYSGTWYAMAKKDPEGLFLQDNVVAQFTVDE
27 NGQMSATAKGRVRLFNNWDVCADMIGSFTDTEPAKF KMKYWGVASFLQKGNDHWWVDTDYDTYALHYS
28 CRELNEDGTCADSYSFVFSRDPKGLPPEAQKIVRQRQIDLCLDRKYRVIVHNGFCs

```

Multiple sequence alignment by MUSCLE (version 3.8) at EBI

Result

1	Chicken	-----MAYTWRALLLLALAFLGSS-	
	MAERDCRVSSFKVKENFDKNRYSGTWYAMAKKDPE		
2	Human_RBP4	-----MKWVWALLLLAALGSGR-----	
	AERDCRVSSFRVKENFDKARFSGTWYAMAKKDPE		
3	Atlantic_salmon	-MQALHVLSTLLSILTANAQT----LRPGKCP-QP-	
	PVQANFDAARYLGKWEIKKLP--		
4	Southern_house_mosquito	MYKSPQVFAAALLVLGLSSAVVYGVYDRPCR-	
	TEISVVQNFCLDRYLGWYELQRYE--		
5	Apolipoprotein	-----	
	YAGRWEIKRYE--		
6	Riverine_mosquito	----MHSSLLAIVLLATVAATVTGLLTDSACP-	
	EGVKVKQNFSLKDYVGRWEIKRYE--		
7			: * **
8			: .
9	Chicken	GLFLQ---DNVVAQFTVDENGQMSATAKGRVRLFNNWDVCADMIGSFTDT--	
	-EDPAKFK		
10	Human_RBP4	GLFLQ---DNIVAEFSDVETGQMSATAKGRVRLNNWDVCADMVGTFTDT--	
	-EDPAKFK		
11	Atlantic_salmon	-VVFQKG-ECTTATYSLESPGVGV--LNRELLADNTVSVITGYAKAKDP--	
	-SEPAKLE		
12	Southern_house_mosquito	-QPFQTKVDCTTANYGLLDSATVSV-	
	RNSAFSLINGTSSEAIGTAVLSFPEQEIVQAKLN		
13	Apolipoprotein	-QFYEKDLDCVVAEYQKTGDNISIV-	
	KNGAFSLANNTRVVADGTAVVSYPDDTTHPAKLS		
14	Riverine_mosquito	-QFYEKDLDCVVAEYQPREEGGITV-ANGAFSLANNTRVVGQGVGIISYPE-	
	-AKDGKLS		
15			: : * : : . . *
			. * : .

```

16
17 Chicken
   MKYWGVASFLQKGNDHVVVDTDYDTYALHYSRELNEDGTCADSYSFVFSRDPKGLPPE
18 Human_RBP4
   MKYWGVASFLQKGNDHVIWVDTDYDTYAVQYSCRLLNLDGTCADSYSFVFSRDPNGLPPE
19 Atlantic_salmon
   VTF FEDSP-----PGNYWLSTDYEGHSVVYSCTDIL--
   GTFHADFAWILSREST-LSEE
20 Southern_house_mosquito
   VSFFGAPN-----DRSNYWIDTDYENFAIVWSCEPLPQDQS--
   SEGFWFLSRERK-FTDD
21 Apolipoprotein
   VAFFGAKA-----
   DRSNYWLDTDYTSFAVVWSCEPFRRDPSKNVLGFWIFSRNPT-FPTD
22 Riverine_mosquito
   VAFFGAKP-----
   DRSNYWLDTDYTSYAVVFSCEPYK DASKNVLGFWIFSRQPT-FPTD
23
   :  ::                .::*:...***  .::  **:                :
   ::*:...  .  ::  :
24
25 Chicken
   AQKIVRQRQIDLCLDRKYRVIVHNGFCS-----
26 Human_RBP4
   AQKIVRQRQEELCLARQYRLIVHNGYCDGRSERNLL--
27 Atlantic_salmon
   K--LEELYNVFTSNGIDIDGMTVTNQSQELCADMPLWA
28 Southern_house_mosquito
   KDANERAFGAIRKYI-DQSEIRFTNQADERCPDF-----
29 Apolipoprotein
   EAVVKRVDEL-----
30 Riverine_mosquito
   ETTVKHVQELVKQYG-DESKFEITNQSDERCPRSYV--
31

```

Q6

Sequence clustering pattern

Phylogenetic Tree

This is a Neighbour-joining tree without distance corrections.

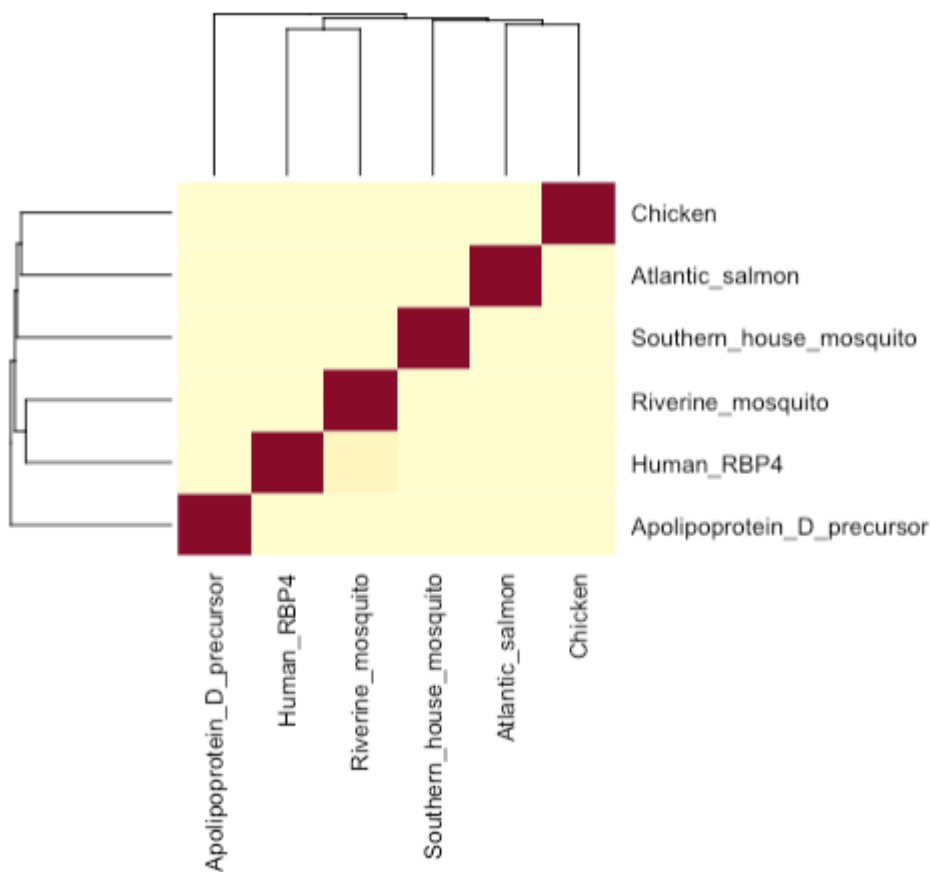
Download Phylogenetic Tree Data

Branch length: ☒ Cladogram ☐ Real



Q7

Heatmap figure with 6 samples



Q8

3 Unique hits info

Species: Sander vitreus, Homo sapiens, Escherichia coli

PDB_ID	Evalue	Identity	Technique	Resolution	Source
5F6Z	4.18E-15	41.026	X-RAY DIFFRACTION	2.25	Sander vitreus
2HZQ	6.03E-12	32.558	X-RAY DIFFRACTION	1.8	Homo sapiens
1QWD	1.91E-12	29.944	X-RAY DIFFRACTION	1.75	Escherichia coli

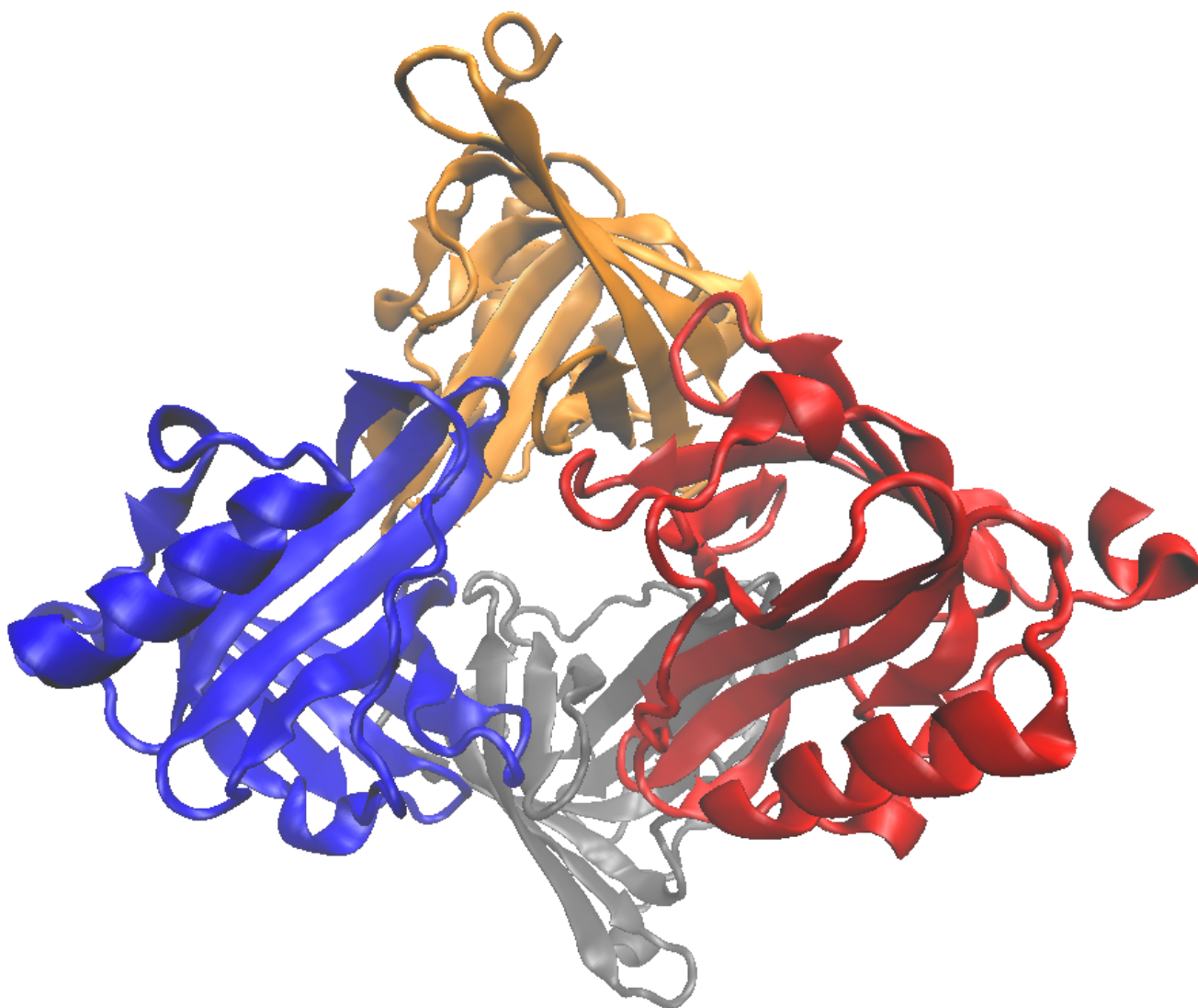
Q9

Structure Info

This structure is likely to be similar in structure to the Apolipoprotein D precursor given the medium sequence similarity (>40%).

In the figure below the Sander cyanin Fluorescent Protein chain A is colored blue and corresponds to the Apolipoprotein D precursor subject of this report.

Structure figure



Q9

Link to ChEMBL

https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2364702/

ChEMBL Info

CHEMBL details 1 binding Assay (CHEMBL2364702) and 15 functional assays. No information of ligand efficiency and Associated Compounds.

Binding assay

Molecule ChEMBL ID	Molecule Name	Molecule Type	Max Phase	First Approval	USAN Stem	Mechanism Of Action	Target ChEMBL ID	Target Name	Mechanism Type	Target Type	Target Organism
 CHEMBL1201131	PIPERONYL BUTOXIDE	Small molecule	4	2000	No Data	Cytochrome P450 inhibitor	CHEMBL2364702	Cytochrome P450	INHIBITOR	PROTEIN FAMILY	Pediculus humanus capitis

An analogue of piperonyl butoxide facilitates the characterisation of metabolic resistance

Using examples of resistant insects with well-characterised resistance mechanisms, a combination of PBO and analogue allows identification of the metabolic mechanism responsible for conferring resistance. The relative potency of PBO as both an esterase inhibitor and an oxidase inhibitor is also discussed. Copyright © 2008 Society of Chemical Industry

Cite: Moores, Graham D., et al. "An analogue of piperonyl butoxide facilitates the characterisation of metabolic resistance." Pest Management Science: formerly Pesticide Science 65.2 (2009): 150-154.
<http://europepmc.org/abstract/MED/18951417>