

Fahim Al Shahrear  
A12015448

### Find A Gene Project

1. Protein Name- Human KIF11

Species- human

Accession number- P52732

Function-This gene encodes a motor protein that belongs to the kinesin-like protein family. Members of this protein family are known to be involved in various kinds of spindle dynamics. The function of this gene product includes chromosome positioning, centrosome separation and establishing a bipolar spindle during cell mitosis.

2. Method: TBLASTN (2.7.1) search against chinese hamster

Database: Expressed Sequence Tags (est)

Organism: chinese hamster (

Chosen match: Accession number-BM800579.1 Homo sapiens cDNA clone. See below for alignment details.

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Translated BLAST: tblastn

blastn blastp blastx tblastn tblastx

Enter Query Sequence

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

P52732

Clear Query subrange

From To

Or, upload file Choose File No file chosen

Job Title P52732:RecName: Full=Kinesin-like protein... Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database Nucleotide collection (nr/nt)

Organism Chinese hamster (taxid:10029) exclude

Optional Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

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

Optional

Limit to Sequences from type material

Optional

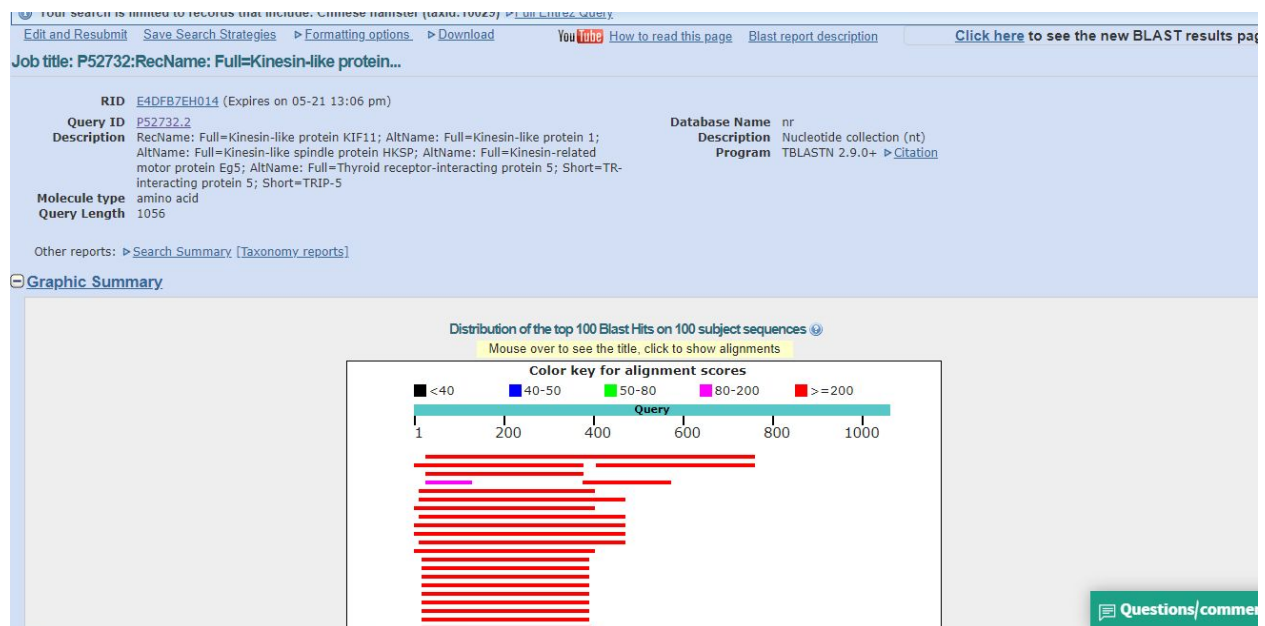
Entrez Query Enter an Entrez query to limit search

YouTube Create custom database

BLAST Search database Nucleotide collection (nr/nt) using Tblastn (search translated nucleotide databases using a protein query)

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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"/>	PREDICTED: Cricetulus griseus kinesin-like protein KIF11 (LOC113838949), mRNA	1307	1307	69%	0.0	86.46%	<a href="#">XM_027434448.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin-like protein KIF11 (LOC113839111), transcript variant X1, mRNA	710	710	35%	0.0	93.09%	<a href="#">XM_027434561.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin-like protein KIF11 (LOC113839111), transcript variant X2, mRNA	683	683	33%	0.0	93.14%	<a href="#">XM_027434562.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin-like protein KIF11 (LOC103159021), transcript variant X2, mRNA	570	570	33%	0.0	80.11%	<a href="#">XM_027433884.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin-like protein KIF11 (LOC113838018), mRNA	344	344	18%	2e-110	86.29%	<a href="#">XM_027433815.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin family member 3A (Kif3a), transcript variant X2, mRNA	318	318	36%	1e-94	45.94%	<a href="#">XM_027414893.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin family member 3A (Kif3a), transcript variant X7, mRNA	319	319	43%	2e-94	41.88%	<a href="#">XM_027427530.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin family member 3A (Kif3a), transcript variant X5, mRNA	319	319	37%	3e-94	45.68%	<a href="#">XM_027427528.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin family member 3A (Kif3a), transcript variant X3, mRNA	320	320	43%	7e-94	41.88%	<a href="#">XM_027414902.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin family member 3A (Kif3a), transcript variant X6, mRNA	321	321	44%	1e-93	41.75%	<a href="#">XM_027427529.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin family member 3A (Kif3a), transcript variant X4, mRNA	321	321	44%	3e-90	41.75%	<a href="#">XM_027427527.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin family member 3A (Kif3a), transcript variant X1, mRNA	320	320	43%	6e-90	41.88%	<a href="#">XM_027414885.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin family member 3A (Kif3a), transcript variant X8, mRNA	318	318	37%	2e-89	45.68%	<a href="#">XM_027427531.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin family member 3B (Kif3b), transcript variant X4, mRNA	304	304	35%	1e-86	43.85%	<a href="#">XM_027421466.1</a>
<input type="checkbox"/>	PREDICTED: Cricetulus griseus kinesin family member 3B (Kif3b), transcript variant X4, mRNA	304	304	35%	1e-86	43.85%	<a href="#">XM_003502315.4</a>

## Alignment details-

Cricetulus griseus kinesin-like protein KIF11 (LOC113839111), transcript variant X1, mRNA

Sequence ID: [XM\\_027434561.1](#) Length: 1414 Number of Matches: 1

## Related Information

Range 1: 242 to 1369

Score	Expect	Method	Identities	Positives	Gaps	Frame
710 bits(1833)	0.0	Compositional matrix adjust.	362/376(96%)	371/376(98%)	0/376(0%)	+2

Query 1 MASQPNSSAKKKKEKGKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADK 60

MASQP+SS+KKKEEKGKNIQVVVRCRPFNLAERKA+AHS+VECD RKEVSVRT GL DK  
 Sbjct 242 MASQPSSSSKKKEEKGKNIQVVVRCRPFNLAERKANAHSVVECDHARKEVSVRTAGLTDK 421

Query 61 SSRKTYTFDMVFGASTKQIDVYRSVVCILDEVIMGYNCTIFAYGQTGTGKTFTMEGERS 120  
 +SRKTYTFDMVFGASTKQIDVYRSVVCILDEVIMGYNCTIFAYGQTGTGKTFTMEGERS  
 Sbjct 422 TSRKTYTFDMVFGASTKQIDVYRSVVCILDEVIMGYNCTIFAYGQTGTGKTFTMEGERS 601

Query 121 PNEEYTWEEDPLAGIIPRTLHQIFEKLTNGTEFSVKVSLLEIYNEELFDLLNPSSDVSE 180  
 PNE YTWEEDPLAGIIPRTLHQIFEKLTNGTEFSVKVSLLEIYNEELFDLL+PS+DVSE  
 Sbjct 602 PNEAYTWEEDPLAGIIPRTLHQIFEKLTNGTEFSVKVSLLEIYNEELFDLLSPSTDVSE 781

Query 181 RLQMFDDPRNKRGVIIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVFS 240  
 RLQMFDDPRNKRGVIIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVFS  
 Sbjct 782 RLQMFDDPRNKRGVIIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVFS 961

Query 241 VTIIHMKETTIDGEELVKIGKLNLDLAGSENIGRSGAVDKRAREAGNINQSLLTLGRVIT 300  
 VTIIHMKETTIDGEELVKIGKLNLDLAGSENIGRSGAVDKRAREAGNINQSLLTLGRVIT  
 Sbjct 962 VTIIHMKETTIDGEELVKIGKLNLDLAGSENIGRSGAVDKRAREAGNINQSLLTLGRVIT 1141

Query 301 ALVERTPHVPYRESKLTRILQDSLGGRTRTSIIATISPASlnleetlstleYAHRAKNIL 360  
 ALVERTPH+PYRESKLTRILQDSLGGRTRTSIIATISPASLNLEETLSTLEYAHRAKNI+  
 Sbjct 1142 ALVERTPHIPYRESKLTRILQDSLGGRTRTSIIATISPASLNLEETLSTLEYAHRAKNIM 1321

Query 361 NKPEVNQKLTKKALIK 376  
 NKPEVNQKLTKKALIK  
 Sbjct 1322 NKPEVNQKLTKKALIK 1369

### 3. Chosen Sequence-

>A. Crisetulus Griseus (Sequence taken from BLAST Result)

NKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVFSVTIIHMKETTIDGEELVKIGKLNLD  
 LAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVERTPHVPYRESKLTRILQDSL  
 GRTRTSIIATISPASlnleetlstleYAHRAKNILNKPEVNQKLTKKALIKKEYTEEIERL

Name- Crisetulus Griseus

Species- Chinese Hamster

Eukaryota; Metazoa; Ecdysozoa; Nematoda; Chromadorea; Spirurida; Dracunculoidea;  
 Anguillicolidae; Anguillicola.

4. A BLASTP search against NR database (see setup in first screen-shot below) yielded a top hit result is to a protein from *Cricetulus griseus* (Chinese Hamster). See additional screen shots below for top hits and selected alignment details:

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Standard Protein BLAST

blastn blastp **blastx** tblastn tblastx

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

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☐ Align two or more sequences [v](#)

**Choose Search Set**

Database  [v](#) [v](#)

Organism  [v](#) ☐ exclude [+](#)

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

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

Optional

**Program Selection**

Algorithm

☐ Quick BLASTP (Accelerated protein-protein BLAST)

☒ blastp (protein-protein BLAST)

☐ PSI-BLAST (Position-Specific Iterated BLAST)

**We are beta testing a New Results page**

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Putative conserved domains have been detected, click on the image below for detailed results.

Query seq.  
Superfamilies

125250375500625750871

C045283



Sequences producing significant alignments:

Select: All None Selected: 0

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/>	kinesin-like protein KIF11 [Cricetulus griseus]	222	952	69%	2e-61	71.35%	<a href="#">XP_027289685.1</a>
<input type="checkbox"/>	PREDICTED: kinesin-like protein KIF11 [Gorilla gorilla gorilla]	234	661	62%	8e-61	74.72%	<a href="#">XP_018889975.1</a>
<input type="checkbox"/>	kinesin-like protein KIF11 [Pan paniscus]	232	561	48%	6e-60	63.59%	<a href="#">XP_003825410.1</a>
<input type="checkbox"/>	kinesin-like protein KIF11 [Pan troglodytes]	232	561	48%	6e-60	63.59%	<a href="#">XP_507923.4</a>
<input type="checkbox"/>	kinesin-like protein KIF11 [Homo sapiens]	232	561	48%	6e-60	63.59%	<a href="#">NP_004514.2</a>
<input type="checkbox"/>	unnamed protein product [Homo sapiens]	232	679	55%	6e-60	63.59%	<a href="#">BA036923.1</a>
<input type="checkbox"/>	KIF11 isoform 1 [Pan troglodytes]	232	560	48%	7e-60	63.59%	<a href="#">PNI02320.1</a>
<input type="checkbox"/>	kinesin-related protein [Homo sapiens]	232	638	50%	7e-60	63.59%	<a href="#">CAA59449.1</a>
<input type="checkbox"/>	KIF11 isoform 2 [Pongo abelii]	230	604	48%	2e-59	63.43%	<a href="#">PNI089443.1</a>
<input type="checkbox"/>	kinesin-like protein KIF11 [Pongo abelii]	230	604	48%	2e-59	63.43%	<a href="#">XP_002821023.1</a>
<input type="checkbox"/>	PREDICTED: kinesin-like protein KIF11 [Ceratotherrus simum simum]	230	718	55%	4e-59	87.05%	<a href="#">XP_004427888.1</a>
<input type="checkbox"/>	PREDICTED: LOW QUALITY PROTEIN: kinesin-like protein KIF11 [Nomascus leucogenys]	230	550	45%	4e-59	62.67%	<a href="#">XP_003255272.1</a>
<input type="checkbox"/>	PREDICTED: kinesin-like protein KIF11 [Colobus angolensis palliatus]	229	600	46%	5e-59	63.13%	<a href="#">XP_011803290.1</a>

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▼ Next ▲ Previous ▲ Descriptions

kinesin-like protein KIF11 [Cricetus griseus]

Sequence ID: [XP\\_027289685.1](#) Length: 349 Number of Matches: 7

Range 1: 9 to 173 [GenPept](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
222 bits(565)	2e-61	Compositional matrix adjust.	122/171(71%)	143/171(83%)	15/171(8%)

Query 94	EEKLHDAASKLLNTVEETTKDVSLH----	SKLDR-KSBJCT----	LETTQKHLQETKLQ	144
	EE++ ++A K+ +EE V+GL ++LD+ KS+ T	LETTQKHLQETKLQ		
Sbjct 9	EEQIVESAERI-GALEEELSKVTGLFVDSKNELDQCKSDLQTKTQELETTQKHLQETKLQ			67
Query 145	LVKEEYITSALESTEEKLHDAASKLLNTVEETTKDVSLHSLDRKQUERYKAVDQHNAE			204
	LVKEEY++SALE TEEKLHDAASKLL+TV+ETT+DVSLHSLDRK ++A+D+HNAE			
Sbjct 68	LVKEEYSSALERTEEKLHDAASKLLSTVKETTRDVSGLHSLDRK-----RAIDEHNAE			122
Query 205	AQDIFGKNLNSLFNNMEELIKDGSQKAMLEHKTFLGNLSSSSVSALDT			255
	AQDIFGKNLNSLFNNMEELIKDGS+KQKAMLE HKTFLGNL+SSSSVSALDT			
Sbjct 123	AQDIFGKNLNSLFNNMEELIKDGSQKAMLEHKTFLGNLSSSSVSALDT			173

Range 2: 114 to 237 [GenPept](#) [Graphics](#) ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps
189 bits(481)	1e-49	Compositional matrix adjust.	97/129(75%)	111/129(86%)	5/129(3%)

Query 321	KAVDQHNAEAQDIFGKNLNSLFNNMEELIKDGSQKAMLEHKTFLGNLSSSSVSALDT			380
	+A+D+HNAEAQDIFGKNLNSLFNNMEELIKDGS+KQKAMLE HKTFLGNL+SSSSVSALDT			
Sbjct 114	RAIDEHNAEAQDIFGKNLNSLFNNMEELIKDGSQKAMLEHKTFLGNLSSSSVSALDT			173
Query 381	QUERYITVALGSLTIPENVSTHVSQIFNMILKEQSLAAESKTVLQELINLKTDLSS			440
	+TT ALG+L SIP+HVS V+DI +MILKEQSLAA+SKTVL+ LIN L+TDLL S			
Sbjct 174	-----VTTTALGTLMSIPQNVARSVTQISDMILKEQSLAAQSKTVLRGLNGLETDLGS			228
Query 441	LEMILITTV 449			
	L+ IL V			
Sbjct 229	LKTILAPGV 237			

Range 3: 234 to 349 [GenPept](#) [Graphics](#) ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps
-------	--------	--------	------------	-----------	------

Related Information

[Gene - associated gene details](#)

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

## 5. Re-labeled sequences for alignment:

> Human sp|P52732.2|KIF11\_HUMAN

MASQPNSSAKKKEEKGKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADKSSRK  
TYTFDMVFGASTKQIDVYRSVVCILDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWE  
DPLAGIIPRTL

>Hamster XP\_027289685.1 kinesin-like protein KIF11

MNGKLTVQEEQIVESAEKIGALEEELSKVTGLFVDSKNELDQCKSDLQTKTQELETTQKHLQETK  
LQLVKEEYVSSALERTEEKLHDAASKLLSTVKETTRDVSGLHSLDRKRAIDEHNAEAQDIFGKN  
LNSLFNNMEELIKDGSQKAMLEHDK

> Gorilla XP\_018889975.1:569-719 PREDICTED: kinesin-like protein KIF11

LLSSLEMILSPTVVSILKINSQKHFKTSLTVADKIEDQKKELDGFLSILCNNLHELQENTICSLVE  
SQKQCGNLTEDLKTIKQTHSQELCKLMNLWTERFCALEEEKCENIQKPLSSVQENIQKSKDIVNK  
MTFHSQKFCADSDFGSQE

> Bonobo monkey XP\_003825410.1 kinesin-like protein KIF11 [Pan paniscus]

MASQPNSSAKKKEEKGKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADKSSRK  
TYTFDMVFGASTKQIDVYRSVVCILDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWE  
DPLAGIIPRTL

> Chimpanzee XP\_507923.4:375-580 kinesin-like protein KIF11 [Pan troglodytes]

IKEYTEEIERLKRD LAAAREKNGVYISEENFRVMSGKLT VQEEQIVELIEKIGAVEEELNRVTELF  
MDNKNELDQCKSDLQNK TQELETTQKHLQETKLQLVKEEYITSALESTEEKLHDAASKLLNTVE  
ETTKDVSGLH

Re-labeled sequences for alignment:

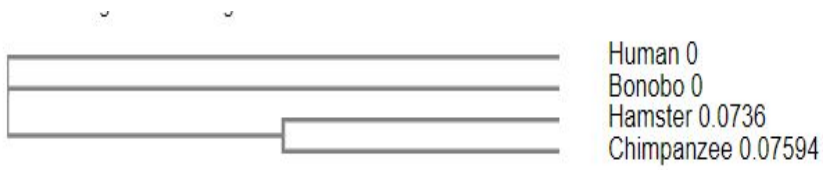
Human           ----- MASQPNSSAKKKEEKGKNIQVVVRCRPFNLAERKAS  
Bonobo           -----MASQPNSSAKKKEEKGKNIQVVVRCRPFNLAERKAS  
Hamster          -----MNGKLT VQEEQIVESAEKIGALEEELS  
Chimpanzee  
IKEYTEEIERLKRD LAAAREKNGVYISEENFRVMSGKLT VQEEQIVELIEKIGAVEEELN  
                  .: .: .: \*: \*   .: \* : .

Human  
AHSIVECDPVRKEVSVRTGGLADKSSRKTYTFDMVFGASTKQI-DVYRSVVCPI LDEVIM  
Bonobo  
AHSIVECDPVRKEVSVRTGGLADKSSRKTYTFDMVFGASTKQI-DVYRSVVCPI LDEVIM  
Hamster  
KVTGLFVDS-KNELDQCKSDLQTKTQELETTQKHLQETKLQLVKEEYVSSALERTEEKLH  
Chimpanzee  
RVTELFMDN-KNELDQCKSDLQNK TQELETTQKHLQETKLQLVKEEYITSALESTEEKLH  
                  .: \*   .: \*:   ... \*   \*:   \*   .: .: .: .: \*:   .:   \*: :

Human           GYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEE DPLAGIIPRTL-----  
Bonobo           GYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEE DPLAGIIPRTL-----  
Hamster  
DAASKLLSTVKETTRDVSGLH SKLDRKRAIDEHNAEAQDIFGKNLNSLFNNMEELIKDGS  
Chimpanzee      DAASKLLNTVEETTKDVSGLH-----  
                  .   .: .:   .: \*   .: :

Human           -----  
Bonobo           -----  
Hamster          AKQKAMLEDHK  
Chimpanzee       -----

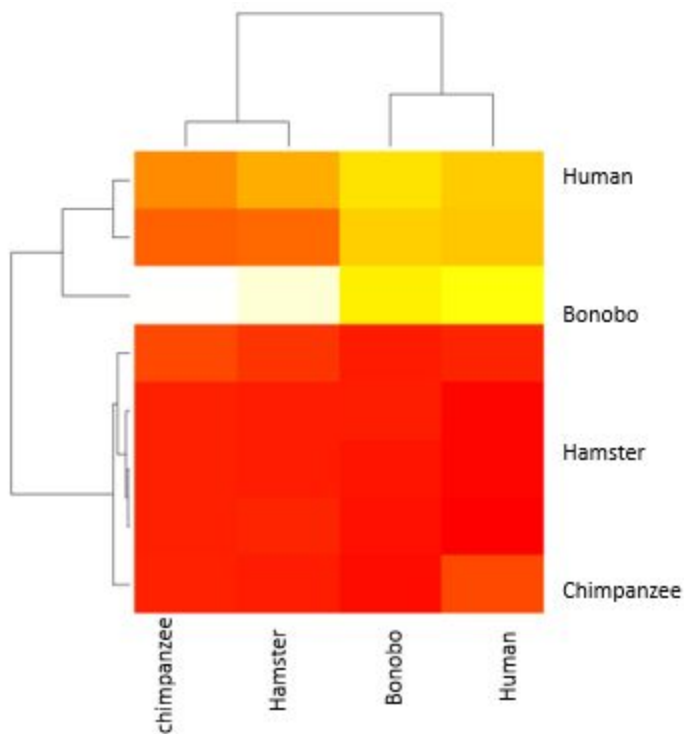
## 6. Phylogenetic Tree



## Tree Data

```
(  
  Human:0.00000,  
  Bonobo:0.00000,  
  (  
    Hamster:0.07360,  
    Chimpanzee:0.07594)  
  :0.81102);
```

## 7. Heatmap Data



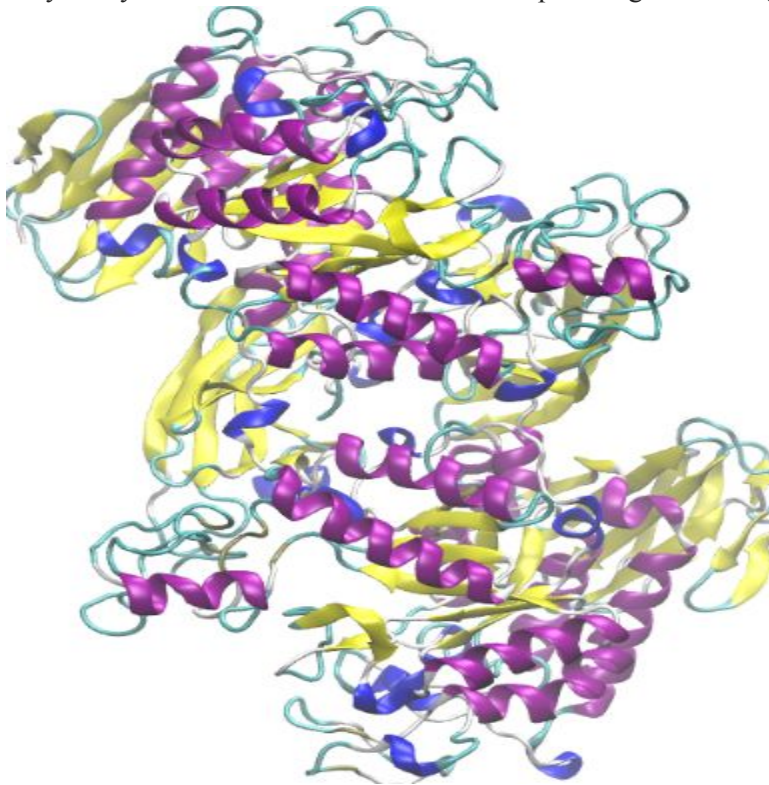


8.

ID	Technique	Resolution	source	Evalue	Identity
5GHD	X-ray diffraction	1.68	Cavia Porcellus	7.34 e -54	85.4
2GRT	X-ray diffraction	1.94	Mesocricetus Auratus	3.24e-52	82.3
7HFG	X-ray diffraction	2.1	Phodopus Sungorus	5.69e-58	81.6

9.

Very likely to be similar in structure to novel protein given the high sequence similarity (>80%)



10. ChEMBL details 31 targets ; No ligand efficiency data.

Status: Results Ready Edit Search

Show Full Query

31 Targets  
0 Selected - Select All  
Browse Activities

Table Heatmap CSV TSV

Filters

Records per page: 20 Show/Hide Columns Showing 1-20 out of 31 records

Organism Taxonomy L1

Eukaryotes 31

Organism Taxonomy L2

Mammalia 29

Apicomplexa 1

Arthropoda 1

Organism Taxonomy L3

ChEMBL ID	E-Value	Positives %	Identities %	Score (bits)	Score	Length	Name	UniProt Accession	Type
<input type="checkbox"/> CHEMBL3632454	No Data	No Data	No Data	No Data	No Data	No Data	Kinesin-like protein KIF15	Q9NS87	SIN PRO

[https://www.ebi.ac.uk/chembl/g/#blast\\_search\\_results/eyJzZXF1ZW5jZSI6Ik5LREVWWVFJTjEVLRFBS1JUVFVBVEwNTkFZU1NSU0hTVkZTViRjSE1LRVRUSURHRUVMVktJR0tMTkxWRFxuTEFHU0VOSUdSU0dBVkJLUkFSRUJHTkI0UUVNMFRMR1JWSVRBTjZFUlRQSFZQWVJFU0tMVFJJTFEU0xHXG5HUIRSVFNJSUFUSVNNQQXNsbmxiZXRsc3R5ZVlBSFJBS05JTE5LUEVWTiFLTFRLS0FMSUtFWVRFRUJFUkxibjI9](https://www.ebi.ac.uk/chembl/g/#blast_search_results/eyJzZXF1ZW5jZSI6Ik5LREVWWVFJTjEVLRFBS1JUVFVBVEwNTkFZU1NSU0hTVkZTViRjSE1LRVRUSURHRUVMVktJR0tMTkxWRFxuTEFHU0VOSUdSU0dBVkJLUkFSRUJHTkI0UUVNMFRMR1JWSVRBTjZFUlRQSFZQWVJFU0tMVFJJTFEU0xHXG5HUIRSVFNJSUFUSVNNQQXNsbmxiZXRsc3R5ZVlBSFJBS05JTE5LUEVWTiFLTFRLS0FMSUtFWVRFRUJFUkxibjI9)