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Find a Gene Project

[Q1]

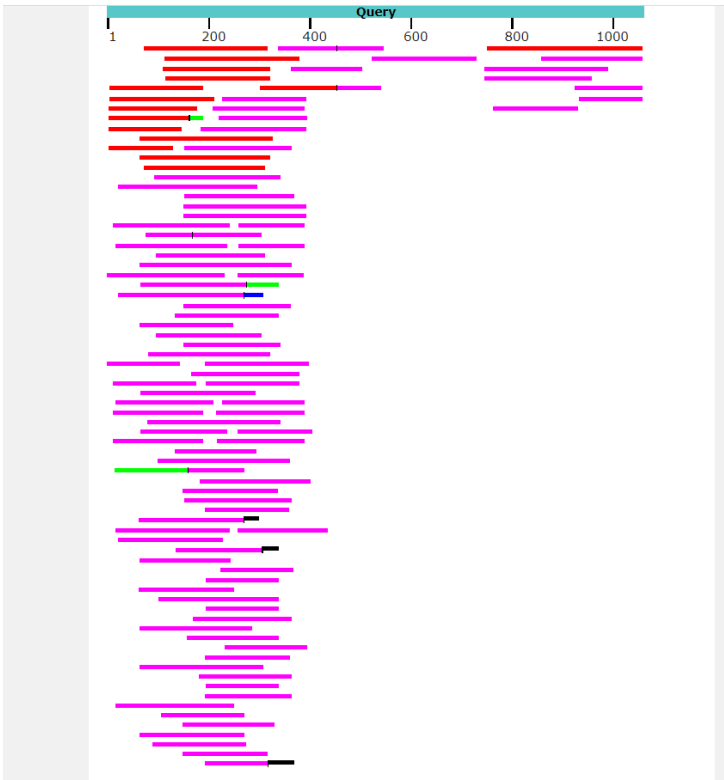
Name: KIF11
Accession: NP_004514.2
Species: Homo Sapiens

[Q2]

Method: TBLASTN against homo sapiens EST
Database: Expressed Sequence Tags
Organism: chicken

The screenshot shows the NCBI TBLASTN search interface. At the top, there are tabs for 'blastn', 'blastp', 'blastx', 'tblastn' (selected), and 'tblastx'. Below the tabs, the title 'Translated BLAST: tblastn' is displayed. The main search area is divided into two sections: 'Enter Query Sequence' and 'Choose Search Set'. In the 'Enter Query Sequence' section, the 'Enter accession number(s), gi(s), or FASTA sequence(s)' field contains 'NP_004514.2'. There is a 'Query subrange' section with 'From' and 'To' fields. Below this, there is an 'Or, upload file' section with a 'Choose File' button and a 'No file chosen' status. The 'Job Title' field contains 'NP_004514:kinesin-like protein KIF11 [Homo...'. In the 'Choose Search Set' section, the 'Database' dropdown is set to 'Expressed sequence tags (est)'. The 'Organism' dropdown is set to 'chicken (taxid:9031)'. There are checkboxes for 'Exclude' (Models (XM/XP), Uncultured/environmental sample sequences) and 'Limit to' (Sequences from type material). The 'Entrez Query' field is empty. At the bottom, there is a 'BLAST' button and a checkbox for 'Show results in a new window'.

Chosen match: Accession BU380362.1, a 830 base pair clone from *gallus gallus*



<input checked="" type="checkbox"/>	gPGC_EST09025 Embryonic gonadal PGC cDNA Library Gallus gallus cDNA 5' mRNA sequence	Gallus gallus	157	157	28%	4e-40	34.11%	1348	DR419183.1
<input checked="" type="checkbox"/>	603601513F1 CSEQCHN54 Gallus gallus cDNA clone ChEST5773 5' mRNA sequence	Gallus gallus	150	150	21%	8e-40	41.18%	706	BU282538.1
<input checked="" type="checkbox"/>	603499116F1 CSEQCHN65 Gallus gallus cDNA clone ChEST413p4 5' mRNA sequence	Gallus gallus	117	186	25%	4e-39	36.49%	808	BU333462.1
<input checked="" type="checkbox"/>	603582989F1 CSEQCHN75 Gallus gallus cDNA clone ChEST534b24 5' mRNA sequence	Gallus gallus	150	191	26%	4e-39	38.15%	830	BU380362.1
<input checked="" type="checkbox"/>	603504004F1 CSEQCHN51 Gallus gallus cDNA clone ChEST425h1 5' mRNA sequence	Gallus gallus	148	148	20%	1e-38	42.66%	775	BU261065.1
<input checked="" type="checkbox"/>	AM068009 Chicken immune 3 - CSEQRBN33 Gallus gallus cDNA clone C0000485A07_T7 mRNA sequence	Gallus gallus	145	145	19%	4e-38	40.87%	695	AM068009.1
<input checked="" type="checkbox"/>	604139583F1 CSEQCHN59 Gallus gallus cDNA clone ChEST970e21 5' mRNA sequence	Gallus gallus	145	145	17%	5e-38	41.62%	700	BU408102.1
<input checked="" type="checkbox"/>	603407203F1 CSEQCHN69 Gallus gallus cDNA clone ChEST317e2 5' mRNA sequence	Gallus gallus	142	142	19%	2e-37	40.00%	617	BU350011.1
<input checked="" type="checkbox"/>	603505385F1 CSEQCHN53 Gallus gallus cDNA clone ChEST430e17 5' mRNA sequence	Gallus gallus	144	144	17%	2e-37	44.63%	688	BU380362.1

Download

GenBank

Graphics

Sort by: E value

NextPreviousDescriptions

603582989F1 CSEQCHN75 Gallus gallus cDNA clone ChEST534b24 5', mRNA sequence

Sequence ID: [BU380362.1](#) Length: 830 Number of Matches: 2

Range 1: 4 to 708

GenBank

Graphics

Next MatchPrevious Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
150 bits(378)	4e-39	Compositional matrix adjust.	95/249(38%)	136/249(54%)	17/249(6%)	+1
Query	23	VRCRPFNLAERKASAHSEVCEDPVRKEVSVRTGGLADSSRKTYTFDMVFGASTKQIDVY	82			
		+RCRP E + P +V V S K +T+D VF S +Q +V+				
Sbjct	4	LRCRPLVPKETSEGCQMLCSFVPGEPQVIV-----GSDKAFTYDYVFDPSVEQEEVF	159			
Query	83	RSVVCPILDEVIMGVNYCTIFAYGQTGTGKTFTEGERSPNEEYTWEEDPLAGIIPRTLHQ	142			
		+ V P++ + GYN T+ AVGQTG+GKT++M G + ++E+ DP G+IPR +				
Sbjct	160	NTAVAPLIRIGFKGYNATVLAYGQTGSGKTYSMGGTYTASQEH----DPSMGVIPRVIKL	327			
Query	143	IF-EKLTDNGETFSVKVSLLEIYNEELFDLLNPSSDVSRLLQMFDDPRNKRGVIIKGLLE	201			
		+F EK EF +KVS LEIYNE++ DLL S + S ++ + +DP K G+ I GL E				
Sbjct	328	LFKEKEQRQDWEFVLKVSYLEIYNEDILLCCSSRRSSQISIREDP--KEGIKIVGLTE	501			
Query	202	ITVHNKDEVYQILEKGAARKTTAATLMNAYSSRSHSVFSVTIHM-KET-TIDGEELVKIG	259			
		V + LE+G RT A+T MN+ SSRSH++F++ I KET T L				
Sbjct	502	RNVACARDTVSCLEQGNCRVASTAMNSQSSRSHAIFTICIDQNKETMTRTAVSLQSYT	681			
Query	260	KLNLVDLAG 268				
		L L+DL G				
Sbjct	682	WLILLDLRG 708				

[Q3]

LRCRPLVPKETSEGCQMCLSFVPGEPPQVIVGSDKAFTYDYVFDPSVEQEEVF
NTAVAPLIRGIFKGYNATVLAYGQTGSGKTYSMGGTYTASQEHDPSMGVIPRVIKL
LFKEKEQRQDWEFVLKVSYLEIYNEDILDLLCSSRERSSQISIREDPKEGIKIVGLTE
RNVACARDTVSCLEQGNNCRTVASTAMNSQSSRSHAIFTICIDQNKETMTRTAVSLQSYT
WLILDLRG

Name: 603582989F1 CSEQCHN75

Species: *Gallus gallus*

[Q4]

A BLASTP search against NR database yielded the following results:

BLASTP programs search protein databases using a protein query. [more...](#) [Reset page](#) [Bookmark](#)

Enter Query Sequence

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

LRCRPLVPKETSEGCQMCLSFVPGEPPQVIVGSDKAFTYDYVFDPSVEQEEVF
NTAVAPLIRGIFKGYNATVLAYGQTGSGKTYSMGGTYTASQEHDPSMGVIPR
VIKL
LFKEKEQRQDWEFVLKVSYLEIYNEDILDLLCSSRERSSQISIREDPKEGIKIV
GLTE

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 ☐ exclude [Add organism](#)

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

Exclude ☐ 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

The top alignment not from the same species is that of the *atlantisia rogersi*

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"/>	chromosome-associated kinesin KIF4 isoform X1 [Gallus gallus]	Gallus gallus	457	457	100%	1e-149	91.91%	1225	XP_015133678.1
<input checked="" type="checkbox"/>	chromosome-associated kinesin KIF4 [Gallus gallus]	Gallus gallus	457	457	100%	1e-149	91.91%	1226	NP_990306.2
<input checked="" type="checkbox"/>	KIF4 protein [Atlantisia rogersi]	Atlantisia rogersi	438	438	100%	3e-148	87.23%	657	NXV79606.1
<input checked="" type="checkbox"/>	hypothetical protein ASZ78_006490 [Callipepla squamata]	Callipepla squamata	453	453	100%	3e-148	90.21%	1191	QXB62671.1
<input checked="" type="checkbox"/>	KIF4 protein [Odontophorus gujanensis]	Odontophorus gujanensis	454	454	100%	3e-148	91.06%	1225	NXJ11164.1
<input checked="" type="checkbox"/>	hypothetical protein CIB84_002715 [Bambusicola thoracicus]	Bambusicola thoracicus	451	451	100%	7e-148	90.64%	1124	POI33532.1
<input checked="" type="checkbox"/>	RecName: Full=Chromosome-associated kinesin KIF4; AltName: Full=Chromokinesin [Gallus...]	Gallus gallus	452	452	100%	1e-147	91.06%	1225	Q90640.1
<input checked="" type="checkbox"/>	chromosome-associated kinesin KIF4A isoform X1 [Numida meleagris]	Numida meleagris	451	451	100%	4e-147	91.06%	1226	XP_021262214.1

KIF4 protein [Atlantisia rogersi]

Sequence ID: [NXV79606.1](#) Length: 657 Number of Matches: 1

Range 1: 15 to 245 [GenPept](#) [Graphics](#)

[Next Match](#)
[Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
438 bits(1126)	3e-148	Compositional matrix adjust.	205/235(87%)	219/235(93%)	4/235(1%)
Query 1	LRCRPLVPKETSEGCQMCLSFVPGEPQVIVGSDKAFTYDYVFDPSVEQEEVNTAVAPLI				60
Sbjct 15	LRCRPLVPKETSEGCQMCLSFVPGEPQV+VG+DK+FTYDYVFDPSVEQEEVNTAVAPLI				74
Query 61	RGIFKGYNATVLAYGQTGSGKTYSMGGTYTASQEHDPSPMGVIPRVIKLLFKEKEQRQDWE				120
Sbjct 75	RGIFKGYNATVLAYGQTGSGKTYSMGGTYTA+QEH+PS+GVIPRVIKLLFKEKEQRQDWE				134
Query 121	FVLKVSYLEIYNEDILDLLCSSRERSQISIREDPKEGIKIVGLTERNVACARDTVSCLE				180
Sbjct 135	FVLKVSYLEIYNEDILDLLCSSRERS+QISIREDPKEGIKIVGLTERNV CA+DTVSCLE				194
Query 181	QGNNCRTVASTAMNSQSSRSHAIFTICIDQNKETMTRTAVSLQSYTWLILLDLRG				235
Sbjct 195	QGNNRTVASTAMNSQSSRSHAIFTICIDQ K+ ++ ++ L L+DL G				245

[Q5]

> **Human_KIF11**

VRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADKSSRKTYTFDMVFGASTKQIDVY
RSVVCPIILDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEEEDPLAGIIPRTLHQ
IFEKLTDNNGTEFSVKVSLLEIYNEELFDLLNPSSDVSERLQMFDDPRNKRGVIIKGLEE
ITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVFSVTIHMKETIDGEELVKIG
KLNLVDLAG

>**Chicken 603582989F1 CSEQCHN75 Gallus gallus cDNA clone**
ChEST534b24 5', mRNA sequence

LRCRPLVPKETSEGCQMCLSFVPGEPQVIVGSDKAFTYDYVFDPSVEQEEVF
NTAVAPLIRGIFKGYNATVLAYGQTGSGKTYSMGGTYTASQEHDPSPMGVIPRVIKLLFKEKEQRQDWE
FVLKVSYLEIYNEDILDLLCSSRERSQISIREDPKEGIKIVGLTE
RNVACARDTVSCLEQGNNCRTVASTAMNSQSSRSHAIFTICIDQNKETMTRTAVSLQSYT
WLILLDLRG

>**Scaled_Quail hypothetical protein ASZ78_006490 [Callipepla squamata]**

LRCRPLVPKETSEGCQTCLSFVPGEPQVIVGSDKAFTYDYVFDPSVEQEEVNTAVAPLI
RGVFRGYNATVLAYGQTGSGKTYSMGGTYTASQEHDPSPMGVIPRVIKLLFKEKEQRQDWE
FVLKVSYLEIYNEDILDLLCSSRERSQISIREDPKEGIKIVGLTERNVACARDTVSCLE
QGNNRSTVASTAMNSQSSRSHAIFTICIDQKKKNDKNSSFHSLHLVDLAG

>**Marbled_wood_quail KIF4 protein [Odontophorus gujanensis]**

LRCRPLVPKETSEGCQMCLSFVPGEPQVIVGSDKAFTYDYVFDPAVEQEEVNTAVAPLI
RGIFKGYNATVLAYGQTGSGKTYSMGGTYTASQEHDPSPMGVIPRVIKLLFKEKEQRQDWE
FVLKVSYLEIYNEDILDLLCSSRERSQISIREDPKEGIKIVGLTERNVACARDTVSCLE

QGNNsRTVASTAMNSQSSRSIAFTICIDQKKKNDKNSSFHskLHLVdLAG

>Northern_bobwhite hypothetical protein H355_010971 [Colinus virginianus]

LRcRPLVPkETSEGCQTCLsFVPGEpQVIVGSDKAFTYDYVFDPSVEQEeVFNTAVAPLI

RGIfKGYNATVLAyGQTGSGKtYSMGGTYtASQEHdPSMGVIpRVIKLLfKEKEQRQDWE

FVLKVSyLEIYNEDILdLLCSSLRERSSQISIREDPKEGIKIVGLTERNVACARDTVSCLE

QGNNsRTVASTAMNSQSSRSIAFTICIDQKKKNDKNSSFHskLHLVdLAG

>Ring_necked_pheasant chromosome-associated kinesin KIF4A isoform X1 [Phasianus colchicus]

LRcRPLVPkETSEGCQMCLsFVPGEpQVIVGSNKAFTYDYVFDPSVEQEeVFNTAVAPLV

RDIFKGYNATVLAyGQTGSGKtYSMGGTYtASQEHdPSMGVIpRVIKLLfKEKEQRQDWE

FVLKVSyLEIYNEDILdLLCSSLRERSSQISIREDPKEGIKIVGLTERNVACAQDTVSCLE

QGNNsRTVASTAMNSQSSRSIAFTICIDQKKKNDKNSSFHskLHLVdLAG

>wild_turkey chromosome-associated kinesin KIF4A isoform X1 [Meleagris gallopavo]

LRcRPLVPkETSEGCQTCLsFVPGEpQVIVGSDKAFTYDYVFDPTVEQEeVFNTAVAPLV

RDIFKGYNATVLAyGQTGSGKtYSMGGSYtASQEHdPSMGVIpRVIKLLfKEKEQRQDWE

FVLKVSyLEIYNEDILdLLCSSLRERSSQISIREDPKEGIKIVGLTERNVACARDTVSCLE

QGNNsRTVASTAMNSQSSRSIAFTICIDQKKKNDKNSSFHskLHLVdLAG

Alignment:

CLUSTAL multiple sequence alignment by MUSCLE (3.8)

```

Human      VRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADKSSRKTYTTFDMVFGASTKQIDVY
Chicken    LRCRPLVPKETSEGCQMCLSFVPGEQVIV-----GSDKAFTYDYVFDPSVEQEEVF
Ring_necked_pheasant LRCRPLVPKETSEGCQMCLSFVPGEQVIV-----GSNKAFTYDYVFDPSVEQEEVF
wild_turkey LRCRPLVPKETSEGCQTCLSFVPGEQVIV-----GSDKAFTYDYVFDPTVEQEEVF
Scaled_Quail LRCRPLVPKETSEGCQTCLSFVPGEQVIV-----GSDKAFTYDYVFDPSVEQEEVF
Northern_bobwhite LRCRPLVPKETSEGCQTCLSFVPGEQVIV-----GSDKAFTYDYVFDPSVEQEEVF
Marbled_wood_quail LRCRPLVPKETSEGCQMCLSFVPGEQVIV-----GSDKAFTYDYVFDPAVEQEEVF
:****:   * . .:  .:  *   : * *   . * *:*** * ..*: * **:

Human      RSVVCPILDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEEDPLAGIIPRTLHQ
Chicken    NTAVAPLIRGIFKGYNATVLAYGQTGSGKTYSMGGTYTASQEH----DPSMGVIPRVIKL
Ring_necked_pheasant NTAVAPLVRDIFKGYNATVLAYGQTGSGKTYSMGGTYTASQEH----DPSMGVIPRVIKL
wild_turkey NTAVAPLVRDIFKGYNATVLAYGQTGSGKTYSMGGSYTASQEH----DPSMGVIPRVIKL
Scaled_Quail NTAVAPLIRGVFRGYNATVLAYGQTGSGKTYSMGGTYTASQEH----DPSMGVIPRVIKL
Northern_bobwhite NTAVAPLIRGIFKGYNATVLAYGQTGSGKTYSMGGTYTASQEH----DPSMGVIPRVIKL
Marbled_wood_quail NTAVAPLIRGIFKGYNATVLAYGQTGSGKTYSMGGTYTASQEH----DPSMGVIPRVIKL
..*. *:  : : ***. *:*****:***: * *   :. :*:   **  *:***.:

Human      IF-EKLTDNGETFSVKVSLLEIYNEELFDLLNPSSDVSERLQMFDDPRNKRGVIIKGLEE
Chicken    LFKEKEQRQDWEFVLKVSYLEIYNEDILDLLCSSRERSSQISIREDPKE--GIKIVGLTE
Ring_necked_pheasant LFKEKEQRQDWEFVLKVSYLEIYNEDILDLLCSSRERSSQISIREDPKE--GIKIVGLTE
wild_turkey LFKEKEQRQDWEFVLKVSYLEIYNEDILDLLCSSRERSSQISIREDPKE--GIKIVGLTE
Scaled_Quail LFKEKEQRQDWEFVLKVSYLEIYNEDILDLLCSSRERSSQISIREDPKE--GIKIVGLTE
Northern_bobwhite LFKEKEQRQDWEFVLKVSYLEIYNEDILDLLCSSRERSSQISIREDPKE--GIKIVGLTE
Marbled_wood_quail LFKEKEQRQDWEFVLKVSYLEIYNEDILDLLCSSRERSSQISIREDPKE--GIKIVGLTE
: * * *   :. * * :*** *****:***: * *   :. :*:   **: * * * *

Human      ITVHNKDEVYQILEKGAARKRTAATLMNAYSSRSHSVFSVTIHMKETIDIGE--ELVKIG
Chicken    RNVACARDTVSCLEQGNNCRTVASTAMNSQSSRSHAIFTICIDQNKETMTRTAVSLQSYT
Ring_necked_pheasant RNVACAQDTVSCLEQGNNCRTVASTAMNSQSSRSHAIFTICIDQKKKNDKNS--SF--HS
wild_turkey RNVACARDTVSCLEQGNNCRTVASTAMNSQSSRSHAIFTICIDQKKKNDKNS--SF--HS
Scaled_Quail RNVACARDTVSCLEQGNNCRTVASTAMNSQSSRSHAIFTICIDQKKKNDKNS--SF--HS
Northern_bobwhite RNVACARDTVSCLEQGNNCRTVASTAMNSQSSRSHAIFTICIDQKKKNDKNS--SF--HS
Marbled_wood_quail RNVACARDTVSCLEQGNNCRTVASTAMNSQSSRSHAIFTICIDQKKKNDKNS--SF--HS
. *   :. . *: *   **. *: * *: *****:***: *   :. :.   .:

Human      KLNLDVLAG
Chicken    WLILLDLRG
Ring_necked_pheasant KLHLVDLAG
wild_turkey KLHLVDLAG
Scaled_Quail KLHLVDLAG
Northern_bobwhite KLHLVDLAG
Marbled_wood_quail KLHLVDLAG
. * *:*** *

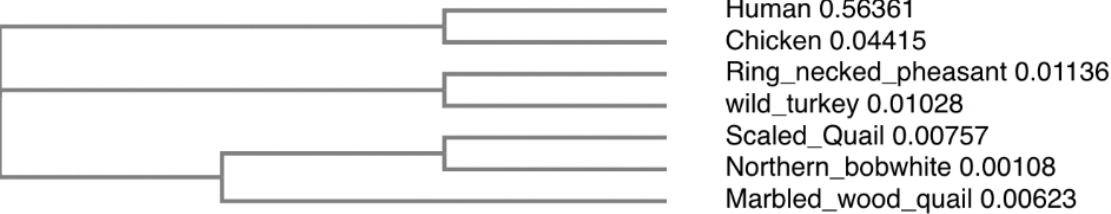
```

[Q6]

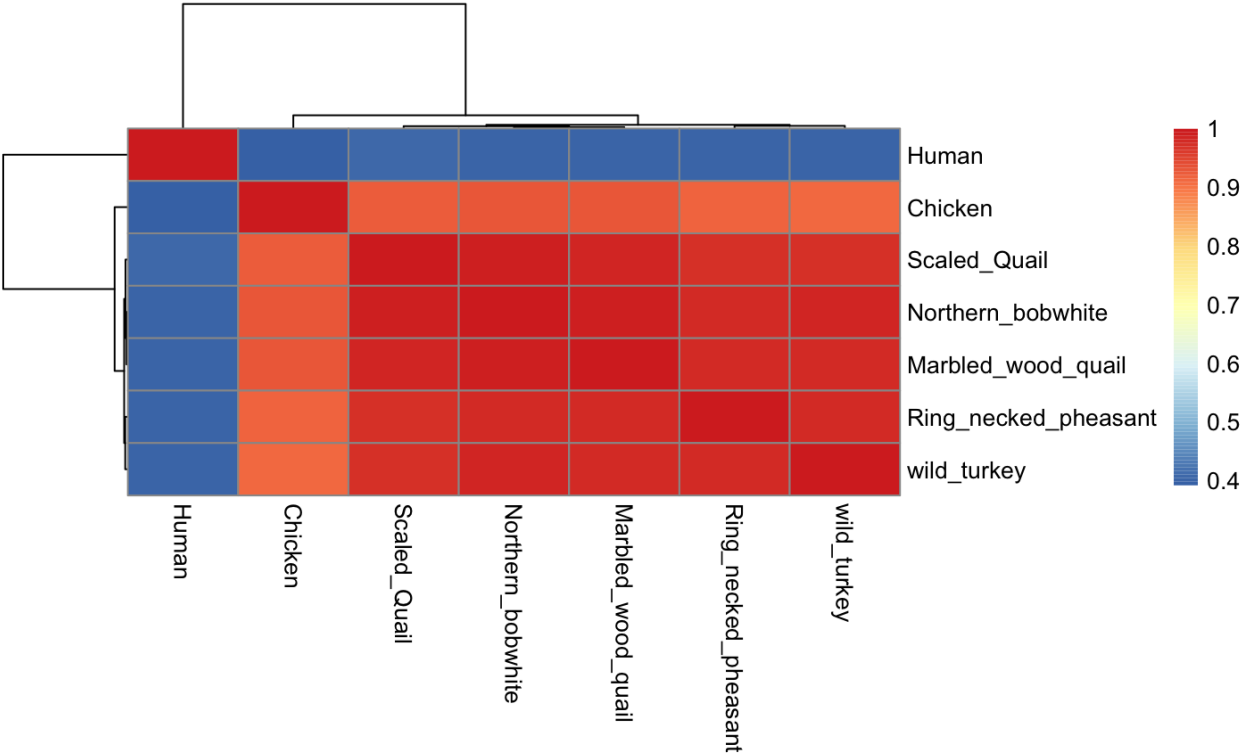
Phylogenetic Tree

This is a Neighbour-joining tree without distance corrections.

Branch length: ☒ Cladogram ☐ Real



[Q7]

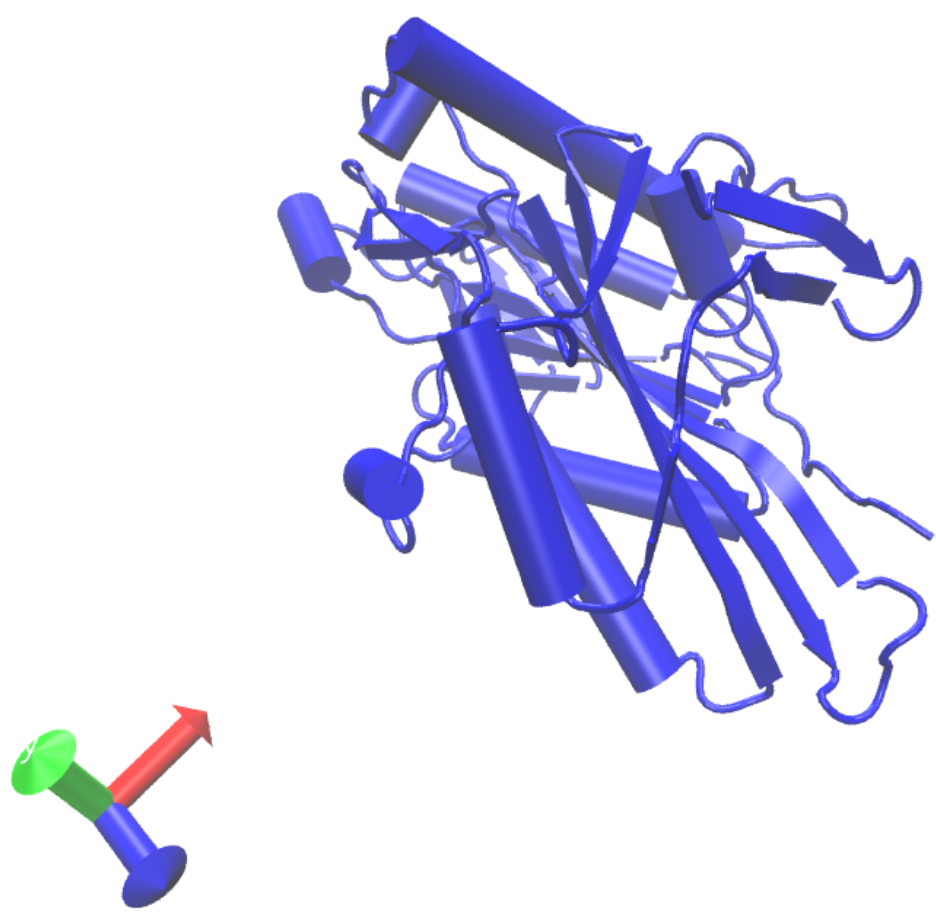


[Q8]

ID	Technique	Resolution	Source	E value	Identity
3ZFC	X-Ray Diffraction	1.80	Mus musculus	6.05e-132	76.170
4A14	X-Ray Diffraction	1.60	Homo sapiens	9.22e-49	40.000
2XT3	X-Ray Diffraction	1.88	Homo sapiens	2.39e-48	40.000

[Q9]

It is possible that this structure is similar to my “novel” gallus gallus protein since the identity is relatively high at 76.17.

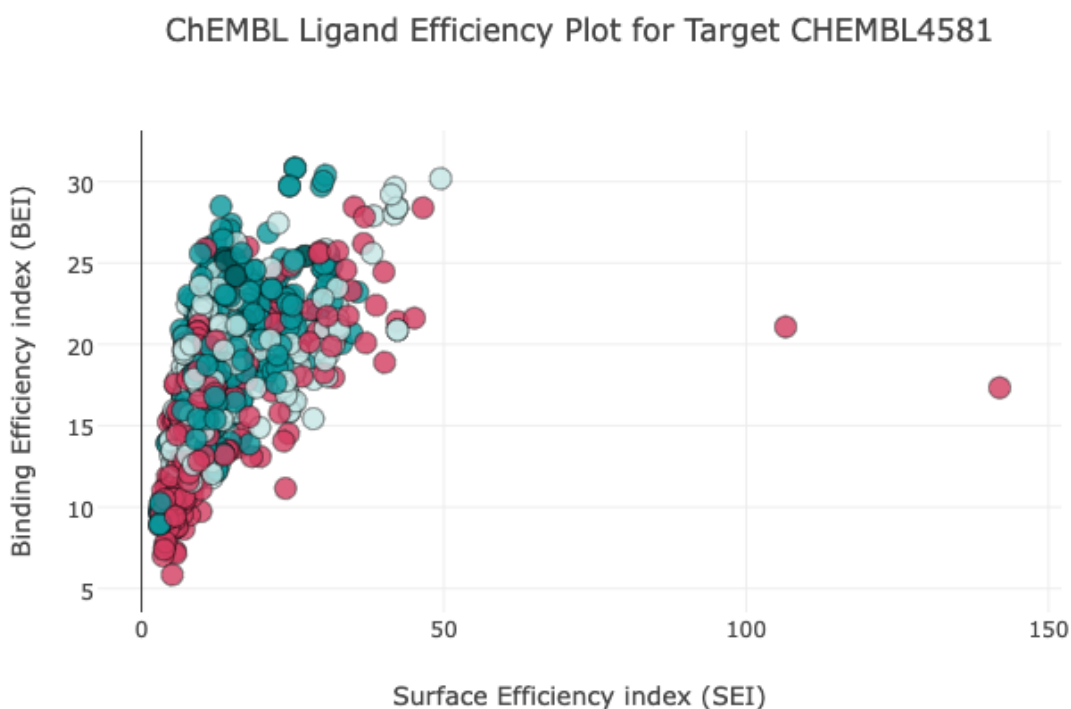


[Q10]

https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4581/

For CHEMBL4581, there are 166 associated binding assays and 8 functional assays

Ligand efficiency:



When experimentally targeting this site with kinesin spindle protein inhibitor ARRY-520 in combination with dexamethasone, there is “a manageable safety profile and encouraging activity in heavily pretreated patients”

Shah JJ, Kaufman JL, Zonder JA, et al. A Phase 1 and 2 study of Filanesib alone and in combination with low-dose dexamethasone in relapsed/refractory multiple myeloma. *Cancer*. 2017 Dec;123(23):4617-4630. DOI: 10.1002/cncr.30892. PMID: 28817190; PMCID: PMC5856158.

<http://europepmc.org/article/MED/28817190>

