

BIMM-143: INTRODUCTION TO BIOINFORMATICS

The find-a-gene project assignment
https://bioboot.github.io/bimm143_S20/

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Questions:

[Q1]

Name: Kinesin family member 11 (KIF11)

Accession: NP_004514

Species: Homo sapiens

Function Known: Encoding a motor protein in which it belongs to the kinesin-like protein family. It is also known that it is involved in many kinds of the dynamics of spindle. Functions in chromosome positioning, centrosome separation and bipolar spindle establishment in mitosis of the cell.

[Q2]

Method: TBLASTN (2.7.1) search against nematode ESTs

Database: Expressed Sequence Tags (est)

Organism: Nematodes (Taxid: 6231)

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blastx
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tblastx

Translated BLAST: tblastn

TBLASTN search translated nucleotide databases using a protein query. [more...](#)

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Enter Query Sequence

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

NP_004514

Query subrange [?](#)

From
To

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Job Title

NP_004514:kinesin-like protein KIF11 [Homo...

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Database

Expressed sequence tags (est) [?](#)

Organism
Optional

nematodes (taxid:6231) ☐ exclude [Add organism](#)

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

[Create custom database](#)

Enter an Entrez query to limit search [?](#)

BLAST

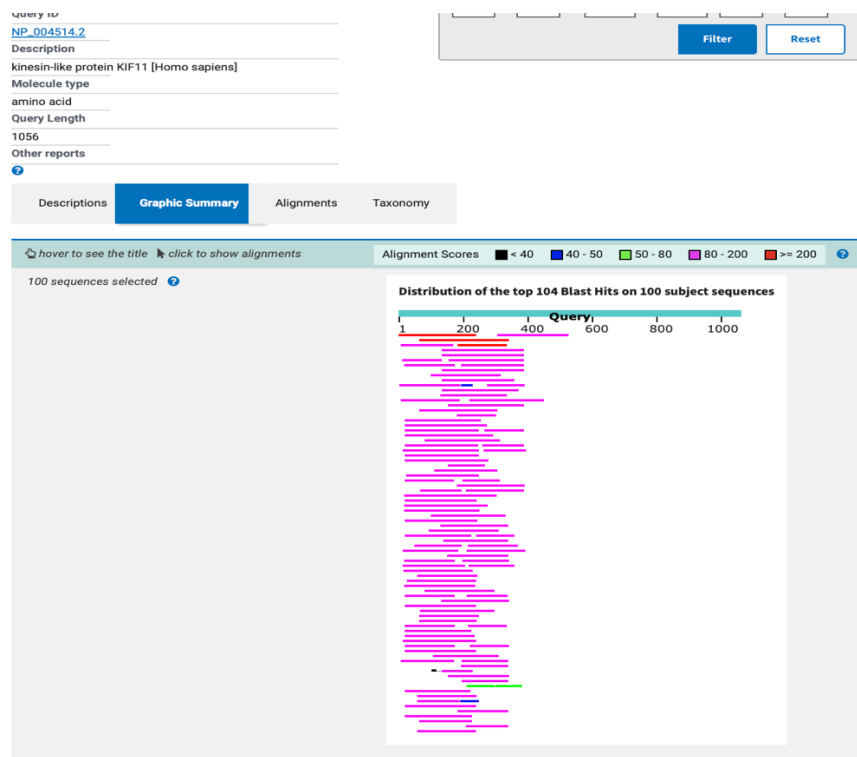
Search database est using Tblastn (search translated nucleotide databases using a protein query)
☐ Show results in a new window

Note: Parameter values that differ from the default are highlighted in yellow and marked with * sign

+ Algorithm parameters

Feedback

Chosen match: Accession JK291331.1, a 757 base pair clone from *Meloidogyne incognita*. See below for alignment details.



Descriptions **Graphic Summary** Alignments Taxonomy

Sequences producing significant alignments

Download Select columns Show 100

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	mjl223k17r1.1 Meloidogyne incognita J2 cDNA library Meloidogyne...	Meloidogyne...	230	230	22%	2e-67	47.13%	757	JK291331.1
<input checked="" type="checkbox"/>	Pd_5pr_67L20 Panagrolaimus davidi 4 degree Panagrolaimus davi...	Panagrola...	206	206	26%	2e-58	45.36%	809	JZ645761.1
<input checked="" type="checkbox"/>	CJ983801 Bursaphelenchus xylophilus mixed-stage library Bursap...	Bursaphel...	200	200	14%	5e-58	64.47%	472	CJ983801.1
<input checked="" type="checkbox"/>	mjl211a09r1.1 Meloidogyne incognita J2 cDNA library Meloidogyne...	Meloidogy...	196	196	23%	4e-55	41.57%	776	JK282786.1
<input checked="" type="checkbox"/>	mjl216g17r1.1 Meloidogyne incognita J2 cDNA library Meloidogyne...	Meloidogy...	195	195	23%	5e-55	41.57%	760	JK287044.1
<input checked="" type="checkbox"/>	mjl207m19r1.1 Meloidogyne incognita J2 cDNA library Meloidogyne...	Meloidogy...	186	186	21%	5e-52	43.53%	738	JK280452.1
<input checked="" type="checkbox"/>	kk03q09.y1 Ascaris suum female ovary Ascaris suum cDNA 5' simil...	Ascaris su...	173	173	18%	7e-48	46.67%	624	BQ095952.1
<input checked="" type="checkbox"/>	mjl212p14r1.1 Meloidogyne incognita J2 cDNA library Meloidogyne...	Meloidogy...	173	173	24%	3e-47	43.02%	783	JK284117.1
<input checked="" type="checkbox"/>	Ls_af1_23b11_T7 Litomosoides sigmodontis adult female 1 (high ...	Litomosoi...	170	170	20%	8e-47	44.95%	620	DN557730.1
<input checked="" type="checkbox"/>	mjl201q24r1.1 Meloidogyne incognita J2 cDNA library Meloidogyne...	Meloidogy...	172	172	21%	1e-46	40.53%	839	JK275977.1
<input checked="" type="checkbox"/>	HTAB-aab12f01.b1 Heterorhabdilis bacteriophora HTAB2_EST.H...	Heterorha...	167	210	21%	6e-46	46.07%	696	ES742822.1
<input checked="" type="checkbox"/>	Pd_5pr_69H21 Panagrolaimus davidi 4 degree Panagrolaimus davi...	Panagrola...	167	167	22%	3e-45	43.98%	755	JZ646412.1
<input checked="" type="checkbox"/>	BJ101792 unpublished oligo-capped cDNA library C. elegans L1 st...	Caenorha...	161	161	19%	9e-44	46.63%	606	BJ101792.1
<input checked="" type="checkbox"/>	Pd_5pr_87P16 Panagrolaimus davidi 4 degree Panagrolaimus davi...	Panagrola...	162	162	21%	3e-43	39.20%	770	JZ652958.1
<input checked="" type="checkbox"/>	HAF_01159 Heterodera avenae female adult Library Heterodera av...	Heteroder...	156	156	22%	1e-41	41.95%	731	JZ145890.1
<input checked="" type="checkbox"/>	HTAB-aae80a09.b1 Heterorhabdilis bacteriophora HTAB2_EST.H...	Heterorha...	156	156	22%	3e-41	42.21%	740	EX913685.1
<input checked="" type="checkbox"/>	CELK050FYF Yuji Kohara unpublished cDNA Caenorhabdilis elega...	Caenorha...	150	150	11%	5e-41	63.33%	360	D67381.1
<input checked="" type="checkbox"/>	mjl225n03r1.1 Meloidogyne incognita J2 cDNA library Meloidogyne...	Meloidogy...	154	154	22%	7e-41	35.02%	713	JK292508.1

Descriptions

Graphic Summary

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Alignment view

Pairwise

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Descriptions

mij223k17r1.1 Meloidogyne incognita J2 cDNA library Meloidogyne incognita cDNA, mRNA sequence

Sequence ID: [JK291331.1](#) Length: 757 Number of Matches: 1

Range 1: 35 to 757 [GenBank](#) [Graphics](#)

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
230 bits(587)	2e-67	Compositional matrix adjust.	115/244(47%)	162/244(66%)	8/244(3%)	+2

Query 1

MASQPNSSAKKKEEKGNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADK

+S AK K K KN+QV VR RP + ER A +IV CD V + VS++ G +D

Sbjct 35

FSSMSTVKAKDKTVKRKNVQVAVRIRPLSDIERSACNKNIVSCDRVARTVSLKAIGFSDS

Query 61

S----SRKTY-TFDMVFGASTKQIDVYRSVVCPIDEVIMGYNCTIFAYGQTGTGKTFTM

S +K + +D +FG + Q++VY V+ P++++VI GYNCT+FAYGQTG+GKT+TM

Sbjct 215

SRFGQGQKCFGPYDKIFGPSTQMEVYEGVLAPLMEDVINGYNCTVFAYGQTGSGKTYTM

Query 116

EGERSPNEEYTWEEDPLAGIIPRTLHQIFEKLTONGTEFSVKVSLLEIYNEELFDLLNPS

EG +E++ W DP AGIIPR L QIF L ++ +++V+VS +E+YNE++FDLLN +

Sbjct 395

EGRHDTSEDFAWNTDPTAGIIPRALDQIFSVLGED-IDYTVRVSYVELYNEQIFDLLNQ

Query 176

SDVSERLQMFDDPRNKRGVIIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRS

E L++FDD +GV I G EE+ V + E++++L +GA KR TA TLMN SSRS

Sbjct 572

ESQLESRLIFDD--KTGVSIAAGAEVIVRSPKEIHELLRRGAEKRRRTATTLNMTSSRS

Query 236

HSVF 239

HSVF

Sbjct 746

HSVF 757

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Descriptions

Alignment details:

>gb|JK291331.1| mij223k17r1.1 Meloidogyne incognita J2 cDNA library
 Meloidogyne incognita
 cDNA, mRNA sequence.
 Length=757

Score = 230 bits (587), Expect = 2e-67, Method: Compositional matrix
 adjust.
 Identities = 115/244 (47%, Positives = 162/244 (66%, Gaps = 8/244 (3%)
 Frame = +2

Query	1	MASQPNSSAKKKEEKGNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADK	60
		+S AK K K KN+QV VR RP + ER A +IV CD V + VS++ G +D	
Sbjct	35	FSSMSTVKAKDKTVKRKNVQVAVRIRPLSDIERSACNKNIVSCDRVARTVSLKAIGFSDS	214
Query	61	S----SRKTY-TFDMVFGASTKQIDVYRSVVCPIDEVIMGYNCTIFAYGQTGTGKTFTM	115
		S +K + +D +FG + Q++VY V+ P++++VI GYNCT+FAYGQTG+GKT+TM	
Sbjct	215	SRFGQGQKCFGPYDKIFGPSTQMEVYEGVLAPLMEDVINGYNCTVFAYGQTGSGKTYTM	394
Query	116	EGERSPNEEYTWEEDPLAGIIPRTLHQIFEKLTONGTEFSVKVSLLEIYNEELFDLLNPS	175
		EG +E++ W DP AGIIPR L QIF L ++ +++V+VS +E+YNE++FDLLN +	
Sbjct	395	EGRHDTSEDFAWNTDPTAGIIPRALDQIFSVLGED-IDYTVRVSYVELYNEQIFDLLNQ	571
Query	176	SDVSERLQMFDDPRNKRGVIIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRS	235
		E L++FDD +GV I G EE+ V + E++++L +GA KR TA TLMN SSRS	
Sbjct	572	ESQLESRLIFDD--KTGVSIAAGAEVIVRSPKEIHELLRRGAEKRRRTATTLNMTSSRS	745
Query	236	HSVF 239	
		HSVF	
Sbjct	746	HSVF 757	

[Q3]

Chosen sequence:

>**M. incognita protein (sequence taken from BLAST result)**
FSSMSTVKAKDKTVKRKNVQVAVRIRPLSDIERSACNKNIVSCDRVARTVSLKAIGFSDS
SRFGQGQKCFGPYDKIFGPSTQMEVYEGVLAPLMEDVINGYNCTVFAYGQTGSGKTYTM
EGRHDTSEDFAWNTDPTAGIIPRALDQIFSVLGEDIDYTVRVSYVELYNEQIFDLLNQT
ESQLESLRIFDDKTKGVSIAGAEVIVRSPKEIHELLRRGAEKRRATTLMNMTSSRS
HSVF

Name: Meloidogyne incognita

Species: Meloidogyne incognita

Eukaryota; Metazoa; Ecdysozoa; Nematoda; Chromadorea; Rhabditida;
Tylenchina; Tylenchomorpha; Tylenchoidea; Meloidogynidae;
Meloidogyninae; Meloidogyne; Meloidogyne incognita group.

[Q4]

Details:

A BLASTP search against NR database (see setup in first screen-shot below) yielded a top hit result is to a protein from *Meloidogyne enterolobii* (nematodes).

See additional screen shots below for top hits and selected alignment details:

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Standard Protein BLAST

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Enter Query Sequence

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

Query subrange [?](#)
From
To

>M. incognita protein (sequence taken from BLAST result)
FSSMSTVKAADKTVKRNQVAVRIRPLSDIERSACNKNIVSCDRVARTVSLKAIGFSDSSRF
GGGQKCFGPYDKIFGPSTQMEVYEGVLAPLMEDVINGYNTVFAYGQTGSGKTYTMEGR
HDTSEDFAWNTPTAGIPRALDQIFSVLSEIDITYVRVSYVELYNEQIFDLLNQTESQLESRL
FDDKTKGVSIAGAEVVRSPKEIHLLRRGAEKRRRTATLMNMTSSRSHSVF

Or, upload file
Choose File no file selected [?](#)

Job Title
M. incognita protein (sequence taken from...
Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Databases
☒ Standard databases (nr etc.): **New** ☐ Experimental databases

[Try experimental clustered nr database](#)
For more info see [What is clustered nr?](#)

Compare
☐ Select to compare standard and experimental database [?](#)

Standard

Database
Non-redundant protein sequences (nr) [?](#)

Organism
Optional

Enter organism name or id—completions will be suggested
☐ exclude

Add organism

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 [?](#)

The top result is to a protein from *Meloidogyne enterolobii* (nematodes)see second screen shot below for alignment details:

Query Length
241
Other reports
[Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#)

Compare these results against the new Clustered nr database [?](#) [BLAST](#)

Descriptions Graphic Summary Alignments Taxonomy

Sequences producing significant alignments									
		Download		Select columns		Show			
<input checked="" type="checkbox"/> select all 100 sequences selected		GenPept		Graphics		Distance tree of results		Multiple alignment	
								MSA Viewer	
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	unnamed protein product [Meloidogyne enterolobii]	Meloidog...	494	494	98%	7e-169	97.48%	753	CAD2147292.1
<input checked="" type="checkbox"/>	unnamed protein product [Meloidogyne enterolobii]	Meloidog...	486	486	98%	3e-165	95.80%	764	CAD2183279.1
<input checked="" type="checkbox"/>	unnamed protein product [Meloidogyne enterolobii]	Meloidog...	480	480	98%	5e-163	94.12%	764	CAD2169206.1
<input checked="" type="checkbox"/>	unnamed protein product [Meloidogyne enterolobii]	Meloidog...	463	463	98%	6e-162	92.44%	376	CAD2147351.1
<input checked="" type="checkbox"/>	unnamed protein product [Meloidogyne enterolobii]	Meloidog...	399	399	98%	3e-136	80.33%	390	CAD2124899.1
<input checked="" type="checkbox"/>	unnamed protein product [Meloidogyne enterolobii]	Meloidog...	391	391	98%	9e-135	79.08%	290	CAD2208809.1
<input checked="" type="checkbox"/>	unnamed protein product [Meloidogyne enterolobii]	Meloidog...	392	392	98%	5e-133	78.66%	439	CAD2177065.1
<input checked="" type="checkbox"/>	unnamed protein product [Meloidogyne enterolobii]	Meloidog...	391	391	98%	1e-122	78.24%	1504	CAD2156593.1
<input checked="" type="checkbox"/>	Kinesin-like protein [Meloidogyne graminicola]	Meloidog...	321	321	98%	2e-103	67.70%	570	KAF7629873.1
<input checked="" type="checkbox"/>	kinesin motor domain-containing protein [Ditylenchus destructor]Ditylench...		278	278	89%	3e-85	61.26%	737	KAI1728869.1
<input checked="" type="checkbox"/>	kinesin motor domain-containing protein [Ditylenchus destructor]Ditylench...		273	273	89%	3e-83	60.09%	739	KAI1711961.1
<input checked="" type="checkbox"/>	kinesin motor domain-containing protein [Ditylenchus destructor]Ditylench...		273	273	89%	6e-83	60.55%	735	KAI1721682.1

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Pairwise

Restore defaults

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100 sequences selected

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GenPept

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Descriptions

unnamed protein product [Meloidogyne enterolobii]

Sequence ID: [CAD2147292.1](#) Length: 753 Number of Matches: 1

Range 1: 1 to 238

GenPept

Graphics

Next Match

Previous Match

Score	Expect	Method	Identities	Positives	Gaps
494 bits(1273)	7e-169	Compositional matrix adjust.	232/238(97%)	236/238(99%)	0/238(0%)
Query 4	MSTVKAKDKTVKRKNVQVAVRIRPLSDIERSACNKNIVSCDRVARTVSLKAIGFSDSSRF				
Sbjct 1	MSTVK+KDKTVKRKNVQVAVRIRPLSDIERS CNKNIVSCDRVARTVSLKAIGFSDSSRF				
Query 64	GQGQKCFGPYDKIFGPSTQMEVYEGVLAPLMEDVINGYNCTVFAYGQTGSGKTYTMEGR				
Sbjct 61	GQGQKCFGPYDKIFGPSTQMEVYEGVLAPLMEDVINGYNCTVFAYGQTGSGKTYTMEGR				
Query 124	HDTSEDFAWNTDPTAGIIPRALDQIFSVLGEDIDYTVRVSYVELYNEQIFDLLNQTESQL				
Sbjct 121	HDTSEDFAWNTDPTAGIIPRALDQIFSVLGEDIDYTVRV YVE+YNEQIFDLLNQTESQL				
Query 184	ESLRIFDDKTKGVSIAAGAEVIVRSPKEIHELLRGAEKRRATTLLMNTSSRSHSV				24
Sbjct 181	ESLRIFDDKTKGVSIAAGAEVIVRSPKE+HELLRGAEKRRATTLLMNTSSRSHSV				23

Related Information

[AlphaFold Structure](#) - 3D structure displays

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GenPept

Graphics

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Descriptions

unnamed protein product [Meloidogyne enterolobii]

Sequence ID: [CAD2183279.1](#) Length: 764 Number of Matches: 1

Range 1: 1 to 238

GenPept

Graphics

Next Match

Previous Match

Related Information

[AlphaFold Structure](#) - 3D structure displays

[Q5]

Re-labeled sequences for alignment:

```
>Original_KIF11| NP_004514.1| Kinesin family member 11 [Homo sapiens]
MASQPNSSAKKKEEGKNIQVVRCPFNLAERKASAHSIVECDPVRKEVSVRTGGLADK
SSRKTYTFDMVFGASTKQIDVRSVVCPILEDEVIMGYNCTIFAYGQTGTGKTFTM
EGERSPNEEYTWEEDPLAGIIPRTLHQIFEKLTDNNGTEFSVKVSLLEIYNEELFDLLNPS
SDVSERLQMFDDPRNKRGVIIKGLLEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRSHSV
```

```
>M.incognita protein (sequence taken from BLAST result)
FSSMSTVKAKDKTVKRKNVQVAVRIRPLSDIERSACNKNIVSCDRVARTVSLKAIGFSDS
SRFGQGQKCFGPYDKIFGPSTQMEVYEGVLAPLMEDVINGYNCTVFAYGQTGSGKTYTM
EGRHDTSEDFAWNTDPTAGIIPRALDQIFSVLGEDIDYTVRVSYVELYNEQIFDLLNQ
ESQLESRLIFDDKTKGVSIAAGAEVIVRSPKEIHELLRGAEKRRATTLLMNTSSRS
HSVF
```


>Dog_roundworm| KHN81034.1| Kinesin-like protein KIF11 [Toxocara canis]
KKKNVQVVVRVRLSDKERAERSHLAVRTNGLAQT VSLKERSSWREFGPFDKVYGIDSSQSTIYMDIVDP
LIKEVIQGYNCTVFAYGQTGTGKTYTMEGEHDPNGSYSWKDDPHMGII PRALMHIFTELDRQKVEEYSVR
VSYVELYNEELYDLLSRSDQQPRLRIFEDAIRKGSVVIAGLEEVAVRERDEVYELLRRGAEKRKTAATW
LNSTSSRSHSV

>Human| pdb|1II6| Chain A, KINESIN-RELATED MOTOR PROTEIN Eg5
MASQPNSSAKKKEEGKKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADKSSRKTYTFDM
VFGASTKQIDVYRSVVCPIIDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEEEDPLAGIIPRTL
HQIFEKLTDNGTEFSVKVSLLEIYNEELFDLLNPSSDVSERLQMFDDPRNKRGVIIKGLEEITVHNKDEV
YQILEKGAARKRTTAATLMNAYSSRSHSV

>Guinea_worm| VDN50419.1| unnamed protein product [Dracunculus medinensis]
QVAVRIRPLNETEKSEKARISLTAYEDKRTIMVKERCANKEFGPFDKVYGMHSSQLEIYTDLVKPLVQEV
LAGYNCTIFAYGQTSTGKTYTMEGIHSHEADLDWKADTTAGIIPRALQHVFSQLEKQPNDYSVRVSYVE
LYNEELYDLLGRSDIEQTRLRLYEDPIRKGSIISSLEEVAVHNRDEVYNLLRKGAEKRRTAATLMNMTS
SRSHSV

>Goldfish| XP_026115923.1| kinesin-like protein KIF11 isoform X1 [Carassius auratus]
SSQLTLPAAKKEEGKGRNIQVVVRCRPFNTVERKSASHTVVECDQNRKEVMVRTGGATDKAARKTYTFDMV
FGPSAKQIEVYRSVVCPIIDEVIMGYNCTVFAYGQTGTGKTFTMEGERSPNEEFTWEEEDPLAGIIPRTLH
QIFEKLSSNGTEFSVKVSLLEIYNEELFDLLSPTPDVTERLQLFDDPRNKRGVTIKGLEEITVHNKDEVY
QILERGAARKRTASTLMNAYSSRSHSV

>Wolverine| VCW67789.1| unnamed protein product, partial [Gulo gulo]
MASQPNSSAKKKEEGKKNIQVVVRCRPFNLAERKANAHSVVECDHVRKEVSVRTGGLADKSSRKTYTFDM
VFGASTKQIDVYRSVVCPIIDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEEEDPLAGIIPRTL
HQIFEKLTDNGTEFSVKVSLLEIYNEELFDLLNPSSDVSERLQMFDDPRNKRGVIIKGLEEITVHNKDEV
YQILEKGAARKRTTAATLMNAYSSRSHSV

Alignment:

CLUSTAL multiple sequence alignment by MUSCLE (3.8)

```
Goldfish|          -
SSQLTLPAAKKEEGKGRNIQVVVRCRPFNTVERKSASHTVVECDQNRKEVMVRTGGATD-
Original_KIF11|
MASQPNSSAKKKEEGKKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLAD-
Human|
MASQPNSSAKKKEEGKKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLAD-
Wolverine|
MASQPNSSAKKKEEGKKNIQVVVRCRPFNLAERKANAHSVVECDHVRKEVSVRTGGLAD-
M.incognita
FSSMSTVKAKDKTVKRKNVQVAVRIRPLSDIERSACNKNIVSCDRVARTVSLKAIGFSDS
Dog_roundworm|      -----KKKNVQVVVRVRLSDKERAERSHLAVRTNGLAQT VSLKE--
----
Guinea_worm|        -----QVAVRIRPLNETEKSEKARISLTAYEDKRTIMVKE--
----
                                **. ** **:.  *.   .   :       .   :  :

Goldfish|          ---KAARKTY-
TFDMVFGPSAKQIEVYRSVVCPIIDEVIMGYNCTVFAYGQTGTGKTFTM
```

Original_KIF11| ---KSSRKTY-
TFDMVFGASTKQIDVYRSVVCPIILDEVIMGYNCTIFAYGQTGTGKTFTM
Human| ---KSSRKTY-
TFDMVFGASTKQIDVYRSVVCPIILDEVIMGYNCTIFAYGQTGTGKTFTM
Wolverine| ---KSSRKTY-
TFDMVFGASTKQIDVYRSVVCPIILDEVIMGYNCTIFAYGQTGTGKTFTM
M.incognita
SRFGQGQKCFGPYDKIFGPESTQMEVYEGVLAPLMEDVINGYNCTVFAYGQTGSGKTYTM
Dog_roundworm| ---
RSSWREFGPFDPKVGIDSSQSTIYMDIVDPLIKEVIQGYNCTVFAYGQTGTGKTYTM
Guinea_worm| ---
RCANKEFGPFDPKVGGMHSSQLEIYTDLVKPLVQEVLAGYNCTIFAYGQTSTGKTYTM

... : .* :.* :.* :.* :.* :.* :.* :.*

*****:*****.:***:**

Goldfish| EGERSPNEEFTWEEDPLAGIIPRTLHQIFEKLSSNGT-
EFSVKVSLLEIYNEELFDLLSP
Original_KIF11| EGERSPNEEYTWEEEDPLAGIIPRTLHQIFEKLTDNGT-
EFSVKVSLLEIYNEELFDLLNP
Human| EGERSPNEEYTWEEEDPLAGIIPRTLHQIFEKLTDNGT-
EFSVKVSLLEIYNEELFDLLNP
Wolverine| EGERSPNEEYTWEEEDPLAGIIPRTLHQIFEKLTDNGT-
EFSVKVSLLEIYNEELFDLLNP
M.incognita EGRHDTSEDFAWNTDPTAGIIPRALDQIFSVLGEDI--
DYTVRVSYVELYNEQIFDLLNQ
Dog_roundworm|
EGEHDPNGSYSWKDDPHMGIIIPRALMHIFTELDRQKVEEYSVRVSYVELYNEELYDLLSR
Guinea_worm|
EGIHSHHEADLDWKADTTAGIIPRALQHVFSQLEKQPNDDYSVRVSYVELYNEELYDLLGR

** .. . * : * . *****: * : * : * : * : * : *

:*:***:::***.

Goldfish|
TPDVTERLQLFDDPRNKRGVTIKGLEEITVHNKDEVYQILERGAAKRKTASTLMNAYSSR
Original_KIF11|
SSDVSERLQMFDDPRNKRGVIIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSR
Human|
SSDVSERLQMFDDPRNKRGVIIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSR
Wolverine|
SSDVSERLQMFDDPRNKRGVIIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSR
M.incognita TESQLESLRIFDD--
KTKGVSIAGAEVIVRSPKEIHELLRRGAEKRRATTATLMNMTSSR
Dog_roundworm|
SDQQQPRLRIFEDAIRKGSVVIAGLEEVAVRERDEVYELLRRGAEKRRKTAATWLNSTSSR
Guinea_worm|
SDIEQTRLRLYEDPIRKGSIIISSLEEVAVHNRDEVYNLLRKGAEKRRKTAATLMNMTSSR

: *.:*: * .. : * . **: *.. .*:*: * .** ** *: * : *

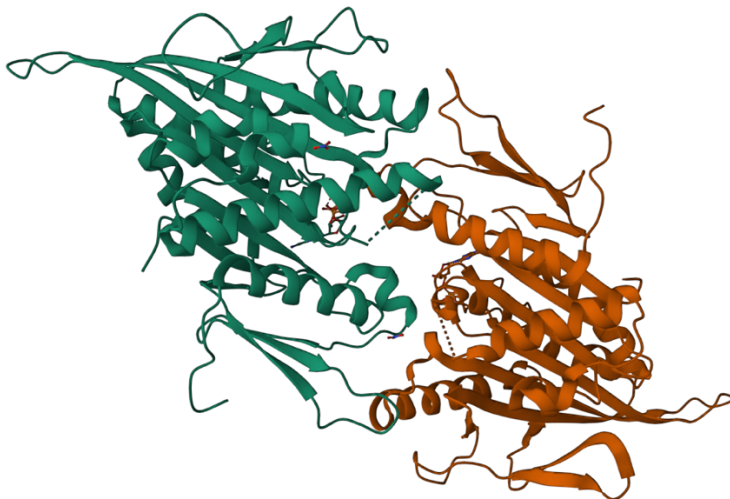
Goldfish| SHSVF
Original_KIF11| SHSVF
Human| SHSVF
Wolverine| SHSVF
M.incognita SHSVF
Dog_roundworm| SHSVF
Guinea_worm| SHSVF

[Q8]

ID	Technique	Resolution	Source	Evalue	Identity
1II6	X-RAY DIFFRACTION	2.10 Å	Homo sapiens	3.105e-64	47
1YRS	X-RAY DIFFRACTION	2.50 Å	Homo sapiens	3.105e-64	47
2FME	X-RAY DIFFRACTION	2.10 Å	Homo sapiens	3.105e-64	47

[Q9]

Not much likely to be similar in structure to *Meloidogyne incognita* given the low sequence similarity (<50%).



[Q10]

CHEMBL details 165 Binding Assays and 2591 Functional Assays; No ligand efficiency data.

[https://www.ebi.ac.uk/chembl/g/ - search_results/](https://www.ebi.ac.uk/chembl/g/-search_results/)

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC245397/>