

Find A Gene Project

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Q1

Name: Kinesin-like protein KIF11 (KIF11)

Accession: P52732

Species: Homo Sapiens

Q2

Method: TBLASTN, search against EST, exclude homo sapeins

Database: Expressed sequence tags (est)

Organism: Exclude Homo Sapeins

BLAST® » tblastn

Translated BLAST: **tblastn**

blastn blastp blastx **tblastn** tblastx

TBLASTN search translated nucleotide databases using a protein query

Enter Query Sequence

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

SP|P52732

Query subrange [?](#)

From

To

Or, upload file 未选择任何文件 [?](#)

Job Title

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

☐ Align two or more sequences [?](#)

Choose Search Set

Database ?

Organism [Optional](#) ☒ 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](#) [YouTube](#) [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

Chosen match: Accession DW624128.1. See below for alignment details.

Job Title

P52732:RecName: Full=Kinesin-like protein...

RID

[TU73UHEU013](#) Search expires on 02-02 01:54 am [Download All](#) ▼

Program

TBLASTN [?](#) [Citation](#) ▼

Database

est [See details](#) ▼

Query ID

[P52732.2](#)

Description

RecName: Full=Kinesin-like protein KIF11; AltName: Full=K ...

Molecule type

amino acid

Query Length

1056

Other reports

[?](#)

Filter Results

Organism

only top 20 will appear ☐ exclude

[+ Add organism](#)

Percent Identity

to

E value

to

Query Coverage

to

Filter

Reset

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download ▼

Select columns ▼

Show 100 ▼

[?](#)

☐ select all 1 sequences selected

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

	Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<input type="checkbox"/>	Rhizoctonia solani EST, clone rsol_all_isotig14362_strain AG1-1B, mRNA sequence	Rhizoctonia solani	444	444	45%	1e-141	48.05%	1681	HG373950.1
<input type="checkbox"/>	CGX41-C02.y1d-s SHGC-CGX Gasterosteus aculeatus cDNA clone CGX41-C02 5', mRNA sequence	Gasterosteus ac...	360	464	32%	2e-120	79.51%	1252	DN685345.1
<input type="checkbox"/>	FS309663 Cp_aO Cynops pyrrhogaster cDNA clone Cp_aO_024_L08 3', mRNA sequence	Cynops pyrrhoga...	424	577	32%	1e-154	84.36%	1055	FS309663.1
<input checked="" type="checkbox"/>	CLJ338-B02.y1d-s SHGC-CLJ2 Gasterosteus aculeatus cDNA clone CLJ338-B02 5', mRNA sequence	Gasterosteus ac...	446	446	31%	2e-145	67.79%	1043	DW624128.1
<input type="checkbox"/>	FS310020 Cp_aO Cynops pyrrhogaster cDNA clone Cp_aO_025_K19 3', mRNA sequence	Cynops pyrrhoga...	422	575	31%	5e-154	86.32%	1027	FS310020.1
<input type="checkbox"/>	AUF_ljOva_19_f11 Ovary cDNA library Ictalurus punctatus cDNA 5' similar to kinesin family member 11, mRNA s...	Ictalurus punctatus	417	417	29%	1e-134	68.71%	942	CK418843.1
<input type="checkbox"/>	ypo4-4-G01 Yellow perch ovarian library 4 Perca flavescens cDNA, mRNA sequence	Perca flavescens	414	414	28%	2e-133	70.21%	965	GO660024.1
<input type="checkbox"/>	CFW85-E12.y1d-s SHGC-CFW Gasterosteus aculeatus cDNA clone CFW85-E12 5', mRNA sequence	Gasterosteus ac...	448	448	27%	2e-145	75.35%	1208	DN675298.1
<input type="checkbox"/>	JGI_CAAV7594 fwd CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (H) Pimepha...	Pimephales pro...	544	544	27%	0.0	87.80%	865	DT277589.1

Chosen match: Accession DW624128.1. See below for alignment details.

Alignment Scores

■ < 40

■ 40 - 50

■ 50 - 80

■ 80 - 200

■ ≥ 200

Distribution of the top 107 Blast Hits on 100 subject sequences



CLJ338-B02.y1d-s SHGC-CLJ2 Gasterosteus aculeatus cDNA clone CLJ338-B02 5', mRNA sequence

Sequence ID: [DW624128.1](#) Length: 1043 Number of Matches: 1

Range 1: 43 to 1020 [GenBank](#) [Graphics](#)

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

Score	Expect	Method	Identities	Positives	Gaps	Frame
446 bits(1146)	2e-145	Compositional matrix adjust.	232/326(71%)	273/326(83%)	0/326(0%)	+1
Query 206	NKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVFSVTIHMKE	TIDGEELVKIGKLNLD	265			
	++DEVYQILE.G.AKR TA.TLMNAYSSRSHSVFSVTIHMKE T.DGEELVKIGKLNLD					
Sbjct 43	DQDEVYQILERGS AKRRTASTLMNAYSSRSHSVFSVTIHMKEITMDGEELVKIGKLNLD	222				
Query 266	LAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVERTPHVPYRESKLTRILQDSL	325				
	LAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVE. PHVPYRESKLTRILQDSL					
Sbjct 223	LAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVEKRPHVPYRESKLTRILQDSL	402				
Query 326	GRTRTSIIATISPAInleettstleYAHRAKNILNKPEVNQKLT	385				
	GRT.TSIIAT.SP.S NLEETLSTLEYA RAKNI.NKPEVNQKLT. LIKEYTEEIERL					
Sbjct 403	GRTKTSIIATVSPSSNLEETLSTLEYASRAKNIMNKPEVNQKLT	582				
Query 386	KRDLAAREKNGVYISEENFRVMVGKLT	445				
	KRDLAAR.KNG.Y.S EN. M G.T E VE ++A.EEE. +VTELF.D.K					
Sbjct 583	KRDLAATRDKNIGYLSAENYESMMGQITSHEVHTVEYSDRIAAMEEIKVTELFVDSKT	762				
Query 446	ELDQCKSDLQNKQTQLETTQKHLQETKLQLVKEEYITSALESTEEKLHDAASKLLNTVEE	505				
	L. C DL K Q LE T + LQ TK +L++ E++ S L +E L.D A +LL+TV+					
Sbjct 763	RLELCAVDLDEKQQRLEETSRDLQHTKEKLMEXEFVCELT	942				
Query 506	TTKDVSGLSKLDLDRKAVDQHNAAEQ	531				
	+T DV GL +LDR K V.QH + Q					
Sbjct 943	STGDVCGLPGLDRXKXVEQHYSGVQ	1020				

Q3

Chosen sequence:

>DW624128.1_1 CLJ338-B02.y1d-s SHGC-CLJ2 Gasterosteus aculeatus cDNA clone

CLJ338-B02 5', mRNA sequence

FXXXXXXXXFGPESRDQDEVYQILERGS AKRRTASTLMNAYSSRSHSVFSVTIHMKEITMD
GEELVKIGKLNLDLAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVEKRPHVPY
RESKLTRILQDSLGGRTKTSIIATVSPSSNLEETLSTLEYASRAKNIMNKPEVNQKLT
KRTLIKEYTEEIERLKRDLAATRDKNIGYLSAENYESMMGQITSHEVHTVEYSDRIAAMEE
EIKKVTELFVDSKTRLELCAVDLDEKQQRLEETSRDLQHTKEKLMEXEFVCELT
LYDTAGRLLSTVDASTGDVCGLPGLDRXKXVEQHYSGVQQSSLSAWX

NAME: Gasterosteus aculeatus

ORGANISM: Gasterosteus aculeatus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
Acanthomorpha; Eupercaria; Perciformes; Cottioidei;
Gasterosteales; Gasterosteidae; Gasterosteus.

Q4

blastnblastpblastxtblastntblastx

BLASTP programs search protein databases using a protein query.

Enter Query Sequence

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

AMEE
EIKKVTELFVDSKTRLELCVDLDEKQQRLEETSRDLQHTKEKLMEXEFVCS
LVQES
LYDTAGRLSTVDASTGDVCGPLGQLDRXKXVEQHYSYGVQQSSLSAWX

Or, upload file

选择文件 未选择任何文件 ?

Query subrange ?

From

To

Job Title

DW624128.1_1 CLJ338-B02.y1d-s SHGC-CLJ2 Gasterosteus...

Enter a descriptive title for your BLAST search ?

☐ Align two or more sequences ?

Choose Search Set

Databases

☒ Standard databases (nr etc.):
 ☐ Experimental databases

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 ?

Details:

A BLASTP search against nr database (see setup in first screen-shot below). The top match is from *Gasterosteus aculeatus aculeatus*.

See screenshots below for alignment details:

Job Title

DW624128.1_1 CLJ338-B02.y1d-s SHGC-CLJ2 Gasterosteus..

RID

[TUCH7CM7016](#) Search expires on 02-02 03:27 am [Download All](#) ▼

Program

BLASTP [?](#) [Citation](#) ▼

Database

nr [See details](#) ▼

Query ID

lcl|Query_6479531

Description

DW624128.1_1 CLJ338-B02.y1d-s SHGC-CLJ2 Gasteroste...

Molecule type

amino acid

Query Length

348

Other reports

[Distance tree of results](#) [Multiple alignment](#) [MSA viewer](#) [?](#)

Filter Results

Organism

only top 20 will appear

☐ exclude

Type common name, binomial, taxid or group name

[+ Add organism](#)

Percent Identity

to

E value

to

Query Coverage

to

Filter

Reset

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

BLAST

×

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

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Select columns ▼

Show 100 ▼ [?](#)

☒ 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"/>	kinesin-like protein KIF11 [Gasterosteus aculeatus aculeatus]	Gasterosteus aculeatus aculeatus	637	637	94%	0.0	96.65%	1060	XP_040035136.1
<input checked="" type="checkbox"/>	kinesin-like protein KIF11 [Pungitius pungitius]	Pungitius pungitius	617	617	94%	0.0	93.60%	1060	XP_037320999.2
<input checked="" type="checkbox"/>	kinesin-like protein KIF11 isoform X1 [Anarrhichthys ocellatus]	Anarrhichthys ocellatus	613	613	94%	0.0	93.29%	1060	XP_031728199.1
<input checked="" type="checkbox"/>	kinesin-like protein KIF11 isoform X2 [Anarrhichthys ocellatus]	Anarrhichthys ocellatus	613	613	94%	0.0	93.29%	1054	XP_031728209.1
<input checked="" type="checkbox"/>	kinesin-like protein KIF11 isoform X1 [Anoplopoma fimbria]	Anoplopoma fimbria	609	609	94%	0.0	91.77%	1062	XP_054456823.1
<input checked="" type="checkbox"/>	kinesin-like protein KIF11 [Cebidichthys violaceus]	Cebidichthys violaceus	607	607	94%	0.0	92.68%	1062	XP_068587987.1
<input checked="" type="checkbox"/>	hypothetical protein VZT92_001339 [Zoarces viviparus]	Zoarces viviparus	600	600	94%	0.0	90.55%	1056	KAK9541282.1
<input checked="" type="checkbox"/>	kinesin-like protein KIF11 [Gasterosteus aculeatus]	Gasterosteus aculeatus	600	600	94%	0.0	90.55%	1057	XP_034464495.1

Alignment view

Pairwise



Restore defaults

100 sequences selected



Download

[GenPept](#) [Graphics](#)**kinesin-like protein KIF11 [Gasterosteus aculeatus aculeatus]**Sequence ID: [XP_040035136.1](#) Length: 1060 Number of Matches: 1[See 2 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)Range 1: 204 to 531 [GenPept](#) [Graphics](#)[Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
637 bits(1644)	0.0	Compositional matrix adjust.	317/328(97%)	320/328(97%)	0/328(0%)
Query 15	DQDEVYQILERGS	AKRRTASTLMNAYSSRSHSVFSVTIHMKEITMDGEELVKIGKLN	LVD 74		
	++DEVYQILERGS	AKRRTASTLMNAYSSRSHSVFSVTIHMKEITMDGEELVKIGKLN	LVD		
Sbjct 204	NKDEVYQILERGS	AKRRTASTLMNAYSSRSHSVFSVTIHMKEITMDGEELVKIGKLN	LVD 263		
Query 75	LAGSENIGRSGAVDKRAREAGNINQSL	TLGRVITALVEKRPHVPYRESKLTRILQDSL	G 134		
	LAGSENIGRSGAVDKRAREAGNINQSL	TLGRVITALVEKRPHVPYRESKLTRILQDSL	G		
Sbjct 264	LAGSENIGRSGAVDKRAREAGNINQSL	TLGRVITALVEKRPHVPYRESKLTRILQDSL	G 323		
Query 135	GRTKTSIIATVSPSSSNLEETLSTLEYASRAKNIMNKPEVNQKLTKRTLIKEYTEEIERL		194		
	GRTKTSIIATVSPSSSNLEETLSTLEYASRAKNIMNKPEVNQKLTKRTLIKEYTEEIERL				
Sbjct 324	GRTKTSIIATVSPSSSNLEETLSTLEYASRAKNIMNKPEVNQKLTKRTLIKEYTEEIERL		383		
Query 195	KRDLAATRDKNGIYLSAENYESMMGQITSHEVHTVEYSDRIAAMEEEIKKVTELFVDSKT		254		
	KRDLAATRDKNGIYLSAENYESMMGQITSHEVHTVEYSDRIAAMEEEIKKVTELFVDSKT				
Sbjct 384	KRDLAATRDKNGIYLSAENYESMMGQITSHEVHTVEYSDRIAAMEEEIKKVTELFVDSKT		443		
Query 255	RLELCAVDLDEKQQRLEETSRDLQHTKEKLMEXEFVCS	ELTVQESLYDTAGRLLSTVDA 314			
	RLELCAVDLDEKQQRLEETSRDLQHTKEKLMEXEFVCS	ELTVQESLYDTAGRLLSTVDA			
Sbjct 444	RLELCAVDLDEKQQRLEETSRDLQHTKEKLMEXEFVCS	ELTVQESLYDTAGRLLSTVDA 503			
Query 315	STGDVCGLPGQLDRXKXVEQHYS	GVQQS 342			
	STGDVCGL +LDR K VEQH S VQQS				
Sbjct 504	STGDVCGLQDKLDRKKKVEQHNSEVQQS	531			