Find A Gene Project

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$\mathbf{Q}\mathbf{1}$

Name: Kinesin-like protein KIF11 (KIF11)

Accession: P52732 Species: Homo Sapiens

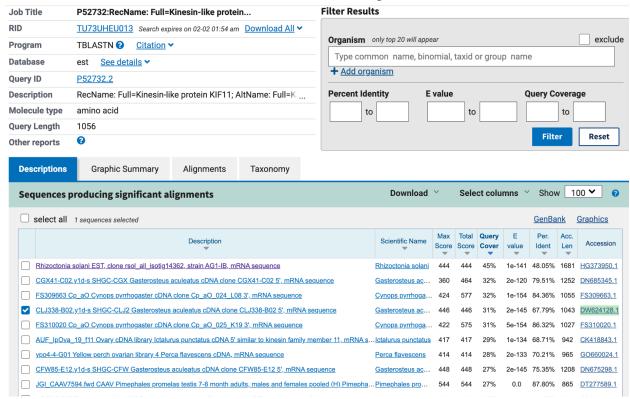
$\mathbf{Q2}$

Method: TBLASTN, search against EST, exclude homo sapeins

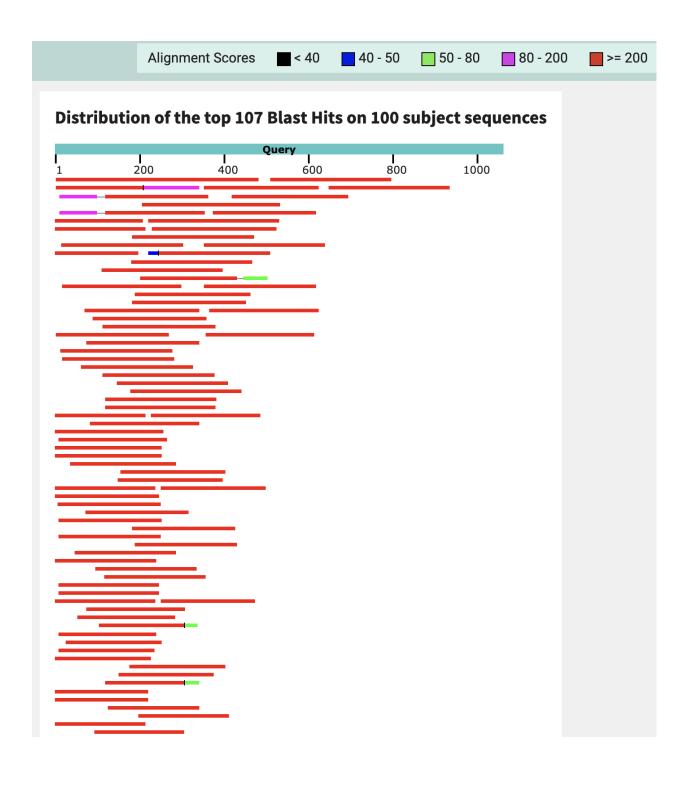
Database: Expressed sequence tags (est) Organism: Exclude Homo Sapeins

BLAST ® » tblastn					
blastn bl	astp	blastx	tblastn	tblastx	Translated BLAST: tblastn
Enter Query Sequence Enter accession number(s), gi(s), or FASTA sequence(s) ② Clear SP P52732 Or, upload file Descriptive title for your BLAST search ② Align two or more sequence ②					
Choose Searce	ch Set				× 2
Organism Optional	♦ Expressed sequence tags (est) Homo sapeins (taxid:9606) Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown ?				
Exclude Optional Limit to Optional Entrez Query Optional	S	equences from	Uncultured/er type material to limit search ?	nvironmental sar	You Tube Create custom database
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.



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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 A Previous Match Identities Positives Method Frame 446 bits(1146) 2e-145 Compositional matrix adjust. 232/326(71%) 273/326(83%) 0/326(0%) +1 Query 206 NKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVFSVTIHMKETTIDGEELVKIGKLNLVD 265 ++DEVYQILE+G+AKR TA+TLMNAYSSRSHSVFSVTIHMKE T+DGEELVKIGKLNLVD Sbjct 43 DQDEVYQILERGSAKRRTASTLMNAYSSRSHSVFSVTIHMKEITMDGEELVKIGKLNLVD 222 Query 266 LAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVERTPHVPYRESKLTRILQDSLG 325 LAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVE+ PHVPYRESKLTRILQDSLG Sbjct 223 LAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVEKRPHVPYRESKLTRILQDSLG 402 Query 326 GRTRTSIIATISPASInleetIstleYAHRAKNILNKPEVNQKLTKKALIKEYTEEIERL 385 GRT+TSIIAT+SP+S NLEETLSTLEYA RAKNI+NKPEVNQKLTK+ LIKEYTEEIERL Sbjct 403 GRTKTSIIATVSPSSSNLEETLSTLEYASRAKNIMNKPEVNQKLTKRTLIKEYTEEIERL 582 Query 386 KRDLAAAREKNGVYISEENFRVMSGKLTVQEEQIVELIEKIGAVEEELNRVTELFMDNKN 445 KRDLAA R+KNG+Y+S EN+ M G++T E VE ++I A+EEE++VTELF+D+K Sbjet 583 KRDLAATRDKNGIYLSAENYESMMGQITSHEVHTVEYSDRIAAMEEEIKKVTELFVDSKT 762 Query 446 ELDQCKSDLQNKTQELETTQKHLQETKLQLVKEEYITSALESTEEKLHDAASKLLNTVEE 505 L+ C DL K Q LE T+ LQ TK+L++ E++ S L +E L+D A+LL+TV+ Sbjct 763 RLELCAVDLDEKQQRLEETSRDLQHTKEKLMEXEFVCSELTLVQESLYDTAGRLLSTVDA 942 Query 506 TTKDVSGLHSKLDRKKAVDQHNAEAQ 531 +T DV GL +LDR K V+QH + Q Sbjct 943 STGDVCGLPGQLDRXKXVEQHYSGVQ 1020

Q3

Chosen sequence:

>DW624128.1_1 CLJ338-B02.y1d-s SHGC-CLJ2 Gasterosteus aculeatus cDNA clone CLJ338-B02 5', mRNA sequence

FXXXXXXFGPESRDQDEVYQILERGSAKRRTASTLMNAYSSRSHSVFSVTIHMKEITMD GEELVKIGKLNLVDLAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVEKRPHVPY RESKLTRILQDSLGGRTKTSIIATVSPSSSNLEETLSTLEYASRAKNIMNKPEVNQKLTK RTLIKEYTEEIERLKRDLAATRDKNGIYLSAENYESMMGQITSHEVHTVEYSDRIAAMEE EIKKVTELFVDSKTRLELCAVDLDEKQQRLEETSRDLQHTKEKLMEXEFVCSELTLVQES LYDTAGRLLSTVDASTGDVCGLPGQLDRXKXVEQHYSGVQQSSLSAWX

NAME: Gasterosteus aculeatus

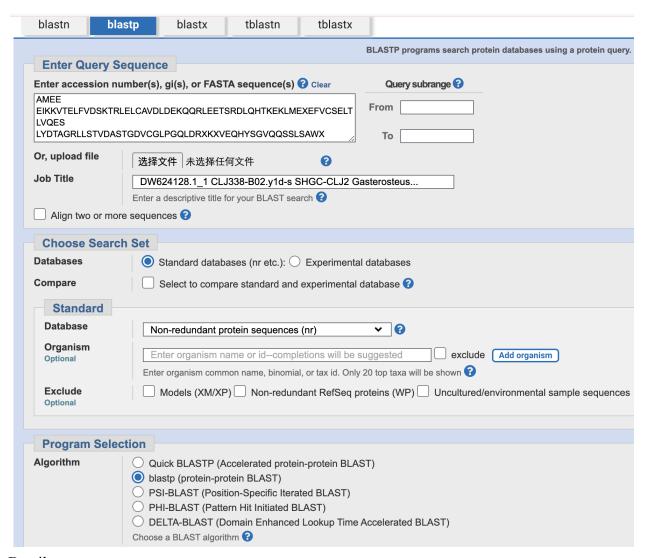
ORGANISM: Gasterosteus aculeatus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Neoteleostei;

Acanthomorphata; Eupercaria; Perciformes; Cottioidei;

Gasterosteales; Gasterosteidae; Gasterosteus.



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:

