

Find a Gene Project Q1-4

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Q1. Tell me the name of a protein you are interested in. Include the species and the accession number. This can be a human protein or a protein from any other species as long as it's function is known.

Name: kinesin family member 11

Accession: NP_004514

Species: Homo sapiens

Function: Enables ATP, microtubule, nucleotide, protein, and protein kinase binding. It also enables microtubule and plus-end-directed microtubule motor activities.

Q2. Perform a BLAST search against a DNA database, such as a database consisting of genomic DNA or ESTs. The BLAST server can be at NCBI or elsewhere. Include details of the BLAST method used, database searched and any limits applied (e.g. Organism).

Method: TBLASTN search against Mus musculus (House mouse) ESTs

Database: Expressed Sequence Tags (est)

Organism: Mus musculus (taxid:10090)

The screenshot displays the NCBI TBLASTN search interface. At the top, there are tabs for different BLAST methods: blastn, blastp, blastx, **tblastn** (selected), and tblastx. The title 'Translated BLAST: tblastn' is shown on the right. Below the tabs, a blue banner reads 'TBLASTN search translated nucleotide databases using a protein query'. The 'Enter Query Sequence' section includes a text box for 'Enter accession number(s), gi(s), or FASTA sequence(s)' containing 'NP_004514', a 'Query subrange' section with 'From' and 'To' fields, and an 'Or, upload file' section with a 'Choose File' button and 'No file chosen' text. The 'Job Title' section contains a text box with 'NP_004514:kinesin-like protein KIF11 [Homo...' and a prompt 'Enter a descriptive title for your BLAST search'. There is also a checkbox for 'Align two or more sequences'. The 'Choose Search Set' section features a 'Database' dropdown menu set to 'Expressed sequence tags (est)', an 'Organism' section with 'Mus musculus (taxid:10090)' and an 'Add Organism' button, and an 'Exclude' section with checkboxes for 'Models (XM/XP)' and 'Uncultured/environmental sample sequences'. There is also a 'Limit to' section with a checkbox for 'Sequences from type material' and an 'Entrez® Query' section with a text box and a 'Create custom database' button. At the bottom, there is a large blue 'BLAST' button and a section for 'Search database est using Tblastn (search translated nucleotide databases using a protein query)' with a checkbox for 'Show results in a new window'.

Figure 1: Blast Method Used

Chosen Match: Accession CN533430.1, a 722 base pair clone from Mus musculus.

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UI-M-HO0-cpw-l-21-0-UI.r1 NIH_BMAP_HO0 Mus musculus cDNA clone IMAGE:30655676 5', mRNA sequence

Sequence ID: [CN533430.1](#)
 Length: 722
 Number of Matches: 1

Range 1: 6 to 722
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[Graphics](#)

Next Match
 Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
489 bits(1260)	4e-165	Compositional matrix adjust.	232/239(97%)	235/239(98%)	0/239(0%)	+3
Query 47	RKEVSVRTGGLADKSSRKTYTFDMVFGASTKQIDVYRSVVC	PILDEVIMGYNCTIFAYGQ	106			
Sbjct 6	RKEVSVRT GL DK+S+KTYTFDMVFGASTKQIDVYRSVVC	PILDEVIMGYNCTIFAYGQ	185			
Query 107	TGTGKTFTMEGERSPNEEYTWEEDPLAGIIPRTLHQIFEKLT	DNGTEFSVKVSLLEIYNE	166			
Sbjct 186	TGTGKTFTMEGERSPNE YTWEEDPLAGIIPRTLHQIFEKLT	DNGTEFSVKVSLLEIYNE	365			
Query 167	ELFDLLNPSSDVSERLQMFDDPRNKRGVIIKGLEEITVHNK	DEVYQILEKGAAKRTTAAT	226			
Sbjct 366	ELFDLL+PSSDVSERLQMFDDPRNKRGVIIKGLEEITVHNK	DEVYQILEKGAAKRTTAAT	545			
Query 227	LMNAYSSRSHSVSVTIHMKETTIDGEELVKIGKLNLDLAG	SENIGRSGAVDKRAREA	285			
Sbjct 546	LMNAYSSRSHSVSVTIHMKXTTIDGEELVKIGKLNLDLAG	SENIGRSGAVDKRAREA	722			

Figure 2: Chosen Match

Q3. Gather information about this “novel” protein. At a minimum, show me the protein sequence of the “novel” protein as displayed in your BLAST results from [Q2] as FASTA format (you can copy and paste the aligned sequence subject lines from your BLAST result page if necessary) or translate your novel DNA sequence using a tool called EMBOSS Transeq at the EBI. Don’t forget to translate all six reading frames; the ORF (open reading frame) is likely to be the longest sequence without a stop codon. It may not start with a methionine if you don’t have the complete coding region. Make sure the sequence you provide includes a header/subject line and is in traditional FASTA format.

Chosen Sequence (FASTA Format): >CN533430.1 UI-M-HO0-cpw-l-21-0-UI.r1 NIH_BMAP_HO0 Mus musculus cDNA clone IMAGE:30655676 5', mRNA sequence
RKEVSVRTAGLTDKTSKKTYYTFDMVFGASTKQIDVYRSVVC
PILDEVIMGYNCTI-
FAYGQTGTGKTFTMEGERSPNEVYTWEEDPLAGIIPRTLHQIFEKLT
DNGTEFSVKVS-
LLEIYNEELFDLLSPSSDVSERLQMFDDPRNKRGVIIKGLEEITVHNK
DEVYQILEK-
GAAKRTTAATLMNAYSSRSHSVSVTIHMKXTTIDGEELVKIGKLNLDLAG
SENIGRS-
GAVDKRAREA

Protein Name: UI-M-HO0-cpw-l-21-0-UI.r1 NIH_BMAP_HO0 Mus musculus cDNA clone IMAGE:30655676 5', mRNA sequence

Species: Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus.

The screenshot shows the EMBOSSTranseq web interface. At the top, there's a header with the logo "EMBOSS TRANSEQ Sequence Translation (ST)" and navigation links: Home, Help & Privacy, Recent Jobs, and Input Form. A "Feedback" button is also present. Below the header, a yellow message bar says: "Welcome to the Job Dispatcher website! If you need assistance or have feedback, please [contact us](#)." The main content area shows "Results for Job ID" followed by the job ID "emboss_transeq-I20260202-065859-0964-6919253-p2m". There are "Copy" and "Resubmission" buttons. Below this is a tabbed interface with four tabs: "Tool Output" (selected), "Tool Output", "Result Files", and "Submission Details". The "Tool Output" tab is active, displaying the title "Raw Tool Output [EMBL-EBI]". Below the title, a message states: "We have not been able to format the results of this job (emboss_transeq-I20260202-065859-0964-6919253-p2m). This could be because the job has failed to complete. Only the following information is available, which might contain clues as to why this has occurred. For more help, please contact us with ideally quoting the URL at the top of this page." A "Help" button is located at the bottom right of this message.

Figure 3: EMBOSSTranseq Search

Q4. Prove that this gene, and its corresponding protein, are novel. For the purposes of this project, “novel” is defined as follows. Take the protein sequence (your answer to [Q3]), and use it as a query in a blastp search of the nr database at NCBI.

- If there is a match with 100% amino acid identity to a protein in the database, from the same species, then your protein is NOT novel (even if the match is to a protein with a name such as “unknown”). Someone has already found and annotated this sequence, and assigned it an accession number.
- If the top match reported has less than 100% identity, then it is likely that your protein is novel, and you have succeeded.
- If there is a match with 100% identity, but to a different species than the one you started with, then you have likely succeeded in finding a novel gene.
- If there are no database matches to the original query from [Q1], this indicates that you have partially succeeded: yes, you may have found a new gene, but no, it is not actually homologous to the original query. You should probably start over.

Description: A BLASTP search against NR database yielded a top hit result to a protein from *Rattus norvegicus* (NP_001162583.1).

Species: *Rattus norvegicus*

Name: kinesin-like protein KIF11 [*Rattus norvegicus*]

Percent Identity: 99.16%. Since the top match has less than 100% identity, this must mean the protein is novel because there is no identical match that is 100% to this specific species in the protein database.

Sequences producing significant alignments

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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> kinesin family member 11, isoform CRA_b, partial [Mus musculus]	Mus musculus	517	517	100%	1e-153	99.58%	1064	EDL41788.1
<input checked="" type="checkbox"/> kinesin-like protein KIF11 [Mus musculus]	Mus musculus	516	516	100%	2e-153	99.58%	1052	NP_034745.1
<input checked="" type="checkbox"/> kinesin-like protein KIF11 [Rattus norvegicus]	Rattus norvegicus	515	515	100%	5e-153	99.16%	1056	NP_001162583.1
<input checked="" type="checkbox"/> kinesin-like protein KIF11 [Rattus rattus]	Rattus rattus	515	515	100%	5e-153	99.16%	1056	XP_032747743.1
<input checked="" type="checkbox"/> rCG48024 [Rattus norvegicus]	Rattus norvegicus	515	515	100%	5e-153	99.16%	850	EDM13198.1
<input checked="" type="checkbox"/> kinesin-like protein KIF11 [Peromyscus maniculatus bairdii]	Peromyscus maniculatus bairdii	514	514	100%	1e-152	98.74%	1055	XP_042118941.2
<input checked="" type="checkbox"/> kinesin-like protein KIF11 [Peromyscus leucopus]	Peromyscus leucopus	514	514	100%	1e-152	98.74%	1055	XP_028738726.1
<input checked="" type="checkbox"/> kinesin-like protein KIF11 isoform X1 [Peromyscus maniculatus bairdii]	Peromyscus maniculatus bairdii	514	514	100%	2e-152	98.74%	1055	XP_042118941.1
<input checked="" type="checkbox"/> kinesin-like protein KIF11 [Arvicanthis niloticus]	Arvicanthis niloticus	514	514	100%	2e-152	99.16%	1054	XP_034350713.1
<input checked="" type="checkbox"/> kinesin-like protein KIF11 [Mastomys coucha]	Mastomys coucha	513	513	100%	2e-152	98.74%	1055	XP_031246053.1
<input checked="" type="checkbox"/> Chain A, KINESIN-LIKE PROTEIN KIF11 [Homo sapiens]	Homo sapiens	500	500	100%	5e-152	97.07%	348	3ZCW_A
<input checked="" type="checkbox"/> Chain A, Kinesin-like protein KIF11 [Homo sapiens]	Homo sapiens	503	503	100%	5e-152	97.07%	382	3WPN_A
<input checked="" type="checkbox"/> Chain A, Kinesin-like protein KIF11 [Homo sapiens]	Homo sapiens	501	501	100%	5e-152	97.07%	367	1Q0B_A
<input checked="" type="checkbox"/> kinesin-like protein KIF11 isoform X1 [Phodopus roborovskii]	Phodopus roborovskii	512	512	100%	5e-152	98.33%	1055	XP_051055532.1
<input checked="" type="checkbox"/> Chain A, Kinesin-like protein KIF11 [Homo sapiens]	Homo sapiens	501	501	100%	5e-152	97.07%	367	5Z07_A
<input checked="" type="checkbox"/> Chain A, Kinesin-like protein KIF11 [Homo sapiens]	Homo sapiens	501	501	100%	5e-152	97.07%	367	6TLE_A
<input checked="" type="checkbox"/> Chain A, KINESIN-RELATED MOTOR PROTEIN Eg5 [Homo sapiens]	Homo sapiens	501	501	100%	5e-152	97.07%	368	1I16_A

Figure 4: BLASTP Search Against NR Dataset