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Find a Gene Project Assignment

1. 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 its function is known. If you do not have a favorite protein, select human RBP4 or KIF11. Do not use beta globin as this is in the worked example report that I provide you with online.

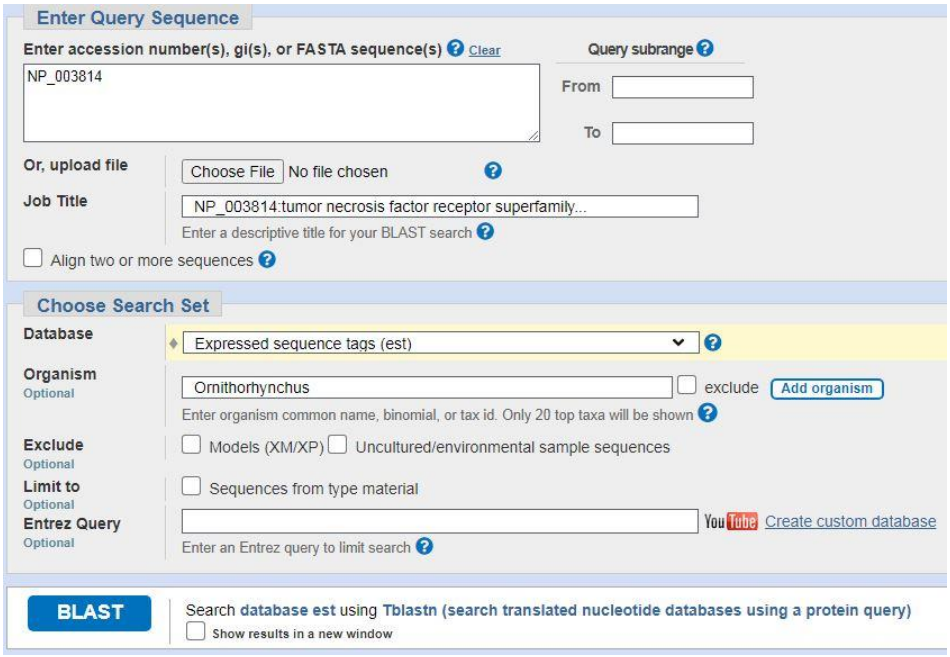
   Name: tumor necrosis factor receptor superfamily, member 6B, decoy
   Accession: NP_003814
   Species: Homo sapiens

2. 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).

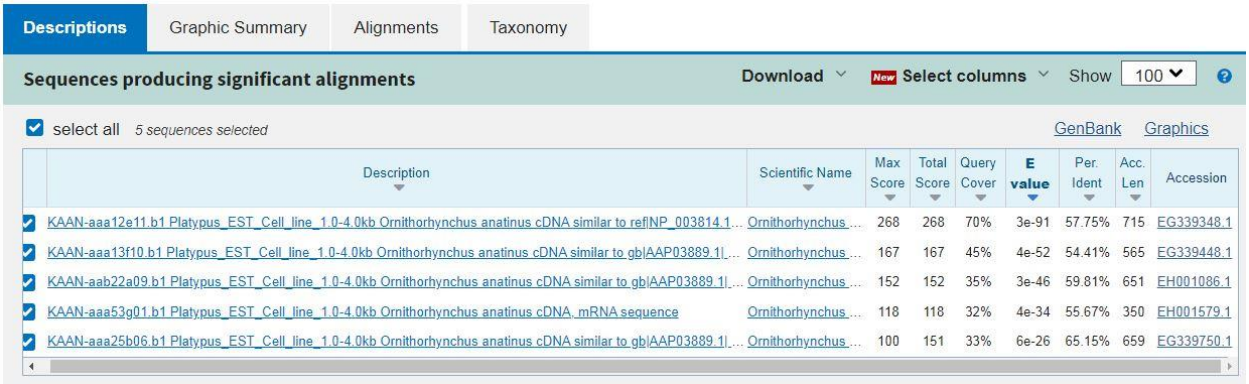
   Method: TBLASTN searched against Ornithorhynchus
   Database: Expressed Sequence Tags (est)
   Organism: Ornithorhynchus (Taxid: 9257)

   Also include the output of that BLAST search in your document. If appropriate, change the font to Courier size 10 so that the results are displayed neatly. You can also screen capture a BLAST output (e.g. alt print screen on a PC or on a MAC press ⌘-shift-4. The pointer becomes a bulls eye. Select the area you wish to capture and release. The image is saved as a file called Screen Shot [].png in your Desktop directory). It is not necessary to print out all of the blast results if there are many pages.

   See search setup in screen-shot below:



The search yielded 5 results, a screen shot of the results is shown below:



Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments — Download — New Select columns — Show 100

select all 5 sequences selected — GenBank — Graphics

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
KAAN-aaa12e11.b1 Platypus_EST_Cell_line_1.0-4.0kb Ornithorhynchus anatinus cDNA similar to ref|NP_003814.1...	Ornithorhynchus...	268	268	70%	3e-91	57.75%	715	EG339348.1
KAAN-aaa13f10.b1 Platypus_EST_Cell_line_1.0-4.0kb Ornithorhynchus anatinus cDNA similar to gb|AAP03889.1|...	Ornithorhynchus...	167	167	45%	4e-52	54.41%	565	EG339448.1
KAAN-aab22a09.b1 Platypus_EST_Cell_line_1.0-4.0kb Ornithorhynchus anatinus cDNA similar to gb|AAP03889.1|...	Ornithorhynchus...	152	152	35%	3e-46	59.81%	651	EH001086.1
KAAN-aaa53g01.b1 Platypus_EST_Cell_line_1.0-4.0kb Ornithorhynchus anatinus cDNA, mRNA sequence	Ornithorhynchus...	118	118	32%	4e-34	55.67%	350	EH001579.1
KAAN-aaa25b06.b1 Platypus_EST_Cell_line_1.0-4.0kb Ornithorhynchus anatinus cDNA similar to gb|AAP03889.1|...	Ornithorhynchus...	100	151	33%	6e-26	65.15%	659	EG339750.1

Chosen match: Accession EG339348.1, a 715 base pair cDNA clone from *Ornithorhynchus anatinus*. See below for alignment details.

Alignment Details:

```
Query: tumor necrosis factor receptor superfamily member 6B precursor [Homo
sapiens] Query ID: NP_003814.1 Length: 300

>KAAN-aaa12e11.b1 Platypus_EST_Cell_line_1.0-4.0kb Ornithorhynchus anatinus
cDNA similar to ref|NP_003814.1| tumor necrosis factor receptor superfamily,
member 6b; decoy receptor 3 [Homo sapiens] ref|NP_116563.1| tumor necrosis
factor receptor superfamily, member 6b; decoy receptor 3 [Homo sapiens]
sp|O95407|TR6B_HUMAN Tumor necrosis fact, mRNA sequence
Sequence ID: EG339348.1 Length: 715
Range 1: 63 to 701

Score: 268 bits(686), Expect:3e-91,
Method: Compositional matrix adjust.,
Identities: 126/213(59%), Positives: 162/213(76%), Gaps: 1/213(0%)

Query  34   PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV  93
            PTY W+D+ T ERL C QCPPGT+V + C R SPT C PCP  HYTQ+WNYL++CRYCNV
Sbjct  63   PTYSWKDSTTQERLQCQQCPPGTYVSQHCSRTSPTQCQPCPTLHYTQYWNYLDKCRYCNV  242

Query  94   LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC  153
             CG +EEE   C ATHNR C+C+ G++A+  FC+EH++CP G+GV++ GTP++NT+CQ C
Sbjct  243  FCGAQEEEVHPCSATHNRVCQCQPGYYAYMDFCIEHSTCPLGSGVVSQGTPTKNTECQEC  422

Query  154  PPGTFsasssssEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECER  213
            P GTFS +SS +E CQ H+NCT LG+ +NVPG+  HDTLCT C  F L++  PG ++CE+
Sbjct  423  PRGTFSDNSSRTEPCQSHQNCTLLGMKVNVPGNRFHDTLCTRCDNFQLNSSEPGNKDCEQ  602

Query  214  AVIDFVAFQDISIKRLQRLLQAL-EAPEGWGPT  245
            A+IDFVA+QDI +KRL RL Q L EAP   G T
Sbjct  603  ALIDFVAYQDIPLKRLLRLQQVLGEAPGAAGQT  701
```

3. 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

```
> O. anatinus protein (sequence taken from BLAST results)
TKKLGTFVLAVTFPMGSNNPPTYSWKDSTTQERLQCQQCPPGTYVSQHCSRTSPTQCQPCPTLHYTQYWNYLDKCRYCN
VFCGAQEEEVHPCSATHNRVCQCQPGYYAYMDFCIEHSTCPLGSGVVSQGTPTKNTECQECPRGTFSDNSSRTEPCQSH
QNCTLLGMKVNVPGNRFHDTLCTRCDNFQLNSSEPGNKDCEQALIDFVAYQDIPLKRLLRLQQVLGEAPGAAGQTRGFQ
V
```

Here, tell me the name of the novel protein, and the species from which it derives. It is very unlikely (but still definitely possible) that you will find a novel gene from an organism such as S. cerevisiae, human or mouse, because those genomes have already been thoroughly annotated. It is more likely that you will discover a new gene in a genome that is currently being sequenced, such as bacteria or plants or protozoa.

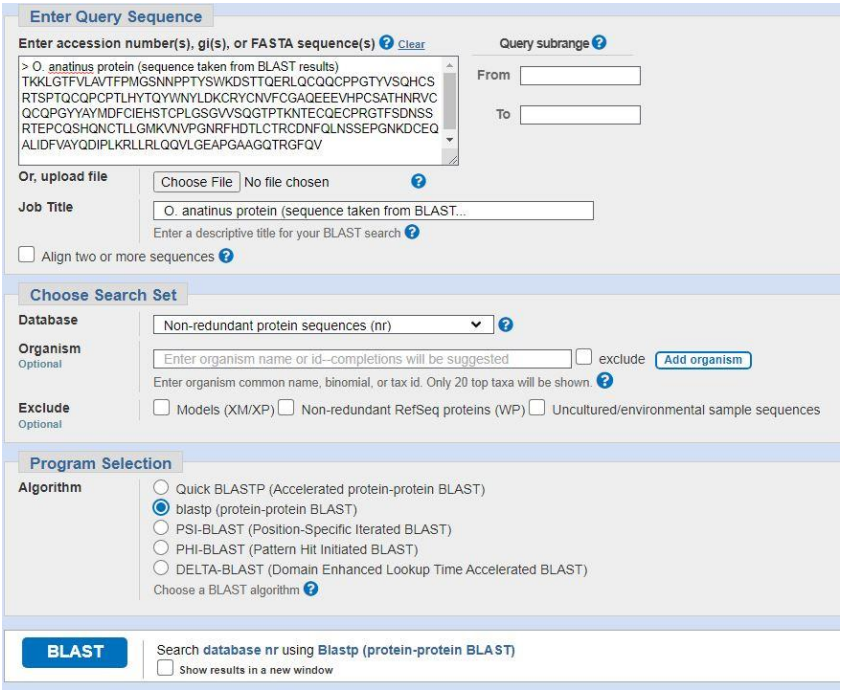
Name: Ornithorhynchus tumor necrosis factor receptor superfamily, member 6B, decoy
Species: Ornithorhynchus anatinus
Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Prototheria; Monotremata; Ornithorhynchidae; Ornithorhynchus

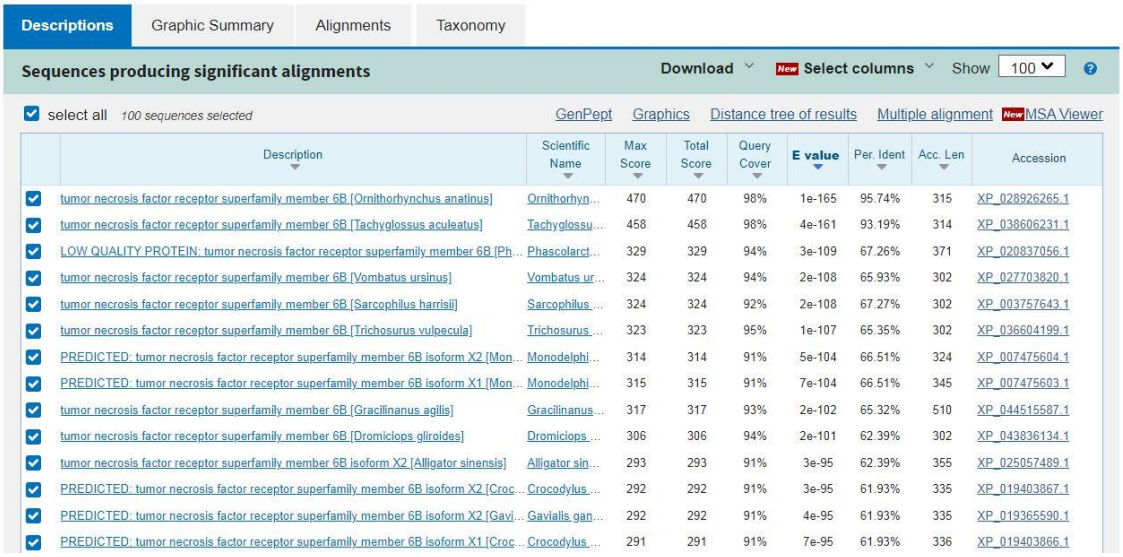
4. Prove that this gene, and its corresponding protein, are novel. For the purposes of this project, "novel" is defined as follows. Take the protein sequence (your answer to [Q3]), and use it as a query in a blastp search of the nr database at NCBI.
• If there is a match with 100% amino acid identity 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.

Details:

A BLASTP search against NR database was used (see setup in first screen-shot below).
This yielded a top hit result is to a protein from Ornithorhynchus anatinus (Platypus)
See additional screen shots below for top hits and selected alignment details:

The first hit has a 95.74% identity with our query, thus since the percent identify reported is less than 100% it is likely that our gene is novel as defined in the question. So we have succeeded as required.





Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
tumor necrosis factor receptor superfamily member 6B [Ornithorhynchus anatinus]	Ornithorhyn...	470	470	98%	1e-165	95.74%	315	XP_028926265.1
tumor necrosis factor receptor superfamily member 6B [Tachyglossus aculeatus]	Tachyglossu...	458	458	98%	4e-161	93.19%	314	XP_038606231.1
LOW QUALITY PROTEIN: tumor necrosis factor receptor superfamily member 6B [Ph...	Phascolarct...	329	329	94%	3e-109	67.26%	371	XP_020837056.1
tumor necrosis factor receptor superfamily member 6B [Vombatus ursinus]	Vombatus ur...	324	324	94%	2e-108	65.93%	302	XP_027703820.1
tumor necrosis factor receptor superfamily member 6B [Sarcophilus harrisii]	Sarcophilus...	324	324	92%	2e-108	67.27%	302	XP_003757643.1
tumor necrosis factor receptor superfamily member 6B [Trichosurus vulpecula]	Trichosurus...	323	323	95%	1e-107	65.35%	302	XP_036604199.1
PREDICTED: tumor necrosis factor receptor superfamily member 6B isoform X2 [Mon...	Monodelphi...	314	314	91%	5e-104	66.51%	324	XP_007475604.1
PREDICTED: tumor necrosis factor receptor superfamily member 6B isoform X1 [Mon...	Monodelphi...	315	315	91%	7e-104	66.51%	345	XP_007475603.1
tumor necrosis factor receptor superfamily member 6B [Gracilinanus agilis]	Gracilinanus...	317	317	93%	2e-102	65.32%	510	XP_044515587.1
tumor necrosis factor receptor superfamily member 6B [Dromiciops gliroides]	Dromiciops ...	306	306	94%	2e-101	62.39%	302	XP_043836134.1
tumor necrosis factor receptor superfamily member 6B isoform X2 [Alligator sinensis]	Alligator sin...	293	293	91%	3e-95	62.39%	355	XP_025057489.1
PREDICTED: tumor necrosis factor receptor superfamily member 6B isoform X2 [Croc...	Crocodylus ...	292	292	91%	3e-95	61.93%	335	XP_019403867.1
PREDICTED: tumor necrosis factor receptor superfamily member 6B isoform X2 [Gavi...	Gavialis gan...	292	292	91%	4e-95	61.93%	335	XP_019365590.1
PREDICTED: tumor necrosis factor receptor superfamily member 6B isoform X1 [Croc...	Crocodylus ...	291	291	91%	7e-95	61.93%	336	XP_019403866.1

Download GenPept Graphics

tumor necrosis factor receptor superfamily member 6B [Ornithorhynchus anatinus]

Sequence ID: XP_028926265.1 **Length:** 315 **Number of Matches:** 1

Range 1: 17 to 250 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
470 bits(1209)	1e-165	Compositional matrix adjust.	225/235(96%)	227/235(96%)	1/235(0%)

```
Query  4    LGTFVLAVTFPMGSNNPPTYSWKDSTTQERLQCQQCPPGTYVSQHCSRTSPTQCQPCPTL  63
            GTFVLAVTFPMGSNNPPTYSWKDSTTQERLQCQQCPPGTYVSQHCSRTSPTQCQPCPTL
Sbjct  17   FGTFVLAVTFPMGSNNPPTYSWKDSTTQERLQCQQCPPGTYVSQHCSRTSPTQCQPCPTL  76

Query  64   HYTQYWNYLDKCRYCNVFCGAQEEEVHPCSATHNRVCQCQPGYYAYMDFCIEHSTCPLGS  123
            HYTQYWNYLDKCRYCNVFCGAQEEEVHPCSATHNRVCQCQPGYYAYMDFCIEHSTCPLGS
Sbjct  77   HYTQYWNYLDKCRYCNVFCGAQEEEVHPCSATHNRVCQCQPGYYAYMDFCIEHSTCPLGS  136

Query  124  GVVSQGTPTKNTECQECPRGTFSDNSSRTEPCQSHQNCTLLGMKVNVPGNRFHDTLCTRC  183
            GVVSQGTPTKNTECQECPRGTFSDNSSRTEPCQSHQNCTLLGMKVNVPGNRFHDTLCTRC
Sbjct  137  GVVSQGTPTKNTECQECPRGTFSDNSSRTEPCQSHQNCTLLGMKVNVPGNRFHDTLCTRC  196

Query  184  DNFQLNSSEPGNKDCEQALIDFVAYQDIPLKRLLRLQQVLGEAPGAAGQTRGFQV  238
            DNFQLNSSEPGNKDCEQALIDFVAYQDIPLKRLLRLQQVLG+  G     +GFQV
Sbjct  197  DNFQLNSSEPGNKDCEQALIDFVAYQDIPLKRLLRLQQVLGKR-GGRRSDQGFQV  250
```