The Translate Tool

The translate tool will take in a nucleotide sequence and translate it to all six possible reading frames. We will use this in Project 1 to help extend what we know of the coding sequence of a protein that we identified through homology from a nucleotide database.

Suppose that you ran a BLAST search with the human ACE protein (NP_000780.1) against a database of uncharacterized genomic sequences from rodents, and found a hit in *Chinchilla lanigera* that you think is interesting. Your original BLAST hit looks like:

Now you want to see if the query sequence contains more of the protein than BLAST is showing you.
1. What are the first three and last three amino acids that you know of in the Chinchilla sequence, from the BLAST results shown above?

2. Now suppose that you upload the sequence to the Translate tool. You get the following output:

Potential ORFs are highlighted in pink. Dashes represent stop codons in that frame.

What reading frame do you think contains the chinchilla homolog of ACE that you found? How can you be sure you are right?

3. What are the first three and last three amino acids in the chinchilla protein that you know of now that you have seen the Translate Tool results? Why?