HOW TO COMPLETE THE WORKSHEETS

1. Use the codon wheel to **translate the DNA sequences** on the worksheet to amino acids.

2. **Type the amino acid sequence** in to the Uniprot Blast search [www.uniprot.org/blast/](http://www.uniprot.org/blast/).

   Press **Run BLAST** to get results (it may take a few seconds for results to appear).

3. When the search results appear, **filter the results** to only show reviewed entries (gold file icon with a star). Each result is known as a “hit.”
4. After filtering the hits should look like this. **Scroll down** to the Overview section.

Look at the info column. This will give you an idea of how reliable your hits are. The Expect value (E-value) indicates the number of random hits you would expect by chance for the given query sequence and the size of the sequence database against which the BLAST is performed.

For example, an E-value of 1.0 means that you would expect on average to get one match in the database for the submitted query simply by chance. The lower the E-value, or the closer it is to zero, the more “significant” the match is. In general, the E-values should be in the range of 0.01 to 0.1 to be statistically significant.

The identity % describes how similar your sequence is to the hit, i.e. whether the amino acids are in the same position when aligned. 100% means the sequences match exactly.
5. **Click on the hit** that you think best matches your sequence. Find out the name of the protein which species the sequence is from (common and species name) and what the protein does. Is the protein found in other species?

You can reduce the amount of information on the screen by unticking the blue display categories on the left hand side of the screen.

If you cannot find all the information you need, try using a Google search or Wikipedia to find out more.

6. To start a new BLAST search click **Edit and resubmit**, and enter your next set of amino acids. Repeat steps 3 to 5.