# Module 9: RNA

## Objective

The objectives of this module are:

1. To determine if the nucleotide sequence under investigation has characteristics to define it as an RNA coding gene.

## Materials

To perform this exercise you will need:

- Access to the internet on a computer equipped with the most recent version of Firefox, Chrome or Safari.
- To have completed the sign up for GENI-ACT described in the Signing Up for GENI-ACT section of the manual.

## Background

Rfam

The Rfam database is similar to Pfam in that multi-sequence alignments are used to build families. However, Rfam uses models built on conserved sequences and secondary structures to search through an unknown sequence for non-coding RNA genes (e.g. rRNAs, tRNAs, and other small RNAs), regulatory motifs within the transcribed regions of protein-coding genes (e.g., riboswitches), and motifs associated with self-splicing RNAs. **This module should be run on the nucleotide sequence of hypothetical genes if no other hits have been found in modules to this point.** If you have good evidence that your gene is functional from other module results, this module will likely not offer any additional information.

Reading: Rfam: annotating non-coding RNAs in complete genomes. S. Griffiths-Jones, S. Moxon, M. Marshall, A. Khanna, S.R. Eddy and A. Bateman. Nucleic Acids Research(2005) Database Issue 33: D121-D124.

## Procedures

1. Navigate to Rfam at http://rfam.sanger.ac.uk .
2. Enter the nucleotide sequence of the gene being annotated.
3. The results will show if any families of RNA were found, the position of the hit along with the score, and the alignment of the sequence to the family.
4. Report the score and record the alignment in the Lab Notebook.