Name:

Date:

RNA Sequencing: Activity 1

1. What do you have to do to prepare a large RNA molecule before it can be sequenced?

2. What are three things researchers can do when they do RNA-seq so that read alignment or mapping will be more successful?

Challenge question

Scenario: You have sequenced only one end of your RNA fragments (i.e., you have single-end data instead of paired-end data). You are trying to align your fragments to the genome. Your technician tells you that the fragment lengths in your sample are about 240 base pairs long.

Does this information about the lengths of your fragments help you align your single-end reads to the genome? Explain your answer.