Recall the definitions: The set of RNA strands S is defined (recursively) by:

Basis Step: $A \in S, C \in S, U \in S, G \in S$ Recursive Step: If $s \in S$ and $b \in B$, then $sb \in S$

where sb is string concatenation. The function rnalen that computes the length of RNA strands in S is defined recursively by:

Basis Step: If $b \in B$ then rnalen(s) = 1Recursive Step: If $s \in S$ and $b \in B$, then rnalen(s) = 1 + rnalen(s)

The function basecount that computes the number of a given base b appearing in a RNA strand s is defined recursively by: