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

$$\begin{array}{ll} \text{Basis Step:} & \texttt{A} \in S, \texttt{C} \in S, \texttt{U} \in S, \texttt{G} \in S \\ \text{Recursive Step:} & \text{If } s \in S \text{ and } b \in B, \text{ then } sb \in S \end{array}$$

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

$$\begin{array}{llll} & & \mathit{rnalen} : S & \to \mathbb{Z}^+ \\ \text{Basis Step:} & \text{If } b \in B \text{ then} & \mathit{rnalen}(b) & = 1 \\ \text{Recursive Step:} & \text{If } s \in S \text{ and } b \in B, \text{ then} & \mathit{rnalen}(sb) & = 1 + \mathit{rnalen}(s) \end{array}$$

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

$$\begin{array}{llll} & & \mathit{basecount} : S \times B & \to \mathbb{N} \\ \text{Basis Step:} & \text{If } b_1 \in B, b_2 \in B & \mathit{basecount}(\ (b_1, b_2)\ ) & = \begin{cases} 1 & \text{when } b_1 = b_2 \\ 0 & \text{when } b_1 \neq b_2 \end{cases} \\ \text{Recursive Step:} & \text{If } s \in S, b_1 \in B, b_2 \in B & \mathit{basecount}(\ (sb_1, b_2)\ ) & = \begin{cases} 1 + \mathit{basecount}(\ (s, b_2)\ ) & \text{when } b_1 = b_2 \\ \mathit{basecount}(\ (s, b_2)\ ) & \text{when } b_1 \neq b_2 \end{cases} \end{array}$$