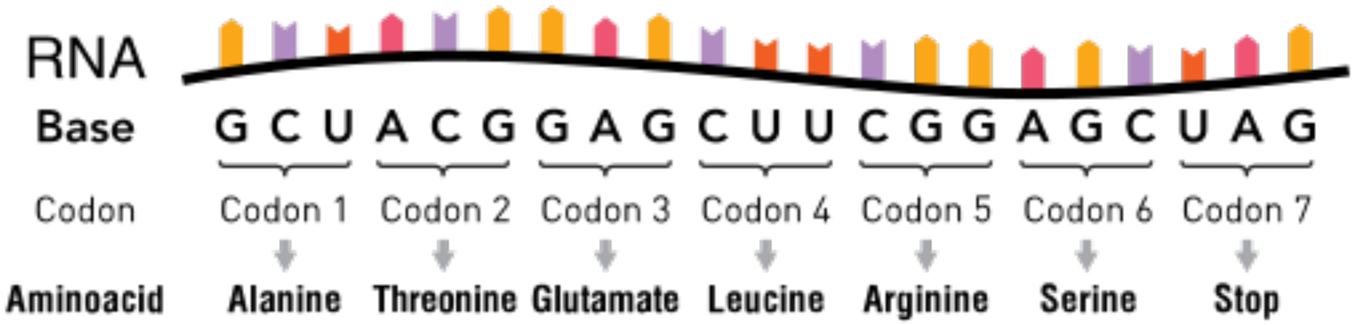
CONCEPT: tRNA, rRNA, AND THE CODON CODE

Codon Code

- Translation is the process of converting nucleotides to amino acids
    - □ There are 4 nucleotides and 20 amino acids - therefore translation is not 1:1
    - □ A **codon** is a ____________________________ of three nucleotides that encodes for a single amino acid
        - A **start codon** (AUG) encodes for a specially labeled methionine as the starting amino acid
        - A **stop codon** (UAA, UAG, and UGA) do not code for amino acids, but signal to stop translation
    - □ The genetic code is **redundant (degenerate)** = multiple combinations of nucleotides encode for one amino acid
        - 64 total nucleotide combinations (4x4x4) encode for only 20 amino acids
        - Lessens the effect of a single mutation
    - □ There are __________________ **reading frames,** each beginning with a different nucleotide within the first codon
        - Only one reading frame specifies the correct protein
        - **Frameshift mutations** are mutations that disrupt the correct reading frame
    - □ This code is nearly universal, but not entirely
        - Mitochondria use AGA as a stop codon, and UGA to encode for the amino acid tryptophan

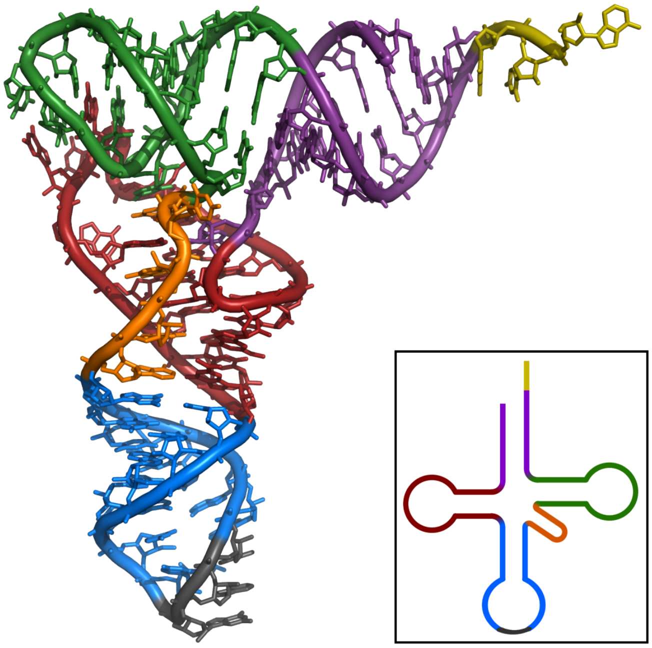
EXAMPLE: Three nucleotides encode for a single amino acid, or signal (start/stop) sequence



tRNA Processing

- tRNAs are the ______________________ molecules responsible for matching amino acids with the proper codon
    - □ tRNAs are 75-80 nucleotides in length
        - Form two double helices in an “L” shape
    - □ The structure of a tRNA contains two main parts: *anticodon region* and the *amino acid binding region*
        - **Anticodon:** region on tRNA made of nucleotides that is complementary to the codon
        - *Amino acid binding region:* 3’ end of the tRNA, which is single-stranded, and attaches to an amino acid

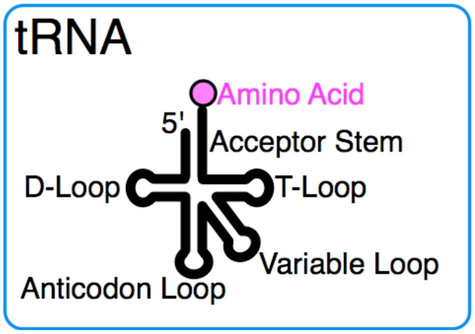
EXAMPLE: A tRNA molecules. Orange is the amino acid binding site, and blue is the anticodon site



- □ tRNAs need to be _________________________________, but their processing is different than that of mRNAs
    - Examples include: Addition of methyl groups, replacement of 3’ Uracils with CCA sequence
    - Some contain introns, but not all
    - There are around 50 nucleotide modifications commonly found in tRNAs
- □ Some tRNAs attach to only one amino acid, some attach to multiple – tRNAs to amino acids are not 1:1
- □ The **wobble hypothesis** allows for a mismatch between the codon and the anticodon at the third position

- tRNAs work by bringing amino acids to the ribosome and acting as an intermediate between mRNA and amino acids
    - **Aminoacyl tRNA synthetase** attaches amino acids to the ________________ tRNA via catalyzing an ester bond
        - Attaches to the 3' end of the tRNA
        - When the amino acid is attached the tRNA is said to be "active" or "charged"
        - There is one synthase for each amino acid (20 total)
    - Certain factors allow for the ________________________________ of the correct amino acid to the correct tRNA
        - The amino acid has the highest affinity for the active site of the tRNA synthase
        - *Proofreading* occurs when the tRNA tries to "fit" into a specific pocket
            - Correct amino acids are excluded and allowed to fully bind to the tRNA

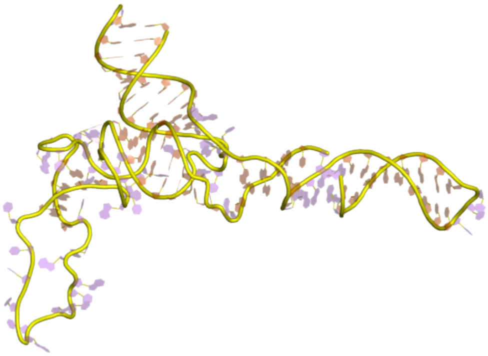
EXAMPLE: Amino acid attached to a tRNA



<u>rRNA Processing and Ribosomal Formation</u>

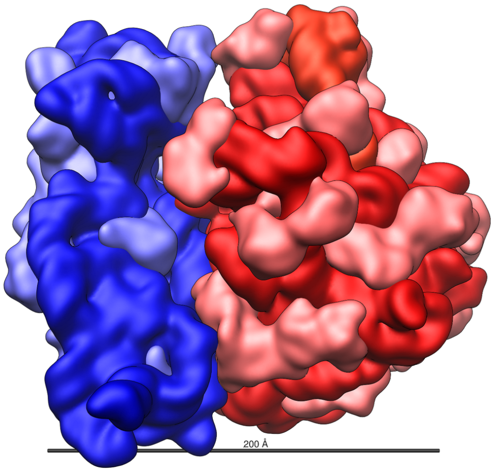
- rRNAs (ribosomal RNA) form the majority of the _________________, which is responsible for translation RNA into protein
    - In prokaryotes there are three rRNAs (16S, 23S, and 5S rRNAs)
        - Each are coded for in the same transcript
    - In eukaryotes, there are four rRNAs (5S, 5.8S, 28S, and 18S)
        - The 5S, 5.8S and 28S are encoded on the same transcript
    - The rRNAs must be _____________________ and cleaved into individual rRNAs before forming the ribosome
        - Processing includes making modifications to the nucleotides (ex: addition of methyl groups)
        - Also includes forming complex structures and conformational changes
    - rRNAs make up around 70-80% of the cell's total RNA

EXAMPLE: Structure of the 5s rRNA



- The ribosome consists of ______________ subunits: the *small* subunit and the *large* subunit
  - □ In prokaryotes the small subunit is built with the 16S rRNA and the large subunit with the 23S and 5S rRNAs
  - □ In eukaryotes the small subunit is built with the 18S rRNA and the large subunit with the 5S 5.8S and 28S rRNAs
  - □ *Small nuclear RNAs (snoRNA)* ______________________ the pre-rRNA (unprocessed rRNA transcript)
    - Bind to pre-rRNA and help them complex with proteins to form snoRNPs
    - snRNPs help to position the rRNAs for the chemical reactions necessary for processing
  - □ The ribosome is formed through processed rRNAs and proteins

EXAMPLE: The large subunit (red) and small subunit (blue) fit together to form the ribosome



PRACTICE

1. Which of the following is not true about the codon code?
    a. One sequence (AUG) initiates transcription
    b. The number of codons is more than the number of amino acids
    c. Out of three possibilities there is only one correct start site (frame) for each gene
    d. Anticodons are encoded in the DNA of the gene

2. Aminoacyl tRNA synthetase is an ezyme that is responsible for doing what?
    a. Forming the tRNA into its cloverleaf structure
    b. Binding the tRNA anticodon and mRNA codon together
    c. Attaching the amino acid onto the tRNA
    d. Attaching the amino acid onto the growing polypeptide chain

3. Which of the following rRNAs make up the small subunit of the eukaryotic ribosome?
    a. 18S
    b. 5S
    c. 16S
    d. 28S