

Ribonucleic Acid (RNA)

- Ribonucleic acids are polyribonucleotides. They contain mainly four nucleotides; AMP, GMP, CMP, **UMP**.
- The nucleotides forming the structure of RNA are interconnected as in DNA by phosphodiester bonds.
- RNA molecules are synthesized in a process termed **transcription** where **the sequence of bases in each RNA molecule is controlled by base sequence in one strand of DNA (template strand)**.

Types of RNA:

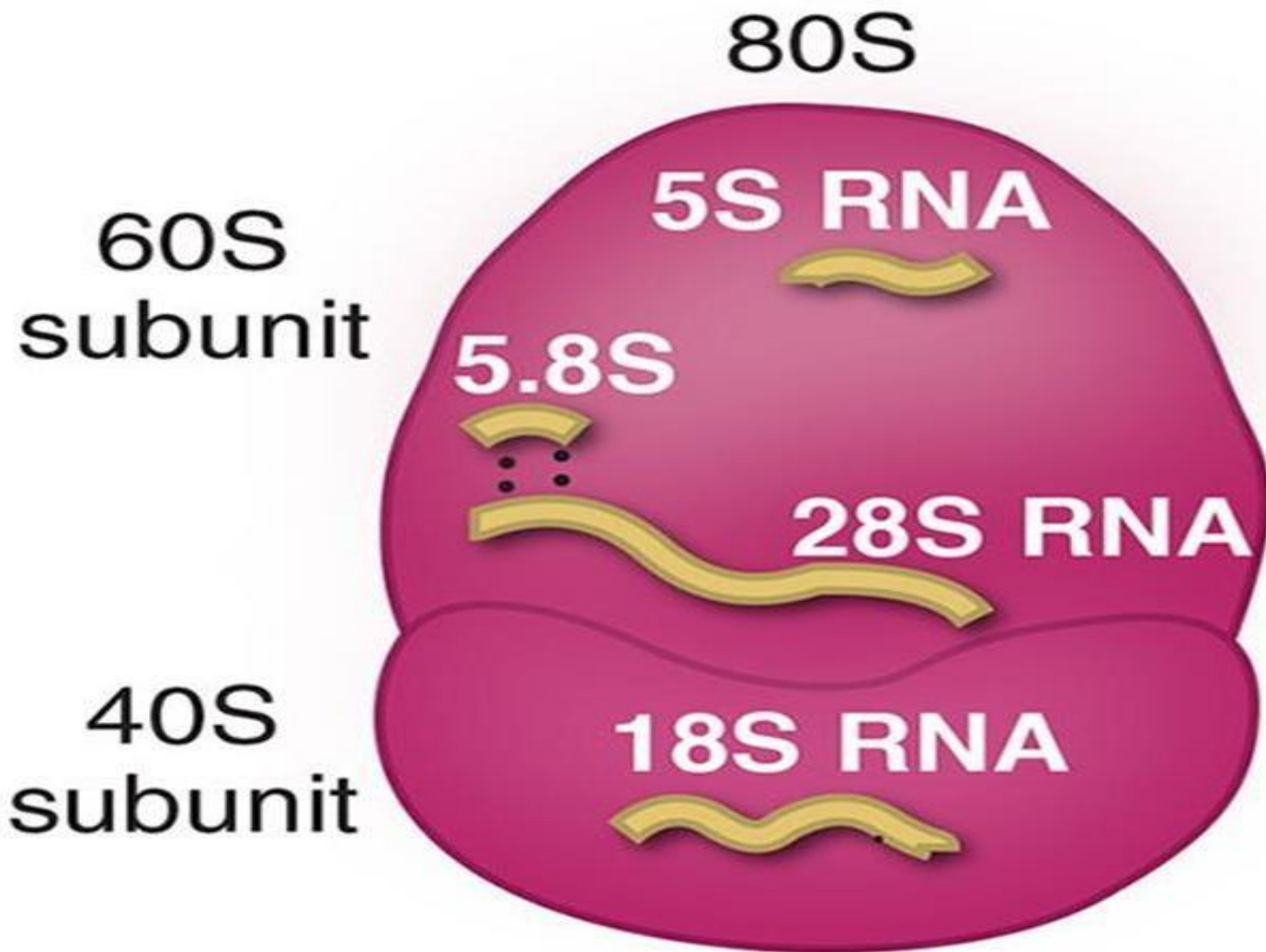
- **Three main types of RNA are formed and all are related to protein synthesis:**
 - 1- Ribosomal RNA (rRNA) molecules form 80% of cellular RNA.**
 - 2- Transfer RNA (tRNA) form 15% of cellular RNA.**
 - 3- Messenger RNA (mRNA) molecules form 5% of cellular RNA.**

Ribosomal RNA (r RNA):

- **rRNA are found in association with several proteins as components of the ribosomes , which are the complex structure that serve as the site for protein synthesis by interacting with the mRNA and tRNA.**

- Eukaryotic **80S** ribosome consists of two **nucleoprotein** subunits of unequal size, the **60S** subunit and the **40S** subunit:
- The 60 S ribosomal subunit: Consists of about 50 polypeptides combined with three subtypes of ribosomal RNA (5S, 5.8S , 28S rRNA)
- The 40 S ribosomal subunit: Consists of 35 polypeptides combined with one r RNA (18S)
- Both 60S and 40 S combine together to form the 80 S full ribosomal subunit.

Eukaryotic Ribosome



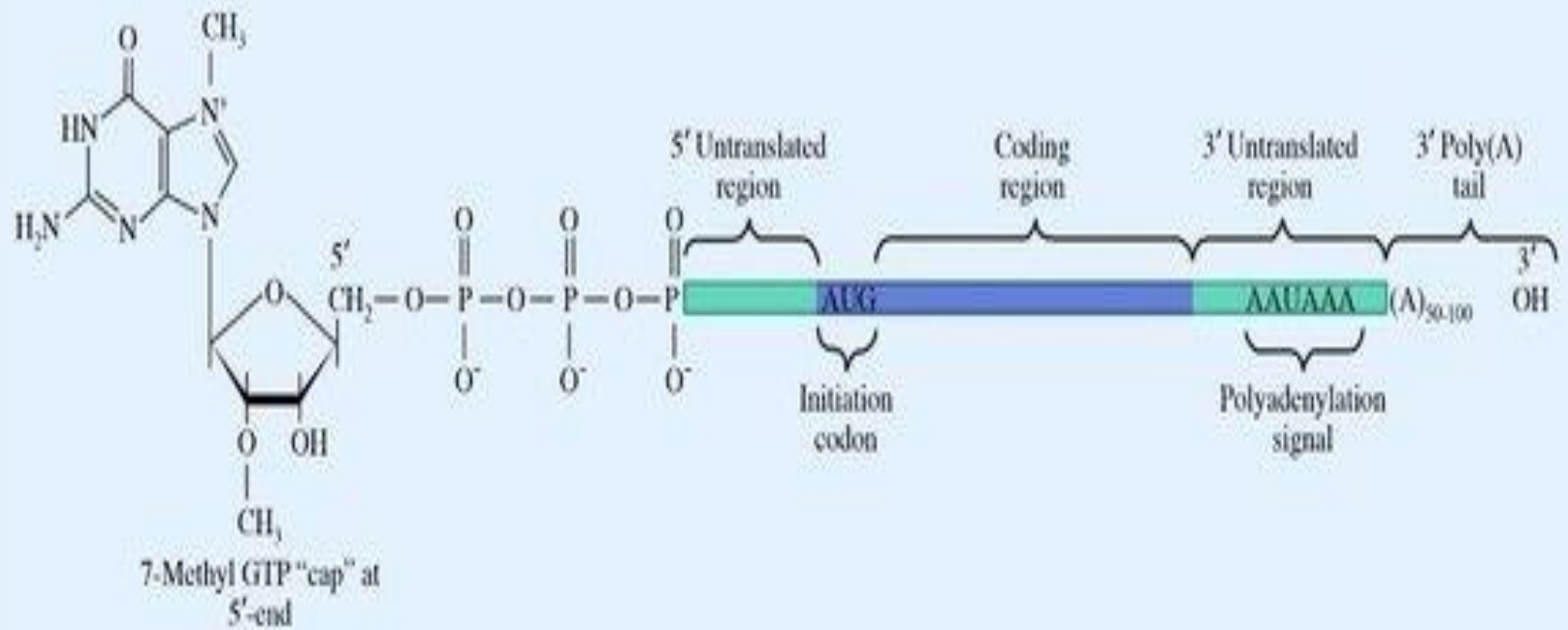
- **S= Svedberg unit (sedimentation or S unit): it is the unit that measures the sedimentation velocity of different particles depending on their molecular weight as well as the size of the particles by using high speed centrifuge.**
- **Because the S values are determined both by shape as well as molecular mass, their numeric values are not strictly additive.**

Messenger RNA (mRNA)

- It forms about 5 % of the total RNA. mRNA is synthesized in the nucleus as a **single strand** with base sequence **complementary to a specific DNA region called gene** (that codes the information of certain protein). Every three nitrogenous base in mRNA form one **codon** specific for one amino acid.

● Eukaryotic mRNA has the following features:

- It contains coding regions (**exons**) that can be translated, and untranslated regions in between exons called **introns**.
- It contains noncoding segments called untranslated regions (**UTRs**) at both their 5' & 3' ends.
- At the 5' ends there is 7- methylguanosine triphosphate cap and at its 3' ends there is a poly A tail, these modified ends are created by post-transcription modification process in the eukaryotic cells

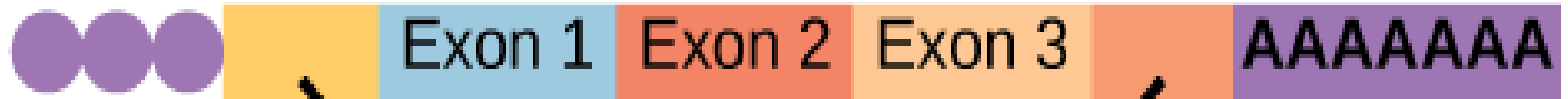


Primary RNA transcript



RNA processing

Spliced RNA



5' cap

5' untranslated region

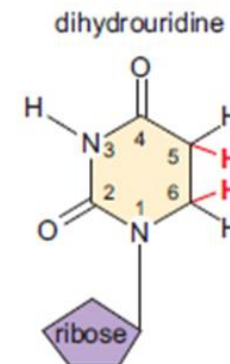
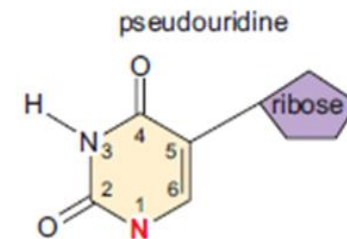
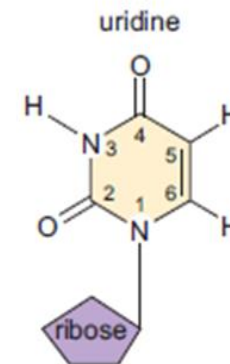
3' untranslated region

Poly-A tail

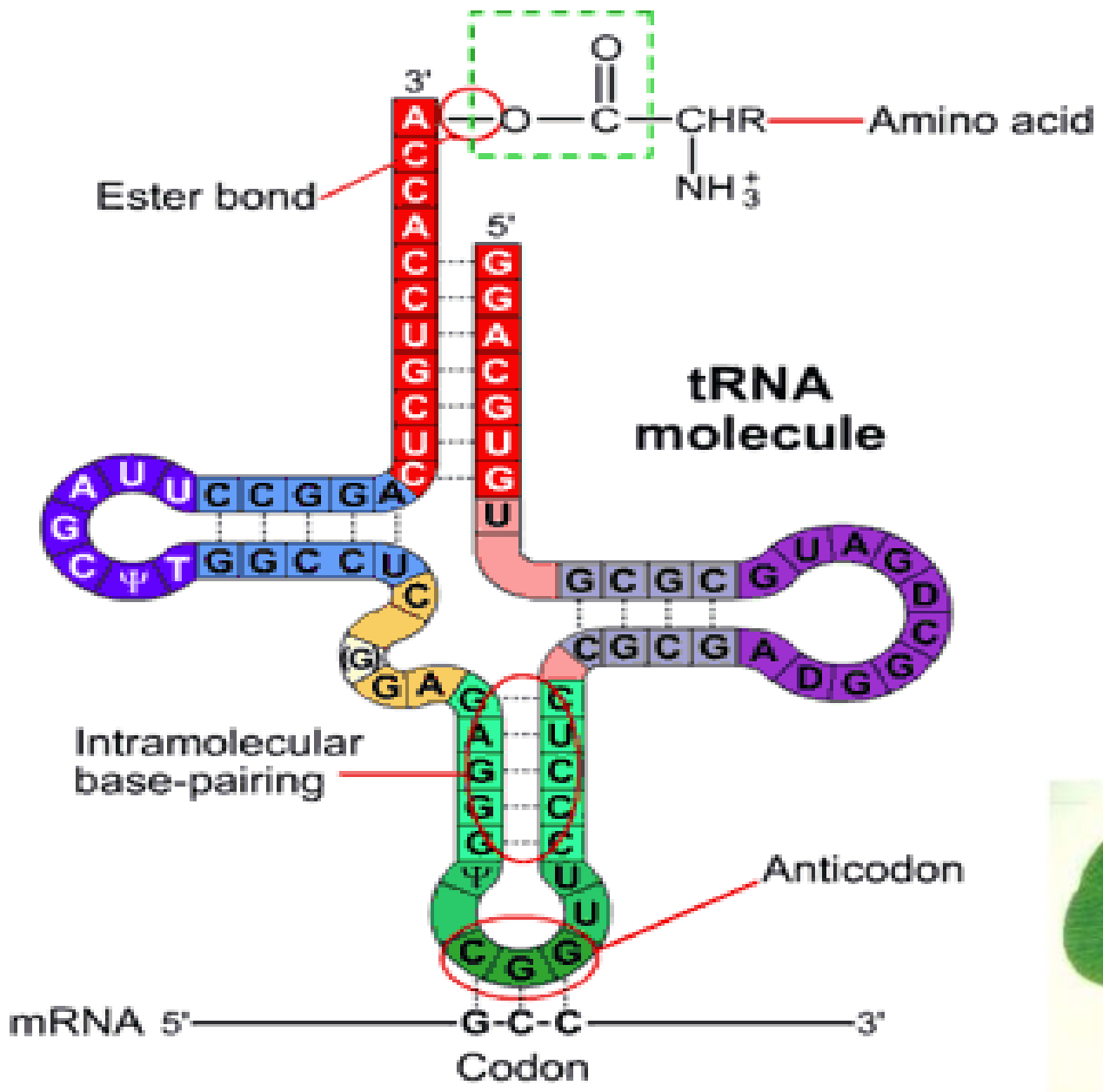
Transfer RNA (tRNA)

- It forms about 15 % of the total RNA. Each tRNA consists of 70-90 nucleotides. The main role of t RNA is to **carry and transport amino acids to the ribosome** during protein synthesis. tRNA consists of single strand folded to have the shape of cloverleaf appearance with four loops & an acceptor arm

- A striking aspect of tRNAs is the presence of several unusual bases in their primary structure. These unusual features are created post-transcriptionally by enzymatic modification of normal bases in the polynucleotide chain. For example, pseudouridine (Ψ U) is derived from uridine by an isomerization in which the site of attachment of the uracil base to the ribose is switched from the nitrogen at ring position 1 to the carbon at ring position 5. Likewise, dihydrouridine (D) is derived from uridine by enzymatic reduction of the double bond between the carbons at positions 5 and 6.



- Other unusual bases found in tRNA include hypoxanthine, thymine, and methylguanine. These modified bases are not essential for tRNA function, but cells lacking these modified bases show reduced rates of growth. This observation suggests that the modified bases lead to improved tRNA function. For example, hypoxanthine plays an important role in the process of codon recognition by certain tRNAs.



- The acceptor arm of tRNA is at the 3' end and has the specific sequence CCA. Amino acids are carried on the 3' end.
- There are at least 20 species of tRNA molecules in every cell, at least one (and often several) corresponding to each of the 20 amino acids required for protein synthesis.
- The different loops of tRNA are named according to their unique structures as follow:

- **Loop I** : contains the unusual base dihydrouracil so termed the D-loop
- **Loop II (Anticodon loop)**: It contains three bases known as the anticodon .It has anticodon sequence that can form base pairing with complementary codon of mRNA to put amino acid in it correct position during protein synthesis.
- **Loop III**: contains from 3-12 bases and it is the major site for variation in tRNA, so termed the variable loop.
- **Loop IV**: contains the unusual thymine and pseudouridine bases, so termed the **TΨC** loop as it contains this specific sequence.