

## UNIT 6 - NUCLEIC ACIDS & PROTEIN SYNTHESIS

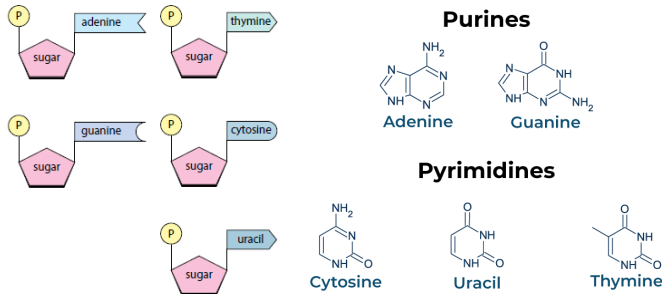
### Key features of DNA:

- ↳ Its ability to store information needed to control cell activity
- ↳ Its ability to copy itself accurately

### 'DNA' - 'Deoxyribonucleic Acid'

- ↳ It is a macromolecule made up of nucleotides (so it is a polynucleotide)

**Nucleotide** - a molecule consisting of a nitrogen-containing base, a pentose sugar, and a phosphate group

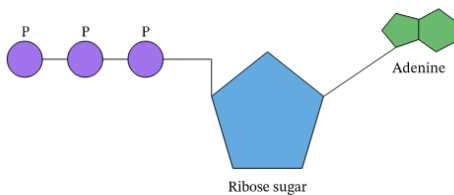


**Nitrogen-containing bases** - can be adenine, guanine, cytosine, or thymine (and uracil instead of thymine in RNA). Adenine always pairs with thymine while cytosine always pairs with guanine (therefore the amount of adenine on one strand of DNA is always equal to the amount of thymine on the OTHER strand)

- ↳ There are purines (large, heavy bases) and pyrimidines (small, light bases). A and G are PURINES while C, T, and U are PYRAMIDINES.
- ↳ Purines and pyrimidines are always paired together. A pair of purines wouldn't fit between the sugar-phosphate backbone, and a pair of pyrimidines wouldn't be able to close the gap between them and form hydrogen bonds.
- ↳ A=T and A=U: they form 2 hydrogen bonds between bases
- ↳ C≡G: they form 3 hydrogen bonds between bases

**Pentose sugars** - they can either be deoxyribose or ribose, depending on whether the nucleotides are part of DNA or RNA

**Phosphate group** - they give nucleic acids their acidic nature



★ The structure of ATP is very similar to that of a nucleotide of RNA

Adenine + Ribose = Adenosine

ATP means Adenosine Triphosphate, so one molecule of ATP has 3 phosphate groups.

**Dinucleotide** - two nucleotides joined together by a phosphodiester bond

**Phosphodiester bond** - a bond joining two nucleotides together; there are 2 ester bonds, one from the shared phosphate groups to either sugar.

**Polynucleotide** - a chain of nucleotides joined together by phosphodiester bonds

### The Structure of DNA

- ↳ It is a double helix made up of two strands that wind around each other
- ↳ The chains run in opposite directions, so are antiparallel: 3'-5' and 5'-3'
- ↳ Each chain has a sugar-phosphate backbone with bases projecting at right angles
- ↳ A complete turn of the DNA double helix occurs every 10 base pairs
- ↳ Any sequence is possible with a single strand, but the other strand **MUST** be complementary

### The Structure of RNA

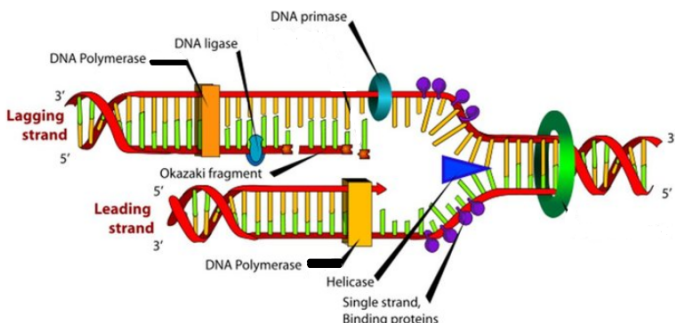
- ↳ RNA has the pentose sugar ribose instead of deoxyribose, and the base uracil instead of thymine
- ↳ RNA is single-stranded and can come in the form of either rRNA (ribosomal RNA), mRNA (messenger RNA), and tRNA (transmission RNA)

### DNA Replication

DNA replication is controlled by enzymes:

- ↳ DNA polymerase synthesizes a new strand of DNA
- ↳ DNA ligase - joins Okazaki fragments
- ↳ DNA helicase - 'unzips' the DNA strands (breaks the hydrogen bonds between bases)

SSB proteins are also involved in keeping the DNA strand from annealing during replication (SSB = Single-Stranded Binding proteins)



- 1) DNA helicase 'unzips' the DNA by temporarily breaking the hydrogen bonds between the bases
  - 2) DNA polymerase then moves in the 5' → 3' direction and uses activated nucleotides (nucleotides free in the cytoplasm with an extra phosphate group) to form a new DNA strand complementary to the template strand
  - 3) DNA polymerase then cleaves off one of the 2 phosphate groups and uses the energy released to create phosphodiester bonds (for the sugar-phosphate backbone) – hydrogen bonds form on their own between the bases
    - DNA polymerase can only work in the 5'-3' direction, so on one strand replication is continuous while, on the other strand, replication is discontinuous resulting in the production of a leading strand in the 5'-3' direction and a lagging strand in the 3'-5' direction. The fragments in the lagging strand are called Okazaki Fragments
  - 4) DNA ligase then runs along the lagging strand and forms phosphodiester bonds between the Okazaki fragments, completing the strand
- ★ This is an example of semi-conservative replication - the method by which a DNA molecule is copied to form 2 identical molecules each containing one strand of the original molecule and one newly-synthesized strand

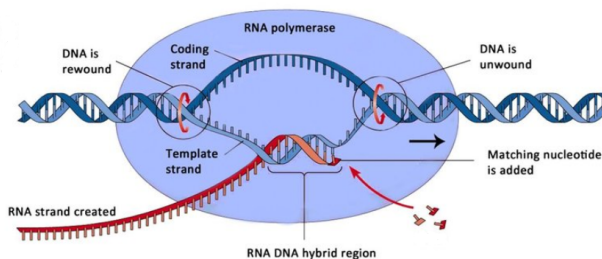
#### Features of the Genetic Code:

- L It is a triplet code, meaning 3 bases code for 1 amino acid. This triplet code is a non-overlapping code, for example, the code AAGTCGCGT can only be read as 'AAG', 'TCG', 'CGT', and not as 'AAG', 'AGT', 'GTC' etc.
- L DNA is a universal code meaning that the amino acid triplets are the same for all living organisms e.g. 'TTC' is one of the codes for lysine in humans, and it is the same in fish, chimpanzees, and every other living organism.
- L DNA is punctuated. It has 'stop' codes (ATT, ATC, & ACT) and a start code (TAC).
- L DNA is a degenerate code meaning that multiple different base combinations can be used for just 1 amino acid e.g. 4 triplet bases 'GAA', 'GAG', 'GAT', and 'GAC' all code for leucine.

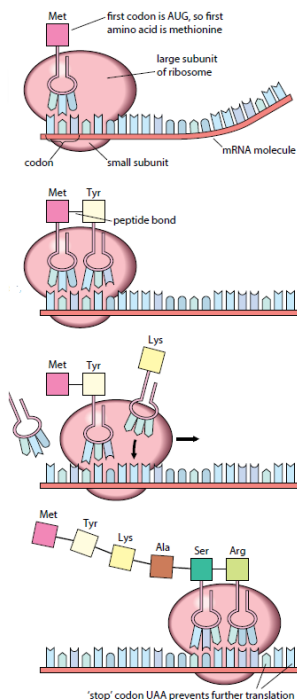
#### Protein Synthesis

##### Transcription - production of an mRNA molecule on DNA

- It occurs inside the nucleus



- L Part of the DNA double helix molecule unwinds and unzips as the hydrogen bonds between bases are broken by DNA helicase
- L Only one of the two DNA strands is selected as a template strand
- L Free RNA nucleotides pair with complementary bases on the template strand
- L RNA polymerase forms phosphodiester bonds between them to form a sugar-phosphate backbone
- L single-stranded mRNA molecule is formed
- L This strand leaves the nucleus through the nuclear pore



##### Translation - the production of a polypeptide at a ribosome from the code on the mRNA strand.

It occurs at the ribosome, outside the nucleus

- L Free tRNA molecules are activated by bonding with corresponding amino acids with the help of an enzyme (aminoacyl tRNA synthetases), as well as energy from ATP
- L mRNA binds to the small ribosomal subunit (6 bases at a time are exposed to the larger subunit)
- L Each tRNA molecule carries a specific amino acid and brings the correct acid to the ribosome
- L tRNA docks at the binding site on the ribosome
- L The anticodon on the tRNA binds with the complementary codon on the mRNA via complementary base pairing
- L A second tRNA molecule binds with the next codon. The two amino acids brought close together form a peptide bond. Once the peptide bond has formed, the first tRNA leaves the ribosome and can be reused. The next tRNA molecule attaches, and this process is repeated until the desired polypeptide is formed.

In prokaryotic cells, translation begins before transcription can even begin to finish. This is because the mRNA is not in the membrane-bound nucleus and is already exposed to the ribosomes.