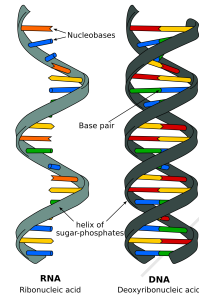
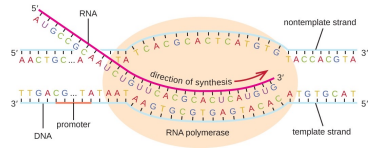


# Nucleic acids and protein synthesis

## DNA replication (S phase)

- semi-conservative replication
- after each DNA replication the end of each DNA molecule is shorter
  - the end-replication problem
- DNA double helix unwinds and the hydrogen bonds between the complementary bases break using DNA helicase
- both of the strands are used as the template and the complementary base pairing occurs between the template strand and free activated nucleotides
- adjacent nucleotides are joined by phosphodiester bonds formed in condensation reaction using DNA polymerase
- steps of replication
- only works in the 5' to 3' direction
- add nucleotide from 3' end of the new strand
- the leading strand is replicated continuously in the 5' to 3' direction
- DNA polymerase
- the second strand which is called the lagging strand is replicated discontinuously in the 5' to 3' direction and forming Okazaki fragments
- DNA ligase join the Okazaki fragment and the leading strand together



## nucleic acid

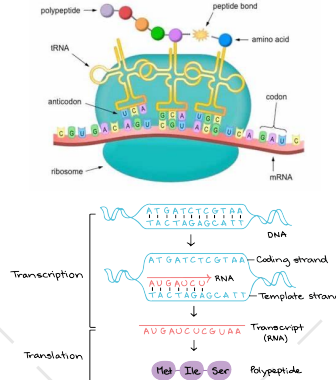
- monomer: nucleotide / polymer: nucleic acid
- ribonucleic acid (RNA)
  - pentose sugar
  - nitrogenous base
    - adenine (purine: two ring structure) complementary base pair with three hydrogen bonds
    - uracil (pyrimidine: single ring structure) complementary base pair with two hydrogen bonds
    - cytosine (pyrimidine) complementary base pair with three hydrogen bonds
    - guanine (purine) complementary base pair with two hydrogen bonds
  - phosphate group
- deoxyribonucleic acid (DNA)
  - pentose sugar
  - nitrogenous base
    - adenine (purine: two ring structure) complementary base pair with three hydrogen bonds
    - thymine (pyrimidine: single ring structure) complementary base pair with two hydrogen bonds
    - cytosine (pyrimidine) complementary base pair with three hydrogen bonds
    - guanine (purine) complementary base pair with two hydrogen bonds
  - phosphate group
- double helix and antiparallel
- Adenosine Triphosphate
  - $ATP + H_2O \rightleftharpoons ADP + H_3PO_4$  (enthalpy change = -30.5 kJ/mol)
- phosphodiester bond
- the ability to store information and can control the behavior of the cell
- the ability to copy itself accurately

## mutation

- change in DNA sequence
- substitution mutation
  - a base replaced by different base
  - sickle cell anaemia
    - CTT → CAT
    - hemoglobin
- deletion mutation
  - frame shift
- addition mutation
  - add a base
- non-sense mutation
  - mutation occurs on the non-coding region like introns

## protein synthesis

- transcription
  - take place in nucleus
  - RNA polymerase transcribe a segment of DNA
  - steps of transcription
    - the hydrogen bonds between the complementary bases break and the DNA uncoils, separating the two strands by DNA helicase
    - one of the DNA strands is used as a template to make the mRNA molecule which is called the template strand
    - free nucleotide bind to the exposed bases via complementary base pairing
    - adjacent nucleotide are joined by phosphodiester bonds to form mRNA by RNA polymerase
  - post-transcriptional modification
    - RNA splicing
    - RNA modification
- genetic code
  - a sequence of 3 consecutive nucleotides that codes for a specific amino acid
  - triplet codes
    - AUG → methionine — START codon
    - UAA / UAG / UGA — STOP codon
    - codon: RNA triplet
  - gene is a sequence of DNA nucleotide that can code for peptide
- transfer RNA
  - clover shape
  - anticodon region
  - amino acid arm
  - 61 different types of tRNA
- translation
  - made in nucleolus
  - ribosomal protein and rRNA
  - ribosome (80s)
    - large subunit: 60s / small subunit: 40s
    - mRNA strand bind to a ribosome
    - ribosome read the first codon
    - tRNA containing the complementary anticodon can bind to the codon forming complementary base pairs
    - a second tRNA binds to the second codon
    - the amino acid in the first codon forms peptide bond with the second amino acid with peptidyl transferase
    - the ribosome moves down the mRNA and continue to elongate the peptide chain until it reaches a STOP codon
  - steps of translation
- central dogma
  - DNA → mRNA → peptide / protein
  - virus: reverse transcriptase (RNA → DNA)



## DNA semi-conservative replication

