Nucleotides: structure and functions

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Composition of Nucleic Acids

Two types of nucleic acids:

RNA – ribonucleic acid - contains ribose

DNA – deoxyribonucleic acid - contains deoxyribose.

Nucleotide structure
Purine and pyrimidine bases found in DNA and RNA
Adenine is a purine base found in DNA and RNA. In nucleosides and nucleotides, adenine is linked to the sugar moiety via a covalent bond between nitrogen #9 of adenine and carbon #1 of the sugar. The ribonucleoside containing adenine is called adenosine. The deoxyribonucleoside containing adenine is called deoxyadenosine.
Nucleosides and nucleotides

**NUCLEOSIDES**

- Adenosine
- Guanosine
- Cytidine
- Uridine

**NUCLEOTIDES**

- Adenosine 5'-monophosphate (AMP)
- Guanosine 5'-monophosphate (GMP)
- Cytidine 5'-monophosphate (CMP)
- Uridine 5'-monophosphate (UMP)
Nucleotide features and functions

• Coenzymes
• Polyfunctional Acids (DNA)
• Role energy metabolism (ATP)
• Physiological mediators (cAMP)
• Activated intermediates (UDP glucose)
  • Absorb ultraviolet light
• Synthetic nucleotides are used in chemotherapy
Nucleotide Functions

Physiological mediators (cAMP)
Nucleotide Functions

Synthetic nucleotides are used in chemotherapy

Thymine

Fluorouracil
All the phosphodiester linkages have the same orientation along the chain, giving each linear nucleic acid strand a specific polarity and distinct 5` and 3` ends.

By definition, the 5` end lacks a nucleotide at the 5` position and the 3` end lacks a nucleotide at the 3` position.

Most often one or more phosphates may be present on one or both ends.
Composition of Nucleic Acids

Two types of nucleic acids:

- RNA – ribonucleic acid - contains ribose
- DNA – deoxyribonucleic acid - contains deoxyribose.
DNA:

Function:
Information storage - very stable

- **Structure:**
  - Long, linear polymers of nucleotides (millions)
    - Usually duplex,
    - Organized with proteins into the chromosomes when cell is dividing.
    - Loosely organized as chromatin in non-dividing cells.
Structure of DNA. DNA double helix - the Watson-Crick base pairing model (1953)

- A and T are matched between the two chains
- G and C are matched between the two chains
- Held together by hydrogen bonding of the bases.
- In DNA (A=T and G=C)

Watson-Crick Anti-Parallel Base Pairing
"The Double Helix"
Two hydrogen bonds form between A and T, while three form between G and C. The bases can pair in this way only if the two polynucleotide chains that contain them are antiparallel to each other.
Watson-Crick Model of DNA

- DNA consists of two helical DNA chains wound around the same axis to form a right-handed double helix.
- The hydrophylic backbones of alternating deoxyribose and phosphate groups are on the outside of the double helix, facing the surrounding water.
- The purine and pyrimidine bases of both strands are stacked inside the double helix, with their hydrophobic and nearly planar ring structures very close together and oriented vertically to the long axis.
- Each nucleotide base of one strand is paired in the same plane with a base of the other strand.
- The offset pairing of the two strands creates a major and minor grooves.
Denaturation of DNA

Two strands of the double helix separate when the **hydrogen bonds** between the paired bases are disrupted.

No **phosphodiester bonds** are broken by such treatment.
**RNA:**

**Function:**
- Information storage and transport (mRNA, viral RNA)
- Info transfer (tRNA)
- Catalysis - ribozymes
- Ribosome
- Regulation - Plasmid copy #, attenuation

**Structure:**
"Single-stranded" But actually lots of intramolecular base pairing to form globular arrangement of short helical structures.
- Primary: - Nucleotide sequence from RNA or DNA
- Secondary: - Watson Crick base pairs
  - Comparative analysis
  - Chemical and Enzymatic probes
  - Computer predictions
- Tertiary: - H-bonds, stacking
  - Crystallography
  - NMR (very few examples)
  - Comparative analysis
  - Crosslinking
tRNA Structure (secondary structure)

All tRNAs have similar sequences of 73 to 93 nucleotides

- 3' end *always terminates* with the sequence CCA, with the 3' hydroxyl of the ribose of the terminal A being the point of covalent attachment of the amino acid

- Contain a number (7-15%) of unique/modified bases. These are post-transcriptionally modified after synthesis by RNA polymerase.

- tRNAs have *cloverleaf* secondary structure due to four base-paired stems

- The cloverleaf contains three non-base-paired *loops*: D, anticodon, and TpsiC loop
tRNA Structure (tertiary structure)

- The tertiary structure of tRNA is best described as a compact "L" shape.
- The *anticodon* is a single-stranded loop at the bottom of the Figure which later base-pairs with the triplet codon.
- The amino acid is attached to the terminal A on the upper right.
- The active sites (*anticodon* and *amino acid*) are maximally separated.
- As in proteins, the tertiary structure is dictated by the primary sequence.
- The tertiary structure is stabilized by base pairing and base stacking.
- Two areas (*anticodon stem* and *acceptor stem*) form double helix.