I. Evidence that DNA is the genetic material

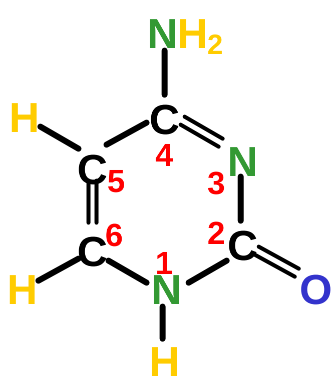
DNA must be able to store and express information, be replicated faithfully, and undergo mutation. It was thought that DNA was not complex enough to do this, so proteins must be the genetic material.

Griffith discovered **transformation**, which imparts genetic properties of one bacterial strain to another. Avery, MacLeod, McCarty showed that it is DNA that is the transforming agent.

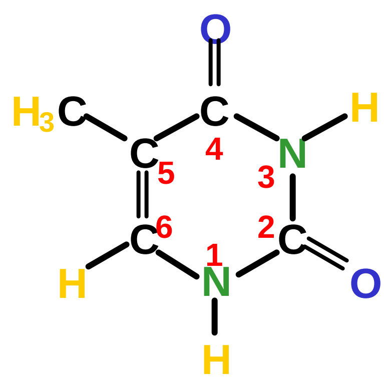
Hershey and Chase showed that the DNA component of phages (bacterial viruses) is transferred to the host during infection, but not the protein component.

II. Building blocks of DNA

bases: **pyrimidines**: 6-member ring, numbered 1-6

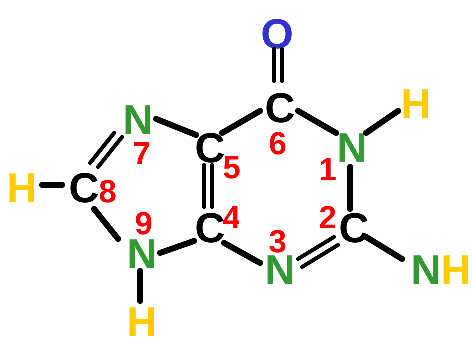


cytosine

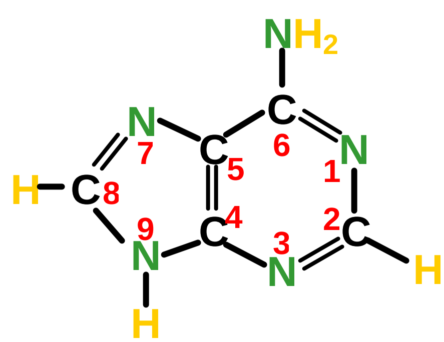


thymine

purines: double-ring of 9 atoms, numbered 1-9

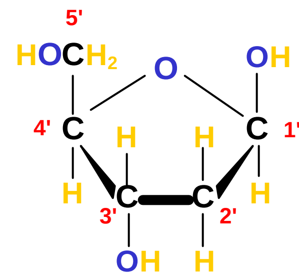


guanine



adenine

sugar **2'-deoxyribose** 5-atom ring with carbons 1' to 4' (the oxygen in the ring is not numbered); the 5th carbon (**5'**) is outside the ring, attached to the 4' carbon.

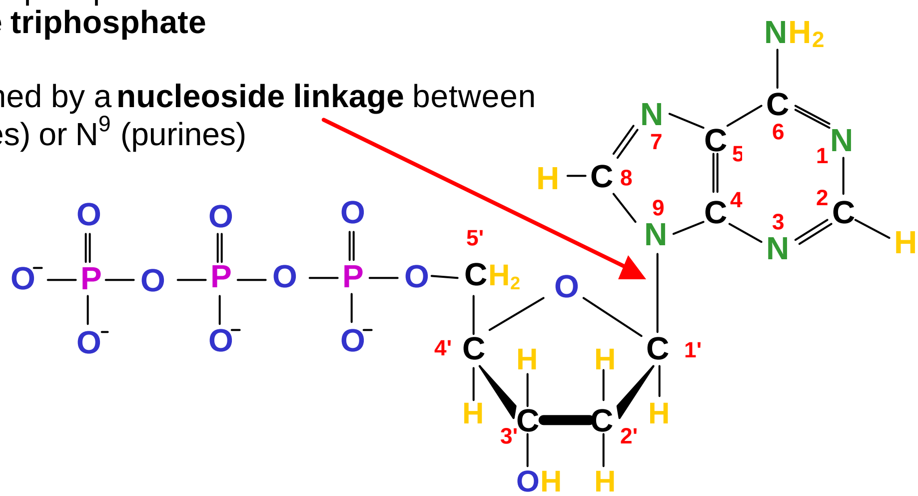


inorganic phosphate (PO_4^{3-})

nucleotide = sugar + base + phosphate(s) on $C^{5'}$

NMP = nucleotide monophosphate
NDP = nucleotide diphosphate
NTP = **nucleotide triphosphate**

The base is attached by a **nucleoside linkage** between $C^{1'}$ and N^1 (pyrimidines) or N^9 (purines)



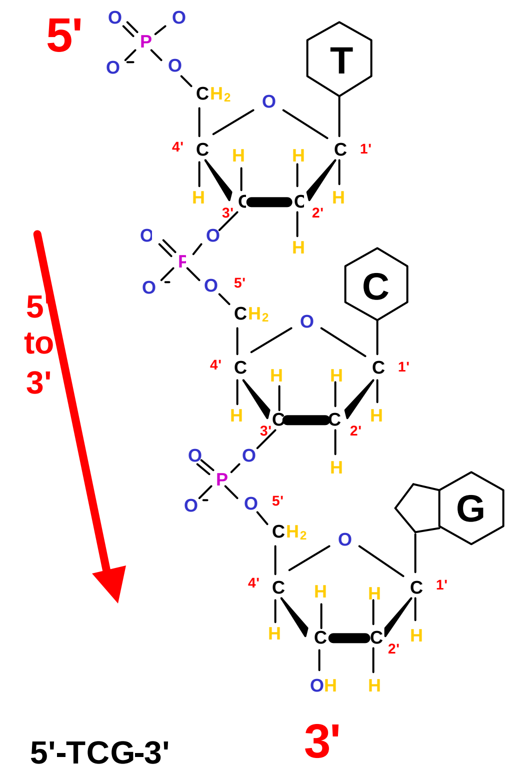
deoxyribonucleotides are denoted with the prefix "d", to distinguish them from **ribonucleotides** (present in RNA and used to provide energy):

ATP = adenosine triphosphate, the main energy storage source in the cell and a building block of RNA
dATP = deoxyadenosine triphosphate, a building block for DNA

III. Polynucleotide chains

A DNA strand is composed of nucleotides connected by **phosphodiester bonds** between the 5' carbon of one sugar and the 3' carbon of another.

A strand therefore has the 5' carbon free at one end (usually with a phosphate group) and the 3' carbon free at the other end (usually with a hydroxyl group). These are referred to as the **5' end** and the **3' end**, respectively.



IV. Clues to the arrangement of DNA strands

Chargaff: (1) pyrimidines always equal purines (C + T = A + G)
(2) T = A and G = C, but A + T may not equal C + G

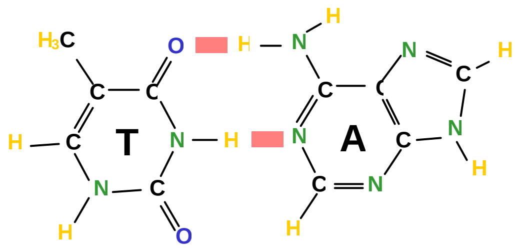
Franklin and Wilkins: X-ray crystallography suggested two components parallel to one another in a helix, to make a long, thin molecule

V. The Watson-Crick model

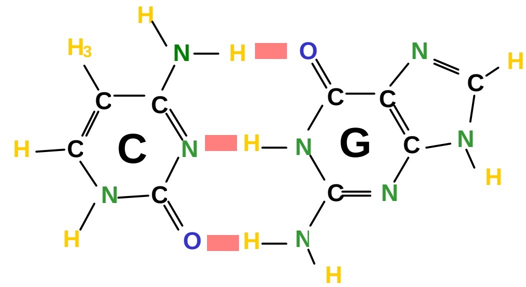
Watson and Crick proposed a **double helix**, with two polynucleotide chains. The sugar-phosphate backbone is on the outside, and the two strands are **anti-parallel**: The 5' end of one strand is opposite the 3' end of the other, so that they run in opposite directions.

The bases are on the inside of the double helix, and are paired through specific **hydrogen bonds**.

A pairs with T, with two H–bonds



G pairs with C, with three H–bonds



Therefore: Each **base-pair** (**bp**) has one purine and one pyrimidine.
G–C base-pairs are stronger than A–T base pairs.

VI. Implications of the structure of DNA

The two strands in DNA are **complementary**; given a base sequence for one strand, we can always write the sequence of the complementary strand.

Double-stranded DNA can be separated into single strands by **denaturing** with heat or alkaline conditions, or by **helicases**, enzymes that disrupt base pairing. Single strands of DNA will **anneal** or **hybridize** to complementary strands.

Genetic information is contained in the sequence of bases along a DNA strand.
Complementary base-pairing ensures accurate replication.
Mutations are alterations to the sequence of bases.