

## The DNA Helix and How It Is Read

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### DNA encodes for two types of information:

- extrinsic: triplet genetic code that specifies structure of proteins, actual structure of DNA does not matter, information carried via transcription and translation
- intrinsic: actual structure of DNA promotes binding of regulatory proteins (for example, *lac* and *lambda* repressors), regions of DNA (the operator) probably form hydrogen bonds with amino acids of regulatory proteins, local structure of DNA important for the identification of these sites

### Basic Structure of DNA:

- determined by x-ray diffraction from stretched natural DNA fibers
- double-ringed purines: adenine (A) and guanine (G)
- single-ringed pyrimidines: thymine (T) and cytosine (C)
- base pairs hydrogen bond across double helix: A forms 2 bonds with T, G forms 3 with C
- major and minor grooves since base pairs do not attach directly across from each other (see diagram on p. 96)

### Differences between A and B DNA:

- use of DNA oligomers (short strands of 4 to 24 bases) in single-crystal x-ray studies helps to determine smaller local variations
- B helix is probably most common form of DNA in nucleus: it is stabilized by hydrogen bonding with a layer of water around it, there is a "zigzag spine of hydration" in the minor groove due to A-T pairs; C-G pairs break up this spine of hydration
- helix probably changes into A form during transcription
- base inclination: tilt of the bases with respect to helical axis
- helical twist: angle from one base pair to the next (corresponds to base pairs per turn and helix rise per base pair)
- propeller twist: angle between planes of two opposite base pairs (p. 98); helps improve stacking of base pairs
- base roll: orientation of the plane of the base pair about its long axis

	A DNA	B DNA
relative humidity	75%	92%
general description	short and fat	slimmer and taller
groove depth	major much deeper	similar depth
base inclination (°)	13.0 +- 1.9	-2.0 +- 4.6
base pairs per turn	10.9	10.0
helix rise per base pair (Å)	2.92 +- .39	3.36 +- .42
helical twist (°)	33.1 +- 5.9	35.9 +- 4.3
propeller twist (°)	15.4 +- 6.2	11.7 +- 4.8
base roll (°)	5.9 +- 4.7	-1.0 +- 5.5

#### Discovery of Z DNA from Single Crystal Studies:

- synthesized short C-G copolymers
- left-handed helix with zigzag backbone
- quite thin and elongated: 12 base pairs per turn
- deep, narrow minor groove and very shallow major groove
- repeating unit really two base pairs: G-C and then C-G
- alternating *syn-anti* conformation (in A and B DNA all the conformations are *anti*); *syn*: guanine has its sugar ring rotated 180 degrees so that it is in towards the minor groove

#### How Code Contributes to Local Structure of DNA:

- floor of major groove has many nitrogen and oxygen atoms that can hydrogen bind with amino acids (minor groove offers less information)
- A-T pair offers a nitrogen atom (hydrogen acceptor), an NH<sub>2</sub> group (donor), and an oxygen atom (an acceptor)
- G-C pair offers a nitrogen atom (acceptor), an oxygen atom (acceptor), and an NH<sub>2</sub> group (donor) [these patterns can also be reversed]
- steric hindrance (especially in the minor groove) between large purine bases contribute to base roll, propeller twist, local helical twist, and other characteristics
- Dickerson's group has determined way to predict these characteristics based on local sequence (p. 111 shows correlation between the predictions and actual characteristics)
- since local sequence can determine localized variations on the DNA structure, these can intrinsically encode information, such as the binding site for a regulatory protein