

23. STRUCTURAL ANALYSIS AND CLASSIFICATION

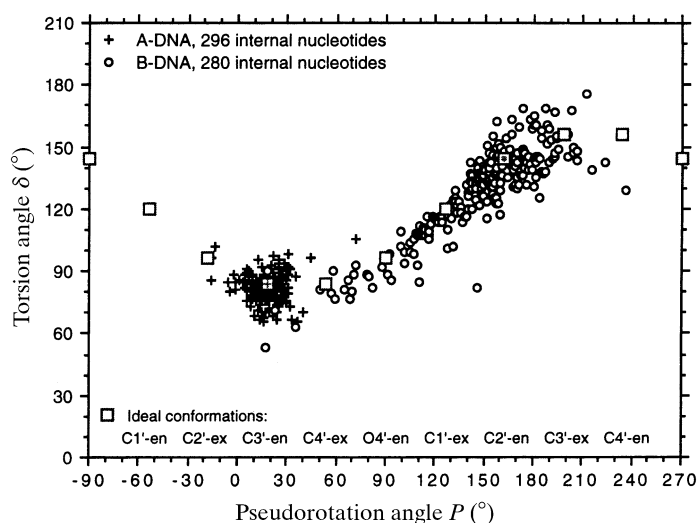


Fig. 23.3.2.6. Plot of observed sugar conformations in 296 nucleotides of A-DNA (crosses) and 280 of B-DNA (open circles). Open squares mark ideal relationships between torsion angle δ (vertical axis) and pseudorotation angle P (horizontal axis) from the expression $\delta = 40^\circ \cos(P + 144^\circ) + 120^\circ$. Deviations from this ideal curve for real helices arise, because the amplitude of pseudorotation (or displacement of one atom from the mean plane of the others) varies from one ring to another. Note the tight clustering of A-DNA points around C3'-endo and the broader distribution of B-DNA conformations.

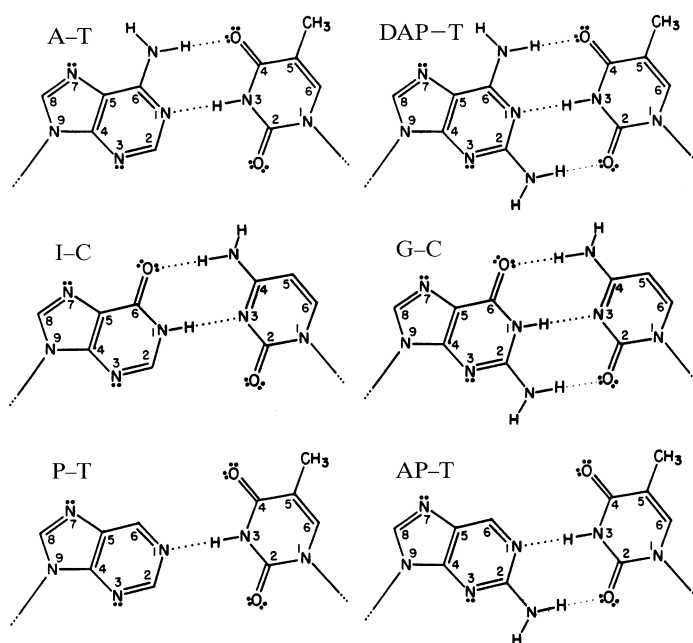


Fig. 23.3.2.8. Alternative purines and pyrimidines, and possible base pairings. Purines: P = purine; AP = 2-aminopurine; A = adenine or 6-aminopurine; DAP = 2,6-diaminopurine (also known as 2aA = 2-aminoadenine); G = guanine; I = inosine. Pyrimidines: T = thymine (uracil if methyl group is absent); C = cytosine. DAP-T is a nonstandard AT-family analogue of G-C, and I-C is a nonstandard GC-family analogue of A-T.

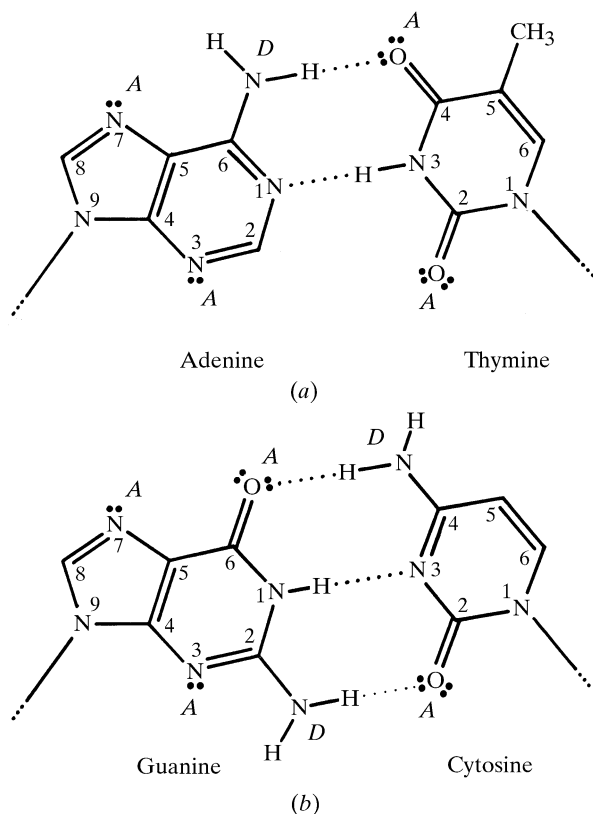


Fig. 23.3.2.7. A-T and G-C base pairs with minor groove edge below and major groove edge above. A is a hydrogen-bond acceptor, D is a hydrogen-bond donor.

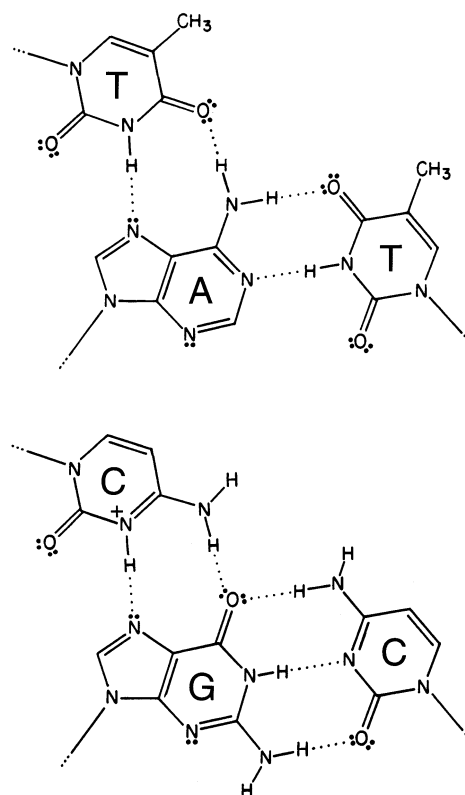


Fig. 23.3.2.9. Watson-Crick pairing of a purine (A or G) with a pyrimidine to its right (T or C), and Hoogsteen pairing of the same purine with a pyrimidine above it. This combination of Watson-Crick and Hoogsteen pairing is found in triple helices or triplexes. Note that Hoogsteen pairing of G and C can only occur at a pH at which C is protonated, because the extra proton is essential for the second hydrogen bond.