

23. STRUCTURAL ANALYSIS AND CLASSIFICATION

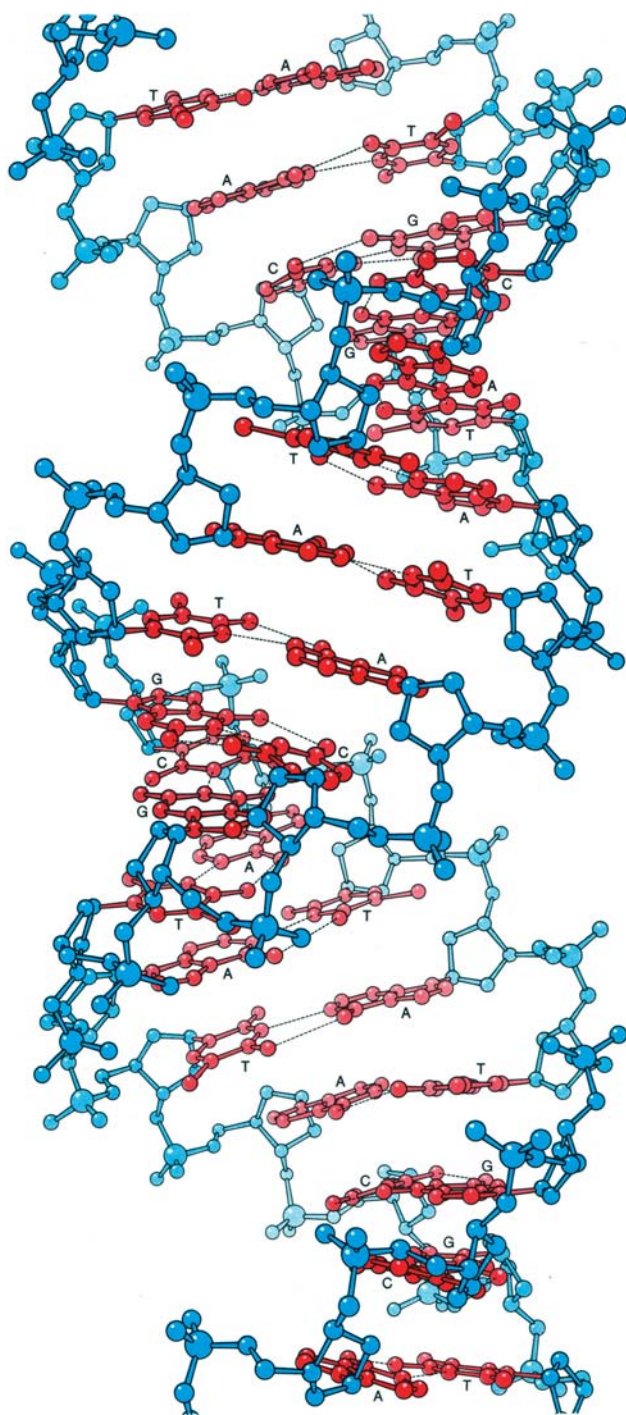


Fig. 23.3.1.2. Infinite A-DNA helix, generated from the X-ray crystal structure of the hexamer G-G-T-A-T-A-C-C (references A2 and A7 in Table A23.3.1.1) by deleting the outer base pair from each end and stacking images of the resulting truncated hexamer so their outer phosphate groups overlapped. This generates an endless helix that exhibits the local structural features of the X-ray crystal structure. Note the degree to which the A helix resembles an antiparallel double-stranded ribbon wound around an invisible helical core (the 'hot wire' axis of Fig. 23.3.1.1). (From Dickerson, 1983.) Reprinted courtesy of the estate of Irving Geis. Rights owned by Howard Hughes Medical Institute.

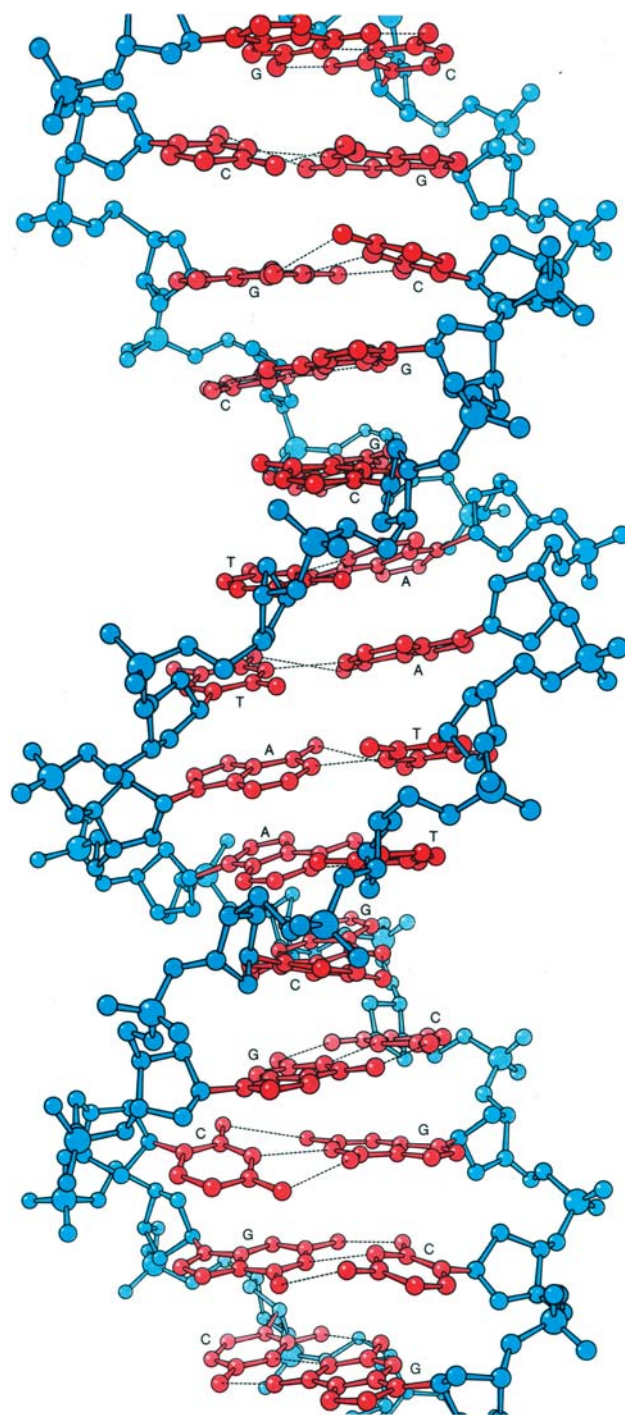


Fig. 23.3.1.3. Infinite B-DNA helix, generated in a similar manner to Fig. 23.3.1.2 from the central ten base pairs of the dodecamer C-G-C-G-A-A-T-T-C-G-C-G (B1-B5). Note that the minor groove is narrow in the AT region facing the viewer at the centre, but appreciably wider in the GC regions on the back side of the helix at top and bottom. Propeller twisting, or deviations of bases from coplanarity within one pair, is one sequence-dependent aspect of DNA that was not suspected from the averaged structures obtained from fibres. (From Dickerson, 1983.) Reprinted courtesy of the estate of Irving Geis. Rights owned by Howard Hughes Medical Institute.