five *exo*. In Fig. 23.3.2.4 (top), pushing the C3′ atom of the C3′-*endo* conformation into the plane of the ring would tend to push C2′ below the ring, passing through a T state and creating a C2′-*exo* conformation. C2′ can, in turn, be returned to the ring plane if C1′ is pushed above the ring, forming C1′-*endo*, and so on, around the ring. In this way, a contiguous series of alternating *endo/exo* conformations is produced, as listed in Table 23.3.2.2.

This ten-conformation *endo/exo* cycle can be generalized to a continuous distribution of intermediate conformations, characterized by a pseudorotation angle, *P* (Altona *et al.*, 1968; Altona & Sundaralingam, 1972), with the ten *endo/exo* conformations spaced 36° apart (Table 23.3.2.2). Fig. 23.3.2.5 shows the calculated potential energy of conformations around the pseudorotation cycle (Levitt & Warshel, 1978). Note that C2′-*endo* and C3′-*endo* are most stable, that the pathway between them along the right half of the circle remains one of low energy, but that a large 6 kcal mol^{-1} potential energy barrier (1 kcal mol^{-1} = 4.184 kJ mol^{-1}) effectively forbids conformations around the left half of the circle.

As Fig. 23.3.2.4 indicates, the main-chain torsion angle, δ, is sensitive to ring conformation, because the C5′—C4′ and C3′—O3′ bonds that define the angle shift as ring puckering changes. The idealized relationship between torsion angle, δ, and pseudorotation angle, *P* (Saenger, 1984), is

$$\delta = 40^\circ \cos(P + 144^\circ) + 120^\circ.$$

Fig. 23.3.2.6 shows the observed torsion angles, δ, and pseudorotation angles, *P*, from X-ray crystal structure analyses of synthetic DNA oligonucleotides: 296 examples from A-DNA and 280 from B-DNA. The most striking aspect of this plot is the radically different behaviour of A- and B-DNA. The prototypical sugar conformation for A-DNA obtained from fibre diffraction modelling, C3′-*endo*, is, in fact, adhered to quite closely in A-DNA crystal structures.

However, B-DNA shows a quite different behaviour. Although earlier fibre diffraction led one to expect C2′-*endo* sugars, the actual experimental distribution is quite broad, extending up the right-hand side of the pseudorotation circle of Fig. 23.3.2.5, through C1′-*exo*, O1′-*endo* and C4′-*exo*, in some cases all the way to C3′-*endo* itself. Indeed, the mean value of δ observed in B-DNA oligomer crystal structures is 128° rather than 144° (Table 23.3.2.1), making C1′-*exo* a better description of sugar conformation in B-DNA than C2′-*endo*. Old habits die hard, however, and the B-DNA sugar conformation is still colloquially termed C2′-*endo*, a designation of historical significance but of little practical value. The apparent greater malleability of the B helix compared to A may indeed be one feature that makes B-DNA particularly suitable for expressing its base sequence to drugs and control proteins *via* local helix structure changes.

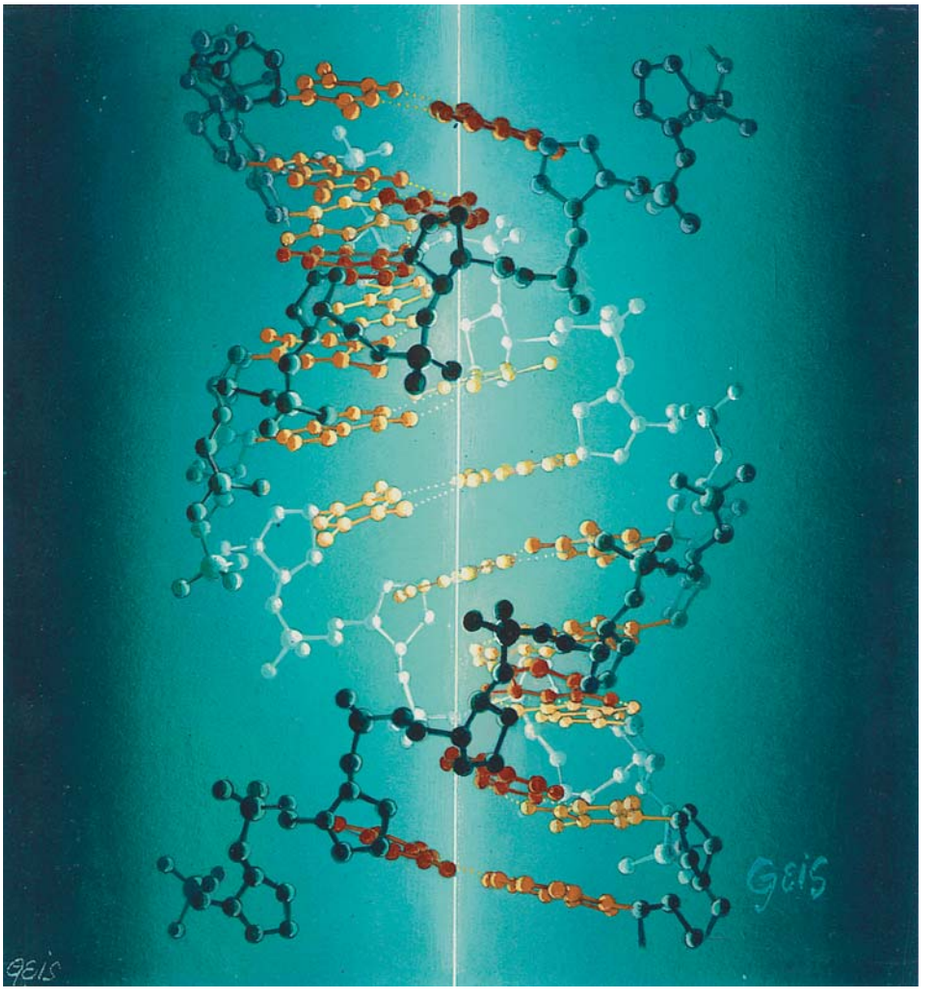

Fig. 23.3.1.1. 'Hot wire' painting of A-DNA by Irving Geis. Geis produced two dramatic paintings of horse-heart cytochrome *c*, in which the sole light source was the central iron atom within the haem, producing a glowing 'molecular lantern' effect. One painting showed this central luminous haem surrounded by hydrophobic side chains; the other featured the polar side chains extending out from the surface. These are to be seen today on the front and back covers of Voet & Voet's *Biochemistry* (Voet & Voet, 1990, 1995). In the present A-DNA painting, Geis chose the imaginary central axis of the helix as a monofilament light source, thereby reversing the conventional illumination: atoms lining the deep major groove glow brightly, whereas the outer surface of the helix is in dark silhouette. Geis struggled with the B helix as an artistic subject, but was never satisfied with the results. Hence, this glowing A-DNA helix represents his nucleic acid artistic legacy. Reprinted courtesy of the estate of Irving Geis. Rights owned by Howard Hughes Medical Institute.

23.3.2.3. *Base pairing*

The key to the biological role of DNA is that one of the two purines can pair with only one of the pyrimidines: A with T, and G with C. Hence, genetic information present in one strand is passed on to the complementary strand. The standard two-base pairs are shown in Fig. 23.3.2.7 along with the conventional numbering of the atoms. Backbone sugar and phosphate atoms are primed while base atoms are unprimed, as, for example, C1′ and N9 at opposite ends of a purine glycosydic bond. The G·C base pair is held together by three hydrogen bonds, whereas an A·T pair has only two. This means that A·T pairs show less resistance to propeller twisting (counter-rotation of the two bases about their common long axis), and this will have an effect on minor groove width, as seen later. The patterns of hydrogen-bond acceptors (*A*) and donors (*D*) on the major and minor groove edges of base pairs are important elements in recognition of base sequence by drugs and control proteins.

references