elastically deformable rod, the energy required for uniform bending is proportional to the rod length and inversely proportional to the square of the radius of curvature[7,8]. The proportionality constant can be evaluated from the persistence length of DNA in solution, and lies between 85 and 170 kcal Å mol^{-1} (refs 5, 8). This means that only 0.25–0.50 kcal of energy would be required per mol of dodecamer to produce the deformation seen in Fig. 1. As a comparison, the barrier to rotation about a single bond in ethane is nearly an order of magnitude greater, 3 kcal mol^{-1}. As crystal packing forces in proteins do frequently lead to different side-chain conformations in crystals where the asymmetric unit contains two molecules[9,10], such forces would be more than adequate to account for the observed curvature.

The probable origin of the crystal packing forces that produce the curvature is to be found in the association of neighbouring molecules up the 2_1 screw axis parallel to c as shown in Fig. 3. The molecules are not stacked on top of one another like cylindrical drums, instead they are staggered, with each molecule overlapping by three base pairs with its neighbours above and below. The overlap involves contact between minor grooves, with hydrogen bonds connecting ring N3 and amino N2 atoms in adjacent guanines from the two helices. (This pairing of guanines in the minor groove has been encountered in the structure of the complex of 9-ethylguanine and 1-methylcytosine[11], and has been proposed as a possible model for the recognition of guanine by asparagine or glutamine side chains of a protein (Fig. 3 of ref. 12).) Specifically, the N2 and N3 of guanine 14 in the upper molecule are hydrogen bonded to N3 and N2 of guanine 24 in the lower, and N2 and N3 of guanine 12 in the upper molecule are bonded to N3 and N2 of guanine 2 in the lower. However, base pairs in neighbouring molecules are sharply canted or tilted relative to one another by 35°, a tilt that brings the last base pair of one helix parallel to, and in packing contact with, the sugar–phosphate backbone of the other helix. The guanine N2 . . . N3 hydrogen bonds are twisted but not broken, and the tilted structure is locked into place by one more hydrogen bond—from the 3′-terminal OH of the upper helix in fig. 3 to the N2 of guanine 22 in the lower helix. The extra stability provided by these five bonds is more than enough to produce a 19° curvature in the helix axis. This interlocking of helix termini, a function of the CGCG sequences with which the molecule begins and ends, is probably also responsible for the unusual ease and rapidity with which crystals of CGCGAATTCGCG can be grown, in comparison with other DNA molecules whose crystallization has been attempted in our laboratory and elsewhere.

The contrast between major and minor from grooves can be appreciated from Figure 4, in which the molecule is viewed from diametrically opposed directions. The ratio of widths of major and minor grooves along the helix axis is almost exactly 7:4, and the minor groove gives, in this space-filling model, the impression of being quite constricted.

The mode of binding of *cis*-dichlorodiamino platinum (II) to DNA is of considerable medical interest because the complex shows promise as a carcinostatic agent in cancer chemotherapy[13,14]. The *cis*-Pt site in the dodecamer is in the vicinity of N7 and O6 of guanines 4 and 16 in the wide groove of the helix. As the *cis*-Pt complex is isomorphous with the native dodecamer only out to 4 Å resolution, it will be refined as an independent structural problem. The *trans*-Pt complex is even less isomorphous as judged by cell dimensions and intensity changes. All three refined structures will ultimately be reported, as a study of the mode of binding of platinum complexes to DNA.

CGCGAATTCGCG was originally synthesized as a substrate for the *Eco*RI restriction endonuclease. Its presence in solutions from which crystals of the endonuclease are being grown leads to a change in crystal form from that of the enzyme alone, fostering the hope that the crystals in the absence of Mg^{2+} contain an abortive binary complex of dodecamer and enzyme suitable for X-ray analysis. If Mg^{2+} is present, the dodecamer is cleaved well by the enzyme (J. Rosenberg, personal communication).

The B helix has been shown here to be the stable conformation of CGCGAATTCGCG in the crystalline state in salt conditions for which CGCG and CGCGCG adopt the left-handed Z configuration. Moreover, the value of 10.1 base pairs per turn and the propeller twist of bases indicate that this crystal structure is close to that which exists in solution. Although the bend in helix axis is probably induced by crystal packing, its presence illustrates the flexibility of the B-DNA structure, and the ease with which the molecule can be continuously deformed to wrap around objects such as the histone core in nucleosomes. Details of the hydration of B-DNA will be of interest as the transitions between B and other forms are generally considered to be a function of water activity[2]. These details, and any sequence-specific modifications of the uniform helix, will be matters of prime concern as refinement continues.

Note added in proof: Further refinement to an R factor of 17.8% has led to a regularization of the O5′-C5′-C4′-C3′ backbone torsion angles to a standard *gauche*⁺ (about +60°) conformation.

1. Wang, A. H.-J. *et al. Nature* **282**, 680–686 (1979).
2. Drew, H., Takano, T., Tanaka, S., Itakura, K. & Dickerson, R. E. *Nature* **286**, 567–573 (1980).
3. Jack, A. & Levitt, M. *Acta crystallogr.* A**34**, 931–935 (1978).
4. Wang, J. C. *Proc. natn. Acad. Sci. U.S.A.* **76**, 200–203 (1979).
5. Levitt, M. *Proc. natn. Acad. Sci. U.S.A.* **75**, 640–644 (1978).
6. Hogan, M., Dattagupta, N. & Crothers, D. M. *Proc. natn. Acad. Sci. U.S.A.* **75**, 195–199 (1978).
7. Schellman, J. A. *Biopolymers* **13**, 217–226 (1974).
8. Camerini-Otero, R. D. & Felsenfeld, G. *Proc. natn. Acad. Sci. U.S.A.* **75**, 1708–1712 (1978).
9. Tulinsky, A., Vandlen, R. L., Morimoto, C. N., Mani, N. V. & Wright, L. H. *Biochemistry* **12**, 4185–4192 (1973).
10. Takano, T. & Dickerson, R. E. in *Interaction Between Iron and Proteins in Oxygen and Electron Transport* (ed. Chien Ho) (Elsevier, Amsterdam, in the press).
11. O'Brien, E. J. *Acta crystallogr.* **23**, 92–106 (1967).
12. Seeman, N. C., Rosenberg, J. M. & Rich, A. *Proc. natn. Acad. Sci. U.S.A.* **73**, 804–808 (1976).
13. Khan, A. (ed. *Proc. 3rd int. Symp. Platinum Coordination Complexes in Cancer Chemotherapy*) Vols 1, 2 (Wadley Institutes of Molecular Medicine, Dallas, 1977).
14. Dorr, R. T. & Fritz, W. L. *Cancer Chemotherapy Handbook* (Elsevier, Amsterdam, 1980).

Corrigenda

The following acknowledgements should have appeared in the letter 'Endotoxin-induced uveitis in rats as a model for human disease' by J. T. Rosenbaum *et al. Nature* **286**, 611–613. 'This work was supported by grant AI 11313 from the NIH. J.T.R. was supported by a fellowship from the Arthritis Foundation.'

In the News and Views article 'X-ray astronomy with the Einstein laboratory' by J. L. Culhane *Nature* **284**, 509–510, reference was made to the 'Harvard Center for Astrophysics'. This should have read 'Harvard/Smithsonian Center for Astrophysics'.

In the News and Views article 'Between the galaxies' by M. G. Edmunds, *Nature* **284**, 213, it was erroneously suggested that the number of intergalactic hydrogen clouds discovered by Sargent *et al.* is considerably *higher* than for galaxies—the correct value was quoted, and the incorrect statement was based on an overestimate of the observed number density of galaxies. Nevertheless, the total mass of the clouds remains small compared with that in galaxies. The author apologises for this error.

In the article '*β*-Chain contact sites in the haemoglobin S polymer' by R. L. Nagel *et al., Nature* **283**, 832–834, the credit for Fig. 2 was omitted. Figure 2 was modified from *The Structure and Action of Proteins* by R. E. Dickerson and I. Geis (Benjamin/Cummings, Menlo Park, 1969).

Errata

In the letter 'Oscillation of $[Ca^{2+}]_i$-linked K^+ conductance in bullfrog sympathetic ganglion cell is sensitive to intracellular anions' by K. Morita *et al., Nature* **283**, 204–205, the column headings for Table 1 should read: 0.5, 1.0 and 3.0 (mM caffeine), not −, 0.5 and 1.0 mM.

In the news item 'Distorting the epidemiology of cancer: the need for a more balanced overview' by R. Peto, *Nature* **284**, 297–300, the caption to the figure on page 299 should have read: Data plotting for 39 countries age-standardized breast cancer death versus total dietary fat (animal or vegetable).