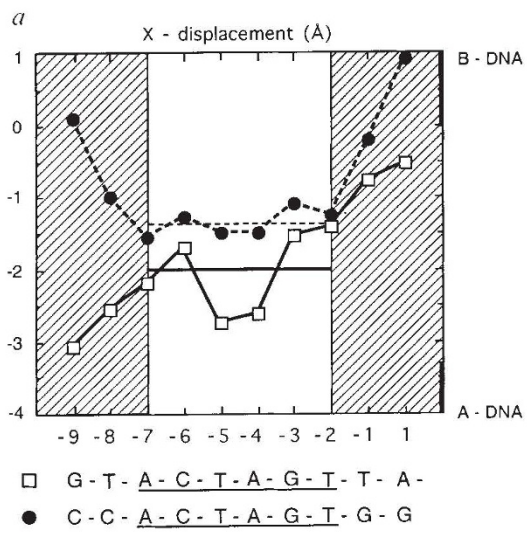
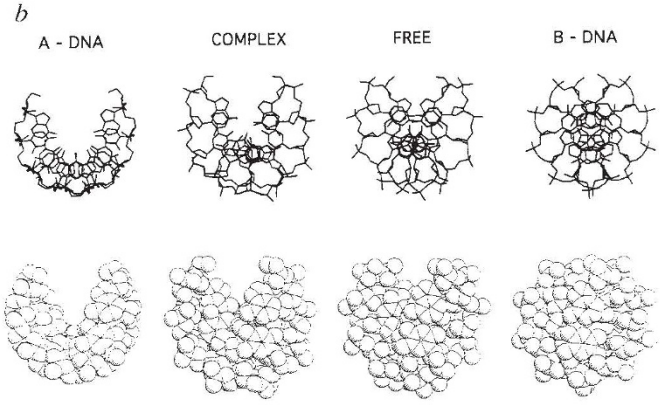


FIG. 2 *a*, X-displacement plots of the free decamer (circles) and the complexed operator (squares). X-displacement is the perpendicular distance from the C6–C8 vector of a base pair to the helix axis[14]. The numbering scheme for the DNA operator half-site is the one used previously and assigns zero to the dyad axis of the *trp* operator[1]. The top strand (from 5′ to 3′ direction and shown at the bottom of the figure) goes from −9 to 1 and that of the complementary strand (not shown) goes from −1 to 9. The same numbering scheme is used for the decamer. Calculations were done with NEWHEL93, provided by R. E. Dickerson. In the free decamer, the calculation of the overall helix axis was based on all 10 bp. In the complexed operator, the local helix based on 10 bp was derived for each of the four crystallographically independent half-sites and the displacement value for each base pair is an average of four independent values (s.d., 0.06–0.26 Å). The regions outside the central 6-bp segment are shaded. Horizontal lines show the corresponding mean values for the ACTAGT regions in the complexed target (continuous line at −2.0 Å) and the free target (broken line at −1.4 Å). The displacement patterns of the complexed and free ACTAGT regions are highly correlated (correlation coefficient, 0.9); that is, the relative displacement of each of the target's 6 bp with respect to its neighbours in the complexed operator is similar to that in the decamer. Whereas the free decamer has a nearly symmetrical pattern, the complex does not, particularly at the terminal base pairs, where asymmetry is imposed by the flanking base pairs and the interacting protein. *b*, Four conformations of the double-helical ACTAGT fragment viewed down the helix axis. Both stick and space-filling drawings are shown. The structures of A-DNA and B-DNA were derived from fibre-based coordinates[16] and are referred to as standard forms. The free structure is the central 6-bp segment in the crystal structure of the decamer. The complexed structure is represented by the corresponding segment in one of the four nearly identical half-sites in the crystal structure of the complex. The cavity down the helix axis is indicative of a deep major groove. The depth of the major groove in the complexed fragment is half way between that in A-DNA and B-DNA, and has been found in the crystal structure of a complex between DNase I and a DNA octameric oligonucleotide[21]. The decanucleotide conformation is intermediate between that of the complexed fragment and standard B-DNA. The projected gap between the two 5′ ends of the two strands is indicative of the degree of helical unwinding: 11 bp per turn for standard A-DNA, 10.9 for the complexed half-site operator, 10.6 for the same segment in the decamer, and 10 for standard B-DNA. The only other cases in which the helices are underwound (10.5 and 10.6 base pairs per turn) are the two DNA decamers CCAACITTGG and CGATCGATCG, which crystallize with packing similar to the present decamer[2,3]. But these two decamers and the *trp* 10-mer differ in their local conformations and other overall features: for example, the central 6-bp regions of the three helices (AACITT, ATCGAT and ACTAGT) show displacement patterns that are distinctly different. The average X-displacement values are −0.5, −0.6 Å and −1.4 Å, respectively, indicating that the deep major groove in the unbound *trp* hexamer is an intrinsic feature of the particular sequence.



ments, display similar features of structure and hydration. We conclude that these are intrinsic properties of this particular DNA target that contribute to its recognition by the *trp* repressor. □

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ERRATUM

High-affinity IgE receptor on eosinophils is involved in defence against parasites

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IN Fig. 4*a* and *b* of this letter, the ordinate axes were both labelled incorrectly: they should read "EPO index" and "ECP index", respectively. □