complex on the basis of the solution structure of the protein (Fig. 3) and data available from mutant studies on Arc and the homologous Mnt repressor[12–15], from methylation protection[15] and from phosphate ethylation interference experiments[16,17]. Arc binds to its operator as a tetramer (B. Brown and J. U. Bowie, cited in ref. 4). The model is shown in Fig. 4*a*, while Fig. 4*b* gives a more detailed view of the β-sheet/DNA interaction. Two Arc dimers bind in successive major grooves of the operator with the possibility of dimer–dimer contacts involving residues in the loop region between the two α-helices.

Specific protein–DNA contacts are known for Mnt repressor, which must bind to DNA in essentially the same way as Arc does. The best evidence for this comes from experiments in which a hybrid Arc–Mnt protein with the six N-terminal residues of Mnt replaced by the nine N-terminal ones of Arc was shown to have the DNA-binding specificity of Arc[13]. Also, the two-dimensional NOE spectra of Mnt indicate that the secondary structure and tertiary fold of Arc and Mnt are the same (M. J. M. B., unpublished results). Therefore, it is likely that contacts to base pairs 5 and 8 made by the Mnt residues His 6 and Arg 10, respectively[4], involve the homologous residues Gln 9 and Arg 13 in the case of Arc; these contacts can be formed in the model (Fig. 4*b*). Furthermore, the N-terminal heptapeptide is sufficiently flexible that it can account for the phosphate ethylation interference data for Arc (compare with Fig. 4*b*). A further contact found for Mnt repressor[15] between Arg 2 (equivalent to Ser 5 in Arc) and base pairs G·C 10 and C·G 11 is probably not present in Arc (ref. 17). Apparently, the conformation of N-terminal residues is different for Arc and Mnt repressors. We note that in the model shown in Fig. 4*b* the contacts of Glu 9 and Arg 13 are made by residues of the inner strands with respect to the dyad axis. For Arg 13 this seems to be the only possibility. Alternative models of the complex in which Glu 9 of the other strand contacts the DNA also seem less likely.

Arc, Mnt and Met repressors seem to be members of the same family of β-sheet DNA-binding proteins. In a recent database search for sequence homology with the Arc repressor[18], the Tra Y proteins of the F episomes and related episomes were found as further members of this family. Thus, the antiparallel β-sheet is the latest addition to a repertoire of structural motifs of DNA-binding proteins that includes the helix–turn–helix[5], zinc-finger[19] and leucine-zipper[20] domains. □

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ERRATA

The LDL receptor pathway delivers arachidonic acid for eicosanoid formation in cells stimulated by platelet-derived growth factor

A. J. R. Habenicht, P. Salbach, M. Goerig, W. Zeh, U. Janssen-Timmen, C. Blattner, W. C. King & J. A. Glomset

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AN error made during the reproduction of Fig. 3*c* in this letter resulted in the incorrect designation of symbols. These should be: □, PDGF; ○, PDGF+LDL; △, PDGF+AA. □

Cortical microstimulation influences perceptual judgements of motion direction

C. Daniel Salzman, Kenneth H. Britten & William T. Newsome

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IN this letter Figs 2 and 3 were transposed. Figure 2 is the two-part graph and Fig. 3 the histogram. □