

Scott, Foresman and Company

The cover illustration depicts the interaction between double helical DNA and the repressor protein complex from phage 434. The repressor is a dimer shown as an alpha-carbon backbone with one subunit in green and the other in yellow. The DNA is represented by a solvent accessible surface calculated considering all of the atoms in the DNA fragment. At the operator's site of interaction, the surface is cut away to reveal anti-parallel red helical tubes passing through the sugar carbon attachment point for each DNA base. The model is based upon the x-ray crystal structure of the complex between the 434 repressor and a 14-base pair operator sequence solved in the laboratory of Stephen C. Harrison at Harvard University. The curvature of the DNA around the repressor is observed in the crystal structure. The DNA model was extended beyond the operator region by joining it with standard model DNA segments on either end.

