The orphaned 3' terminal end in the minor groove of the adjacent duplex where it symmetrically pairs with the 5' terminal guanine to form a d(G(F.G.C)) base-pair. Our findings extend to the minor groove a DNA hydrogen bonding pattern which permits base-pair recognition during homologous recombination.

**PS04.04.16 PHASING IN DRUG-DNA SEQUENCE RECOGNITION: STRUCTURE OF A TRIS (BENZIMIDAZOLE) - DNA COMPLEX.** Stephen Neidle, George R. Clarkson, Emily J. Gray, Yu-Hua Li and Werner Leupin,  The CRC Biomolecular Structure Unit, The Institute of Cancer Research, Sutton, Surrey, SM2 5NG, UK. *Permanent address: Chemistry Department, University of Auckland, New Zealand

Effective recognition of a DNA sequence longer than ca 3-4 base pairs in length requires drug and base pairs to be in register along the complete length of the drug. We have studied this problem in the context of the crystal structure of a complex between a tris(benzimidazole) drug and the oligonucleotide duplex d(CGCAATTGCG). This has been determined to 2.2 Å resolution and refined to 1R of 17.4%. The drug is bound in the minor groove region and covers ca 7' base pairs. There is an extensive set of hydrogen bonds between the imidazole rings and N3/O2 atoms of the ATP base pairs. These have exceptionally high hydrogen-bonding register with the A:T base pair edges. The drug itself is highly twisted in order to achieve maximum hydrogen-bonding register with the A:T base pair edges. The DNA is deformed beyond what has been observed in other minor-groove drug crystal structures, with evidence of local helix unwinding and extension. These changes are necessary for effective DNA recognition of every benzimidazole sub-unit to take place, and thus for each to be in phase with base pairs.

**PS04.04.17 CRYSTAL STRUCTURE OF A 1:1 COMPLEX BETWEEN NETROPSIN AND d(CGCAATTGCG).** Christine M. Nunn, Neil Spink, Elspeth Garman, Stephen Neidle, CRC, Biomolecular Structure Unit, Institute of Cancer Research, 15 Cotswold Road, Sutton, Surrey, SM2 5NG, UK. *Laboratory of Molecular Biophysics, University of Oxford, Oxford, OX1 3QU, UK

DNA minor groove binding drugs such as netropsin, distamycin and pentamidine have been extensively studied bound to DNA dodecamers which contain a central AT-rich base-pair region. In this study the naturally occurring antibiotic netropsin has been co-crystallised with the DNA dodecamer d(CGCAATTGCG) and the structure determined to 2.4 Å resolution. The netropsin molecule displays AT specificity with hydrogen bonding contacts from the amide NH groups of netropsin to adenine N3 and thymine O2 atoms lying along the floor of the groove.

The crystal structure of native d(CGCAATTGCG) has been determined in two previous studies. Within the netropsin: DNA complex the central eight bases of each single strand form Watson-Crick base-pairs and duplexes of the type d(CGCAATTGCG), whilst the terminal 5'-C and G-3' bases are unpaired. The two terminal guanines of each single strand lie within the minor groove of a symmetry-related duplex with hydrogen-bonding interactions via guanine atoms N2 and N3 and atom O4' of the deoxyribose sugar to a C-G base-pair. The terminal unpaired cytosine bases lie within the major groove of adjacent duplexes to form base triplets of the type C-G-C with hydrogen-bonding interactions to a C-G base-pair.

2. See Poster by Wood, Nunn & Neidle.