Guanine-specific binding at an intercalated DNA junction. J.R. Hobbs (a), J.H. Thorpe (a), W.A. Denny (b), P. Charlton (c) and C.J. Cardin (a) (corresponding author) (a) Department of Chemistry, The University of Reading, Whiteknights, Reading RG6 6AD, UK. (b) Auckland Cancer Society Research Centre, Faculty of Medicine and Health Science, The University of Auckland, Private bag 92109, Auckland, New Zealand. (c) Xenova plc, 240 Bath Road, Slough, UK.

Keywords: proteins, nucleic acids.

Some DNA-intercalating tricyclic carboxamides have the unusual ability [1] to poison both topoisomerase I and topoisomerase II [2], the structurally diverse enzymes that may contribute to their unusual dual topoisomerase poisoning ability and their functionally distinct mode of action. The hemi-intercalative binding architecture is two such linked cavities. The DNA superhelix orientation with respect to histone-octamer, dinucleotide step identity, as well as more distant sequence- and environment.

 structural analysis has revealed the general mechanism for DNA-wrapping and provided insight towards the basis of sequence-dependent positioning and stability. Furthermore, in conjunction with the apparent plasticity observed for histone binding of identical sequences and the DNA distortions present in two NCP-constructs containing different 146 bp DNA's, we propose a model for histone octamer movement along the DNA superhelix.