

Table I Preliminary assessment of fit of A10 between DNA base pairs

Sequence	Fit in hydrogen bonding domain	Relative fit in topographical domain	Predicted relative activity*
5'-dTdT-3' · 5'-dAdA-3'	++ 1/2	60	85
5'-dTdC-3' · 5'-dGdA-3'	++	55	75
5'-dCdT-3' · 5'-dAdG-3'	++	55	75
5'-dTdG-3' · 5'-dCdA-3'	++	50	70
5'-dTdA-3' · 5'-dTdA-3'	++	45	65
5'-dCdG-3' · 5'-dCdG-3'	++	45	65
5'-dAdT-3' · 5'-dAdT-3'	++	35	55
5'-dGdC-3' · 5'-dGdC-3'	+	40	50
5'-dGdT-3' · 5'-dAdC-3'	+	35	45
5'-dCdC-3' · 5'-dGdG-3'	±	15	25

* Sum of components of fit.

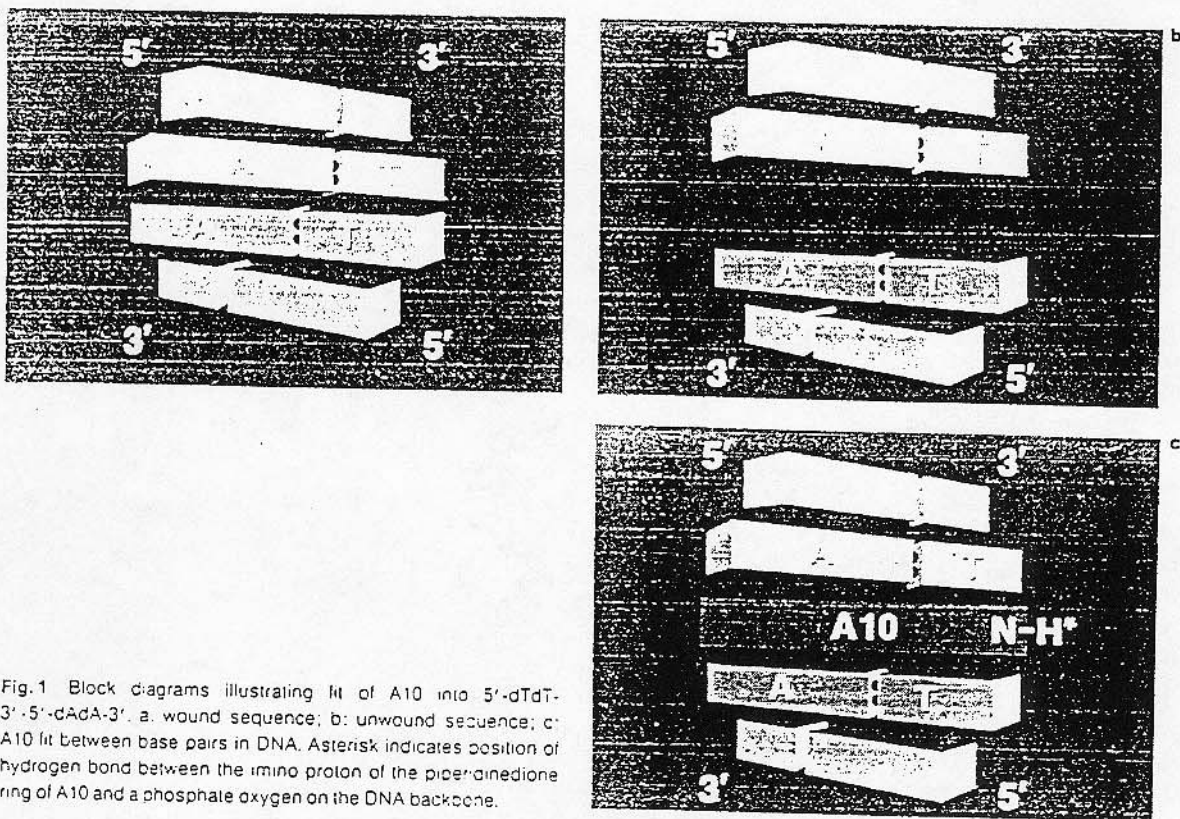


Fig.1 Block diagrams illustrating fit of A10 into 5'-dTdT-3' · 5'-dAdA-3'. a. wound sequence; b: unwound sequence; c: A10 fit between base pairs in DNA. Asterisk indicates position of hydrogen bond between the imino proton of the piperidinedione ring of A10 and a phosphate oxygen on the DNA backbone.