Graphs and structural representations relating to RNA research referenced as 'Dr Fuller'.

Contributors

Fuller, Watson, b.1935

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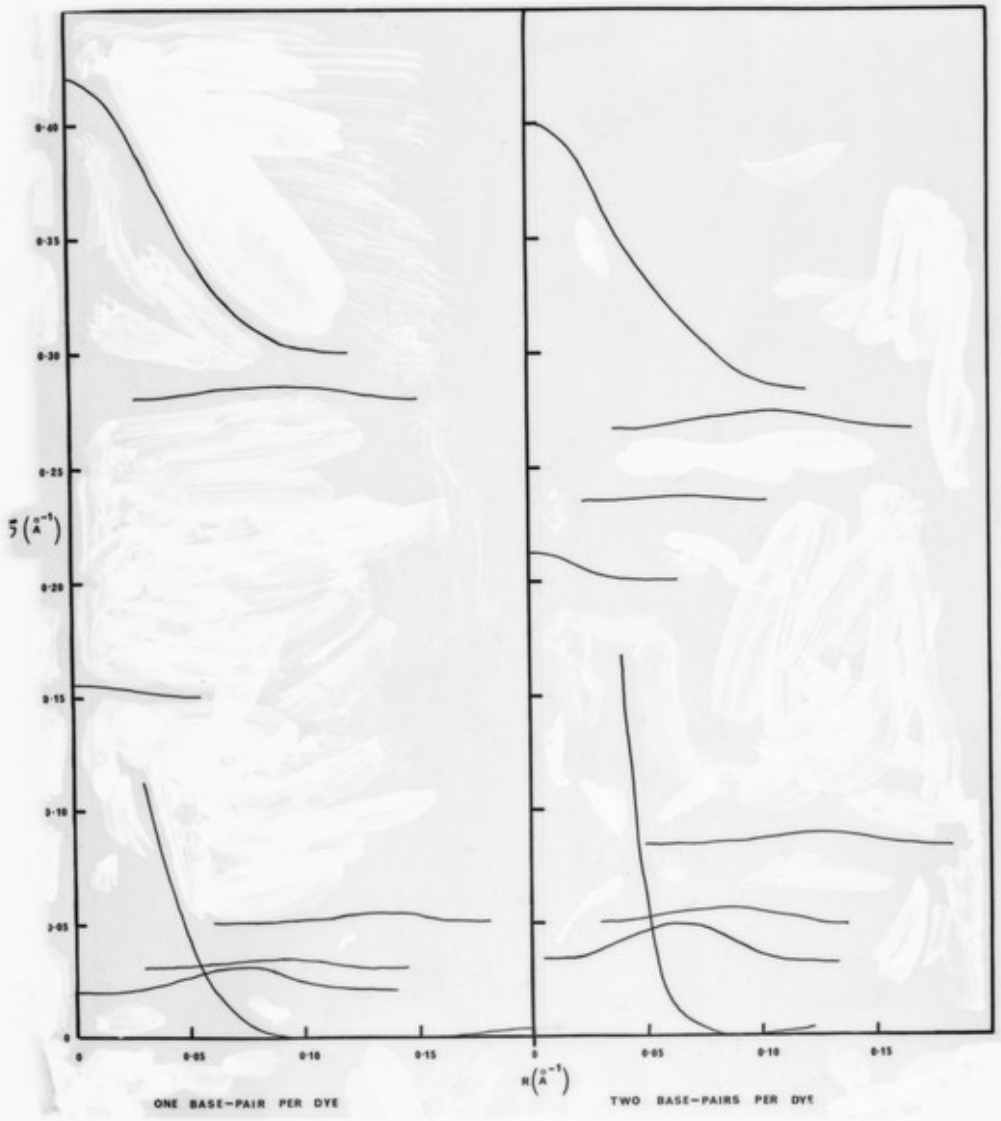
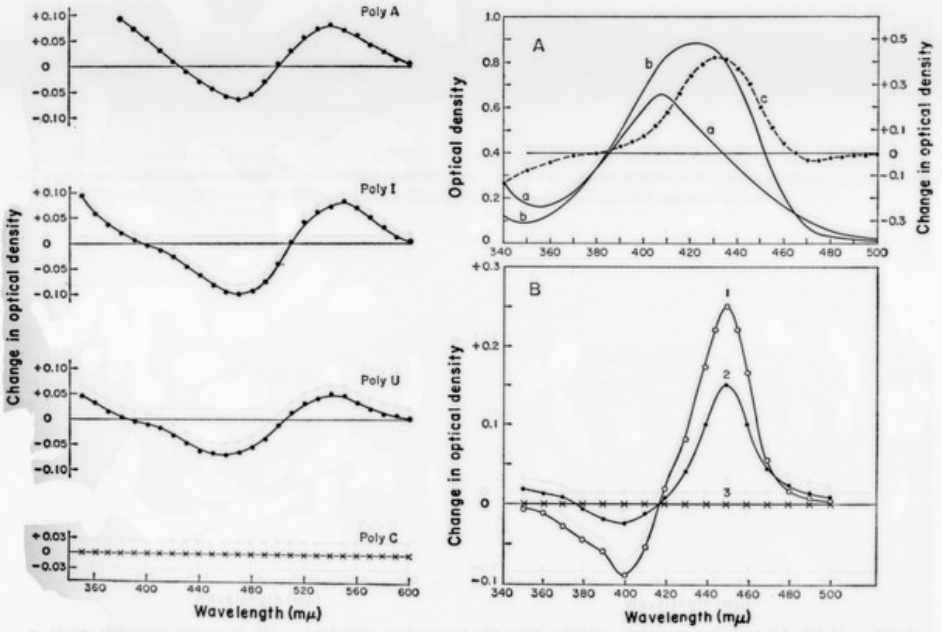
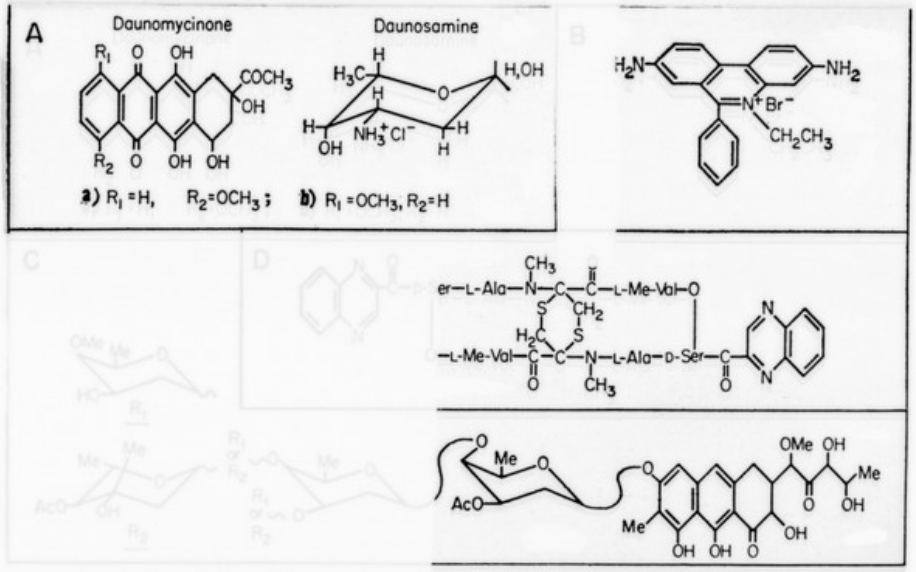

0·40
0·35
0·30
0·25
$S\left(\frac{a^{-1}}{A}\right)$
0·20
0·15
0·10
0·05
0
0
0·05
0·10
0·15
$R\left(\frac{a^{-1}}{A}\right)$
ONE BASE-PAIR PER DYE
TWO BASE-PAIRS PER DYE

flavine) forms complexes by intercala- cytidylic acids. The properties of these chromophores and sugar components tion between adjacent base pairs of complexes of ethidium with mono- (32). Their tumor-inhibiting propertie

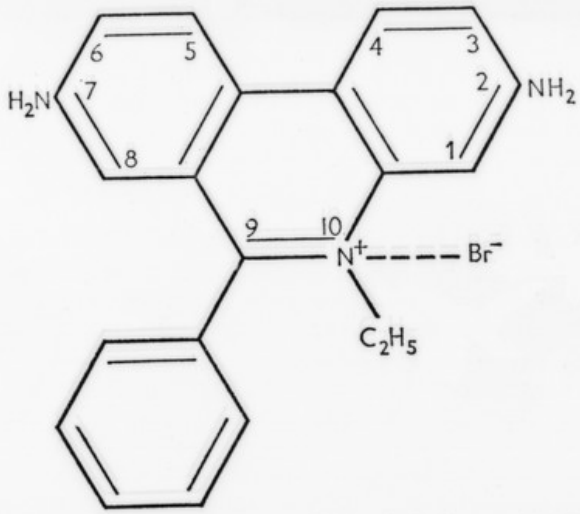


(left). Difference spectra of ethidium solutions read against the same solutions containing polyA, polyI, polyU, and polyC. All measurements were made in 0.1*M* tris-HCl, *p*H 7.9. The concentrations of reactants were: ethidium, 40 μg/ml (100 mμmole/ml) (optical density at 480 mμ = 0.54 1-cm light path); polyA, polyI, polyU, and polyC, 400 μg/ml. Fig. 5 (right). *A*, Effect of Mg^{++} on the spectrum of chromomycin A_3. Curve *a*, chromomycin (100 mμmole/ml) in 0.01*M* tris-HCl, *p*H 7.4, containing 0.01*M* NaCl. Curve *b*, the same, with added $MgCl_2$ (0.05*M*). Curve *c*, the difference spectrum resulting from the addition of $MgCl_2$. *B*, Effect of Mg^{++} on the interaction of chromomycin with DNA. Difference spectra of chromomycin solutions (100 mμmole/ml) read against the same solutions containing DNA (425 mμmole/ml). Curve *1*, native calf-thymus DNA. Curve *2*, heat-denatured calf-thymus DNA in 0.01*M* tris-HCl, *p*H 7.4-0.01*M* NaCl containing 0.03*M* $MgCl_2$. Curve *3*, same as curve *1*, but without $MgCl_2$



Structures of *A*, daunomycin (*35*) (R_1 and R_2 may be as in *a* or *b*); *B*, ethidium bromide (*36*); *C*, chromomycin A_3 (*37*); and *D*, echinomycin (*38*). Nogalamycin is similar in structure to daunomycin, possessing a tetracycline-like chromophore linked to an amino sugar. Olivomycin and mithramycin are closely related to chromomycin, differing by minor variations in their chromophores and sugar components (*32*).

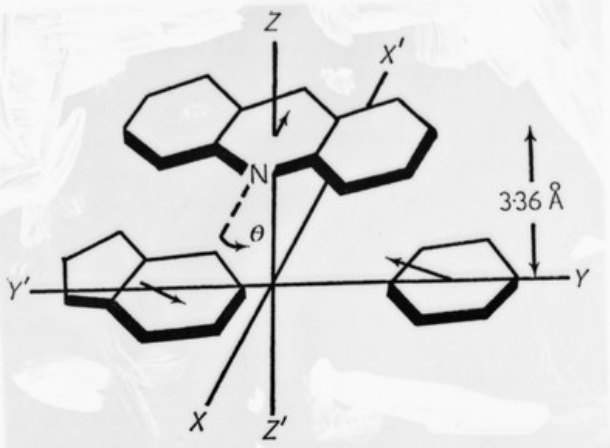
dependent RNA polymerase (see below) have been used to interpret the



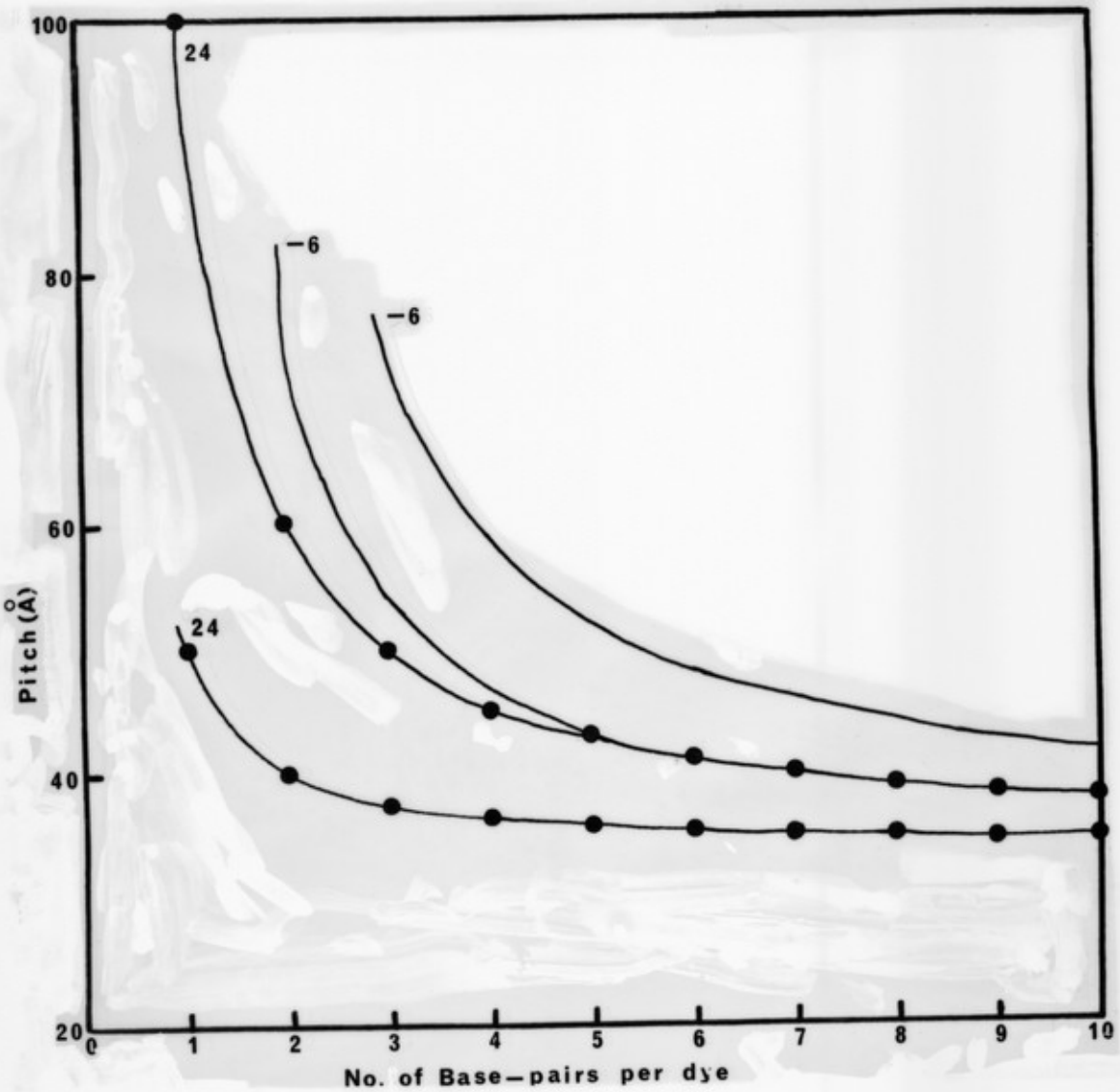
Ethidium bromide: 2:7 diamino-9-phenyl-10-ethyl phenanthridinium bromide.

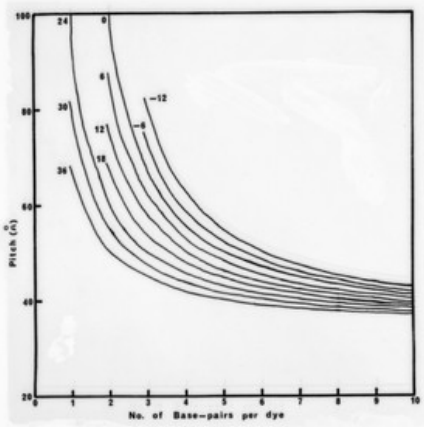
(a) *Nucleic acid preparations*

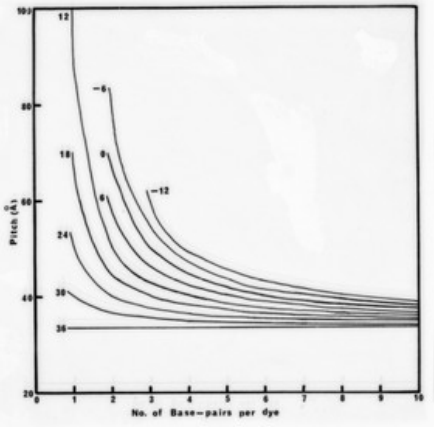
occus lysodeikticus DNA was prepared from spray-dried cells (California C
r Biochemical Research) according to the method of Marmur (1961). After 3



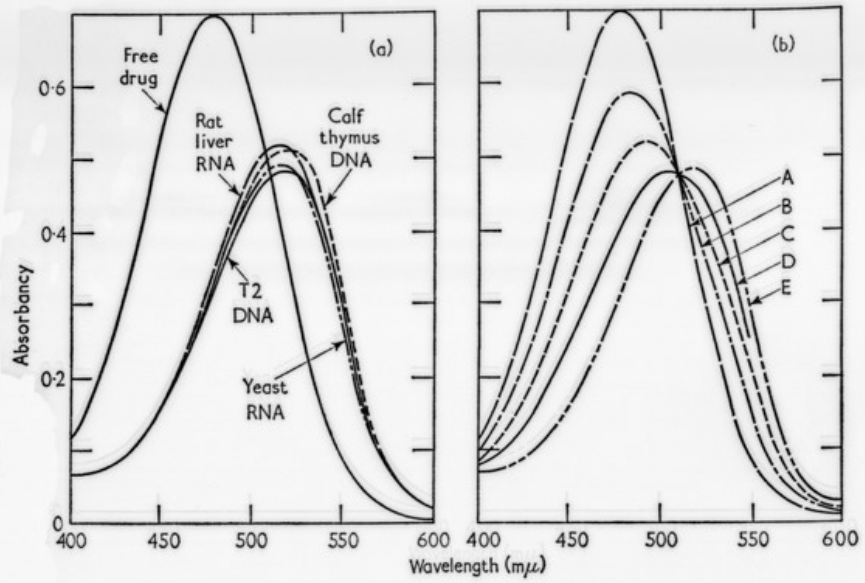
Relative positions of an adenine–thymine base pair and an aminoacridine molecule, as used in the free energy calculations for the intercalated model (I). The skeletons of the molecules are shown and no amino or carboxyl groups are indicated, the ring nitrogen only of the dye being shown. The three dipole moments are represented by short arrows and are not drawn to scale.


100
80
60
40
20
Pitch (Å)
24
-6
-6
24
0
1
2
3
4
5
6
7
8
9
10
No. of Base-pairs per dye


Pitch (Å)
No. of Base-pairs per dye
24
30
36
0
6
12
18
-12
-6


Pitch (Å)
No. of Base-pairs per dye
12
18
24
30
36
-6
-12
9
6

mμ. This effect is evident as a change in colour from yellow-orange to bright pink. Figure 1(a) shows the results when the nucleic acids are present in excess, that is to say, further additions produce no significant change in the spectrum of the drug. Minor diff[redacted] nucleotides, but [redacted]



Effect of nucleic acids on the absorption spectrum of ethidium bromide. Solutions contained $1{\cdot}25\times10^{-4}$ M-ethidium bromide and the absorbancy was measured using a 1-cm light path. In panel (a) the concentration of each nucleic acid was $1{\cdot}5\times10^{-3}$ M. In panel (b) T2 DNA was present at the following concentrations: curve A, zero; B, $1{\cdot}5\times10^{-4}$ M; C, 3×10^{-4} M; D, 5×10^{-4} M; E, $1{\cdot}2\times10^{-3}$ M.

[redacted] increasi[redacted]s of [redacted] tion spectrum of ethidium bromide. The peak can be seen to shift progressively towards a limit (curve E) which represents the spectrum of the drug in a fully complexed form. All the curves pass through an isosbestic point at 510 mμ, indicating that they result from the contributions of two forms of ethidium, free and bound, each

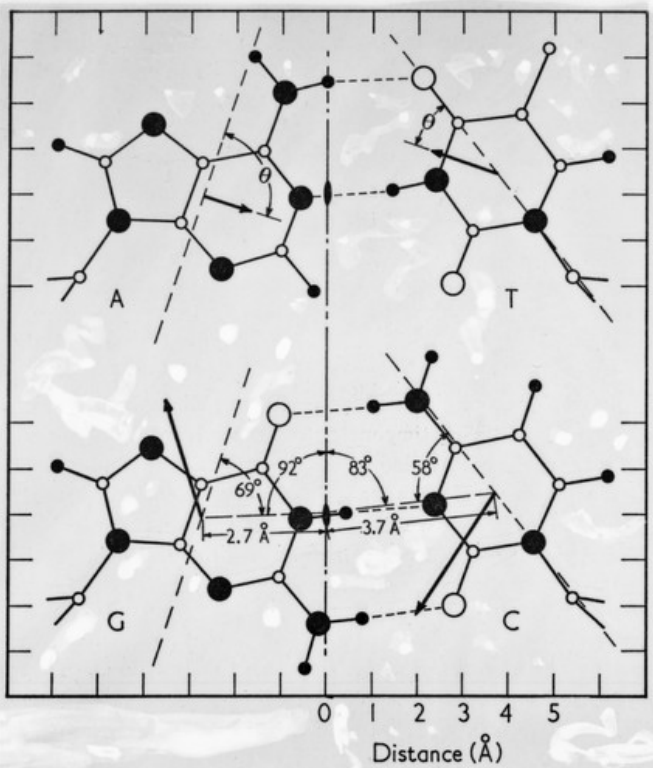
TABLE 3

Comparison of calculated free energy values (in kcal. per repeating unit) for native DNA, model I and model IIa

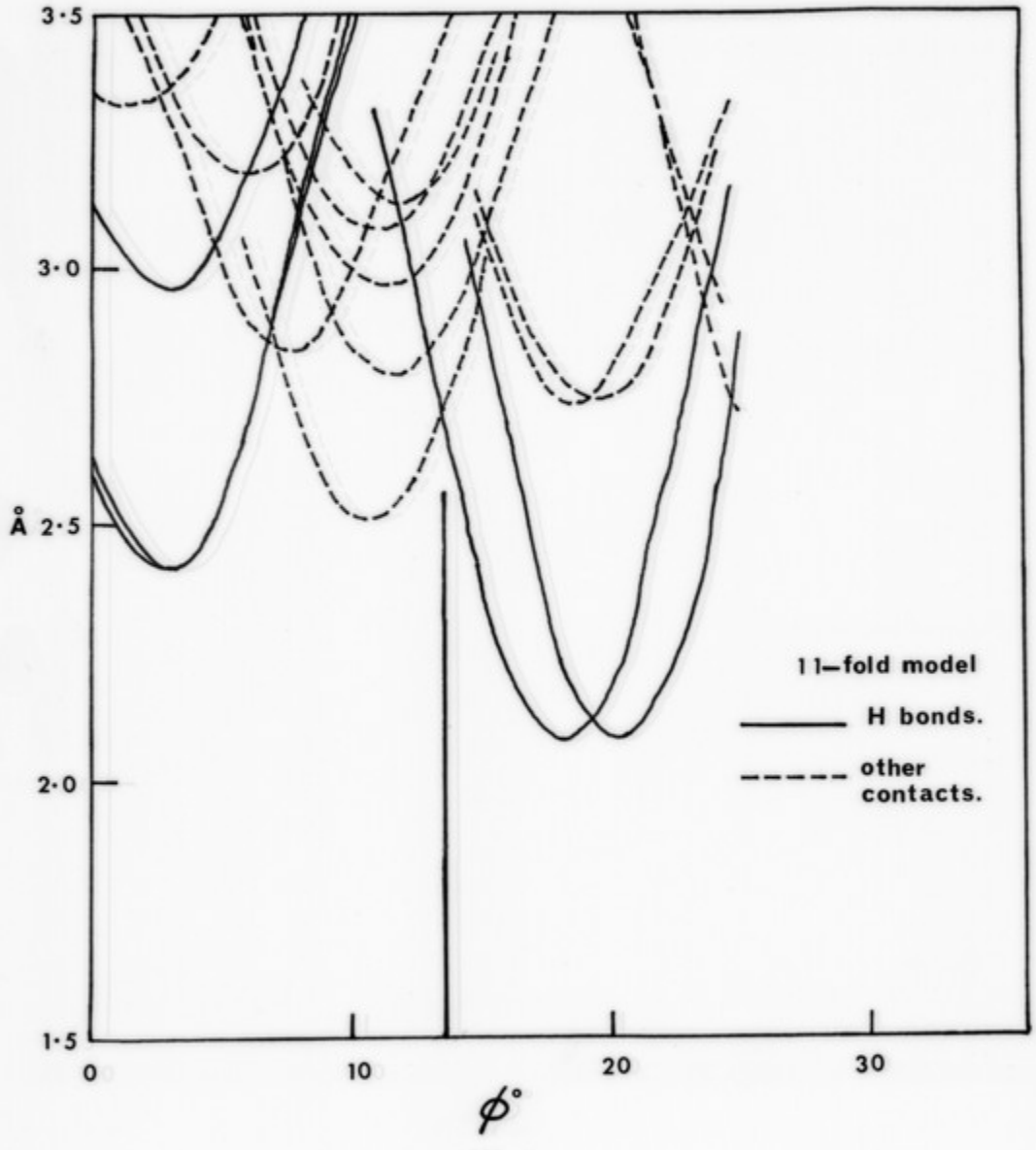
Repeating unit	De Voe & Tinoco (1962) for native DNA	Proflavine intercalated, model I		External attachment of proflavine, model IIa			
	$\epsilon_{ij} = 1{\cdot}0$	$\epsilon_{ij} = 1{\cdot}0$		$\epsilon'_{ij} = 10$		$\epsilon'_{ij} = 35$	
	F_{total}	F_{total}	ΔF	F_{total}	ΔF	F_{total}	ΔF
CG GC	− 35·7	− 48·3	− 12·6	− 39·6	− 3·9	− 36·9	− 1·2
GC GC	− 19·9	− 48·0	− 28·1	− 23·8	− 3·9	− 21·1	− 1·2
TA CG	− 20·5	− 55·3	− 34·8	− 24·4	− 3·9	− 21·7	− 1·2
AT CG	− 13·7	− 55·3	− 41·6	− 17·6	− 3·9	− 14·9	− 1·2
AT GC	− 12·9	− 55·2	− 42·3	− 16·8	− 3·9	− 14·1	− 1·2
TA GC	− 12·5	− 55·2	− 42·7	− 16·4	− 3·9	− 13·7	− 1·2
GC CG	− 7·5	− 48·2	− 40·7	− 11·4	− 3·9	− 8·7	− 1·2
TA AT	− 10·6	− 62·7	− 52·1	− 14·5	− 3·9	− 11·8	− 1·2
AT AT	− 10·2	− 62·7	− 52·5	− 14·1	− 3·9	− 11·4	− 1·2
AT TA	− 3·4	− 62·6	− 59·2	− 7·3	− 3·9	− 4·6	− 1·2

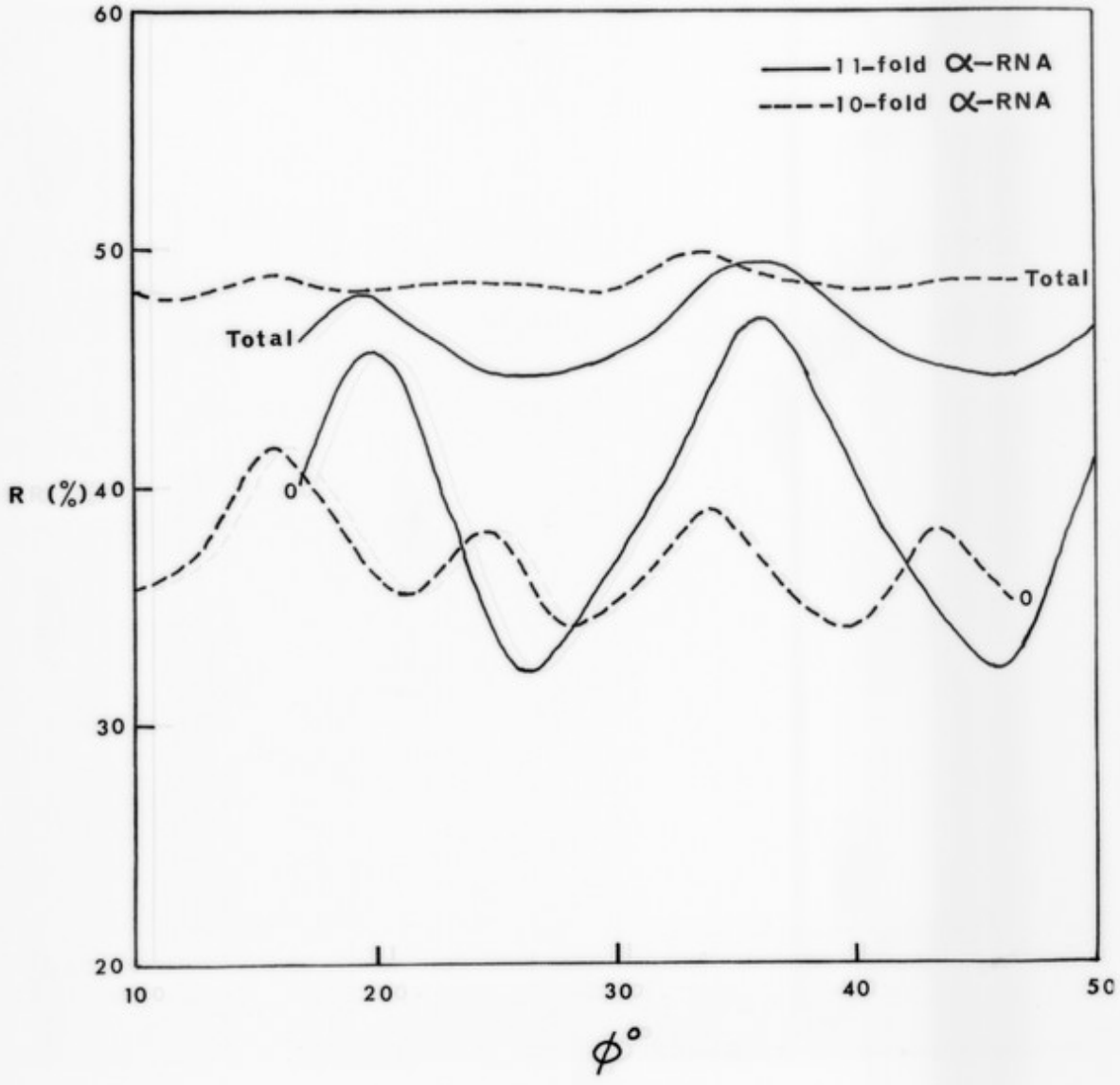
The repeating unit shown is for DNA. Those for the DNA–proflavine complexes are those indicated in Fig. 3 with the appropriate base pairs. See text for explanation of the values chosen for ϵ_{ij} and for ϵ'_{ij}.

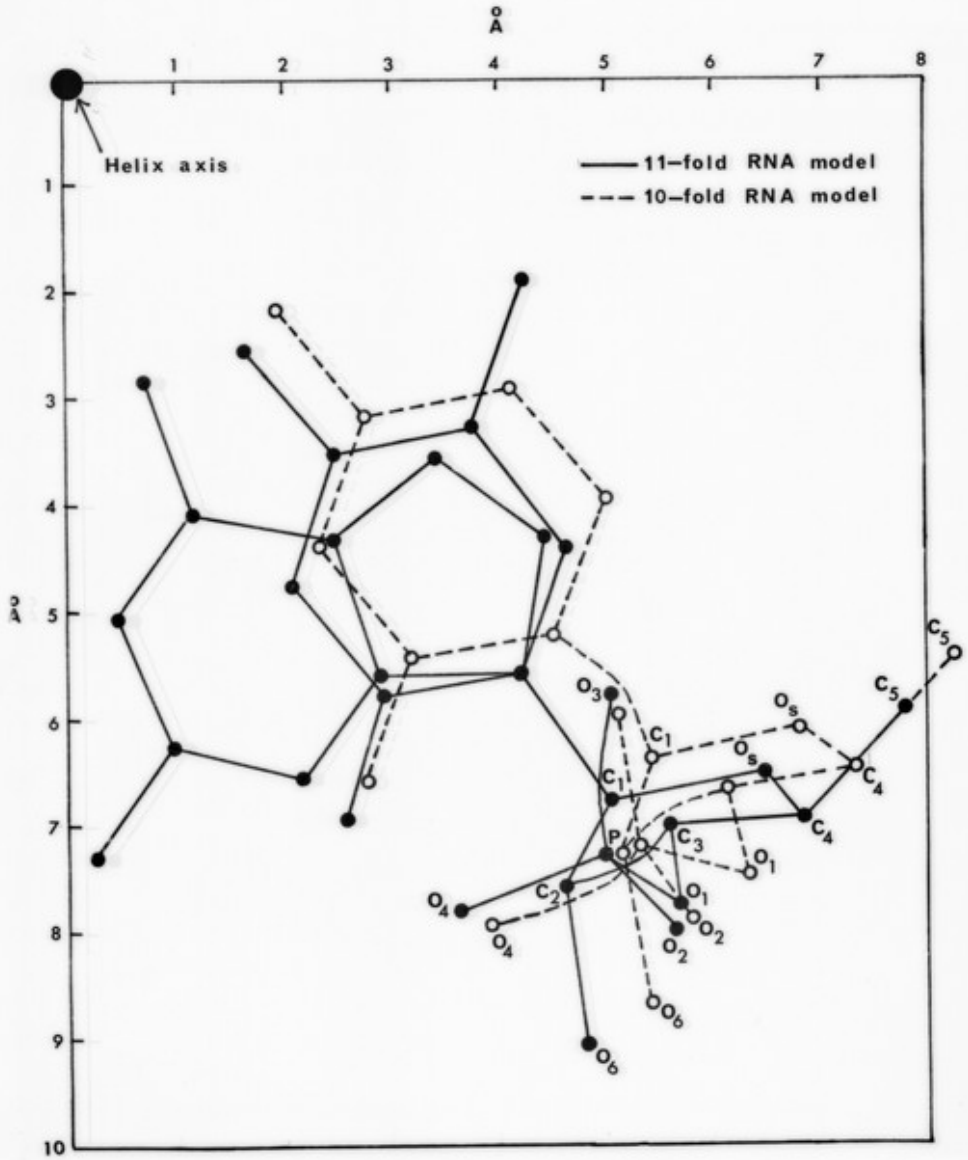
of the intercalated model I. For this model, strong binding would be predicted, on the basis of the results in Table 3, up to $r = 0{\cdot}5$, whereas experimentally it is found that

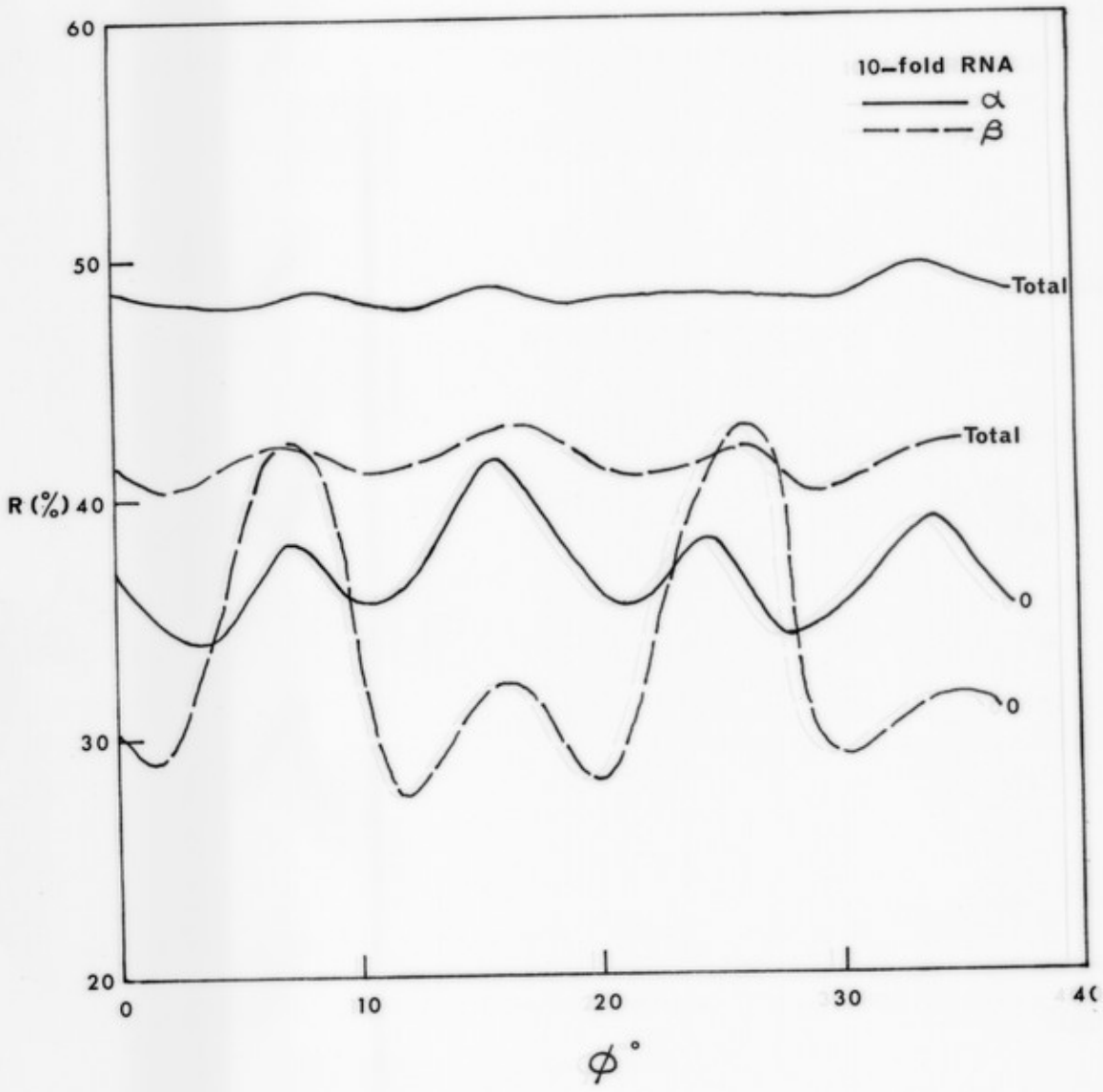


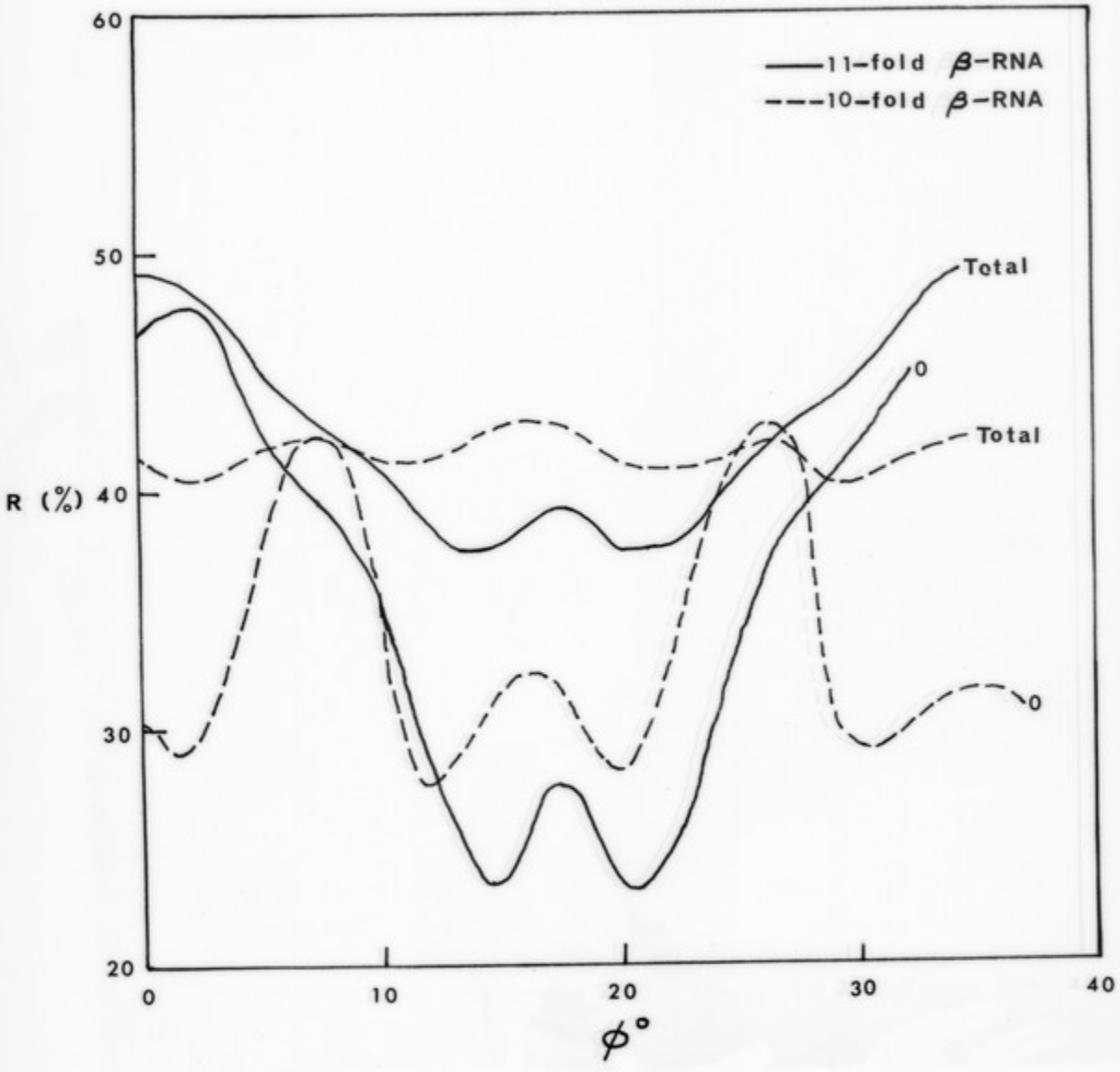
Atom positions in the AT and GC base-pairs of DNA. The figure is in the plane of the bases and of the dyad axis (— - —) and is perpendicular to the helix axis. The calculated dipole moment of each base is drawn to scale, with the positive end located at the position of the point dipole used in the energy calculations. The dipole orientation angle θ is defined. Atom symbols: ● nitrogen. ○ oxygen. ● hydrogen. ○ carbon.


3·5
3·0
Å 2·5
2·0
1·5
0
10
20
30
φ°
11–fold model
H bonds.
other contacts.


11-fold α-RNA
10-fold α-RNA
Total
Total
0
0
R (%)
60
50
40
30
20
10
20
30
40
50
φ°


Å
1
2
3
4
5
6
7
8
Helix axis
11–fold RNA model
10–fold RNA model
Å
1
2
3
4
5
6
7
8
9
10
O3
C1
Os
C5
C4
C3
P
O1
O2
C2
O4
O6


10–fold RNA
α
β
Total
Total
0
0
R (%)
60
50
40
30
20
0
10
20
30
40
φ°


11-fold β-RNA
10-fold β-RNA
Total
0
Total
0
R (%)
60
50
40
30
20
0
10
20
30
40
φ°