

$$L_k = 42$$

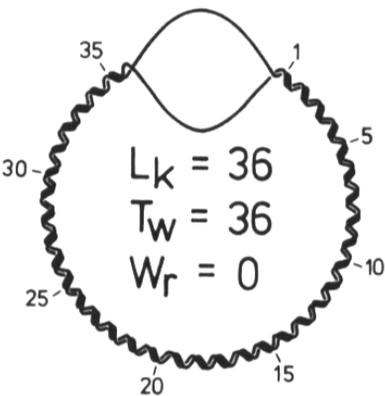
$$T_w = 42$$

$$W_r = 0$$

unstrained relaxed



unwind by six
right handed turns
 $\Delta L_k = -6$



$$L_k = 36$$

$$T_w = 36$$

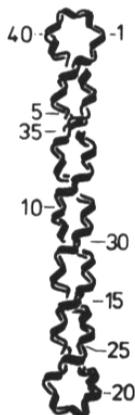
$$W_r = 0$$

"relaxed"

$$L_k = 36$$

$$T_w = 42$$

$$W_r = -6$$



supercoil

partially unwound

The Linking Number (L) of DNA

- The linking number of DNA, a topological property, determines the degree of supercoiling;
- The linking number defines the number of times a strand of DNA winds in the right-handed direction around the helix axis when the axis is constrained to lie in a plane;
- If both strands are covalently intact, the linking number cannot change;
- For instance, in a circular DNA of 5400 basepairs, the linking number is $5400/10=540$, where 10 is the basepair per turn for type B DNA.

The Twist (Tw) of DNA

Twist is a measure of the helical winding of the DNA strands around each other.

**Given that DNA prefers to form B-type helix, the preferred twist = number of basepair/10;
10 is the number of nucleotide in one twist!**

The Writhe (W_r) of DNA

- Writhe is a measure of the coiling of the axis of the double helix.

A right-handed coil is assigned a negative number (negative supercoiling) and a left-handed coil is assigned a positive number (positive supercoiling).

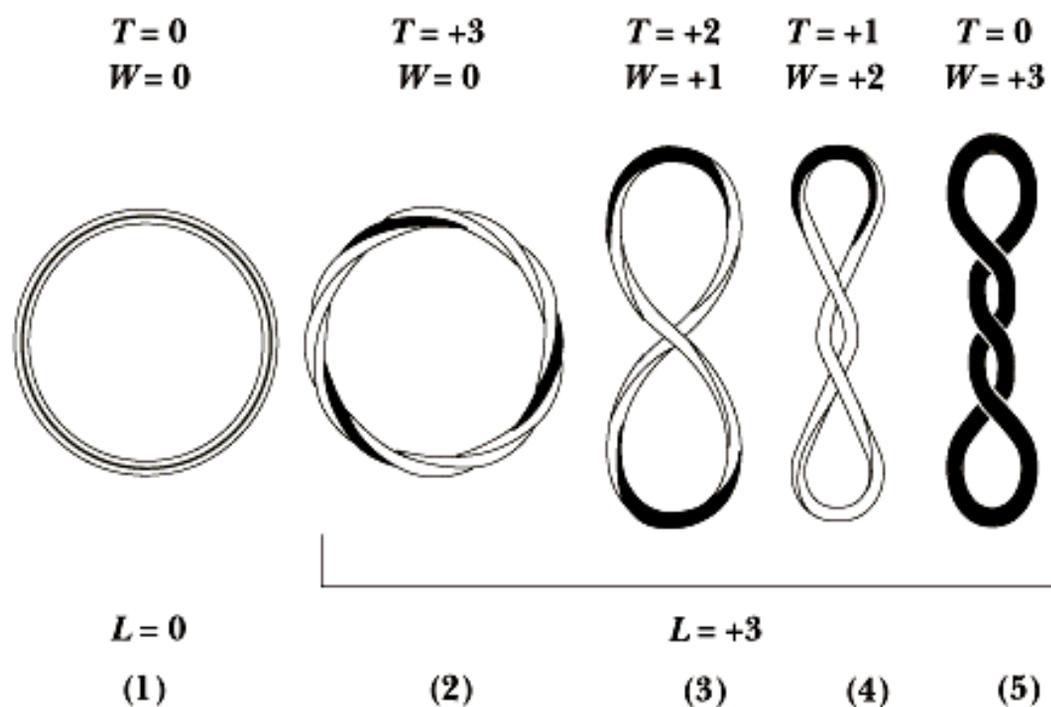
Topology theory tells us that the sum of T and W equals to linking number:

$$**L=T+W**$$

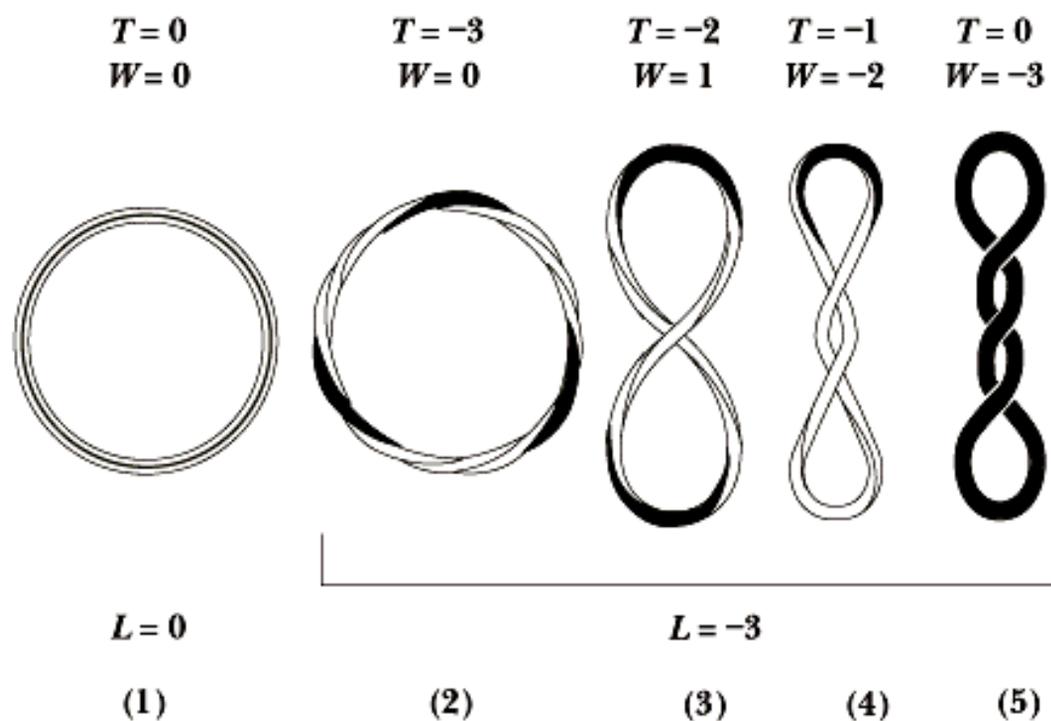
For example, in the circular DNA of 5400 basepairs, the linking number is $5400/10=540$

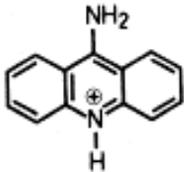
If no supercoiling, then $W=0$, $T=L=540$;

(a) Positive supercoiling

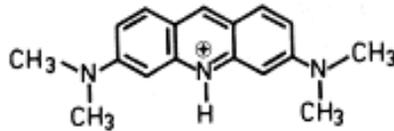


(b) Negative supercoiling

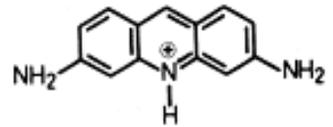




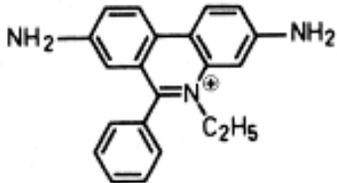
① 9-Aminoacridine



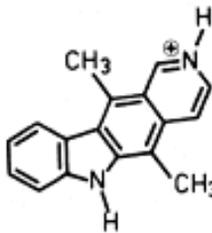
② Acridine orange



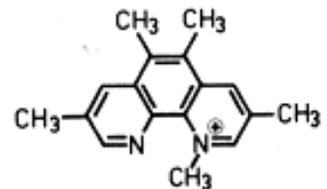
③ Proflavine



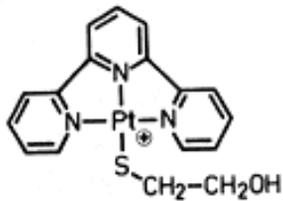
④ Ethidium



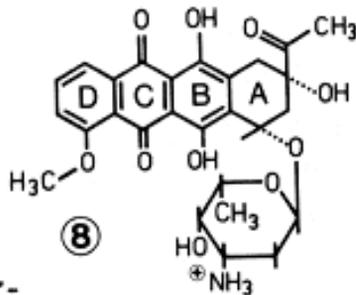
⑤ Ellipticine



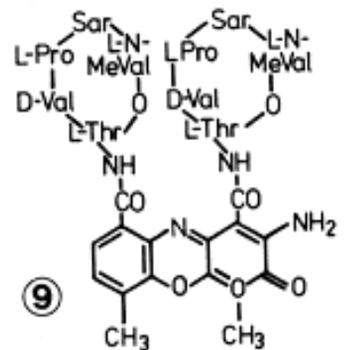
⑥ 3,5,6,8 -Tetramethyl - N -methyl phenanthrolium



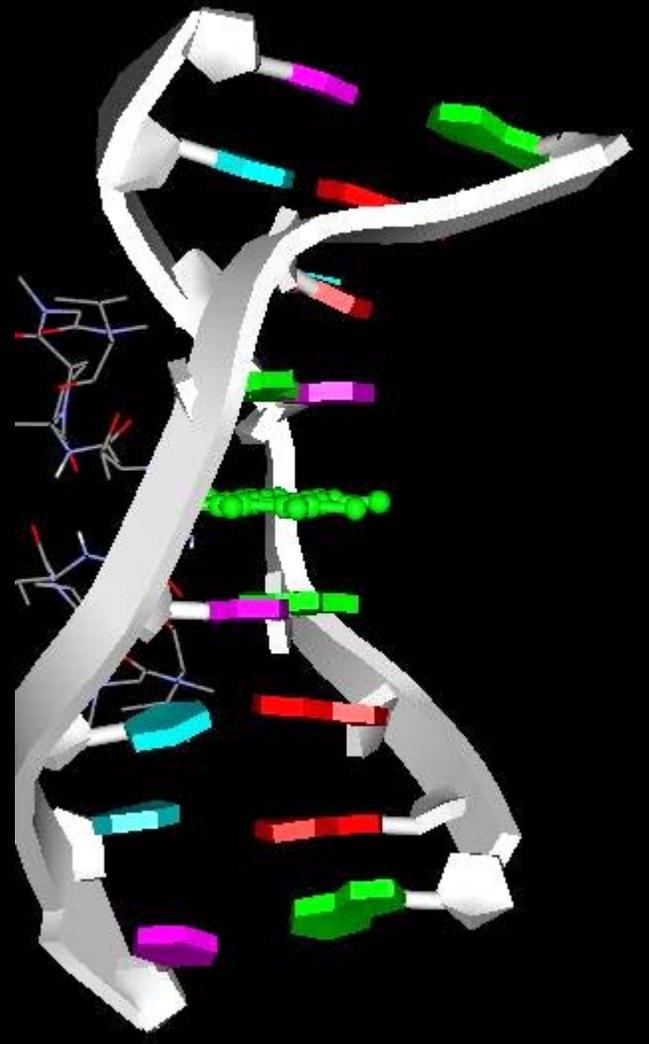
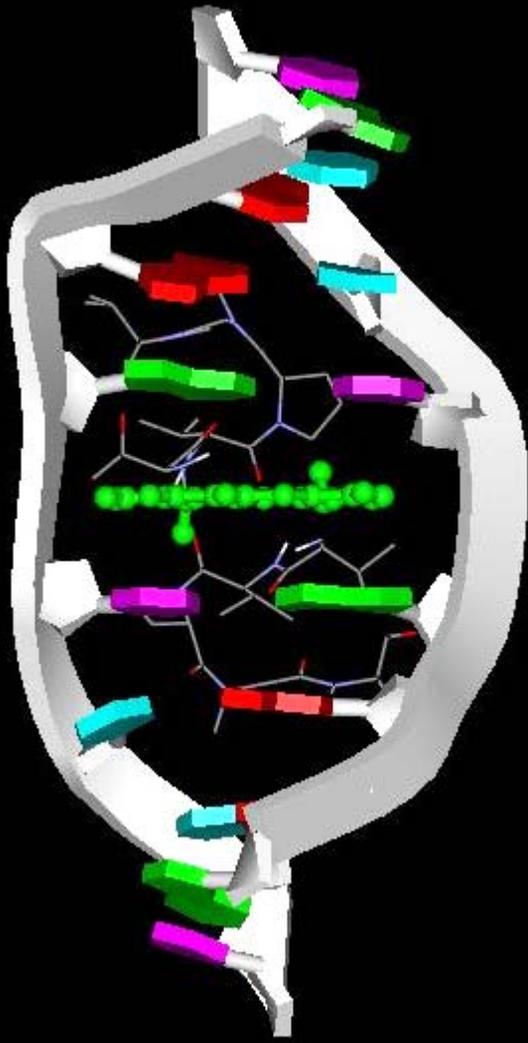
⑦ 2-Hydroxy-ethanethiolato -2,2',2''-terpyridine - platinum (II)

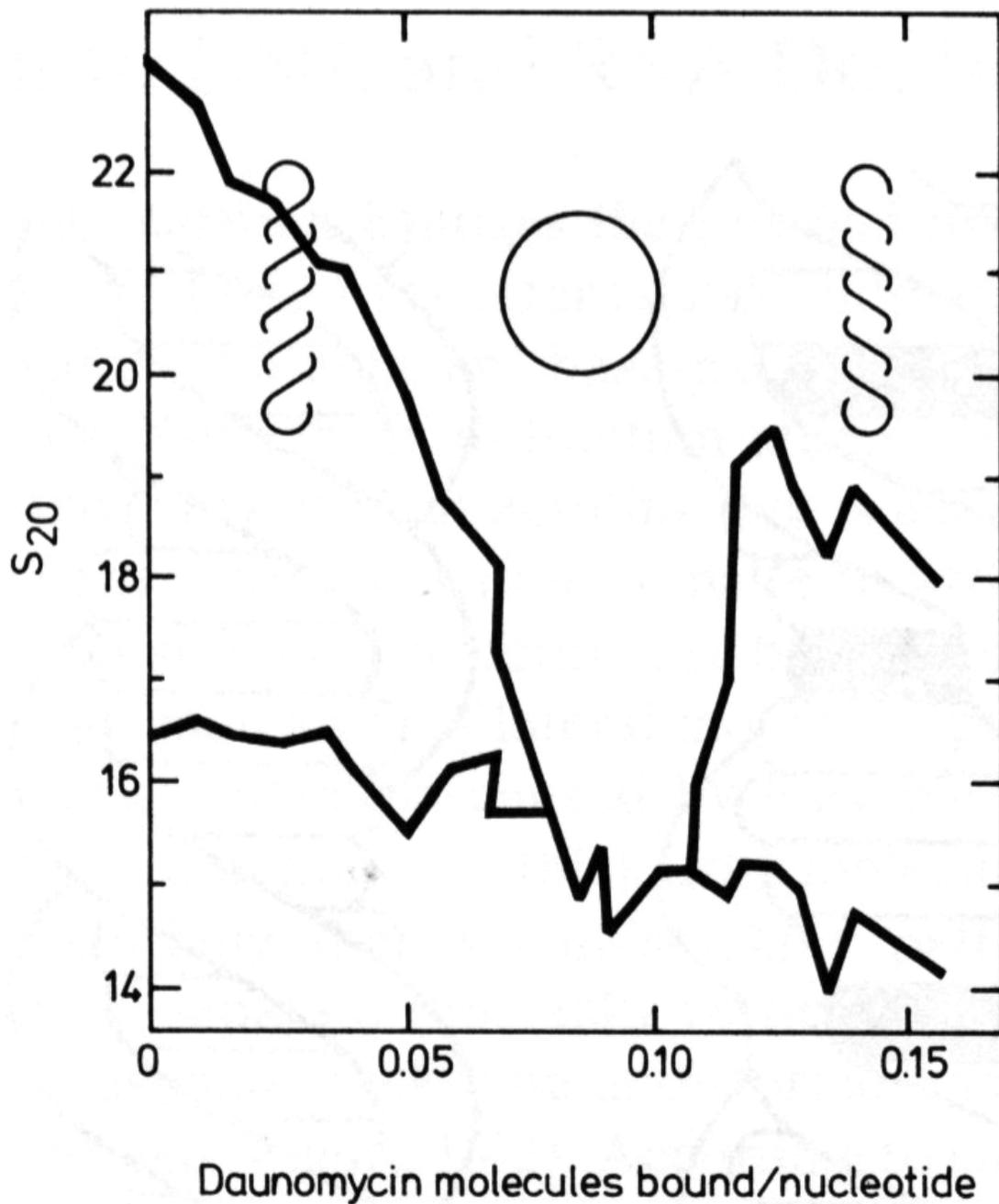


⑧ Daunomycin



⑨ Actinomycin



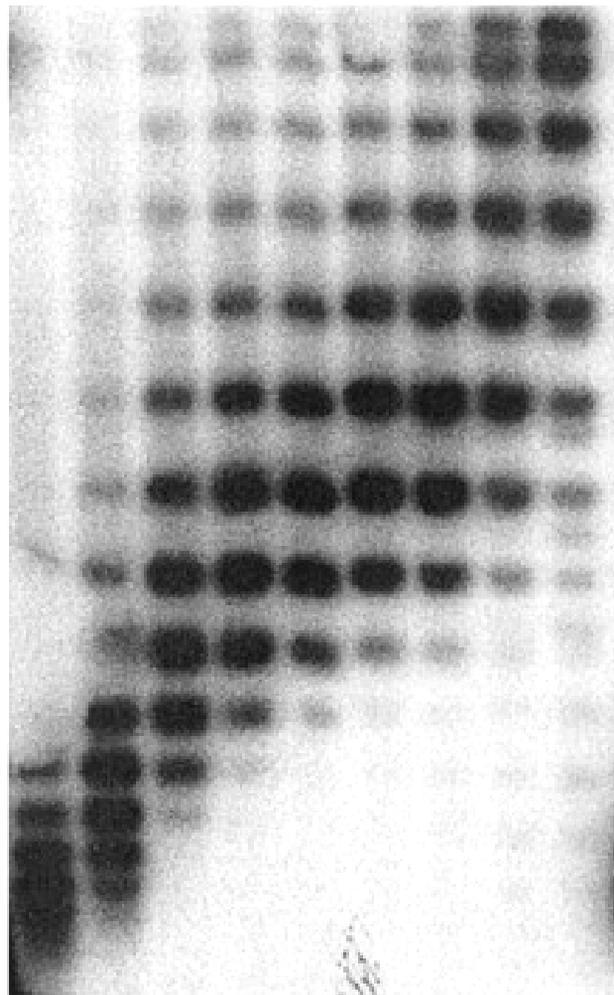


1 2 3 4 5 6 7 8 9 10
 0  30 120

$\sigma = -0.048 \rightarrow$

$\sigma = -0.057 \rightarrow$

$\sigma = -0.077 \rightarrow$



topo IV

+	-
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topo I

+

gyrase

+	-
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<i>topA⁺ parC⁺ gyrA⁺</i>
