БАШКИРСКИЙ ГОСУДАРСТВЕННЫЙ МЕДИЦИНСКИЙ УНИВЕРСИТЕТ

Строение и свойства ДНК

Профессор, д.м.н. Ш.Н.Галимов

Конформации сахаров

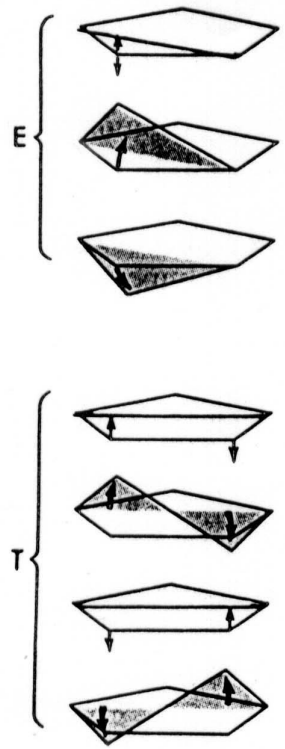


Рис. 2.6. Конформация конверта (E) и твист-конформация (T) пятичленного кольца. В E-конформации четыре атома компланарны, а пятый выступает из плоскости; в T-конформации компланарны три атома, а два отходят в разные стороны от плоскости.

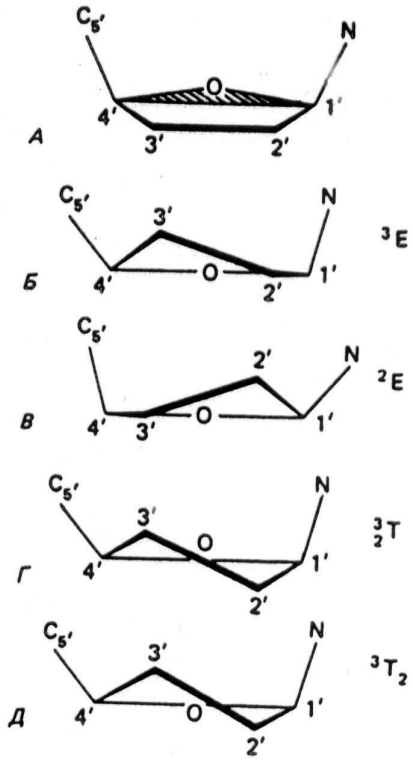
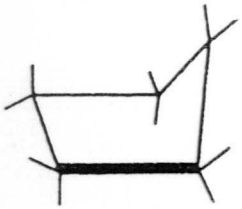


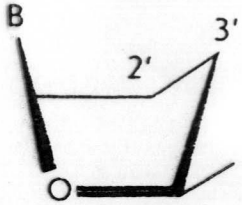
Рис. 2.7. Различные конформации сахара. *А*. Исходное состояние с несуществующим плоским пятичленным сахаром. Треугольник $C_{1'}$—$O_{4'}$—$C_{4'}$ заштрихован. *Б*–*Д*. Плоскость треугольника перпендикулярна плоскости рисунка. *Б*. Конверт $C_{3'}$-*эндо*, или ^3E. *В*. Конверт $C_{2'}$-*эндо*, или ^2E. *Г*. Симметричная твист-конформация, или полукресло $C_{2'}$-*экзо*–$C_{3'}$-*эндо*, или ^3_2T. *Д*. Несимметричная твист-конформация с главным $C_{3'}$-*эндо*-выступом и минорным C_2-*экзо*-выступом, или $^3T_2$.

Конформации сахаров

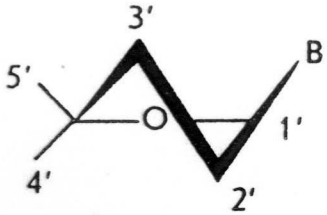


«Конверт» (Е или V)

«Твист» (Т)



3' — эндо



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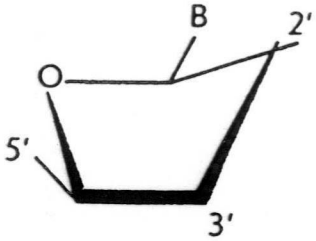
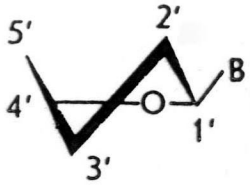


2' — эндо



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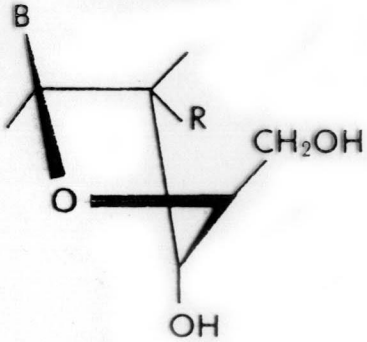

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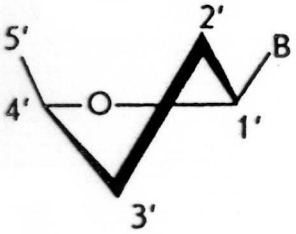

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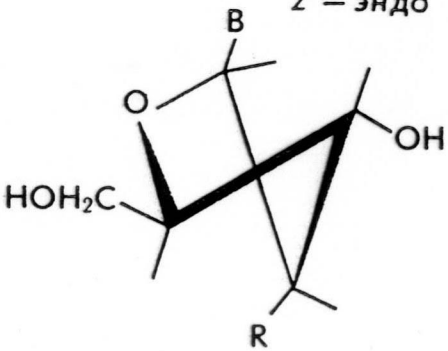

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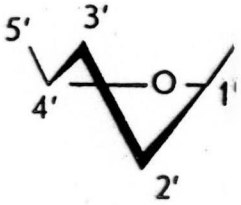


2' — экзо

Син- и анти-конформации нуклеозидов

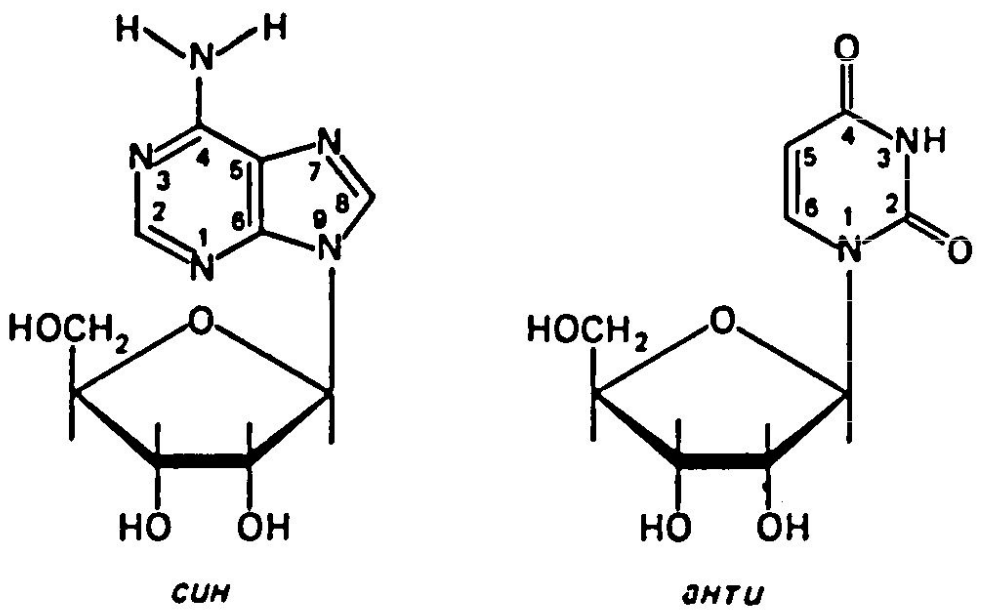


Рис. 10. *Син-* (аденозин) и *анти-* (уридин) конформации нуклеозидов

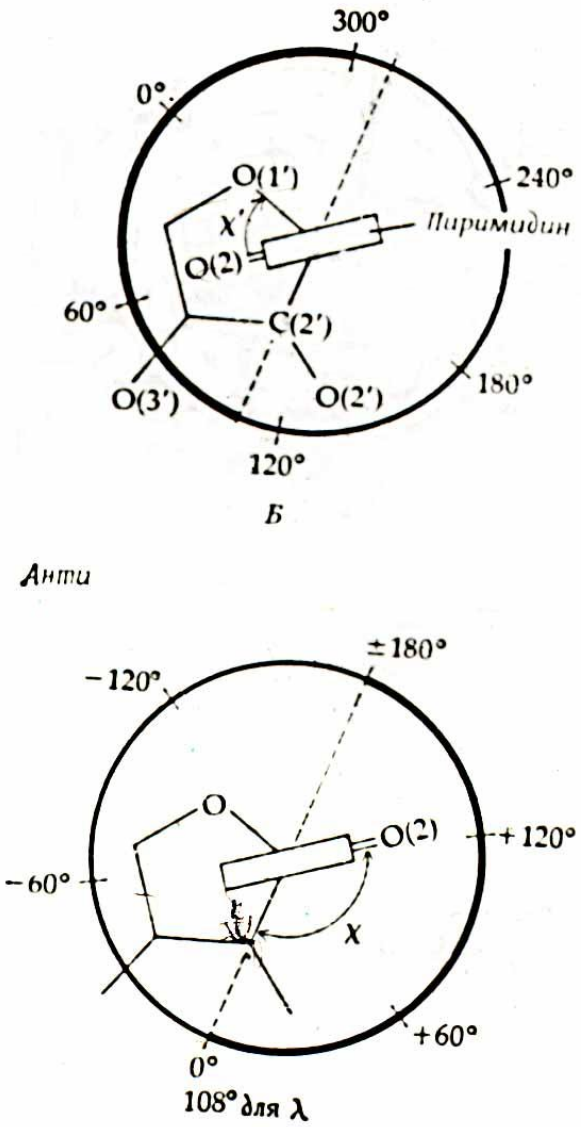


Схема изменения расстояний между фосфатными остатками нуклеозидного звена ДНК при конформаци-

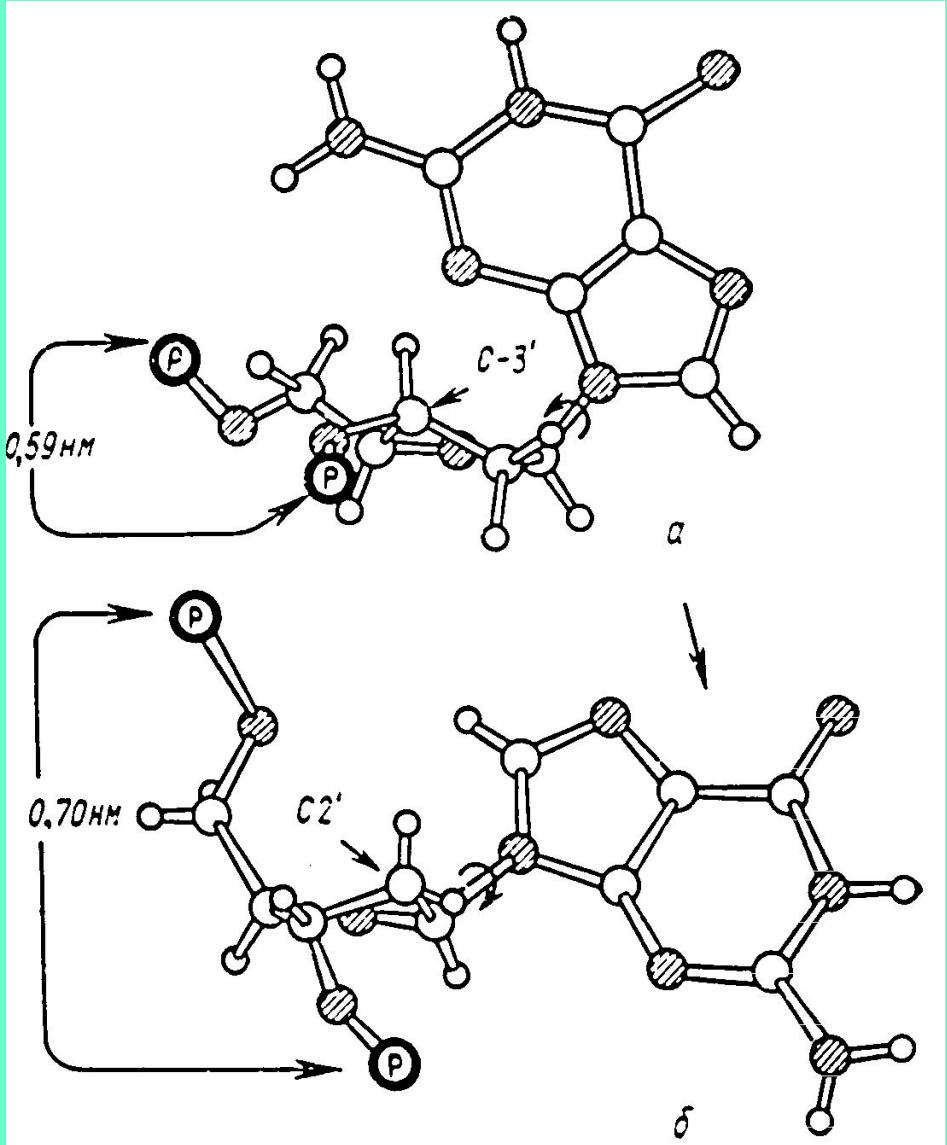
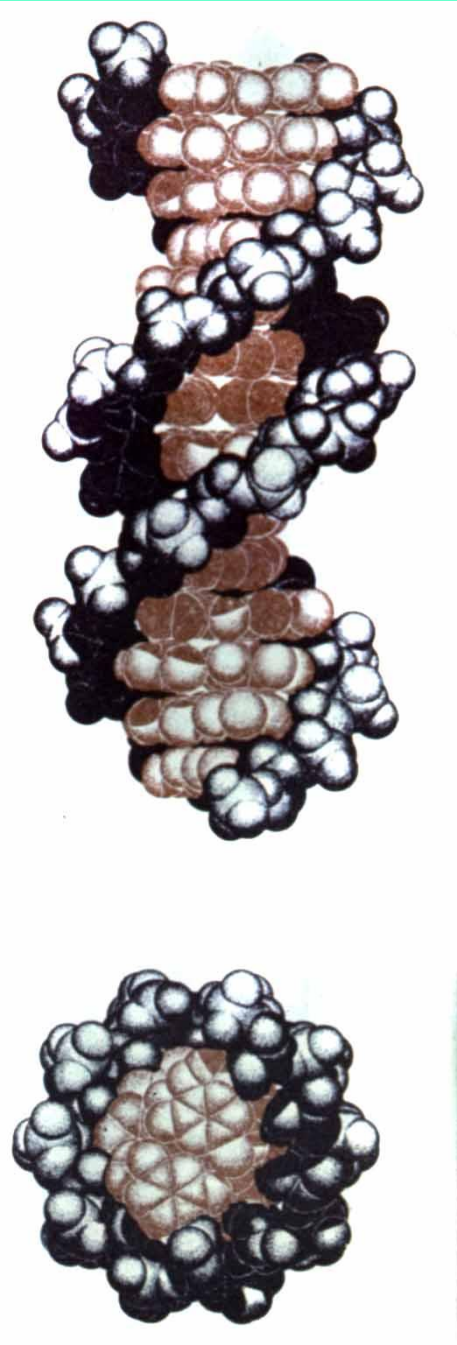
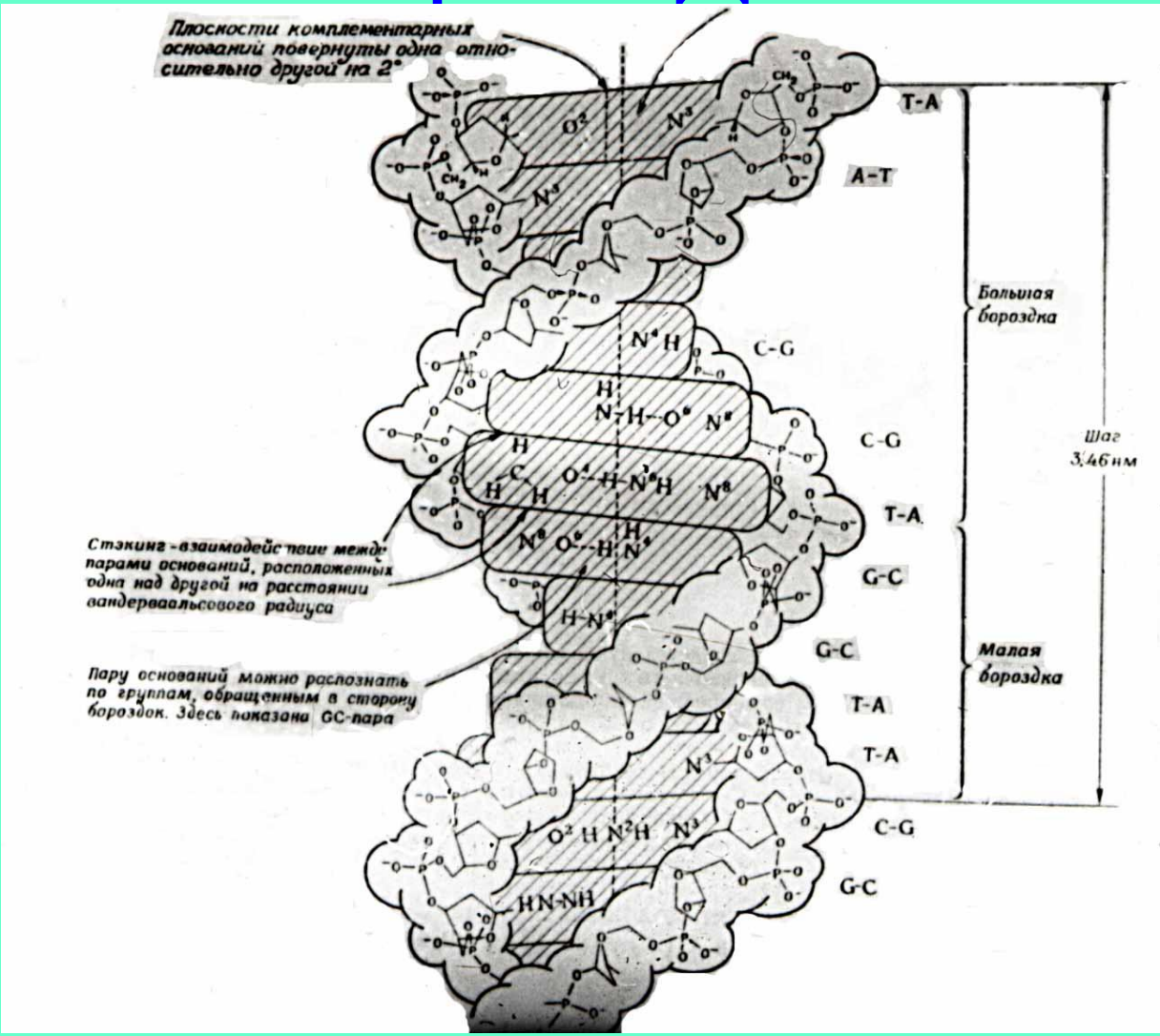


Рис. 11. Схема, показывающая изменение расстояний между фосфатными остатками нуклеотидного звена ДНК при C3'-*эндо*- — C2'-*эндо*-конформационном переходе:

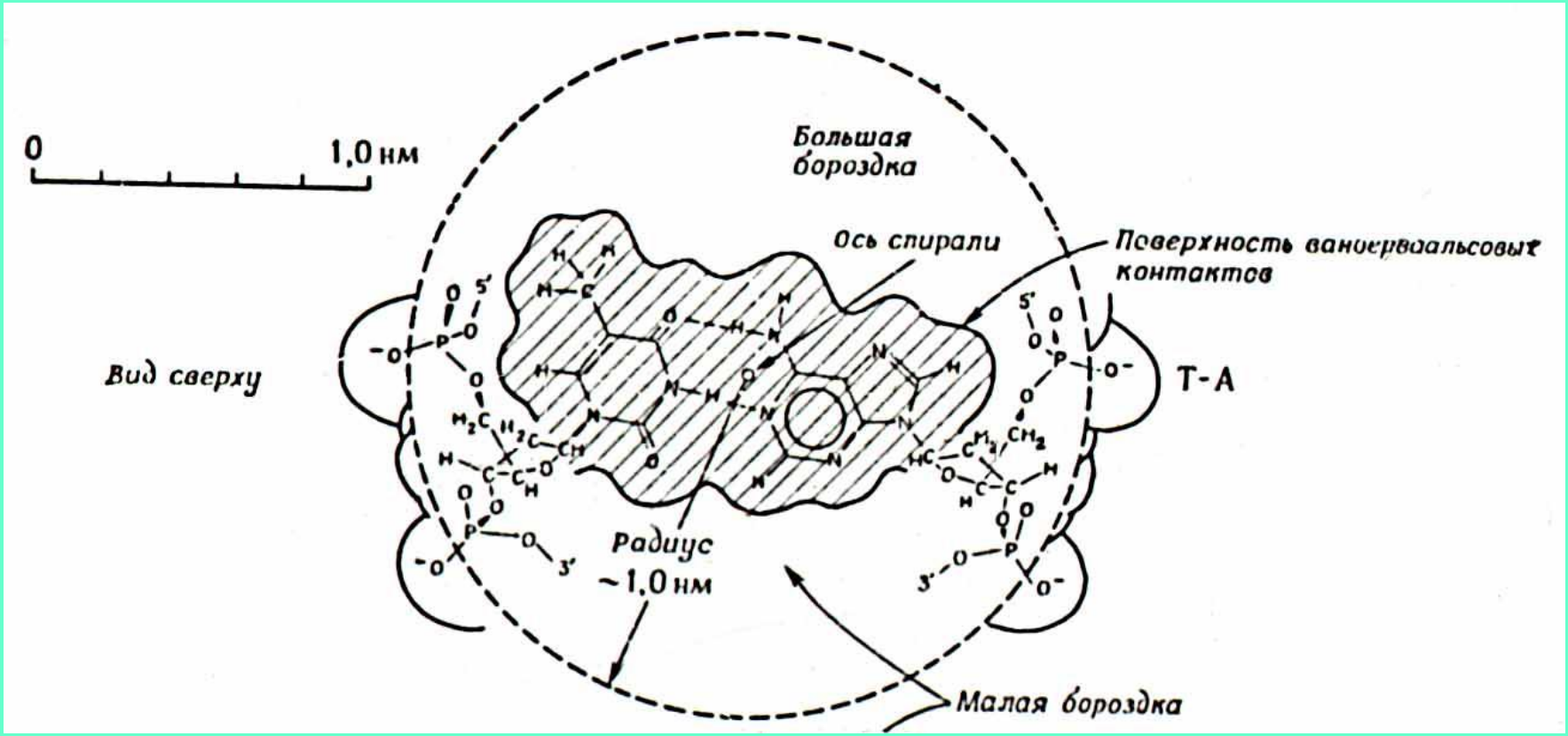
В-форма ДНК



Малая и большая бороздки спирали ДНК



Малая и большая бороздки спирали ДНК



ДНК в А-форме

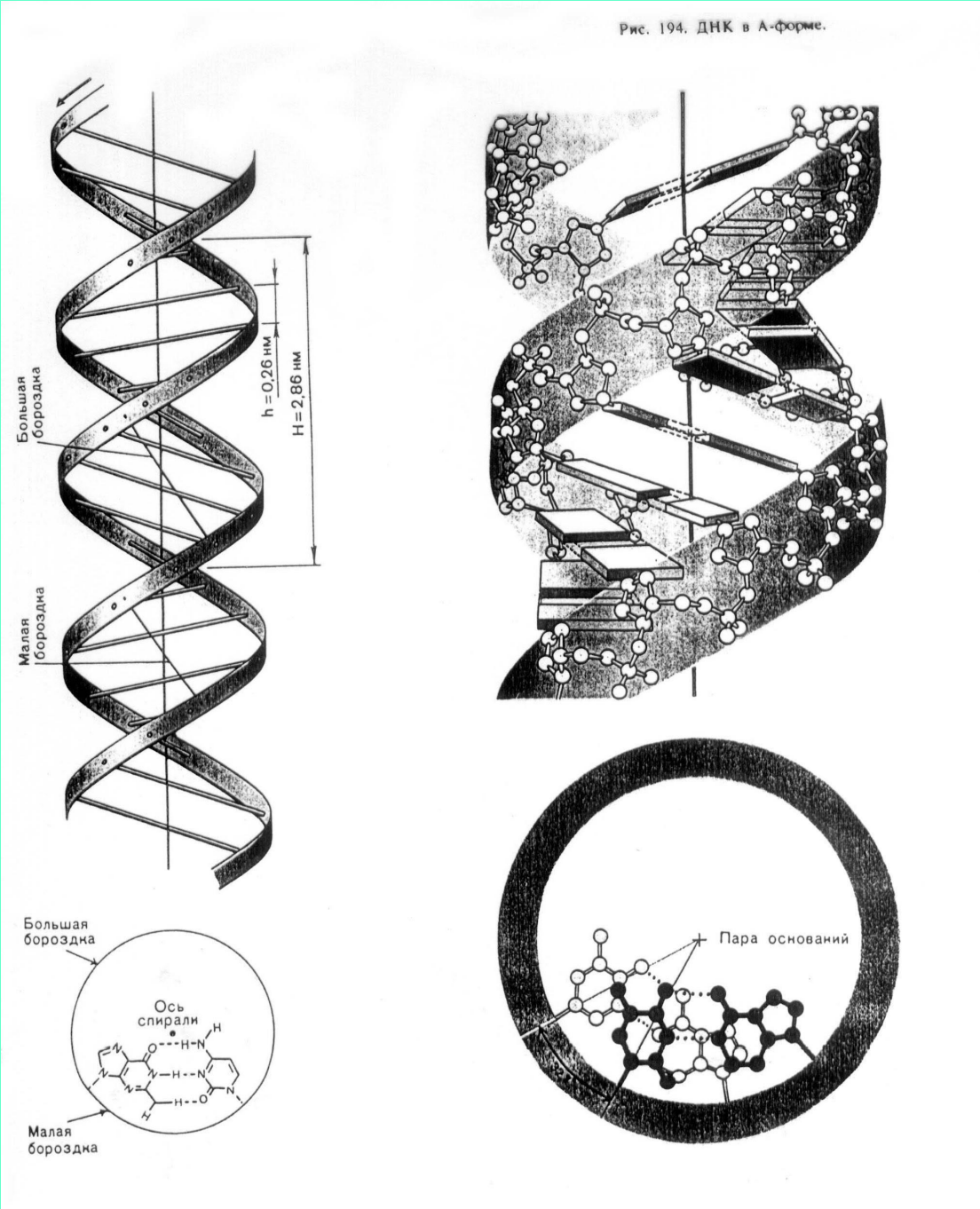
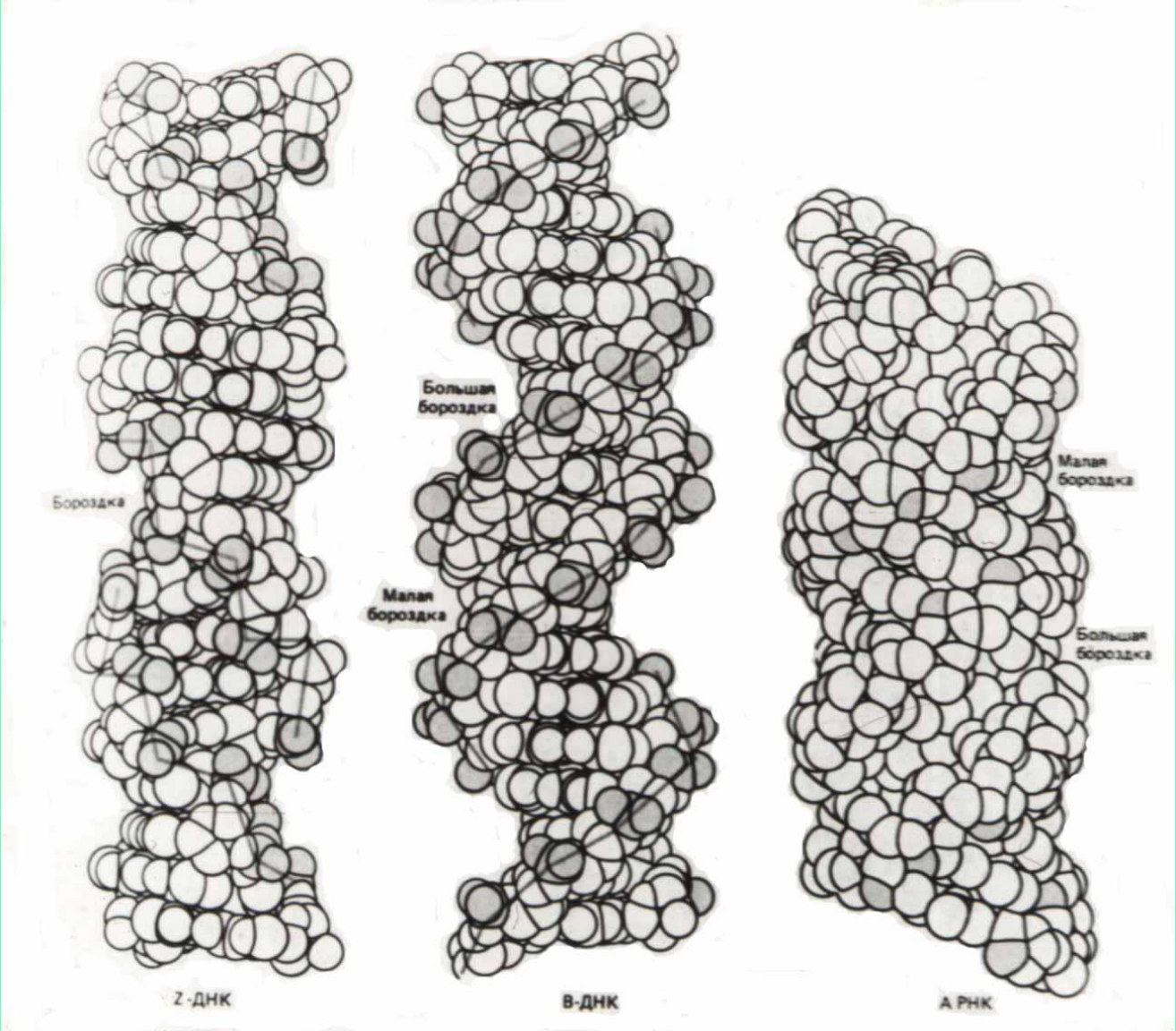


Рис. 194. ДНК в А-форме.

Формы ДНК и РНК



Объёмные модели Z- и B-форм ДНК

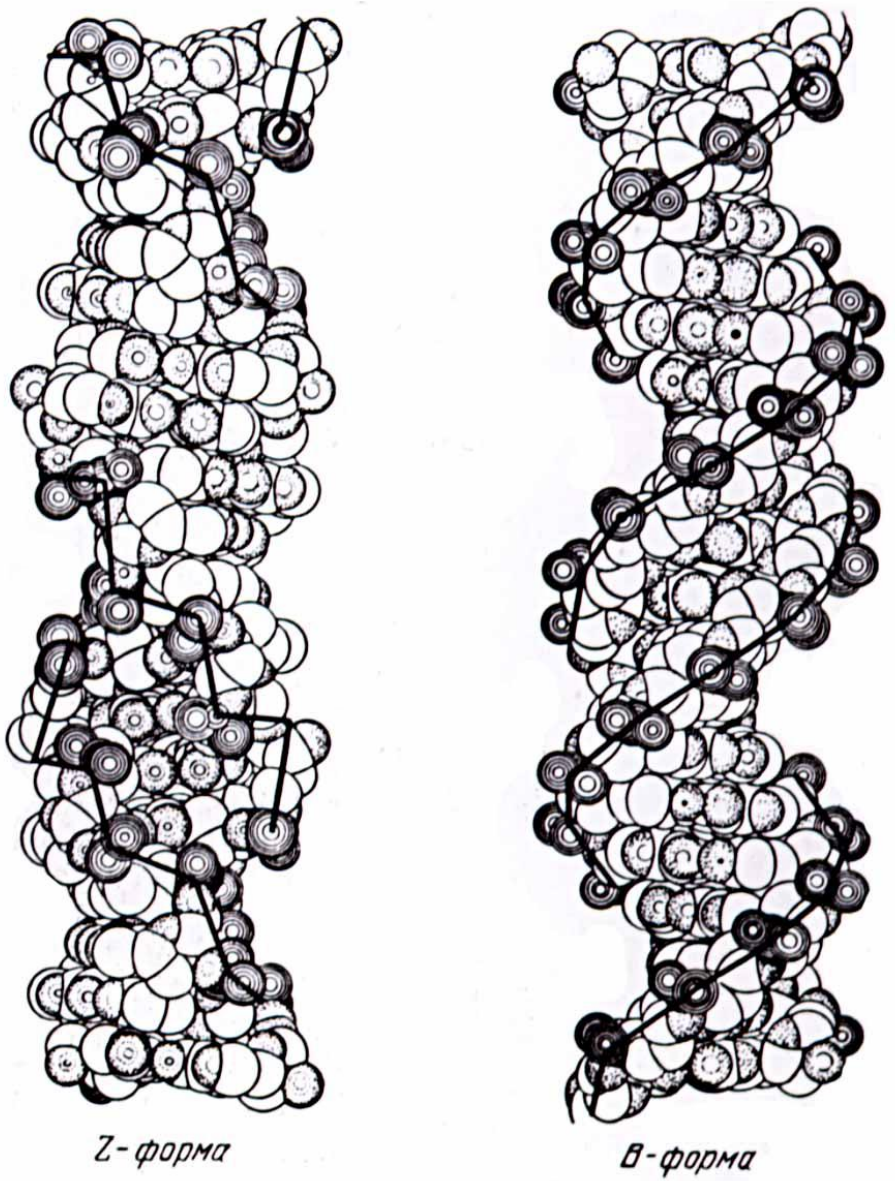
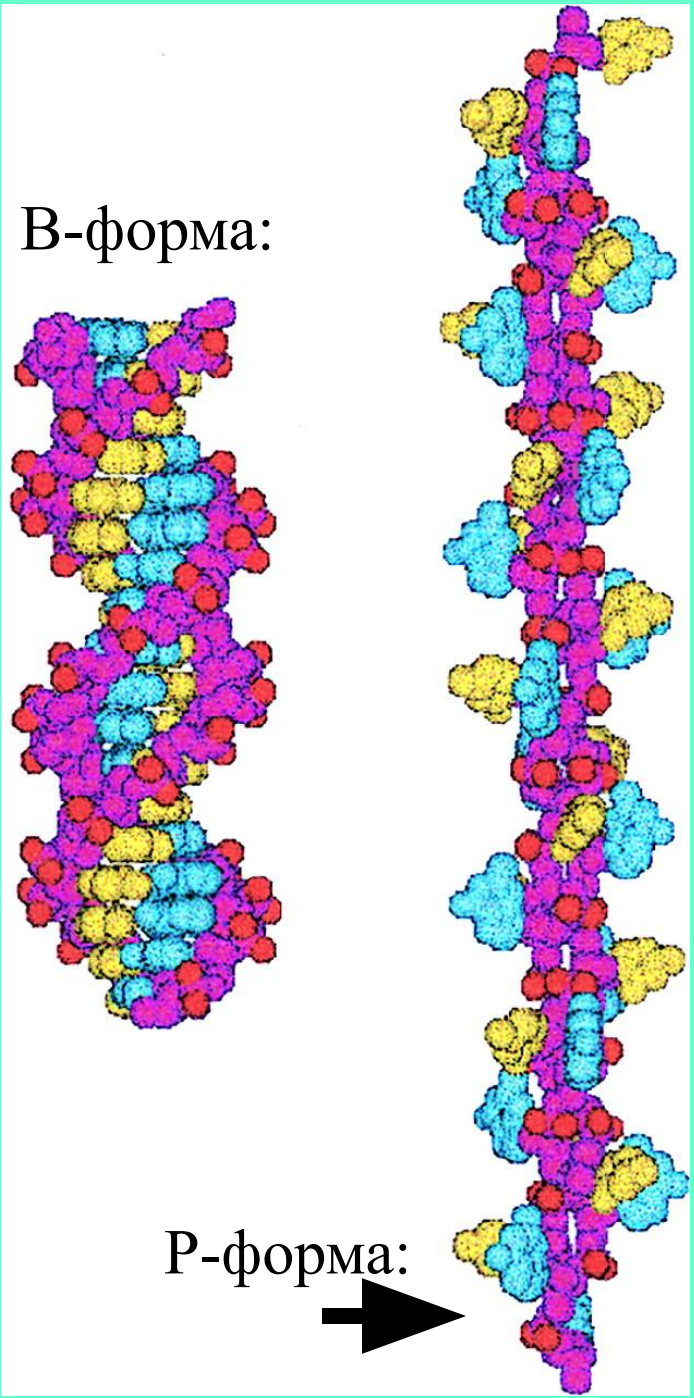


Рис. 34. Так выглядят объемные модели Z- и B-формы ДНК. Черные линии нарисованы, чтобы показать ход сахаро-фосфатной цепи

Z-форма ДНК

ДНК в Р-форме



Отрицательная суперспираль ДНК

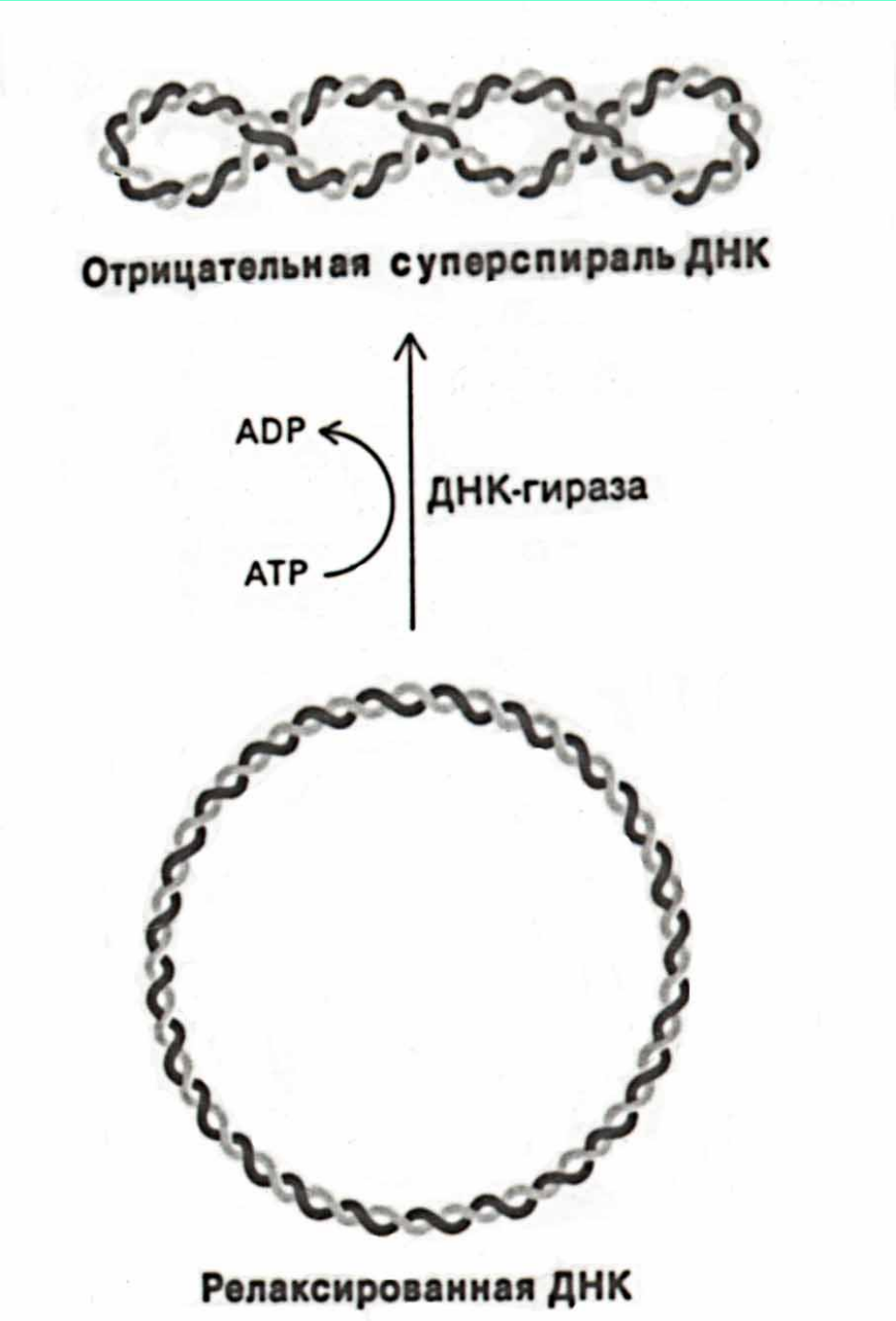


Схема образования отрицательно сверхспира-лизованной кольцевой ковалентно замкнутой ДНК

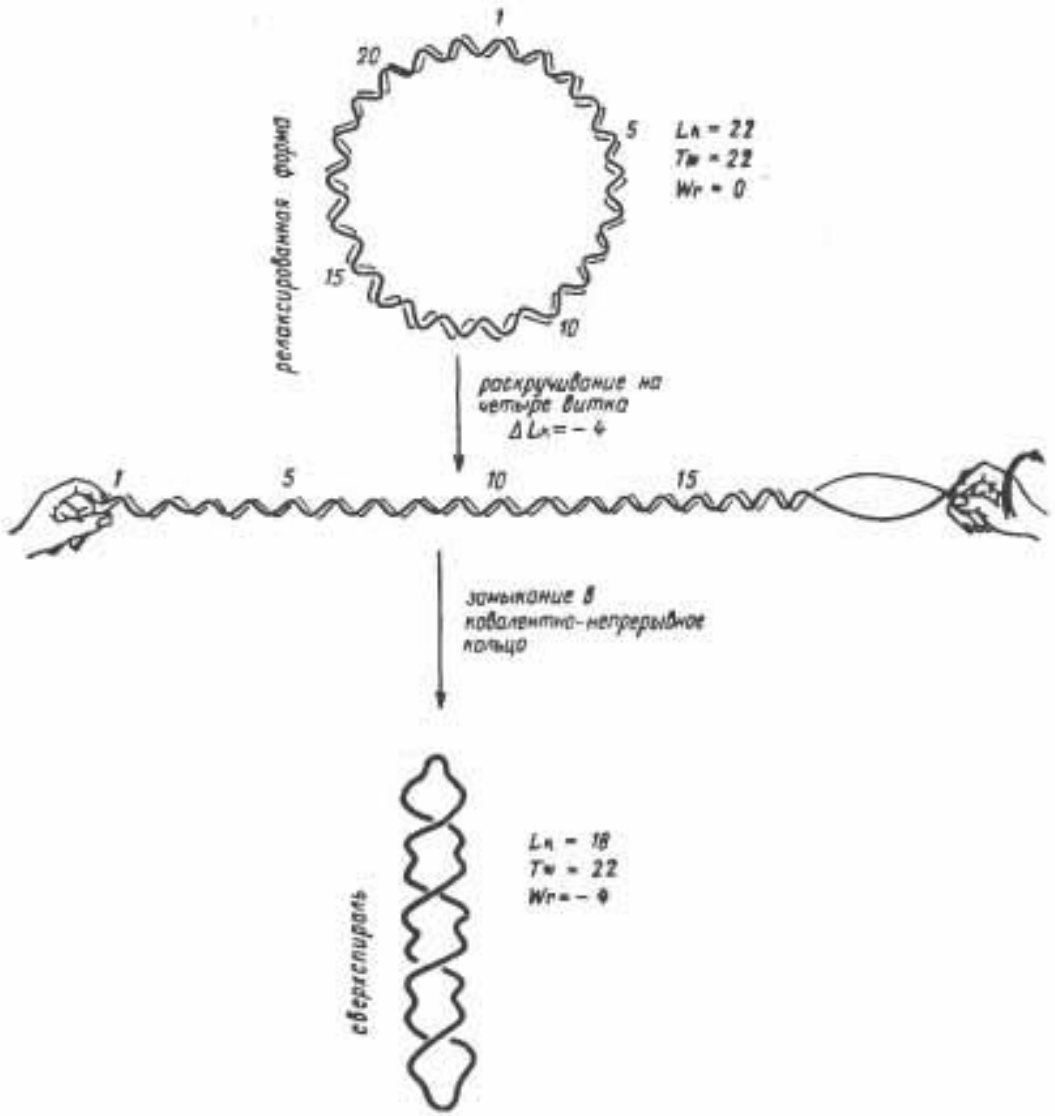
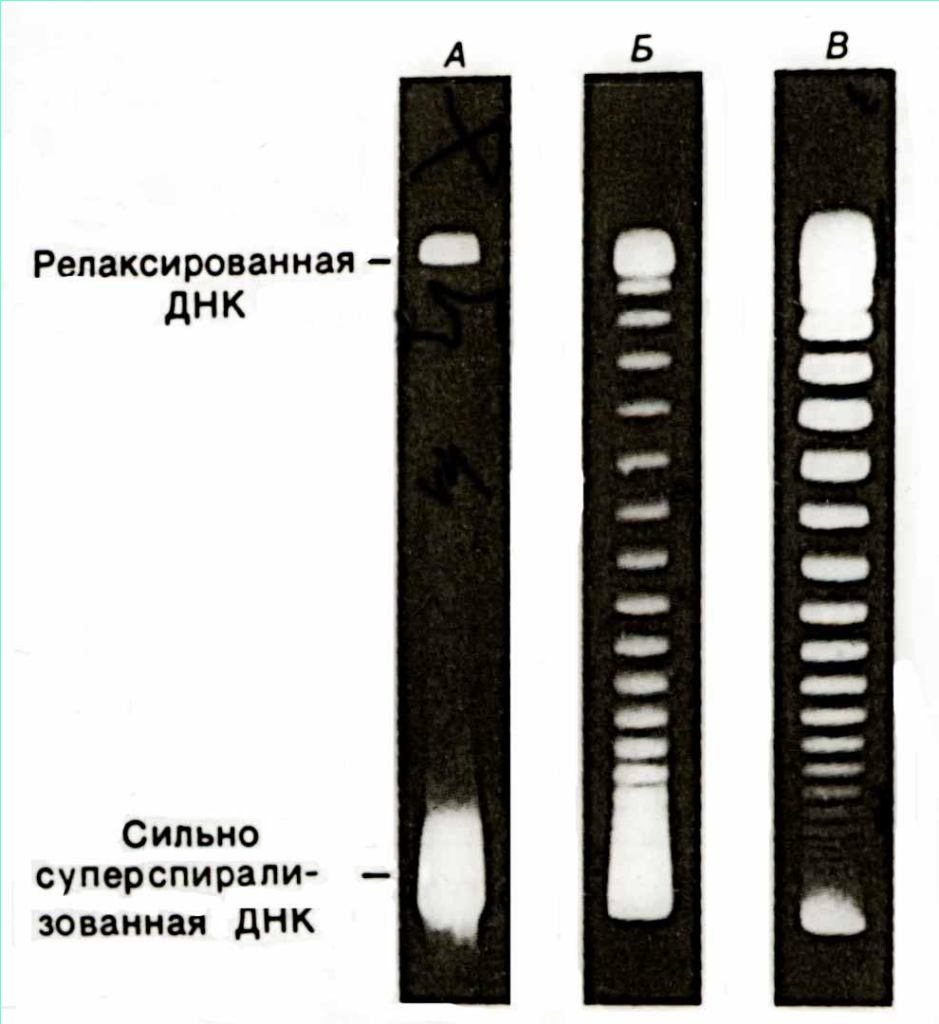


Рис. 18. Схема, иллюстрирующая образование отрицательно сверхспирализованной кольцевой ковалентной замкнутой ДНК

Электрофоретическое разделение топологических изомеров ДНК



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Классификация топоизомераз

TABLE 1 Classification of Topoisomerases

Topoisomerase[a]	Subfamily type	Subunit structure	Size(s) (aa)[b]
Eubacterial DNA topoisomerase I (*E. coli*)	IA	Monomer	865
Eubacterial DNA topoisomerase III (*E. coli*)	IA	Monomer	653
Yeast DNA topoisomerase III (*S. cerevisiae*)	IA	Monomer	656
Mammalian DNA topoisomerase IIIα (human)	IA	Monomer	1001
Mammalian DNA topoisomerase IIIβ (human)	IA	Monomer	862
Eubacterial and archaeal reverse DNA gyrase (*Sulfolobus acidocaldarius*)	IA	Monomer	1247
Eubacterial reverse gyrase (*Methanopyrus kandleri*)[c]	IA	Heterodimer	A, 358 B, 1221
Eukaryotic DNA topoisomerase I (human)	IB	Monomer	765
Poxvirus DNA topoisomerase (vaccinia)	IB	Monomer	314
Hyperthermophilic eubacterial DNA topoisomerase V (*Methanopyrus kandleri*)[d]	IB	Monomer	—[e]
Eubacterial DNA gyrase (*E. coli*)	IIA	A_2B_2 hetero-tetramer	GyrA, 875 GyrB, 804
Eubacterial DNA topoisomerase IV (*E. coli*)	IIA	C_2E_2 hetero-tetramer	ParC, 752 ParE, 630
Yeast DNA topoisomerase II (*S. cerevisiae*)	IIA	Homodimer	1428
Mammalian DNA topoisomerase IIα (human)	IIA	Homodimer	1531
Mammalian DNA topoisomerase IIβ (human)	IIA	Homodimer	1626
Archaeal DNA topoisomerase VI (*Sulfolobus shibatae*)	IIB	A_2B_2 hetero-tetramer	A, 389 B, 530

[a]The source of the most extensively studied family member is given in parentheses. The top portion of the table lists the type I topoisomerases; the bottom portion the type II enzymes.

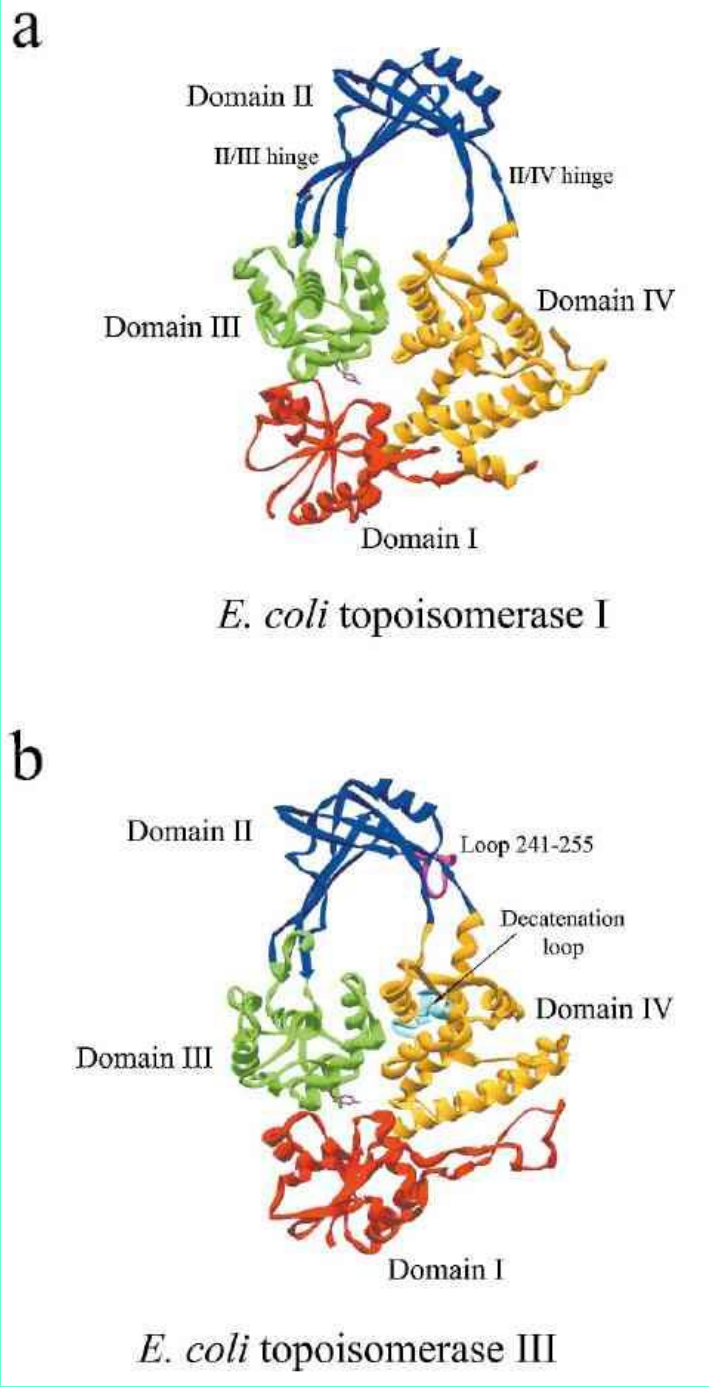
[b]The subunit sizes are those corresponding to the most extensively studied family member.

[c]Included as the only known reverse gyrase with a heterodimeric structure.

[d]Only known representative at present. Probably present in other hyperthermophilic eubacteria.

[e]Gene not yet cloned; purified protein has a molecular size of 110 kDa.

Структура топоизомераз I и III *E. coli*



Пространственная структура гиразы

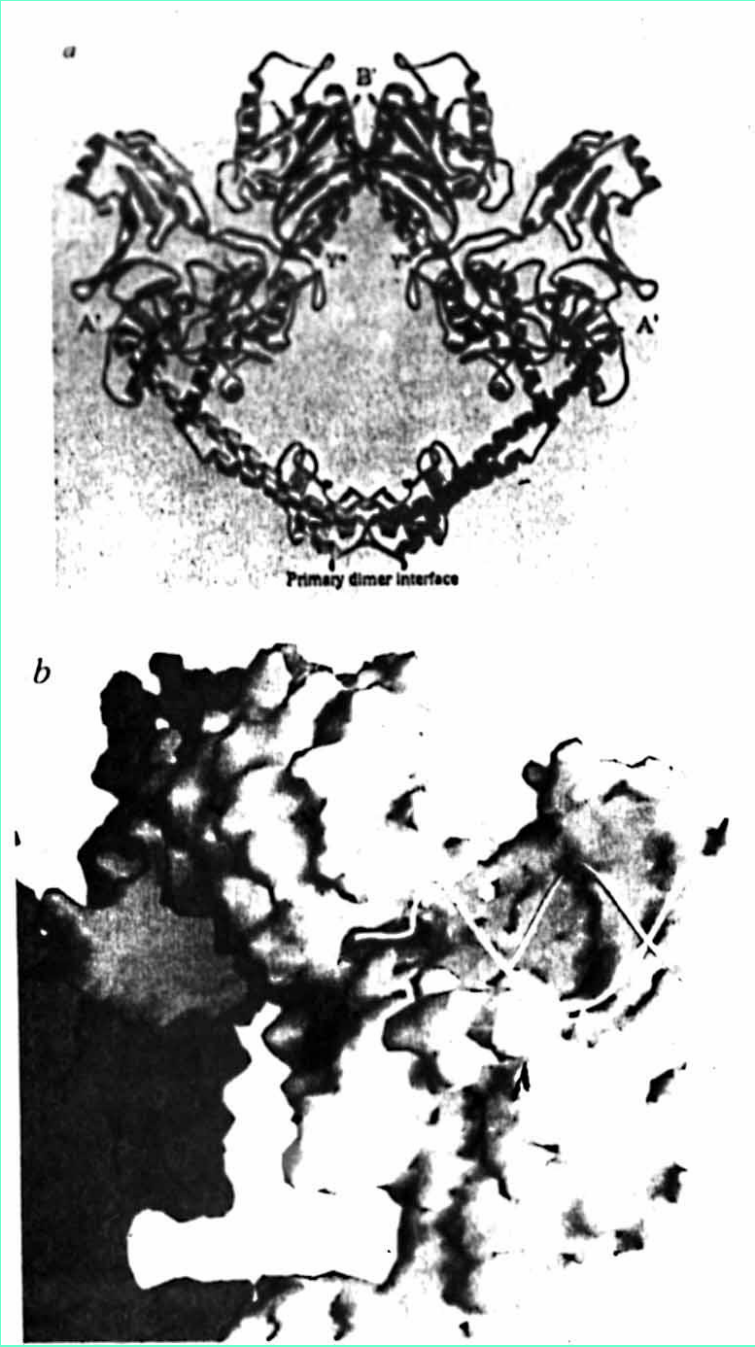
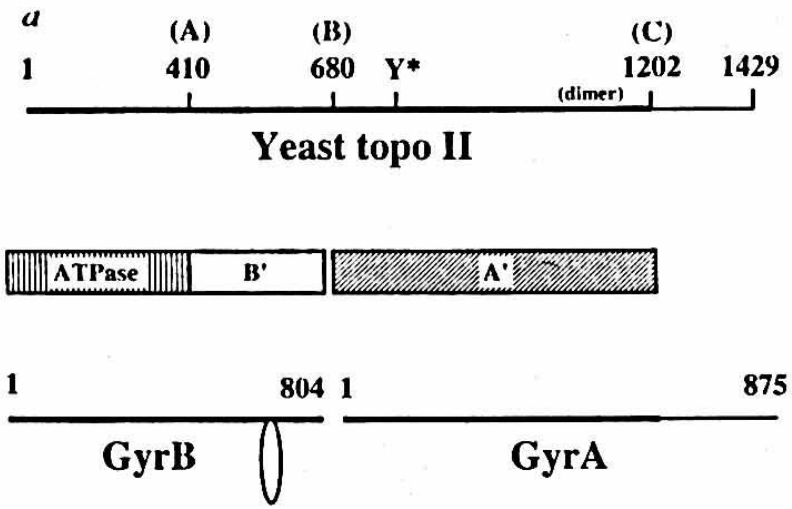


Схема расщепления дуплекса ДНК топоизомеразой II



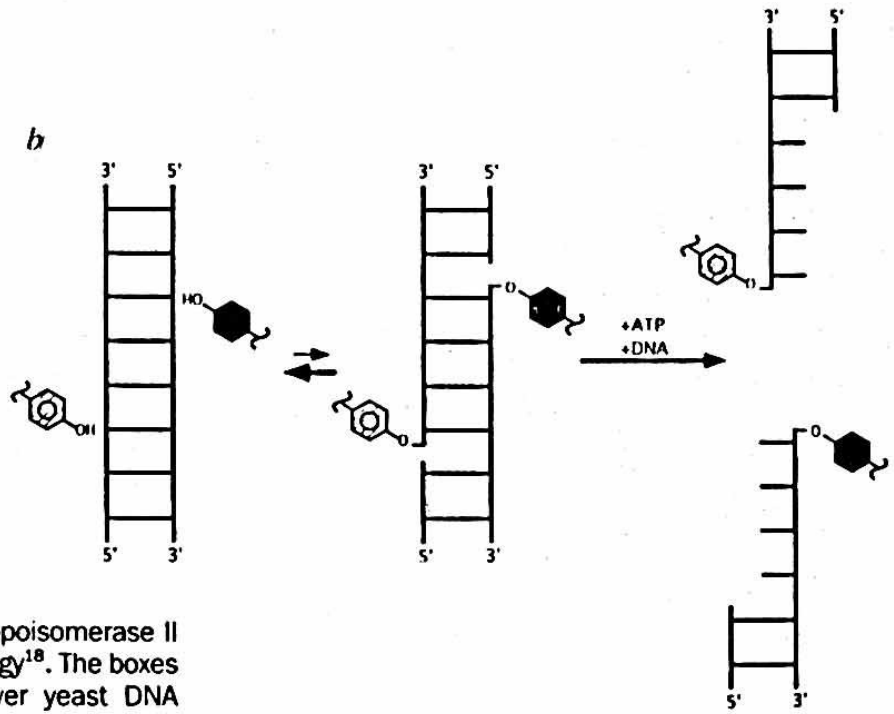


FIG. 1*a*, Schematic alignment of the amino-acid sequences of yeast DNA topoisomerase II (topo II) and *E. coli* DNA gyrase. Overlapping areas indicate regions of homology[18]. The boxes are known proteolytic fragments of gyrase. The numbers and letters over yeast DNA topoisomerase II are the SV8 protease cleavage sites. The dimerization region (defined as the region between residues 1036–1128) and active-site tyrosine positions are labelled dimer and Y*, respectively. *b*, Diagram of DNA topoisomerase II cleavage reaction. The active-site tyrosines (Tyr 783) in the yeast enzyme) are in equilibrium with DNA between cleaved and uncleaved states. ATP binding and perhaps the binding of a second DNA duplex cause the two DNA-linked tyrosines to undergo a significant translocation away from each other to open a gap large enough for the second duplex to pass through.

Молекулярная модель каталитической реакции топоизомеразы II

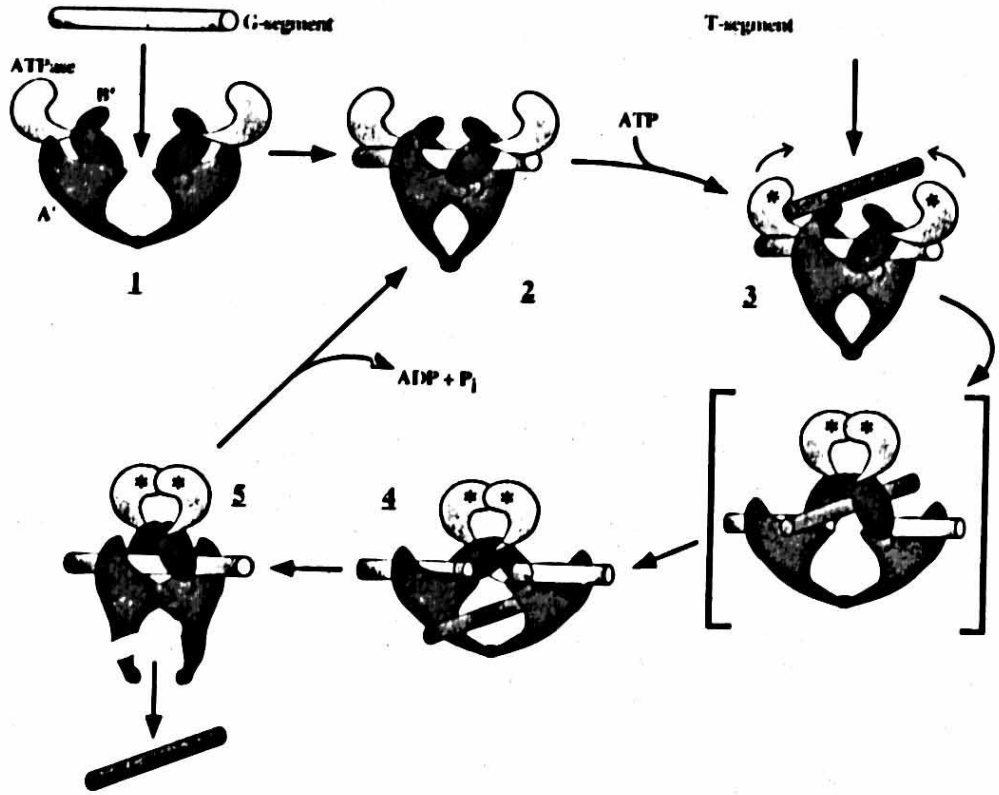


FIG. 5. A molecular model for the catalytic reaction of topoisomerase II. The ATPase domain, B' and A' subfragments are coloured yellow, red and blue, respectively. The G-segment DNA (containing the DNA gate) is grey, and the transported T-segment is green. In (**1**) an unliganded enzyme first binds the G-segment, inducing a conformational change shown in (**2**). Upon binding of ATP (represented by asterisks) and a T-segment (**3**), a series of conformational changes occur in which the G-segment is split by the A' subfragments as they separate from each other. Concomitantly, the ATPase domains dimerize, and the T-segment is transported through the break and into the central hole (**4**). The B' subfragment in front is uncoloured in (**4**) to permit visualization of the DNA behind it. For clarity, the DNA transport step is shown to proceed through a hypothetical intermediate (brackets). Following transport, the G-segments is resealed and the T-segment released from the enzyme through the opening of the dimer interface between A' subfragments (**5**). The interface between the two A' subfragments again dimerizes, and ATP is hydrolysed and released to regenerate the starting state (**2**).