

**БАШКИРСКИЙ ГОСУДАРСТВЕННЫЙ
МЕДИЦИНСКИЙ УНИВЕРСИТЕТ**

Строение и свойства ДНК

Профессор, д.м.н. Ш.Н.Галимов

Конформации сахаров

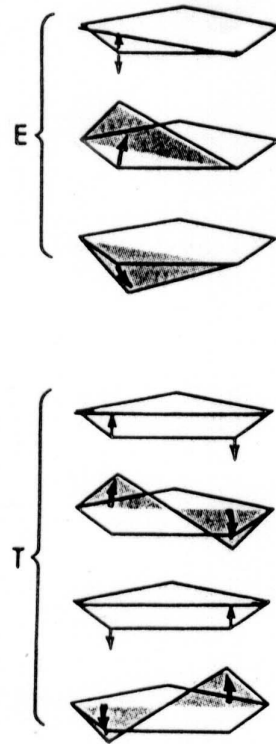


Рис. 2.6. Конформация конверта (E) и твист-конформация (Т) пятичленного кольца. В E-конформации четыре атома компланарны, а пятый выступает из плоскости; в Т-конформации компланарны три атома, а два отходят в разные стороны от плоскости.

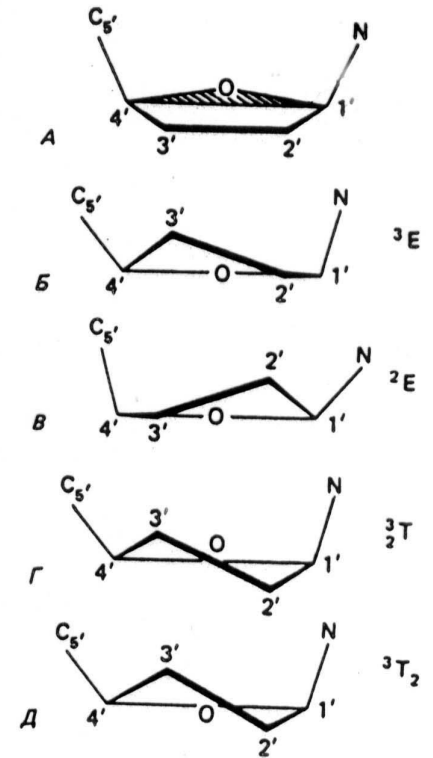
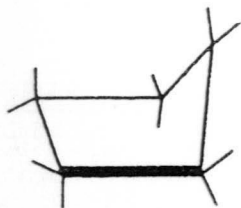
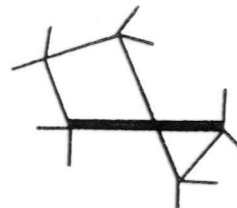


Рис. 2.7. Различные конформации сахара. А. Исходное состояние с несуществующим плоским пятичленным сахаром. Треугольник $C_1-O_4-C_4$ заштрихован. Б-Д. Плоскость треугольника перпендикулярна плоскости рисунка. Б. Конверт C_3 -эндо, или 3E . В. Конверт C_2 -эндо, или 2E . Г. Симметричная твист-конформация, или полукресло C_2 -экзо- C_3 -эндо, или 3T_2 . Д. Несимметричная твист-конформация с главным C_3 -эндо-выступом и минорным C_2 -экзо-выступом, или 3T_2 .

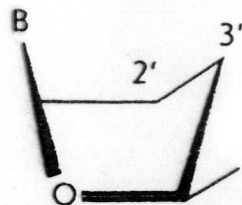
Конформации сахаров



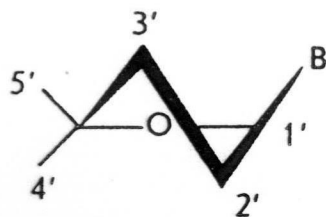
«Конверт» (E или V)



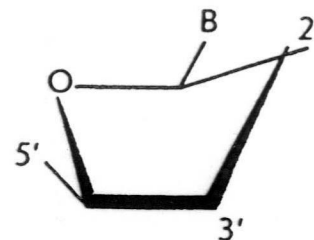
«Твист» (T)



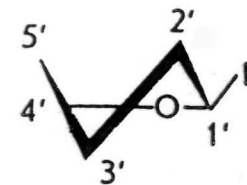
3'-эндо



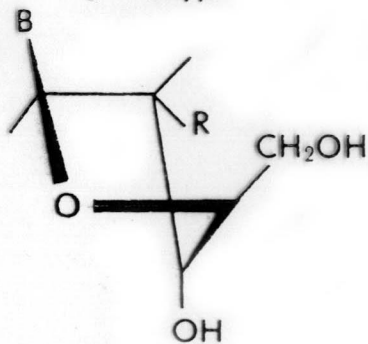
3'-эндо



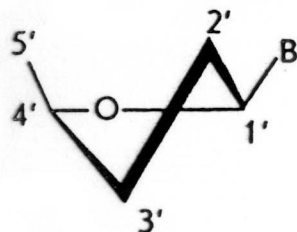
2'-эндо



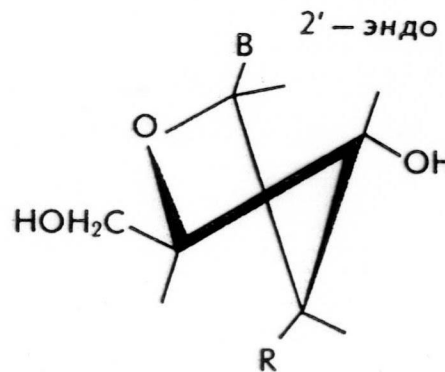
2'-эндо



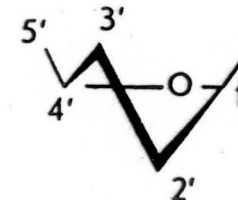
3'-экзо



3'-экзо



2'-экзо



2'-экзо

Син- и анти- конформации

нуклеозидов

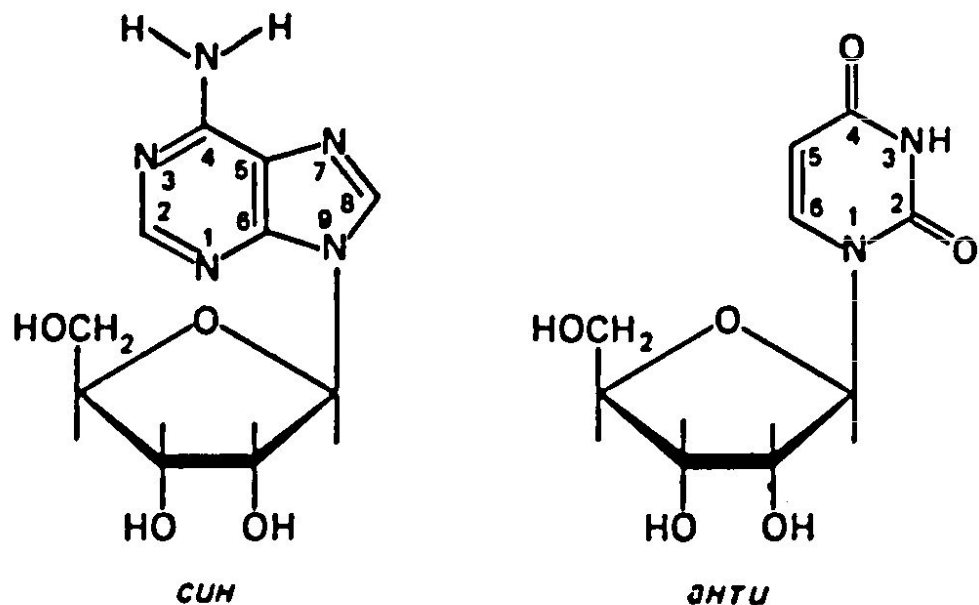
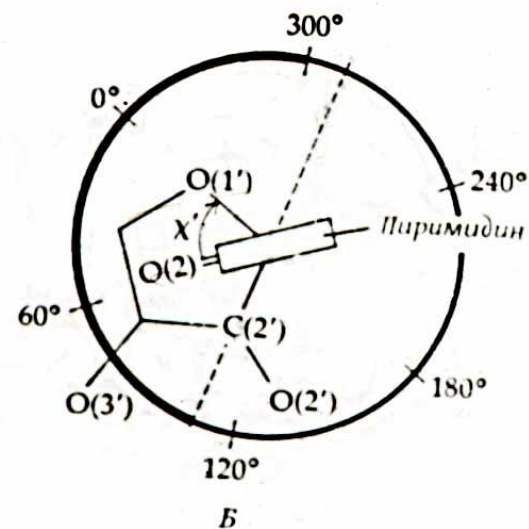


Рис. 10. Син- (аденозин) и анти- (уридин) конформации нуклеозидов



Анти

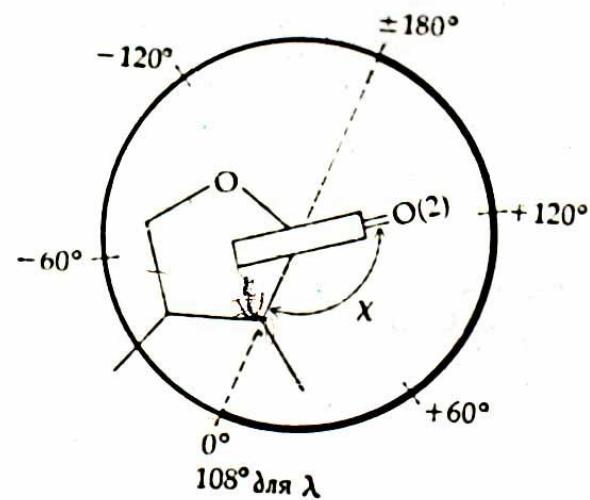


Схема
изменения
расстояний
между
фосфатными
остатками
нуклеозидного
звена ДНК при
конформаци-

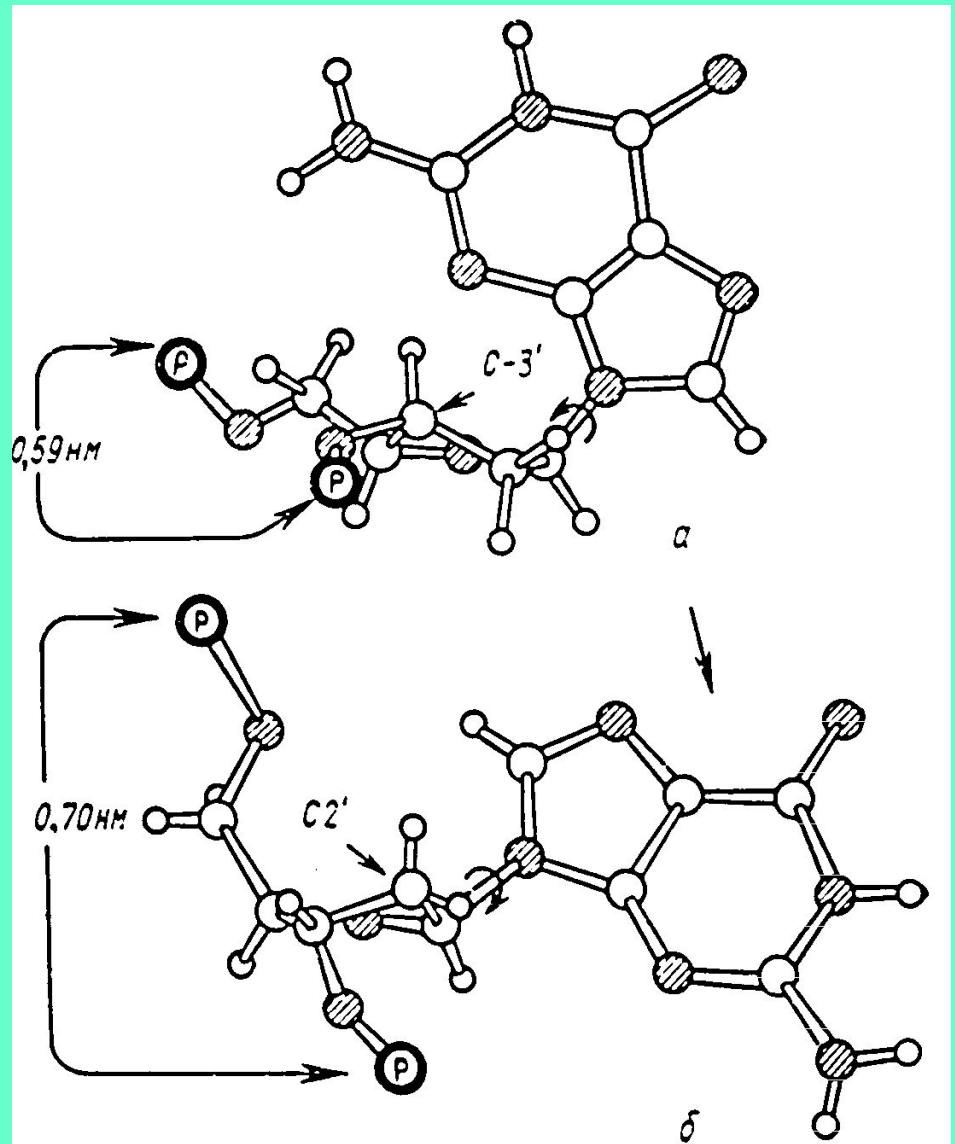
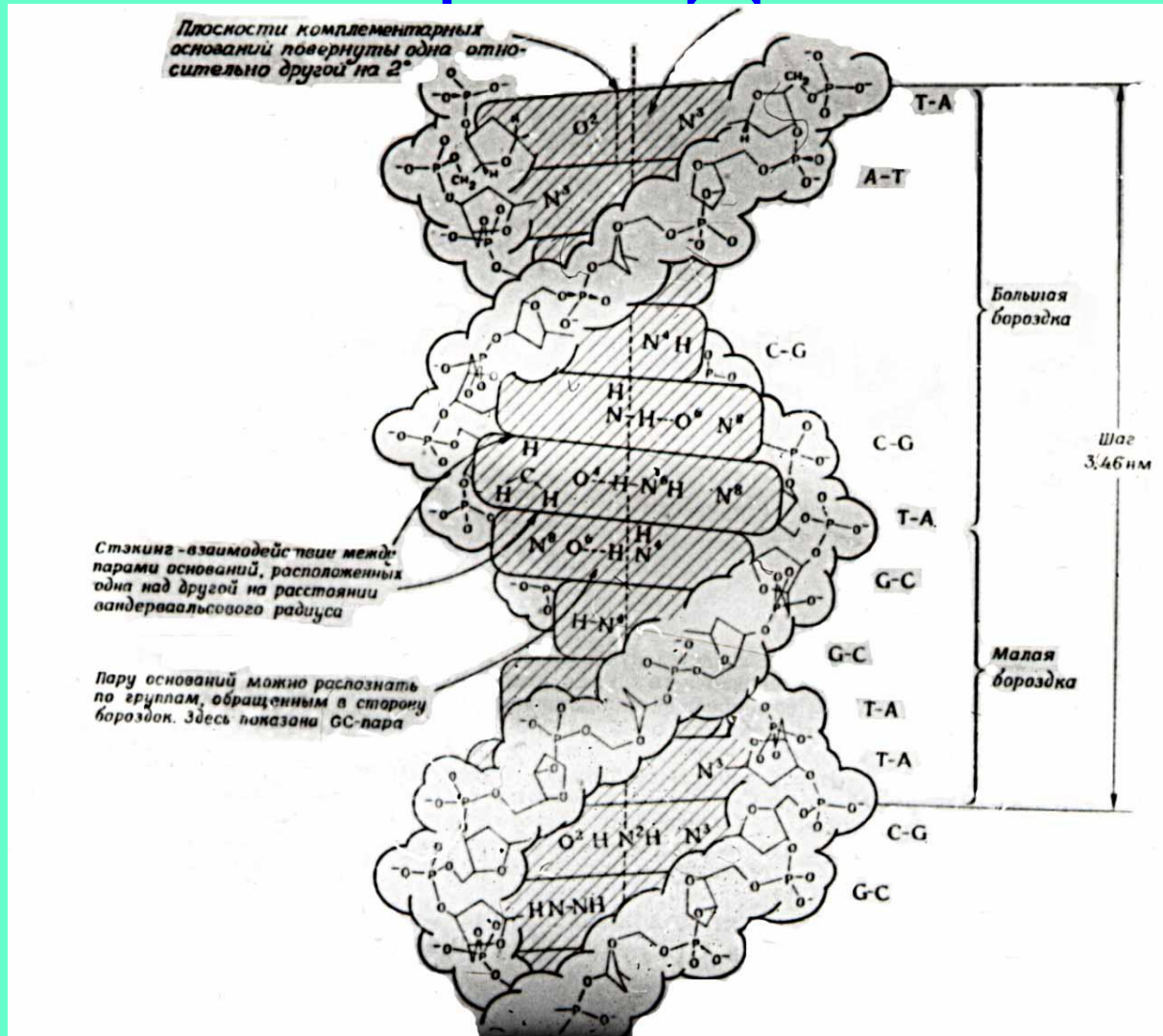


Рис. 11. Схема, показывающая изменение расстояний между фосфатными остатками нуклеотидного звена ДНК при C3'-эндо- — C2'-эндо-конформационном переходе:

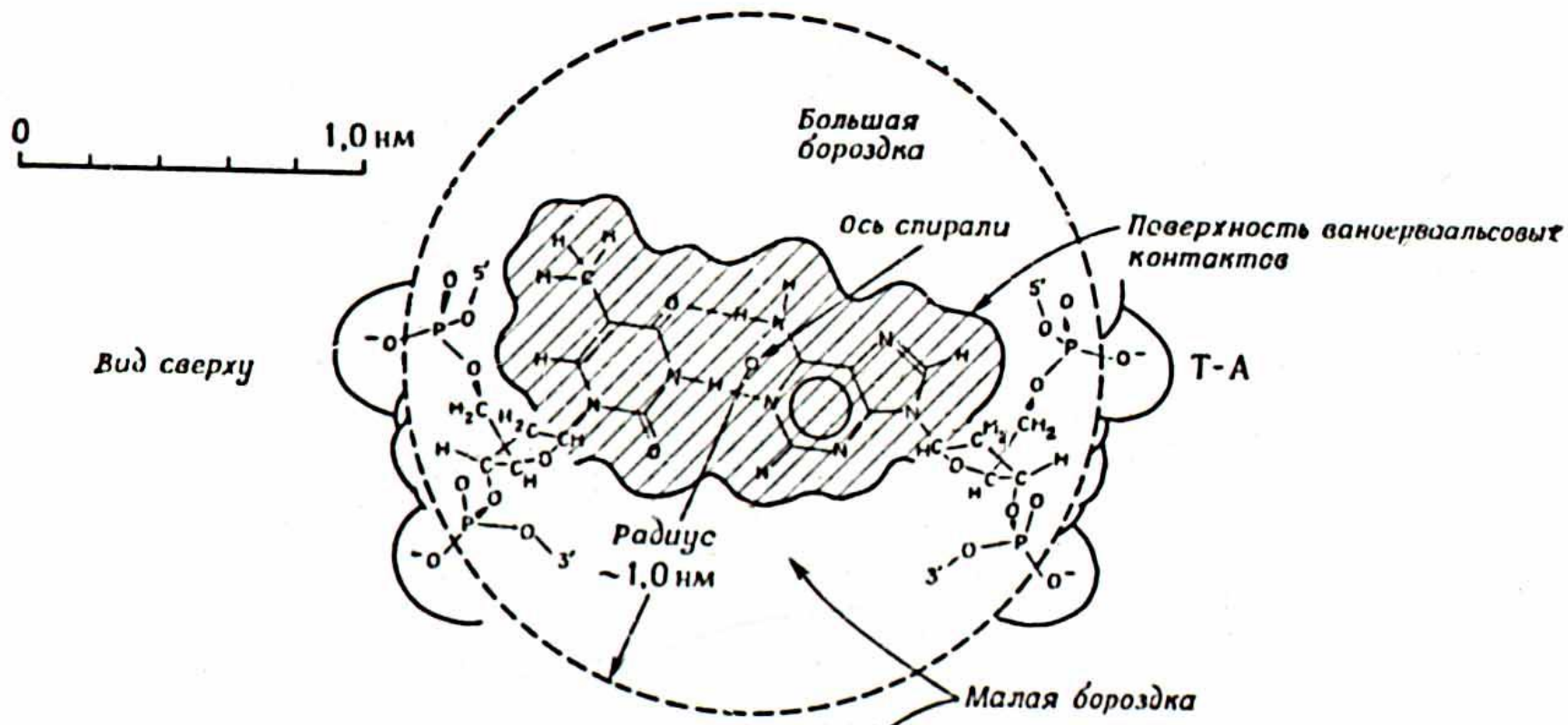
В-форма ДНК



Малая и большая бороздки спирали ДНК



Малая и большая бороздки спирали ДНК



ДНК в А-форме

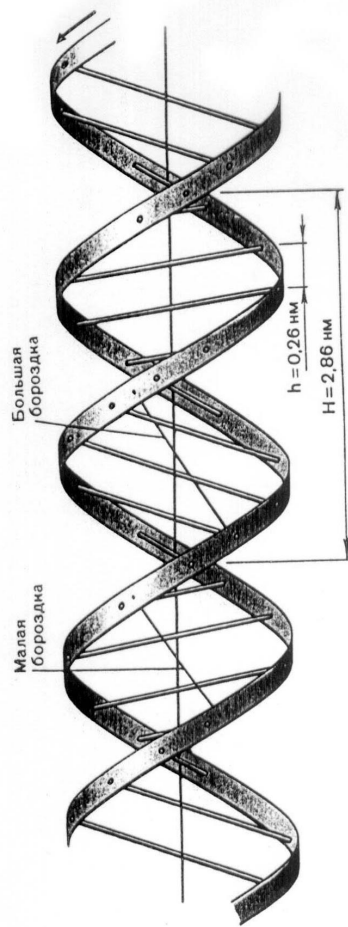
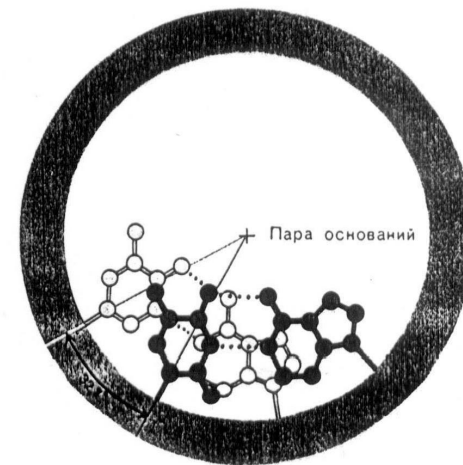
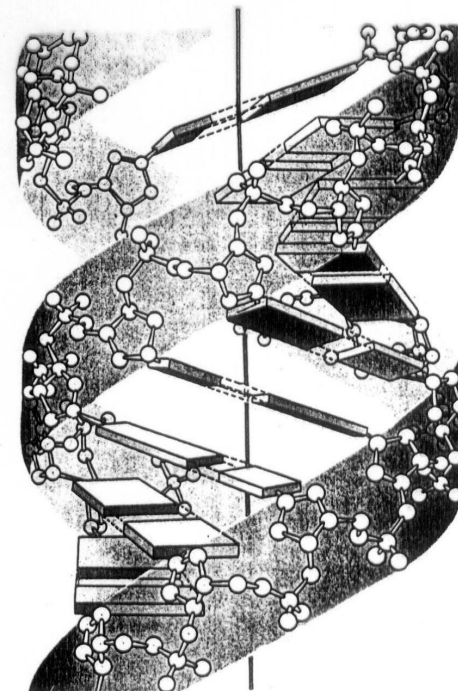
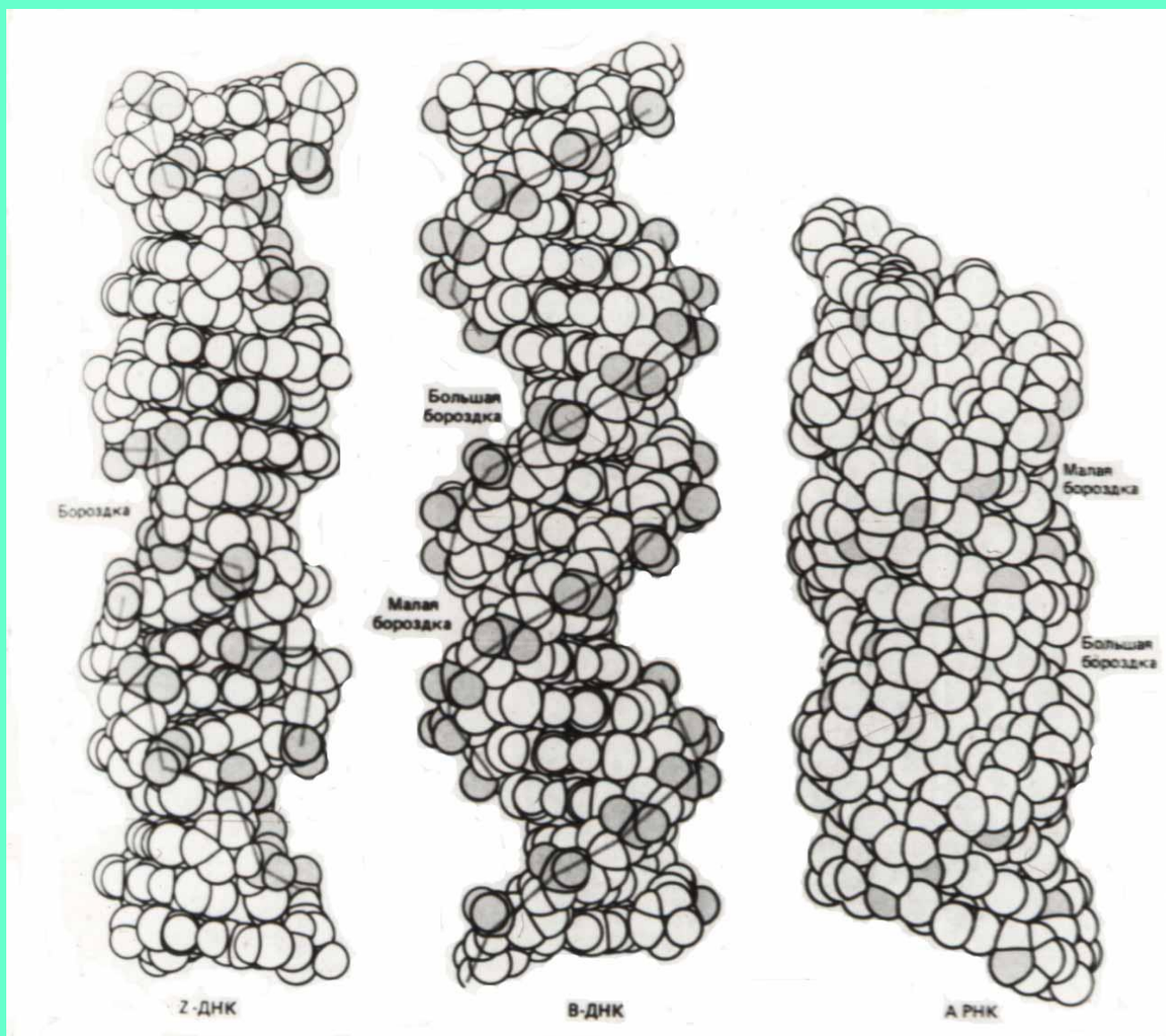


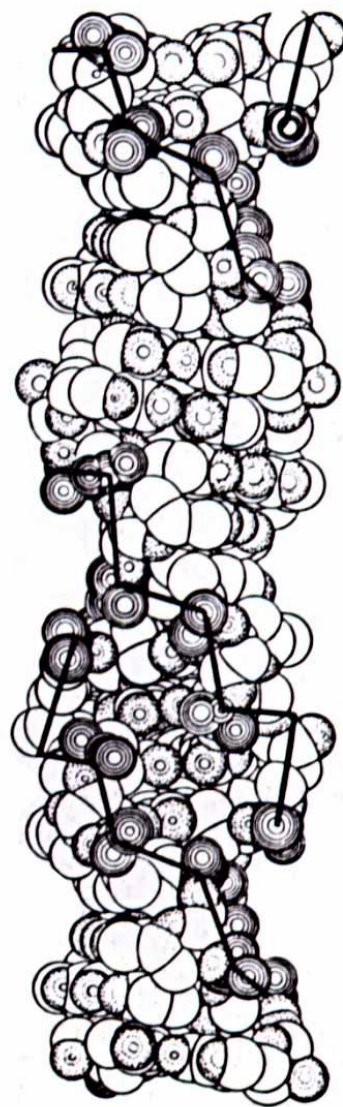
Рис. 194. ДНК в А-форме.



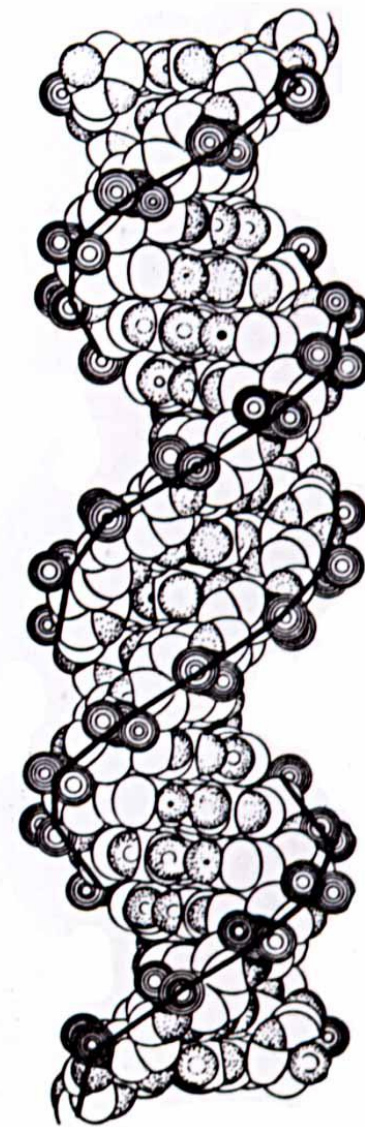
Формы ДНК и РНК



Объёмные модели Z- и В-форм ДНК



Z-форма



B-форма

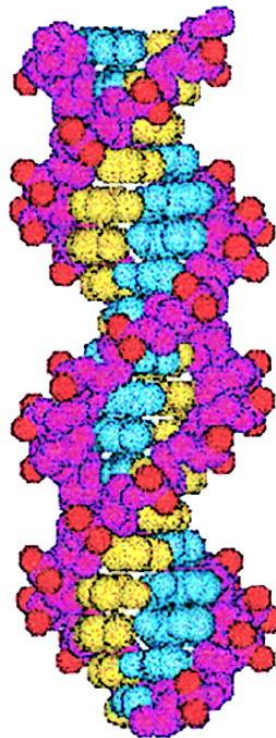
Рис. 34. Так выглядят объёмные модели Z- и B-формы ДНК. Черные линии нарисованы, чтобы показать ход сахаро-фосфатной цепи

Z-форма ДНК

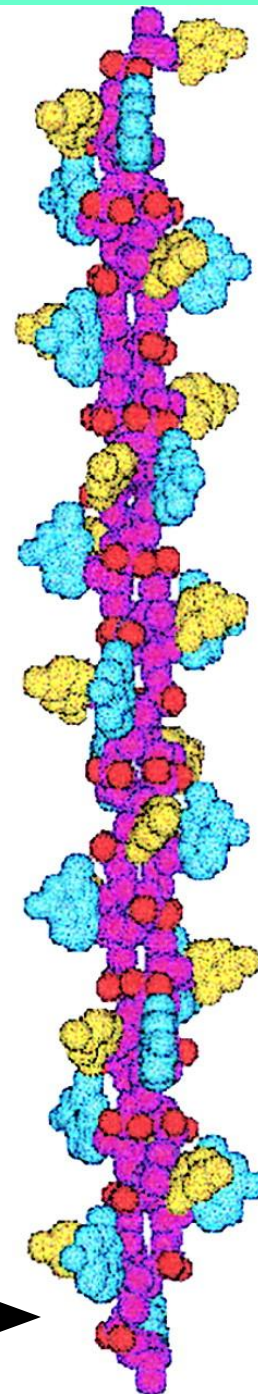


ДНК в Р-форме

В-форма:



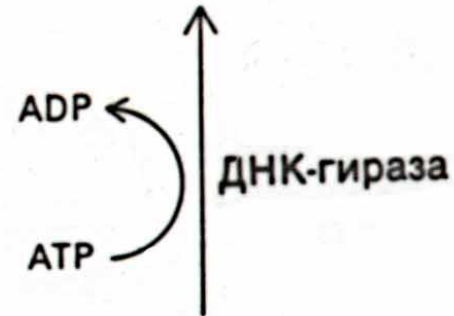
Р-форма:



Отрицательная суперспираль ДНК

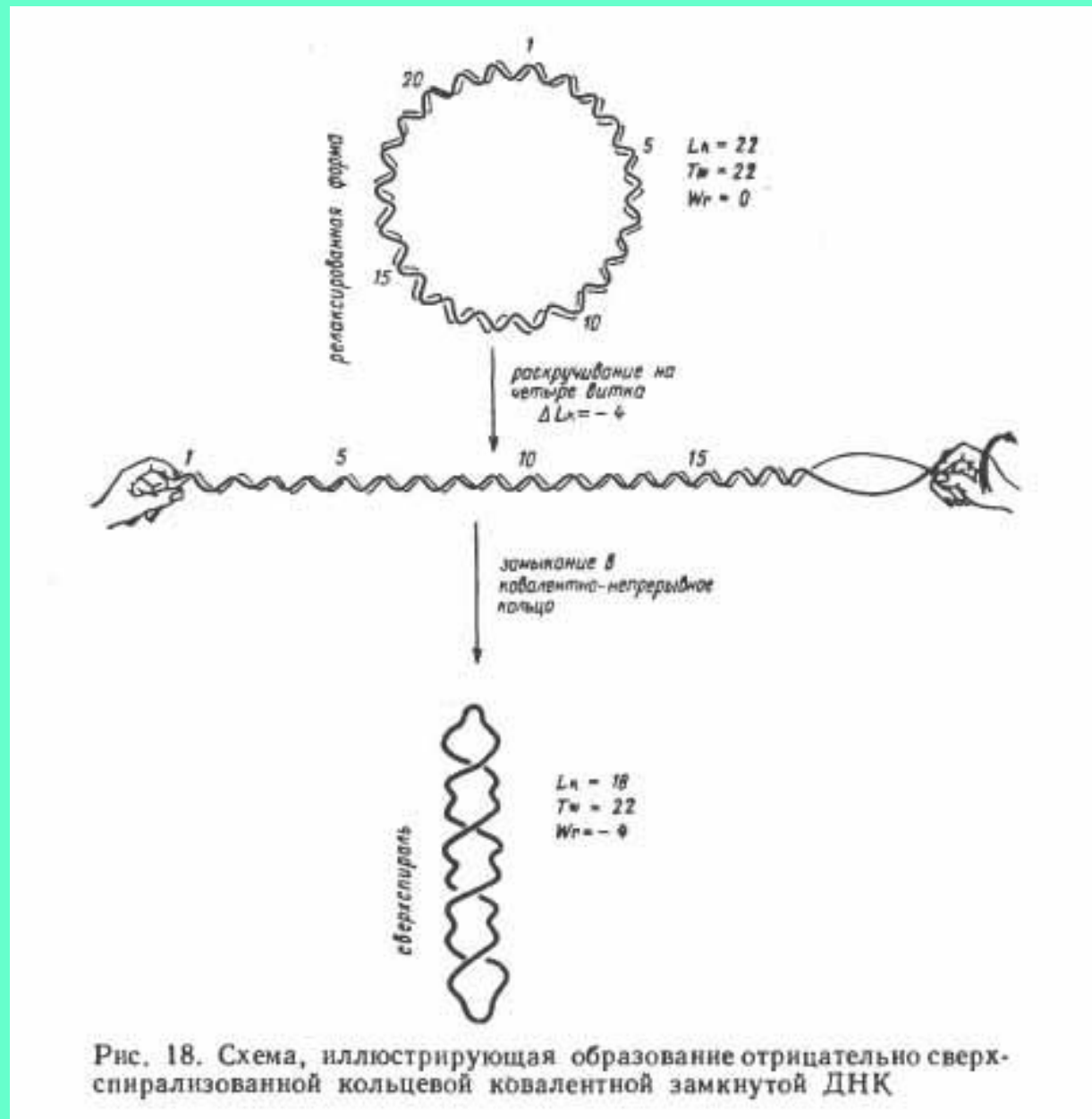


Отрицательная суперспираль ДНК

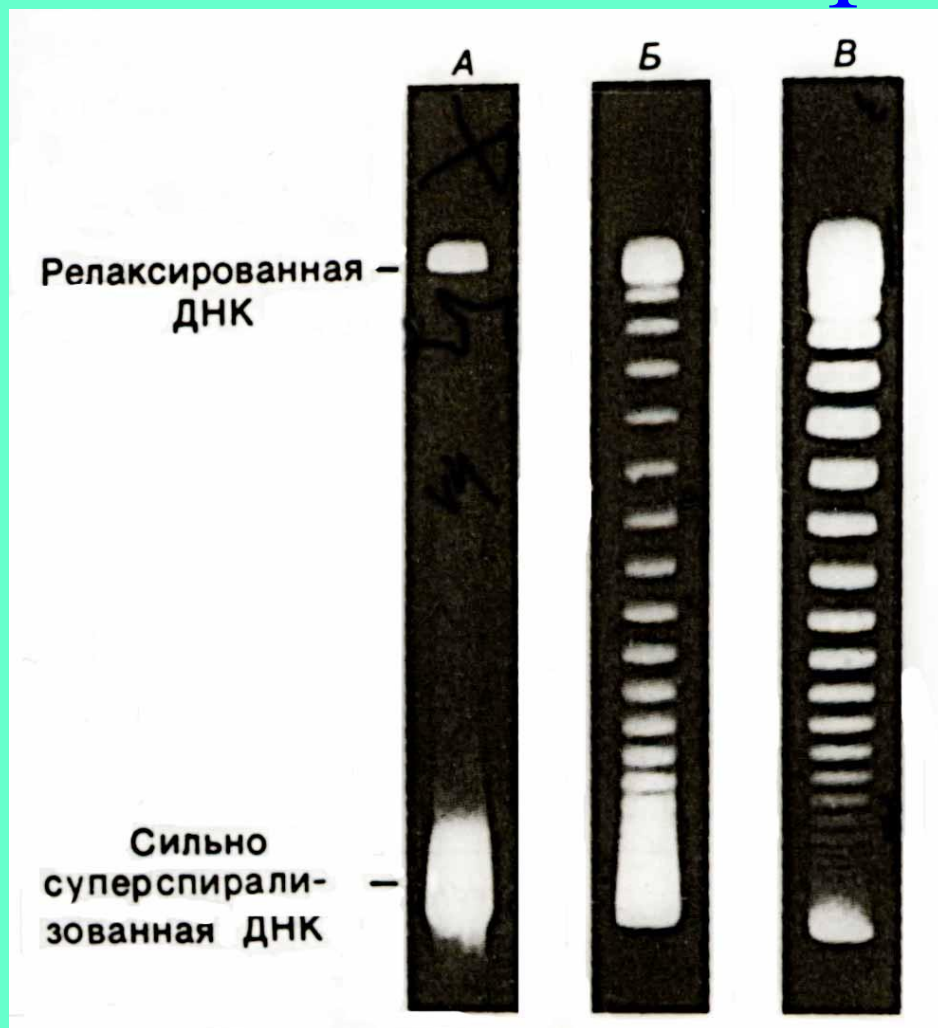


Релаксированная ДНК

Схема
образования
отрицательно
сверхспира-
лизованной
кольцевой
ковалентно
замкнутой
ДНК



Электрофоретическое разделение топологических изомеров ДНК



Классификация ТОПОИЗОМЕРАЗ

TABLE 1 Classification of Topoisomerases

| Topoisomerase ^a | Subfamily type | Subunit structure | Size(s) (aa) ^b |
|---|----------------|--|---------------------------|
| Eubacterial DNA topoisomerase I (<i>E. coli</i>) | IA | Monomer | 865 |
| Eubacterial DNA topoisomerase III (<i>E. coli</i>) | IA | Monomer | 653 |
| Yeast DNA topoisomerase III (<i>S. cerevisiae</i>) | IA | Monomer | 656 |
| Mammalian DNA topoisomerase III α (human) | IA | Monomer | 1001 |
| Mammalian DNA topoisomerase III β (human) | IA | Monomer | 862 |
| Eubacterial and archaeal reverse DNA gyrase (<i>Sulfolobus acidocaldarius</i>) | IA | Monomer | 1247 |
| Eubacterial reverse gyrase (<i>Methanopyrus kandleri</i>) ^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 (<i>Methanopyrus kandleri</i>) ^d | IB | Monomer | — ^e |
| Eubacterial DNA gyrase (<i>E. coli</i>) | IIA | A ₂ B ₂ heterotetramer | GyrA, 875 GyrB, 804 |
| Eubacterial DNA topoisomerase IV (<i>E. coli</i>) | IIA | C ₂ E ₂ heterotetramer | ParC, 752 ParE, 630 |
| Yeast DNA topoisomerase II (<i>S. cerevisiae</i>) | IIA | Homodimer | 1428 |
| Mammalian DNA topoisomerase II α (human) | IIA | Homodimer | 1531 |
| Mammalian DNA topoisomerase II β (human) | IIA | Homodimer | 1626 |
| Archaeal DNA topoisomerase VI (<i>Sulfolobus shibatae</i>) | IIB | A ₂ B ₂ heterotetramer | A, 389 B, 530 |

^aThe 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.

^bThe subunit sizes are those corresponding to the most extensively studied family member.

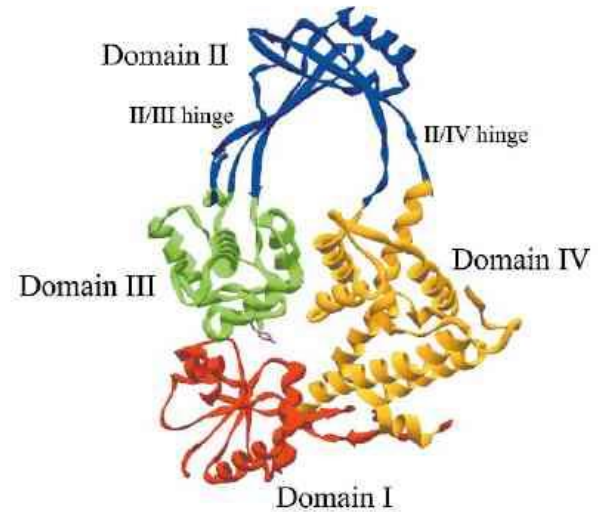
^cIncluded as the only known reverse gyrase with a heterodimeric structure.

^dOnly known representative at present. Probably present in other hyperthermophilic eubacteria.

^eGene not yet cloned; purified protein has a molecular size of 110 kDa.

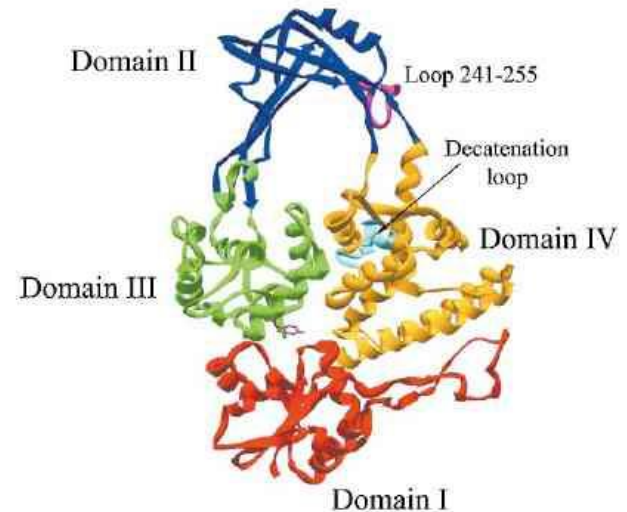
Структура топоизомераз I и III *E. coli*

a



E. coli topoisomerase I

b



E. coli topoisomerase III

Пространственная структура гиразы

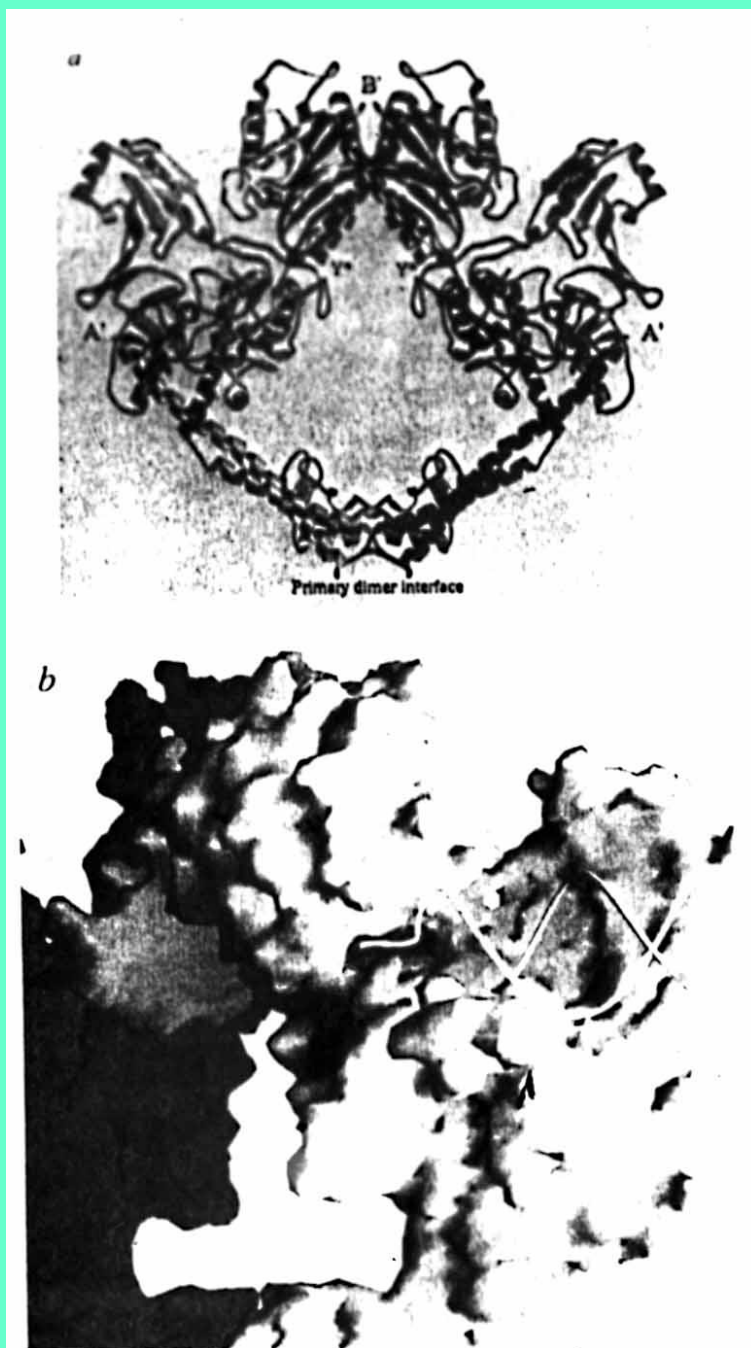


Схема расщепления дуплекса ДНК топоизомеразой II

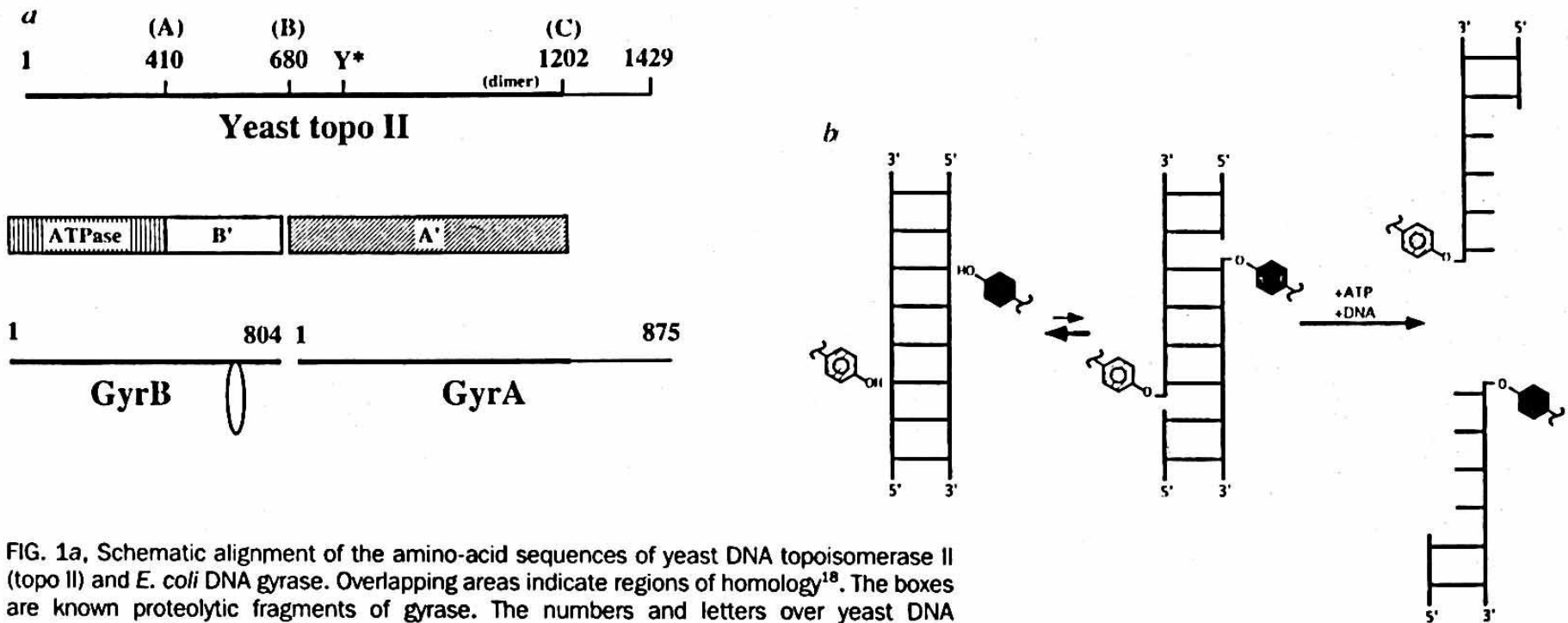


FIG. 1a, Schematic alignment of the amino-acid sequences of yeast DNA topoisomerase II (topo II) and *E. coli* DNA gyrase. Overlapping areas indicate regions of homology¹⁸. The boxes are known proteolytic fragments of gyrase. The numbers and letters over yeast DNA topoisomerase II are the SV8 protease 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

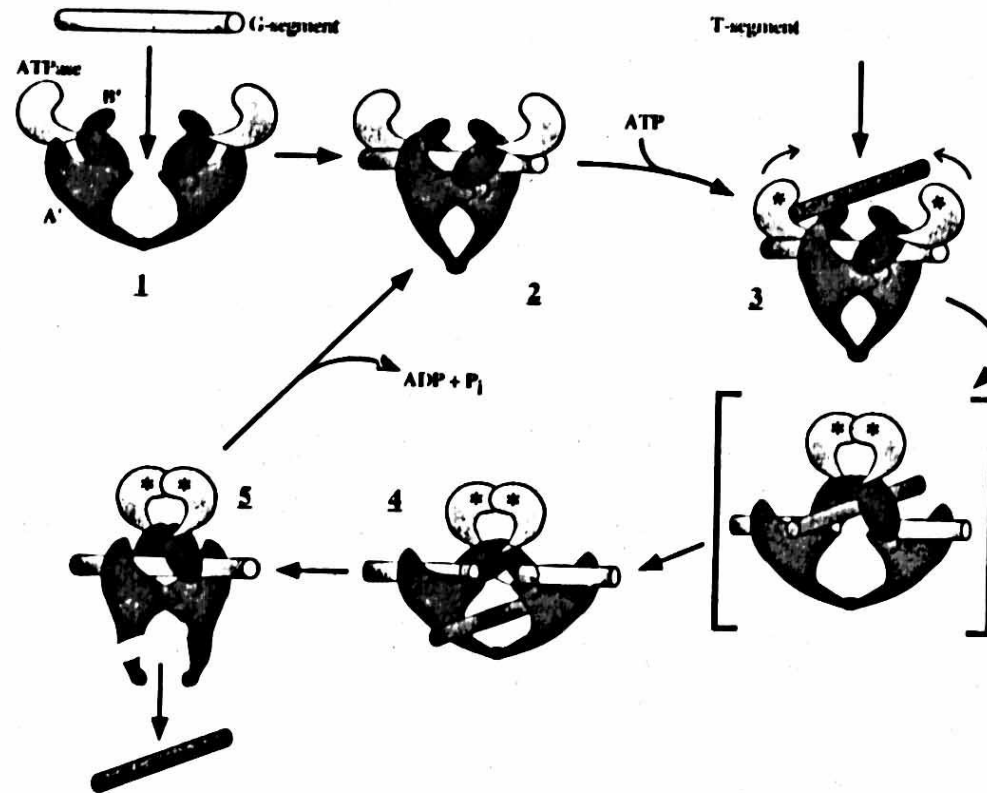


FIG. 5. A molecular model for the catalytic reaction of topoisomerase II. The ATPase domain, B' and A' subfragments are coloured yellow, red and blue, respectively. The G-segment DNA (containing the DNA gate) is grey, and the transported T-segment is green. In (1) an unliganded enzyme first binds the 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).