

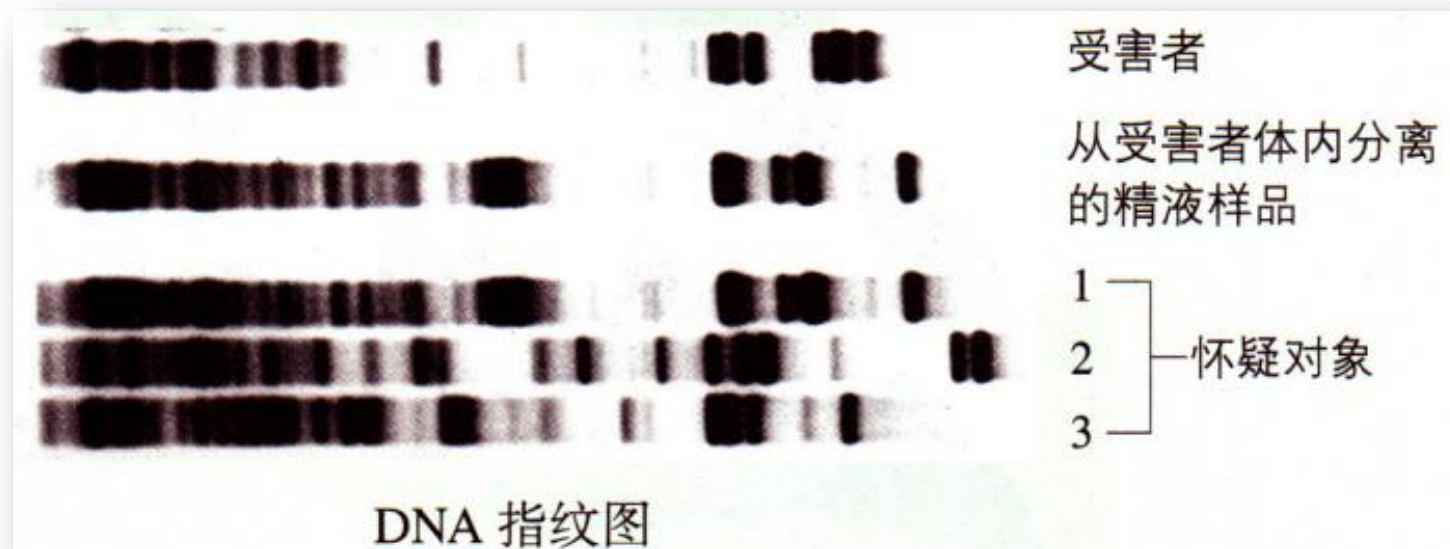
真凶密码



琳达还没回家
Lynda's not home yet.

DNA指纹技术

你能从下面DNA指纹图判断出怀疑对象中谁是罪犯吗？



DNA指纹技术还可以用于亲子鉴定、死者遗骸鉴定等。

DNA为什么能作为遗传物质？

它的哪些结构特点与储存丰富的遗传信息相适应？



人教必修2

第3章 基因的本质

第2节 DNA的结构



一 .DNA双螺旋结构模型的构建

1.构建者:沃森和克里克

克里克: 物理学家, 对X射线晶体衍射图谱的分析十分熟悉, 能够帮助沃森理解晶体结学原理。

沃森: 生物学家, 可以帮助克里克理解生物学内容。



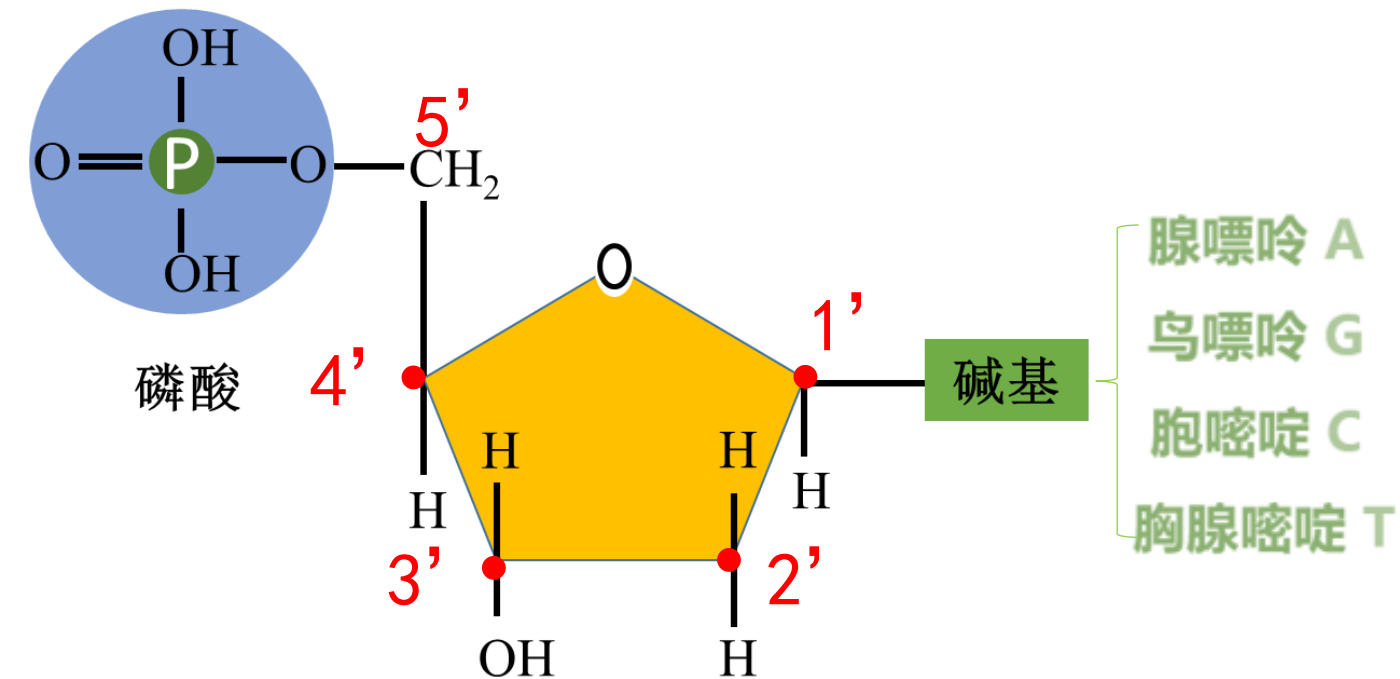
沃森 (左) 和克里克 (右)

2、构建过程

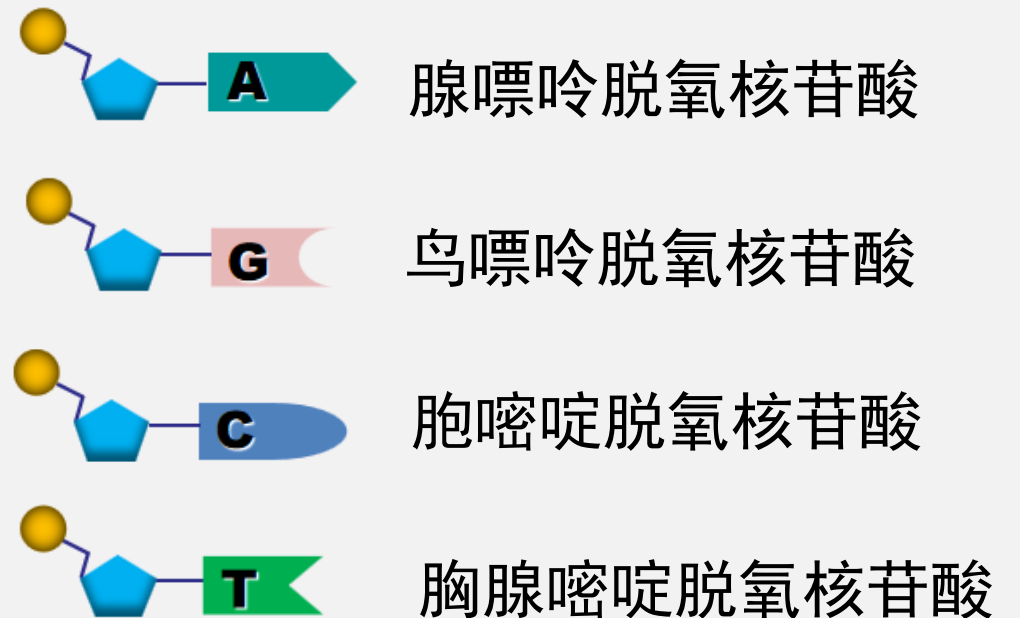
【资料1】当时科学界已经认识到：DNA是以4种脱氧核苷酸为单位连接而成的长链。

1、DNA的基本单位：脱氧核苷酸

脱氧核苷酸的组成： 1分子磷酸 + 1分子脱氧核糖 + 1分子含氮碱基



脱氧核苷酸的种类：4种



活动一、构建四种脱氧核苷酸的模型



请同学们两人为一组，利用材料制作4种脱氧核苷酸，并放在活动单上对应的小框内。（3分钟完成）完成后请同学展示自己制作的模型。



例：腺嘌呤脱氧核苷酸

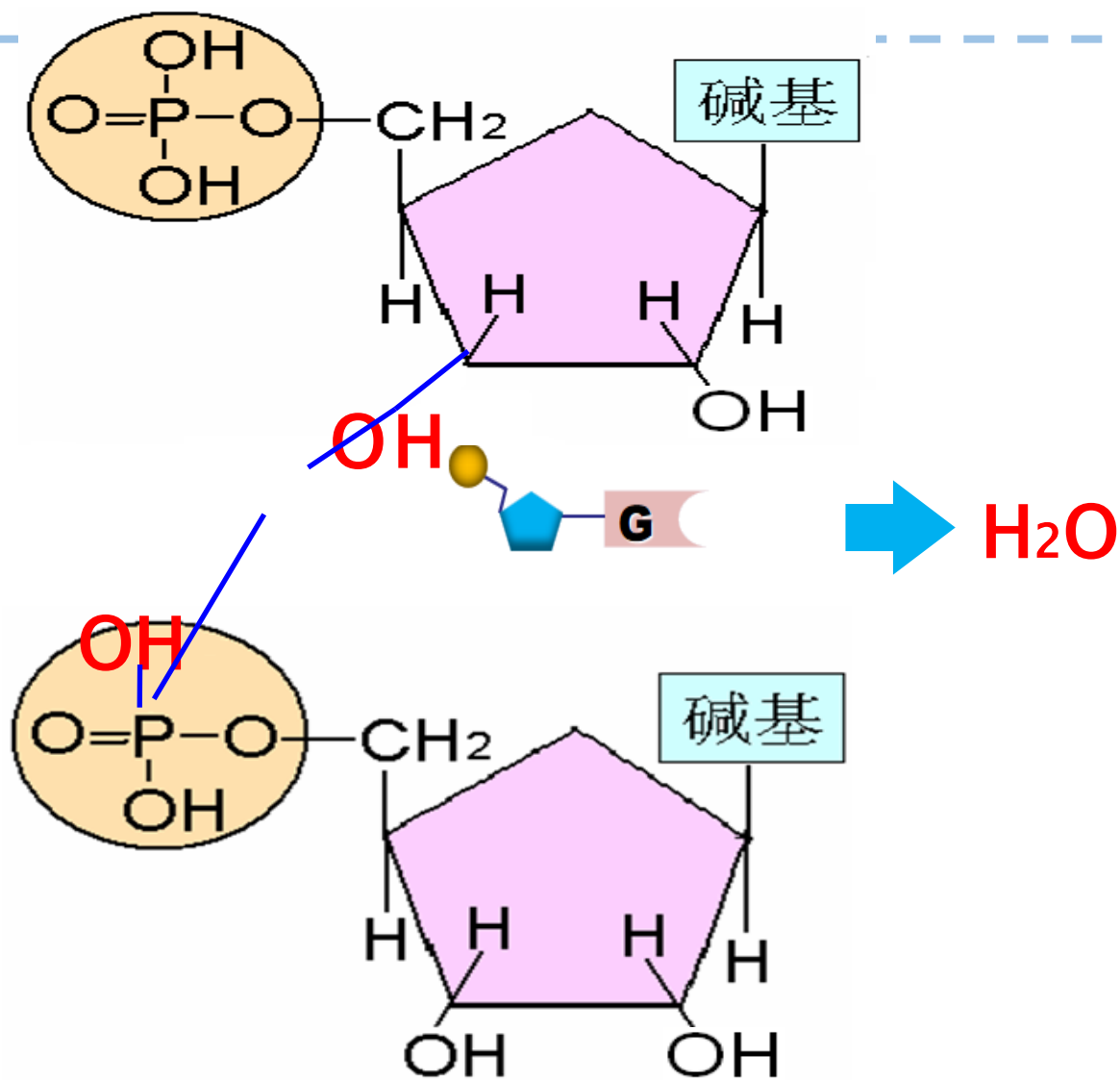
注：碱基模型上有字母，注意区分

构建过程

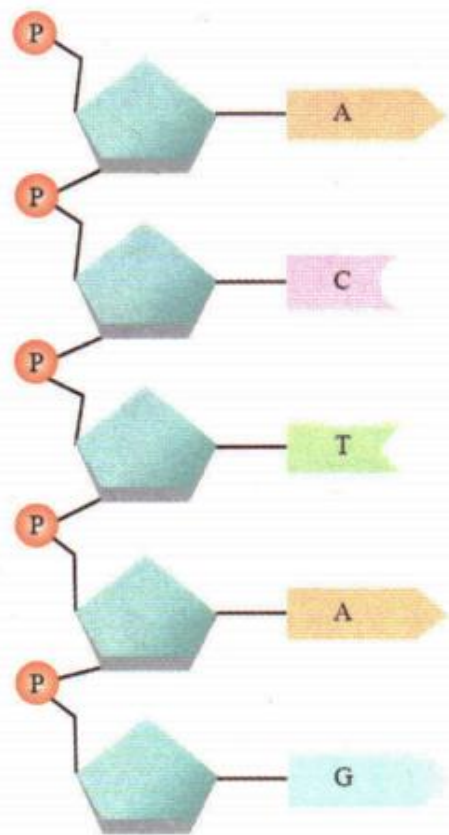
【资料1】当时科学界已经认识到：DNA是以4种脱氧核苷酸为单位连接而成的长链。

DNA的基本单位：**脱氧核苷酸**

脱氧核苷酸是如何连接成长链的呢？



活动二、利用模型构建DNA的一条单链



▲ 图 2-14 核苷酸连接而成的长链

两人为一组，将刚才制作的四个脱氧核苷酸连接成一条单链，并上台展示和介绍。

细棒连接脱氧核糖和磷酸

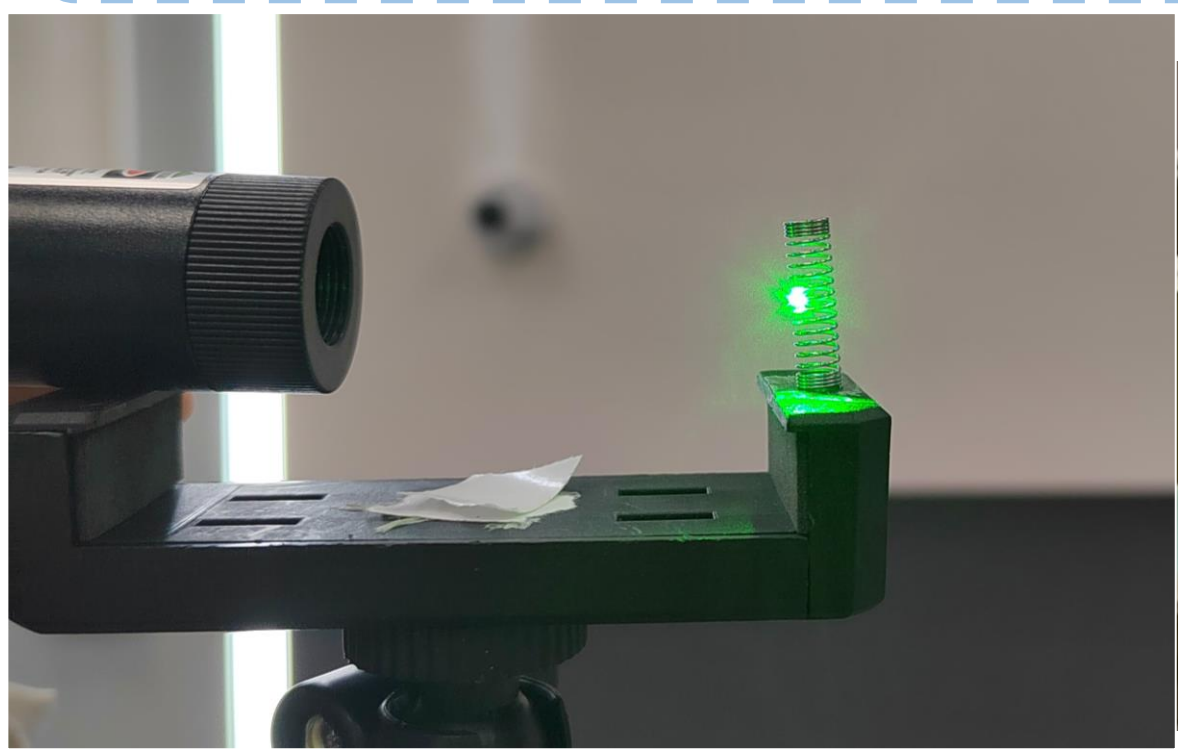


粗棒连接脱氧核糖和碱基



构建过程

【资料2】英国物理学家威尔金斯和他的同事富兰克林利用X射线衍射技术获得了高质量的DNA衍射图谱。

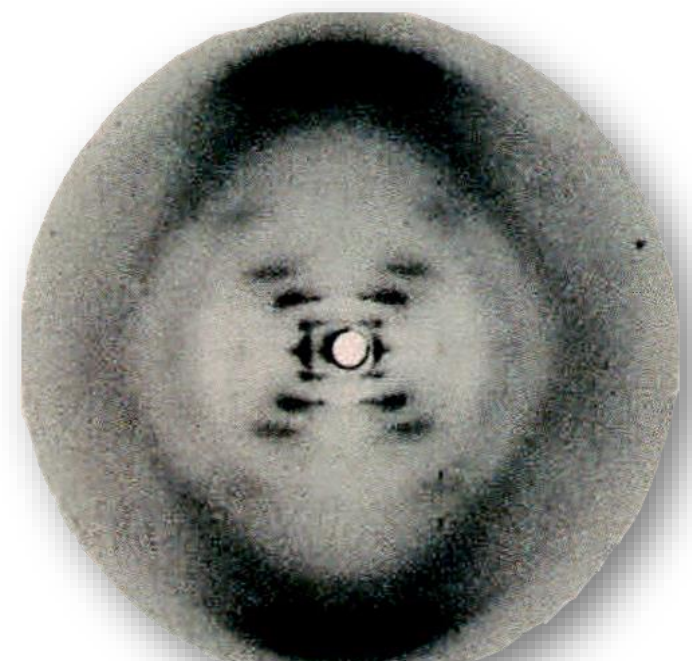
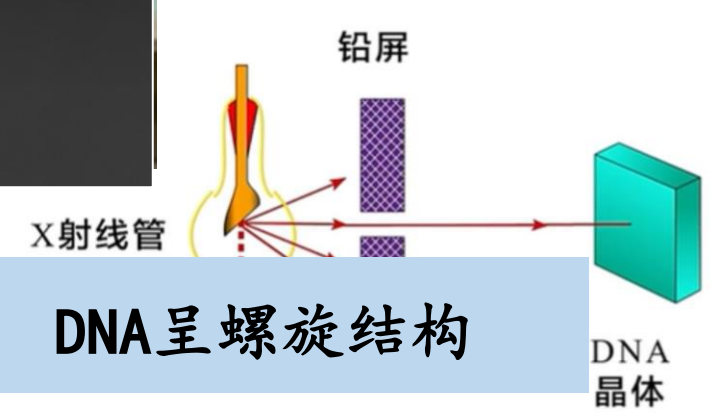


DNA衍射图呈现
“X”形

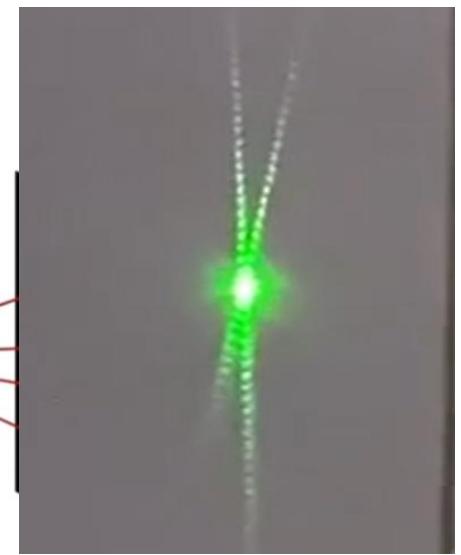
推断
→

DNA呈螺旋结构

找找两个图谱
的相似处？
说明DNA有什么
样的结构？



富兰克林拍摄的DNA衍射图谱



弹簧的类衍射图

【资料3】1952年，奥地利生物化学家查哥夫（E. Chargaff）发现：在DNA中，四种碱基有如下的数量关系：

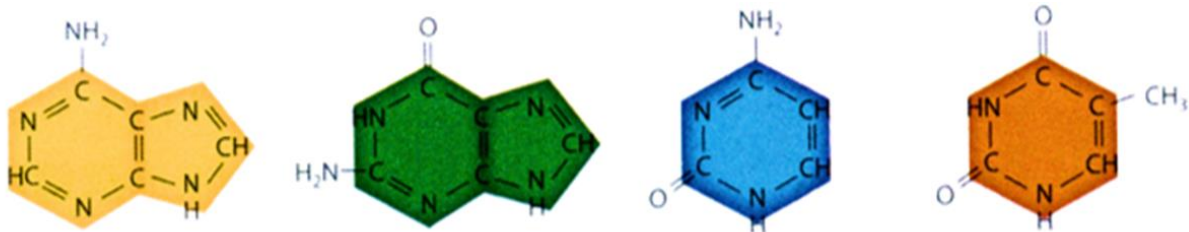
来源	碱基的相对含量			
	腺嘌呤 A	鸟嘌呤 G	胞嘧啶 C	胸腺嘧啶 T
人	30.9	19.9	19.8	29.4
牛	27.9	22.7	22.1	27.3
酵母菌	31.3	18.7	17.1	32.9
结核分枝杆菌	15.1	34.9	35.4	14.6

碱基之间存在怎样的数量关系？

$$A=T$$

$$C=G$$

【资料4】DNA的直径是恒定的，4种碱基的结构如下图所示：



腺嘌呤 (A) 鸟嘌呤 (G) 胞嘧啶 (C) 胸腺嘧啶 (T)

嘌呤是双环化合物，所占空间大，
嘧啶是单环化合物，所占空间小

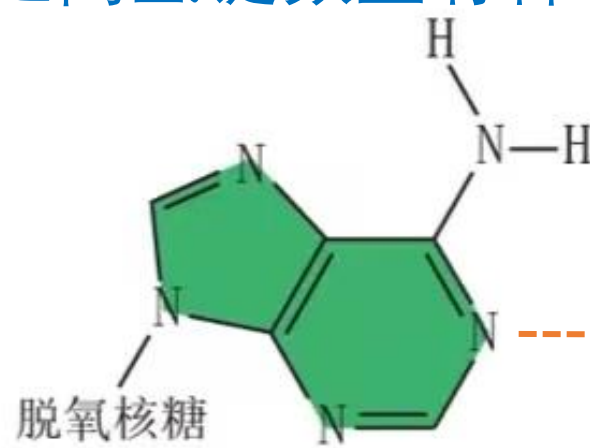
沃森和克里克认为：**A和T配对，C和G配对—碱基互补配对原则**

排列在双螺旋内部

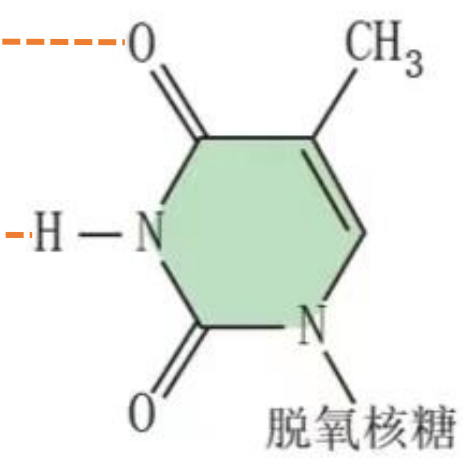
DNA内侧的AT和CG之间是如何配对？
会形成什么化学键？

观察两种碱基对之间氢键数量有什么不同？

腺嘌呤 (A)



胸腺嘧啶 (T)



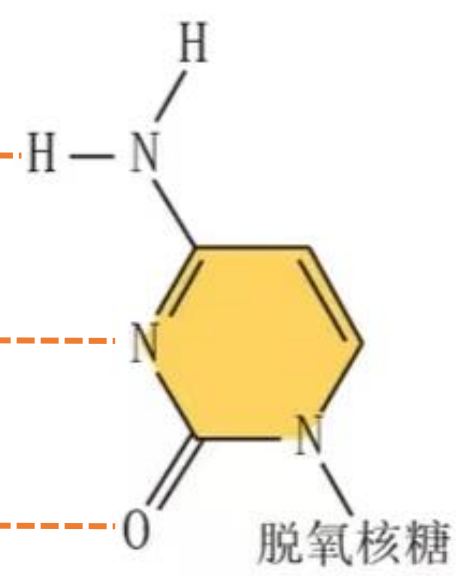
氢键和DNA结构的
稳定有关

氢键

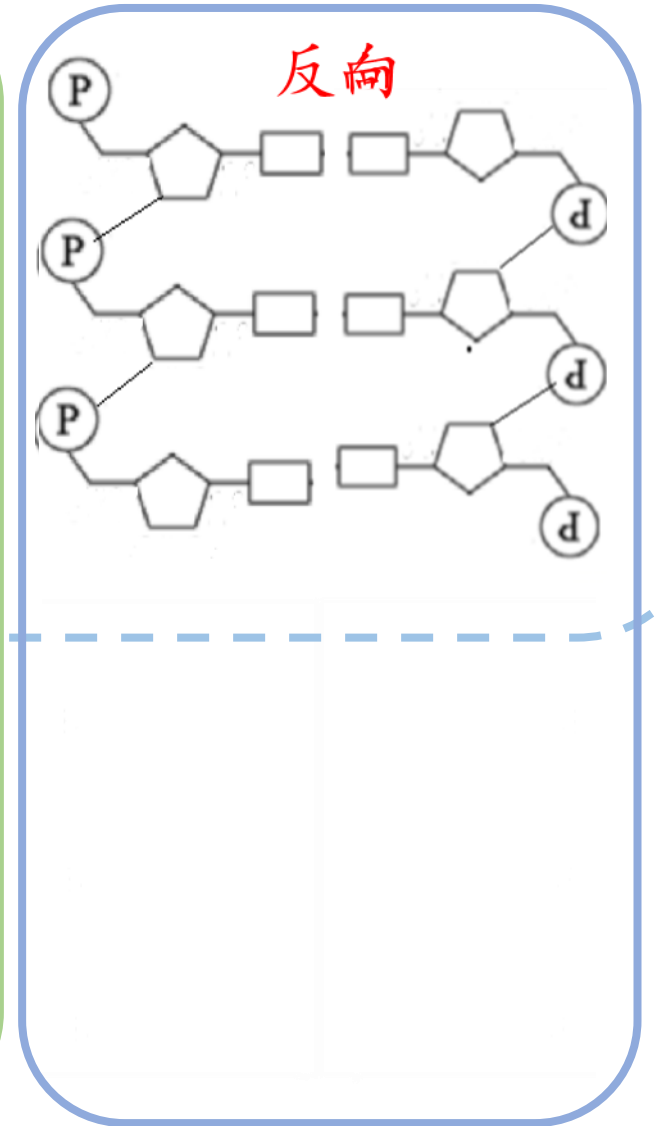
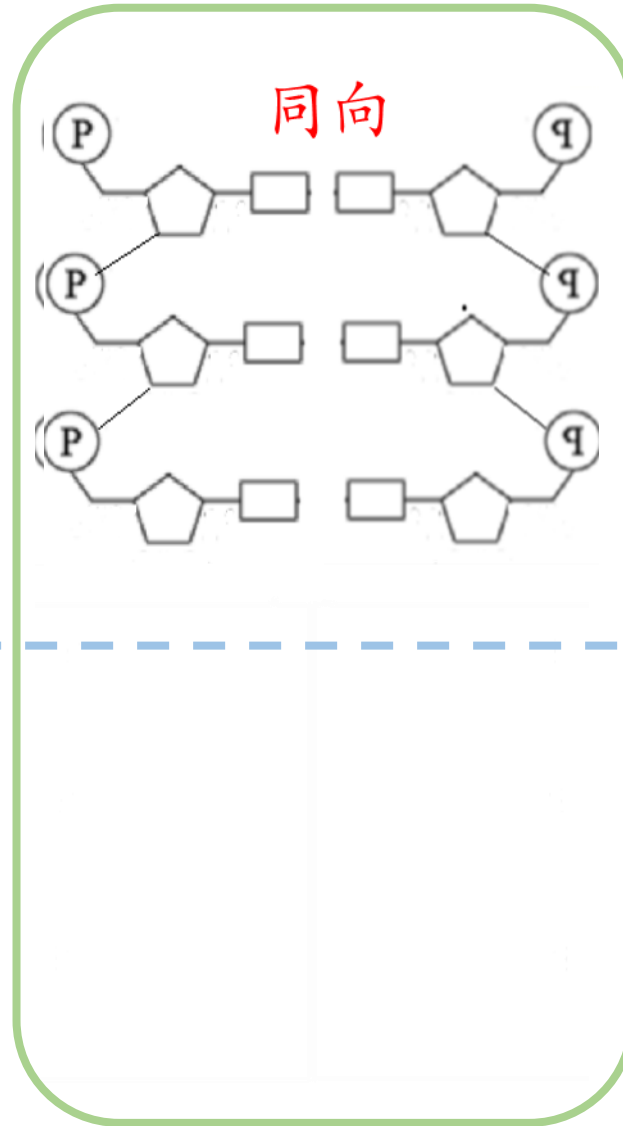
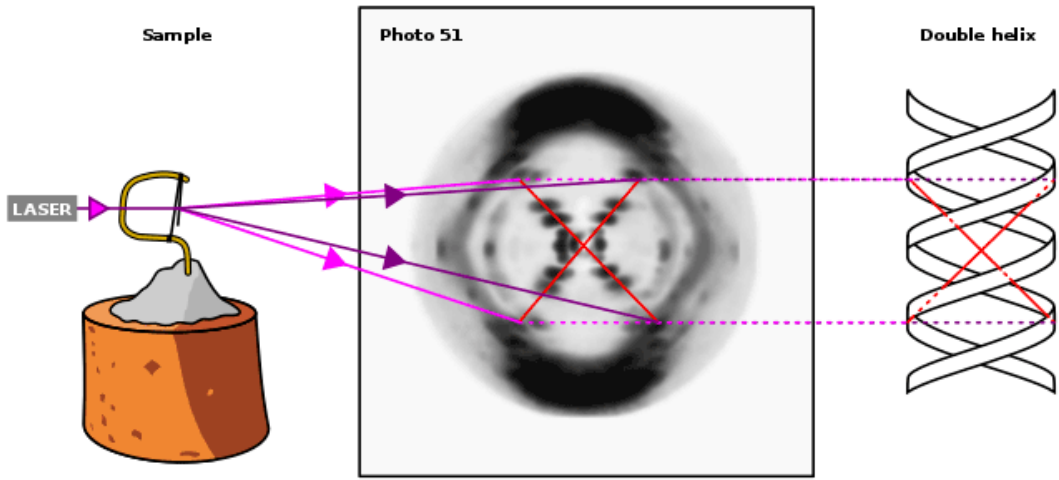
鸟嘌呤 (G)



胞嘧啶 (C)



【资料5】富兰克林和威尔金斯给DNA拍了多张X射线衍射图谱，他们发现DNA翻转180°后的图谱与未翻转的一模一样。



DNA应该是一个轴对称还是中心对称的结构呢？DNA的两条链的方向应该是怎么样的呢？

DNA应该是一个中心对称的结构
由衍射图对比得出DNA两条链
是反向的

构建模型

沃森和克里克将碱基安排在双链螺旋内部，脱氧核糖—磷酸骨架安排在螺旋外部，A与T配对，G与C配对，DNA两条链的方向是相反的。

DNA不是平面结构，会在力的作用下形成双螺旋结构

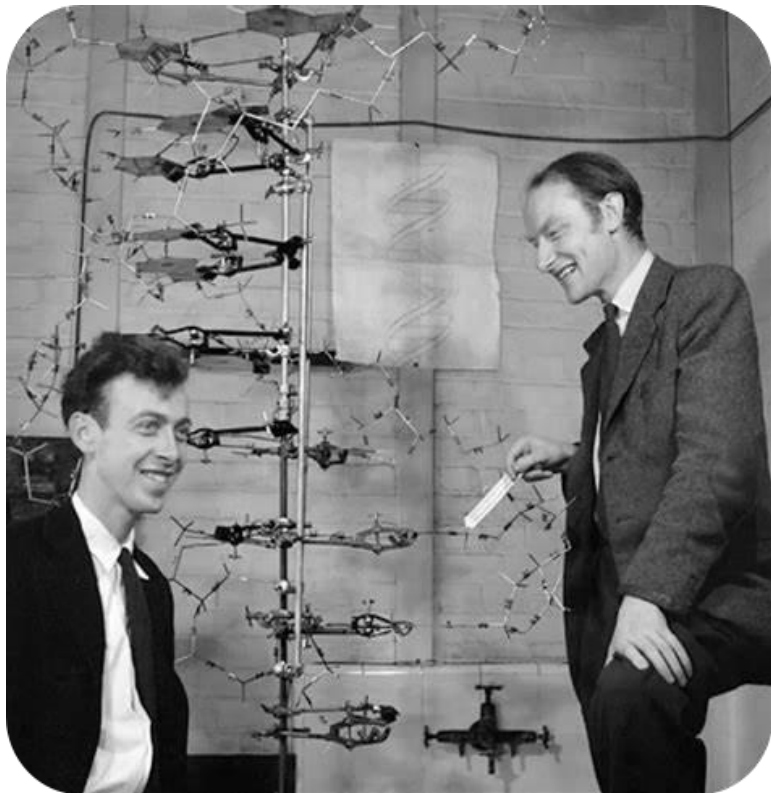


DNA的立体结构



沃森和克里克搭建的DNA双螺旋结构模型

这个金属材料制作的模型与拍摄的X射线衍射照片比较时，发现模型与基于照片推算出的DNA双螺旋结构相符。



equipment, and to Dr. G. E. R. Deacon and the captain and officers of R.R.S. *Discovery II* for their part in making the observations.

¹ Young, F. B., Gerrard, H., and Jevons, W., *Phil. Mag.*, **40**, 149 (1925).

² Longuet-Higgins, M. S., *Mou. Not. Roy. Astro. Soc., Geophys. Supp.*, **6**, 285 (1949).

³ Von Ark, W. S., *Woods Hole Papers in Phys. Oceanog. Meteor.*, **11** (3) (1956).

⁴ Ekman, V. W., *Arkiv. Mat. Astron. Fysik. (Stockholm)*, **2** (11) (1905).

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

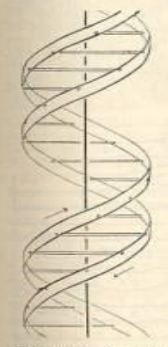
A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey¹. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate di-ester groups joining β -D-deoxy-ribofuranose residues with 3',5' linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's² model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There



This figure is purely diagrammatic. The two ribbons symbolize the chains, and the horizontal rods the pairs of bases linking the chains together. The vertical line marks the fibre axis.

is a residue on each chain every 3-4 A. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical z-coordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally^{3,4} that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

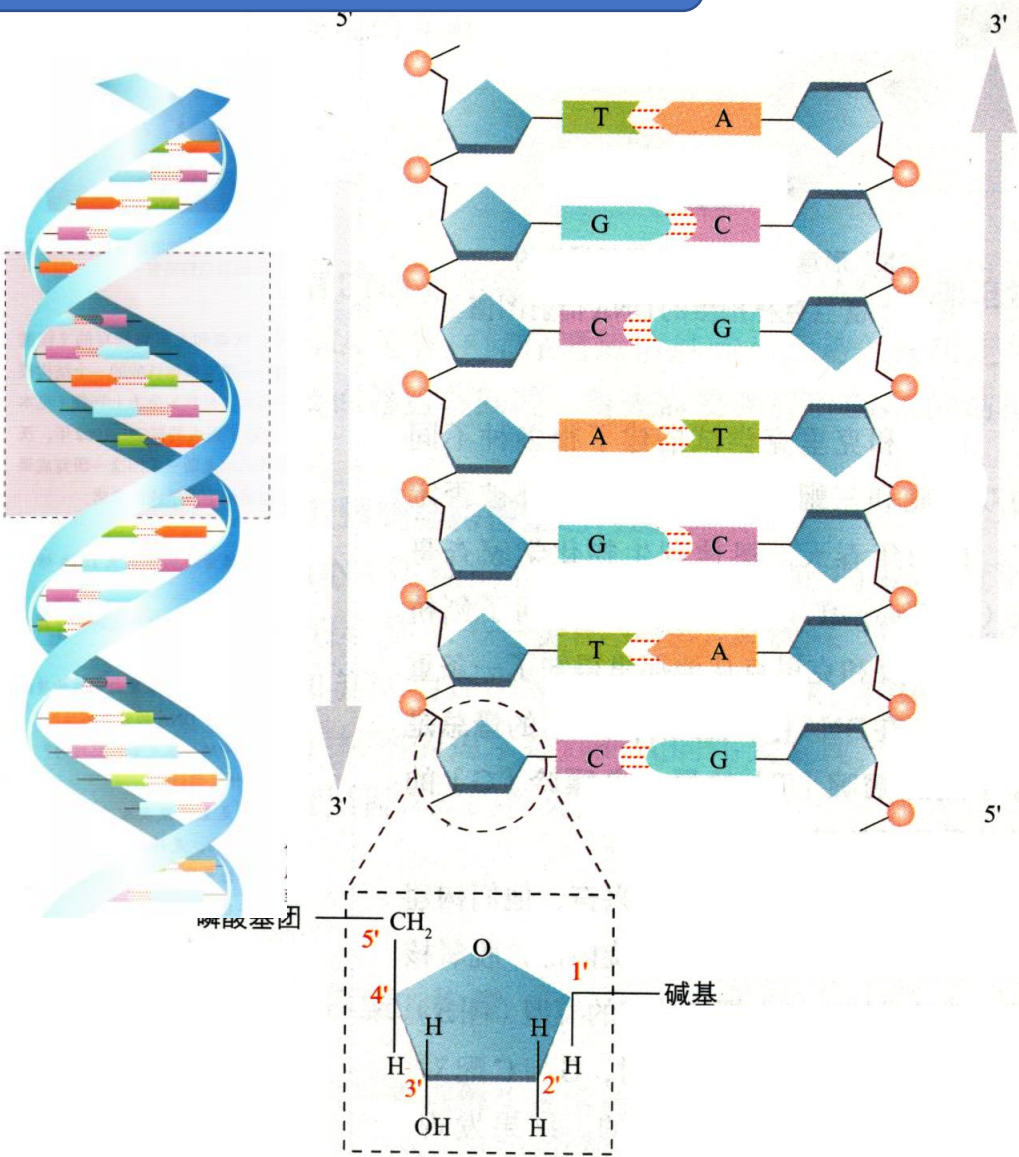
The previously published X-ray data^{5,6} on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at

二.DNA的结构



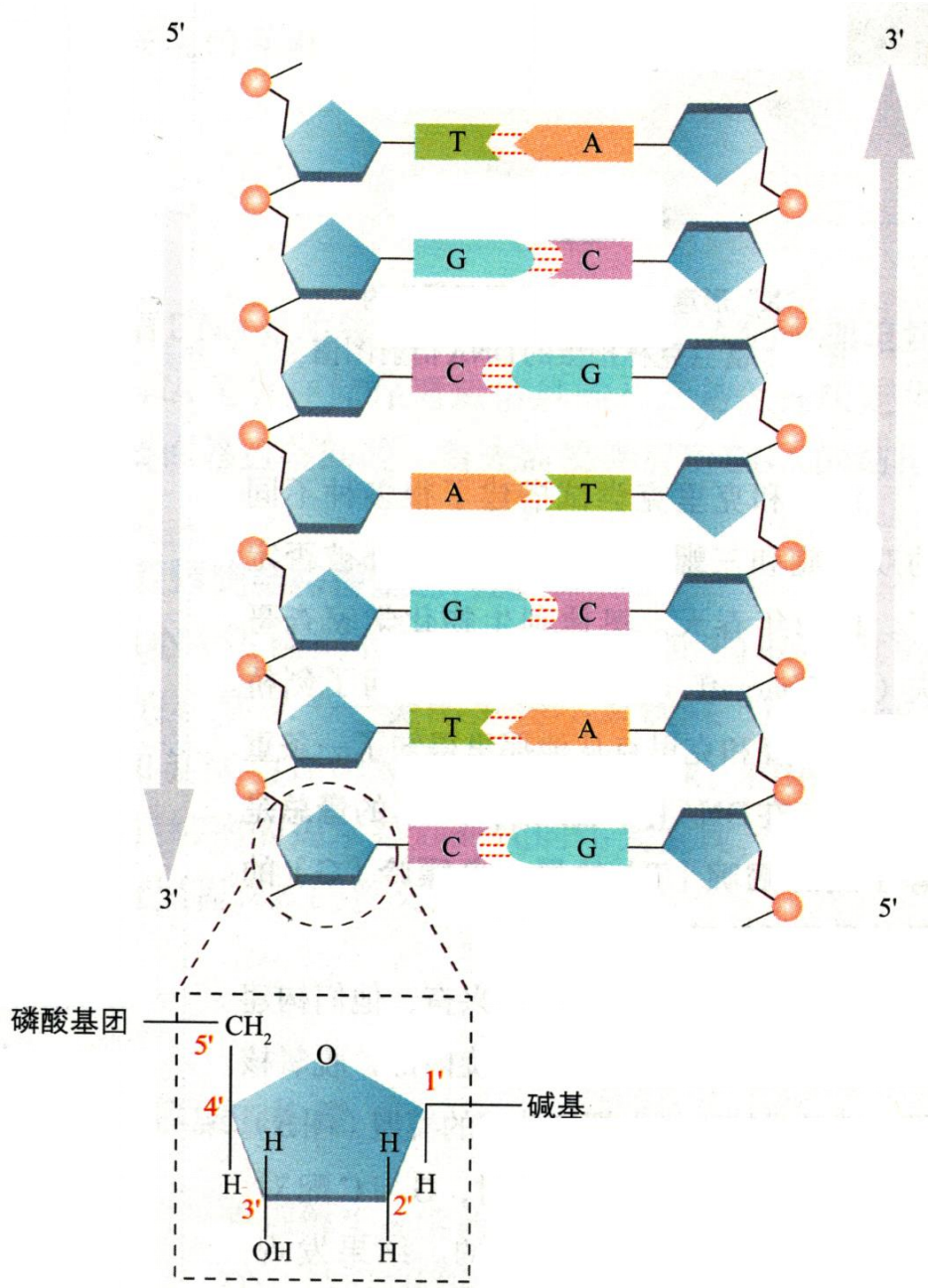
1.DNA分子是由**两条单链**组成的，这两条链按**反向平行方式**盘旋成**双螺旋结构**。

2.DNA分子中的**磷酸**和**脱氧核糖**交替连接排列在外侧，构成**基本骨架**；**碱基**排列在内侧。

3.两条链上的碱基通过**氢键**连接起来，形成**碱基对**，且遵循**碱基互补配对原则**。

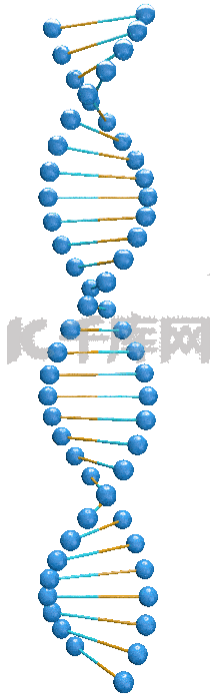
碱基互补配对原则：**A=T** **G≡C**

活动三、构建DNA双螺旋模型



1、请1、3、5排的同学向后转，前后两组同学尝试将两条单链连接成DNA双链，看看两个单链一定能互补成双链吗？如果不能，观察模型并思考是什么原因。

活动三、构建DNA双螺旋模型



DNA的立体结构

2、再收集左右两组的DNA连接成更长的DNA片段，构建成立体的双螺旋结构，并展示。

活动、构建DNA双螺旋模型

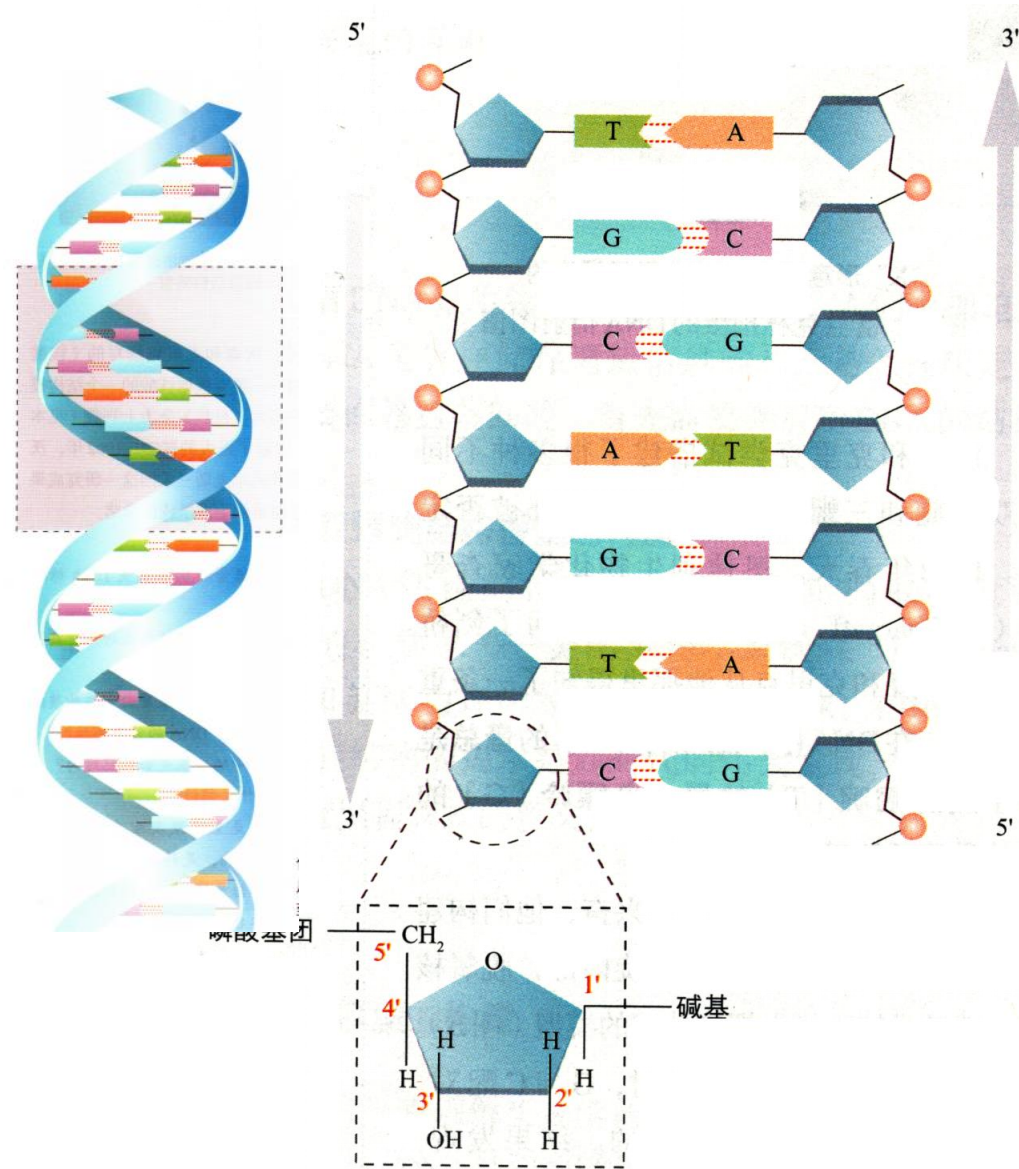
进一步思考：

1、为什么DNA虽然只含有4种脱氧核苷酸却可以储存大量遗传信息？

DNA虽然只含有4种脱氧核苷酸，但是**碱基的排列顺序却千变万化**，使DNA储存了大量的遗传信息

2、碱基互补配对原则对遗传信息的传递有什么意义？

根据碱基互补配对原则，DNA两条链的**碱基之间有准确的一一对应关系**，保证了遗传信息传递的准确性。





1962年诺贝尔生理学及医学奖



威尔金斯

克里克

沃森

DNA结构的科学探究过程给了你哪些启示？

多学科交叉融合、
合作探究、
科学的研究方法、
科学技术的进步、
百折不挠、
善于总结等。

课后探究

- 1、你能够根据DNA的结构特点，设想DNA的复制方式吗？
- 2、生物遗传物质DNA的螺旋方向是左手螺旋还是右手螺旋？
- 3、不同生物的DNA结构都相同吗？