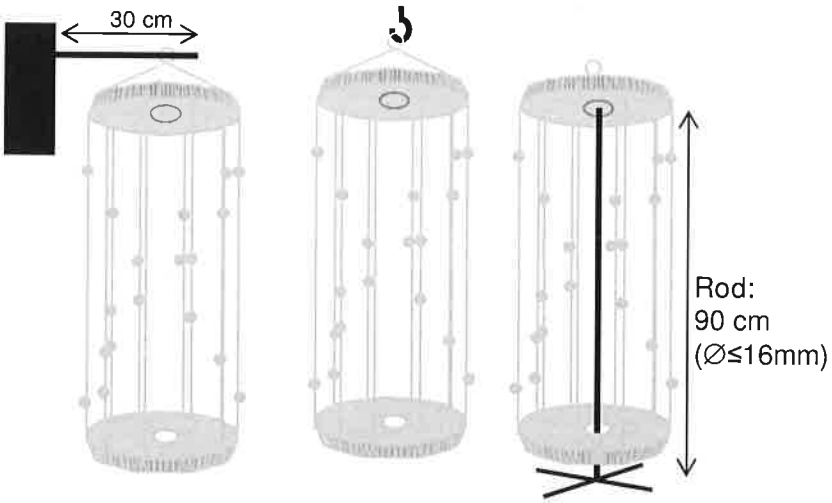
Orbit™ Proview™ DNA Suspension Framework

This pack contains a framework of nylon lines between two wooden plates. It is used to position and support the DNA model.

You need to have one of the following in place to support the framework:

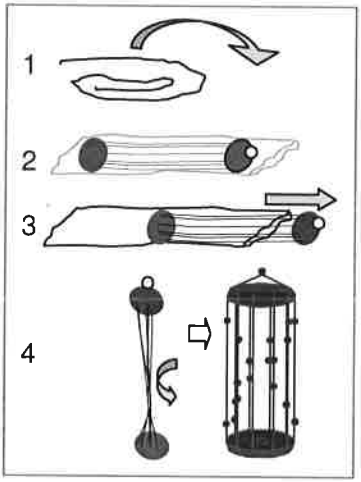
(1) a horizontal strut 1-1.5 cm dia. (2) hook or (3) a stand



PREPARE ONE OF THE SUPPORTS ABOVE BEFORE OPENING THIS PACK

Removing the Framework from the pack.

5. Gently unwind the package.
6. Take hold of the ring or first plate.
7. Gently pull the assembly from the bag.
8. If any of the lines are tangled gently unwind the tangles.



Mount the framework on a hook, strut or stand as shown above

How to make the DNA model is explained in separate instructions.

N.B. The difference between T-A and A-T is that the Adenine and Thymine in the A-T layers will be on the opposite side, or 'strand', of the DNA compared to the T-A layers. And because the two strands have opposite 'directions' (one up and one down in our model) the base pair in Figure 5 has been turned over as well as left-to-right to account for this.

G-C = Guanine-Cytosine. This is the same base pair as Cytosine-Guanine but with opposite orientation as per Figure 6.

If using the retort stand, allow the upright to go between the hydrogen bonds nearest the major groove. See "O" in Fig.6

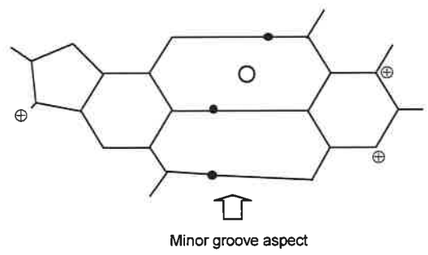


Figure 6. Guanine-Cytosine orientation

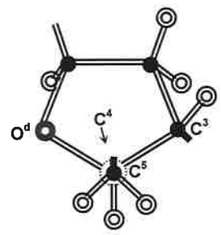
When you have put all the layers on, stand back five yards and look at the spiral effect of the base pairs and check if they seem parallel to each other and equi-distant from each other. The layers should be 7.0 cm apart (6.6 cm to allow for atom/straw thickness). Take the measurement as near the nylon line as you can. A piece of card cut to the right height can help to do this. If necessary, slide the atom centres on the nylon lines up or down.

The base pairs are now ready to be joined by a chain of sugar and phosphate groups.

(7) Attach the Sugar Rings to the Base Pairs.

Examine a sugar ring to ensure you can identify the following details: (see Fig.3)
a. The oxygen (red atom centre) that is part of the ring.
b. The bond with no atom centre on its end (attached to carbon atom 1)
c. The two carbon atoms that have spare prongs.

Carbon atom 5 can be rotated. Rotate the unused prong to bisect the inside angle of the ring at carbon atom 4 when viewed down the carbon-5 carbon-4 axis. i.e. in the diagram, right, the prong points up, half-way between the oxygen and carbon atom 3.



Make sure that all your sugar rings have this structure.

Join a single sugar ring to the top base pair by connecting the spare bond of a sugar ring to the spare prong on the N^j atom on the pentagon. Twist the sugar ring so that the plane of the ring is vertical with its oxygen atom above the level of the base pair.

Orbit™ Proview™ DNA – assembly instructions

Product Reference 0125

This model of DNA has 1.2 pitches (12 base pairs) and if the assembly instructions are carried out it will build a DNA coded for the first part of the protein lysozyme.

The model is assembled out of the pieces from the Orbit™ Molecular Building System. This system uses coloured pieces with prongs on them to represent atoms and tubes to represent bonds.

The tubes are coloured to indicate the type of bond; grey denotes a covalent bond and white a hydrogen bond. The atom centres are coloured to denote the element as follows:

Table 1

	White	Hydrogen univalent	(H^a)
	Red	Oxygen univalent	(O^a)
	White	Hydrogen-bonding hydrogen	(H^b)
	Red	Divalent oxygen	(O^d)
	Blue	Divalent nitrogen	(N^d)
	Black	planar ring carbon	(C^j)
	Blue	planar ring nitrogen	(N^j)
	Black	Tetrahedral carbon	(C^k)
	Purple	Tetrahedral phosphorous	(P^k)

Construction Summary

Unassembled kit contents	Part Assembled kit contents
9 bags of different atom centres 1 bag of various straws 1 suspension framework	12 base pairs 24 sugar rings 22 phosphate groups 1 suspension framework
• Start construction at step (1)	• Start construction at step (4)

Now add sugar rings to each nitrogen atom immediately below and just one line to the left of the one above such that you have a single spiral of sugar rings all with the oxygen atoms **above** their base pair.

Join another sugar ring to the N^j atom on the hexagon of the top base pair. Twist this sugar ring so that the plane of the ring is vertical with its oxygen atom **below** the level of the base pair.

Now add sugar rings to each nitrogen atom immediately below and just one line to the left of the one above such that you have a second spiral of sugar rings all with the oxygen atoms **below** their base pair.

When any base pair is viewed horizontally from the 'minor groove aspect' (Figures. 1, 2, 5 & 6) the sugar rings should be orientated as per Figure 7.

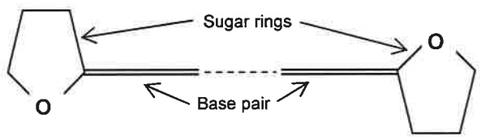


Figure 7. Minor groove aspect of a base pair with sugars in correct orientation.

(8) Attach the Phosphate Groups to the Sugar Rings.

Place the phosphate model with the two O^a atoms (atoms 1 & 2 in Figure 4) on the table nearest you, and one of the O^d atoms (atom 4 in Figure 4) on the table furthest away. Turn the bond attached to atom 4 to point to the left, leaving its open end about 5mm above the table. Now repeat the above, but this time place the other O^d atom in the position of atom 4. To help you can lay a spare tube/bond on the table and bring the end of the bond so it rests upon it.

Looking at the top base pair from the minor groove aspect (Figure 7) join each sugar ring to the sugar ring below it with a phosphate group. Orientate the phosphate groups so that the two O^a atoms on it are pointing away from the centre of the DNA, and away from the minor groove. Repeat this for all base pairs. As you move down the model the minor groove aspect twists with the twist of the helix.

To obtain the best fit you may need to juggle with the position of the carbon 5 atom on the sugar ring and the O^d atoms of the phosphate groups.

If you have made the sugar rings and phosphate groups with care and if, in particular, you have orientated the C_5 atom on the sugar and the empty ended bonds on the phosphate groups as described, then the model will fit together with very little need for final adjustment.

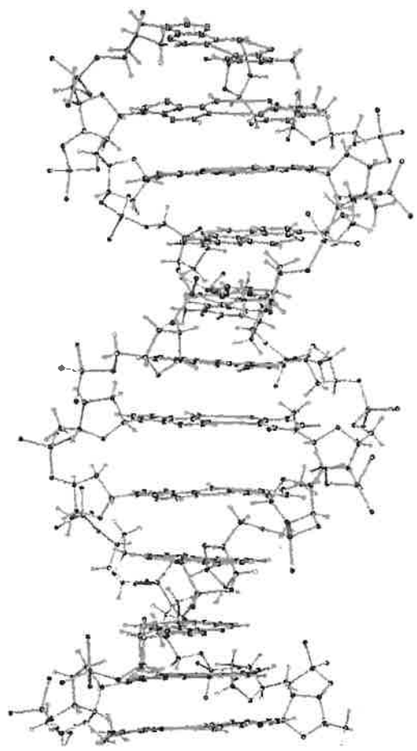


Figure 8. Completed model (excluding plates and lines)

(1) Construct 12 Base Pairs

This DNA model requires:
- 6 Thymine-Adenine pairs
- 6 Guanine-Cytosine pairs

Copy these base pairs from the diagrams below. Make sure that your base pairs are flat. Pay particular care to
- bond lengths
- note that two nitrogen atoms have unused 'prongs' on them

For explanation H^a etc. see table 1

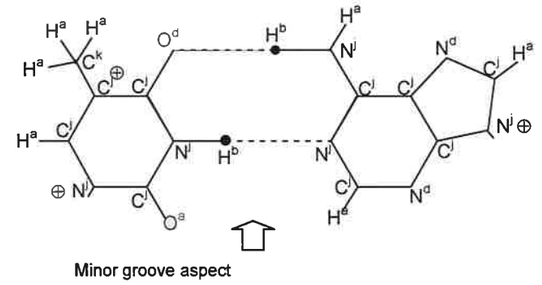


Figure 1. Thymine-Adenine pair

Bond lengths
H—Any atom = 2.0 cm

C—C
C—N
C—O
} = 2.0 cm grey

H^b- - -O
H^b- - -N
} = 3.5cm white

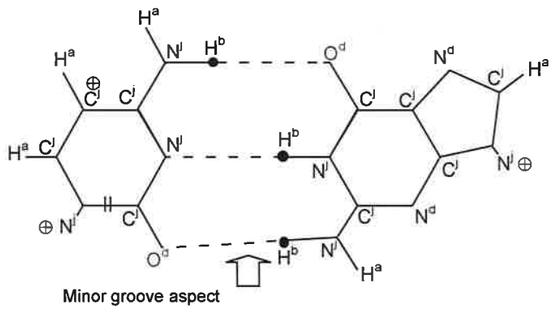


Figure 2. Cytosine-Guanine Pair

(2) Construct 24 Sugar Rings

Follow the diagrams in Figure 3 and note in particular:
- the unused prongs on the C^3 and C^5 atoms
- the bond with an empty end on the C^1 atom
- all bonds are modelled with 2.0 cm tubes
- the pentagon should be planar

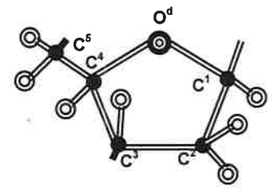
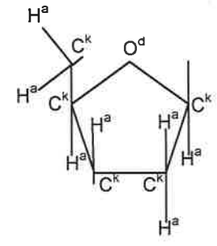


Figure 3. Sugar ring



(3) Construct 22 Phosphate Groups

Follow this diagram and note in particular:
- the bonds with the empty ends on the O^d atoms
- the P-O bonds 3.0cm and the O— bonds 2.0cm
- (the numbers refer to section 8)

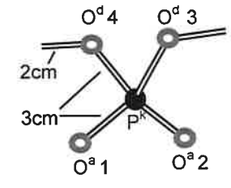


Figure 4. The phosphate group

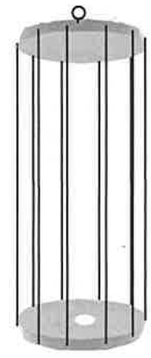
(4) The Suspension Framework

***** PREPARE A HOOK OR STRING TO HANG THE FRAMEWORK OR A RETORT STAND TO SUPPORT IT BEFORE REMOVING THE FRAMEWORK FROM THE BAG. *****

The suspension framework supplied with the model can either be hung from a suitably placed hook or placed over a laboratory stand of at least 90 cm height. The suspension framework consists of:

1. Two plates: one with a ring attached to its top to allow the model to be hung; the other with a hole in its centre to allow it to slip over the retort stand.

2. 10 nylon threads already in place on the above plates. The "Top" end of the model is the plate with the ring attached for hanging. The threads are numbered 1-10.



(5) The Suspension Framework (continued)

Open the bag and remove the pre-assembled framework by gently pulling on the ring or the first plate. Either hang the assembly from a hook or place it over a retort stand, with the hole in the bottom plate going over the stand and the top of the stand fitting into the moulding on the underneath of the top plate.

The atom centres on the nylon lines are arranged in 12 layers of three atoms in each layer. Each layer has two blue and one black atom in it. Table 2 shows where the atoms should be. So the top layer contains an N^j on line 1, a C^j on line 2 and an N^j on line 7.If any lines look slack, turn the white moulding underneath the bottom plate to which the slack line is attached.

Base pair	Nylon Lines									
	10	9	8	7	6	5	4	3	2	1
T-A				N^j					C^j	N^j
T-A			N^j					C^j	N^j	
C-G		N^j					C^j	N^j		
C-G	N^j					C^j	N^j			
A-T	C^j					N^j				N^j
G-C					N^j				N^j	C^j
A-T				N^j				N^j	C^j	
A-T			N^j				N^j	C^j		
G-C		N^j				N^j	C^j			
C-G	N^j				N^j					C^j
C-G				N^j					C^j	N^j
A-T			N^j	C^j					N^j	

Base pairs: T = Thymine, A = Adenine, C = Cytosine, G = Guanine

Table 2. Arrangement of atoms on the string framework

(6) Attach the Base Pairs to the Framework

Each base-pair will be connected to the Framework in three places, by replacing three of its atoms with the atoms attached to the nylon lines. The three atoms on the base pairs correspond to those atoms marked with a ⊕ in Figures 1 and 2.

1st (top) layer

Table 2 shows that the top layer is Thymine-Adenine. Take a Thymine-Adenine pair and orientate it as shown in Figure 1; with the black C^k atom towards the back and the pentagon on the right. If you can, rotate the Framework, such that line 1 is on your left.

Move the Thymine-Adenine pair inside the Framework without turning the base pair over such that the two blue atoms that have spare prongs on them lie next to the same atoms in the top layer of the Framework. If you are using a retort stand for support you will need to open a hydrogen bond and allow the pole between the two hydrogen bonds of the base pair before closing the open bond.

Remove the two blue atoms from the base pair and attach the remainder of the base pair to the two blue atoms on the Nylon lines 1 and 7 thus creating a base pair attached to the nylon lines. Keep the two blue atoms that you removed as spare parts. Remove the black C^j atom and its attendant C^k and H^a atoms from the base pair and reconnect the base pair and the C^k and H^a atoms to the C^j on line 2.

Your first base should now be attached at the top of the Framework and be roughly flat.

Subsequent layers

Refer to Table 2 to see which base pair to use and the information below on how to orientate it. The twist of the helix means that the base pairs gradually rotate around within the Framework, but they should be kept flat whilst doing this.

T-A = Thymine-Adenine, orientate the base pair as per Figure 1.

C-G= Cytosine-Guanine. Orientate the base pair as per Figure 2.

A-T = Adenine-Thymine. This is the same base pair as Thymine-Adenine but with the opposite orientation. This is achieved by flipping the base pair upside down and left to right to look like Figure 5: the black Ck is now at the back-right and the pentagon on the left.

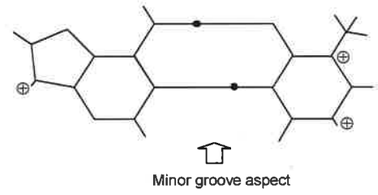


Figure 5. Adenine-Thymine orientation