

+ invite others to the conversation



Read



Juan Benet  
juan@benet.ai



Initiator

**Sharing Menu** a panel to invite others to conversations, trails, etc.

It begins with the content initiator (creator) already populated in the menu, and allows others to be invited. important to select sharing permissions

+ invite others to the conversation



Read



Juan Benet  
juan@benet.ai



Initiator



Francis Crick  
fcrick@mrc.ac.uk



Write



James Watson  
jwat@mrc.ac.uk



Read



**Sharing Menu** a panel to invite others to conversations, trails, etc.

When people are already shared-with, they appear under the initiator (or maybe it is sorted alphabetically or something). Permissions are blue, so that they are perceived as links.

**Rosalind Franklin**  
[+ Add](#)

**Rosalind Franklin**  
rosalind@mrc.ac.uk

**Robert Weinberg**  
weinberg@wit.mit.edu  
francis@mrc.ac.uk

**Robert Sauer**  
James Watson  
jwat@mrc.ac.uk

 **Read** ▾

 **Initiator**

 **Write** ▾

 **Read** ▾

**Sharing Menu** a panel to invite others to conversations, trails, etc.

Add another person or group by entering their name or associated email account. Field auto-completes giving user a contextual menu of options to select from. arrow keys should work. (add appears)

The screenshot shows a sharing menu for a user named Rosalind Franklin. The menu includes a list of users and their email addresses, along with their assigned permissions: Read, Write, or Share. The 'Share' permission is highlighted with a blue border. The menu also includes a 'Read' permission for James Watson, which is not highlighted.

User	Email	Permission
Juan Benet	juan@benet.ai	Read
Francis Crick	fcrick@mrc.ac.uk	Write
James Watson	jwat@mrc.ac.uk	Share
James Watson	jwat@mrc.ac.uk	Read

**Sharing Menu** a panel to invite others to conversations, trails, etc.

Permission selection works similarly, and includes clear, simple explanation of the abilities granted. (permission menu opened automatically after selecting a user, to encourage awareness of permission selection.

The screenshot shows a sharing menu interface. At the top, there is a header with a profile picture of Rosalind Franklin, the name "Rosalind Franklin", a blue "Add" button with a plus sign, a "Share" button with a person icon, and a dropdown arrow. Below the header, there are three user entries, each with a small profile picture, the user's name, their email address, and a set of actions. The first user is Juan Benet (juan@benet.ai), the second is Francis Crick (fcrick@mrc.ac.uk), and the third is James Watson (jwat@mrc.ac.uk). Each user entry has a "Delete" icon (trash can), a "Edit" icon (pencil), a "Write" button with a dropdown arrow, and a "Read" button with a dropdown arrow. The "Write" and "Read" buttons are blue, while the "Delete" and "Edit" icons are grey.

User	Email	Actions
Juan Benet	juan@benet.ai	
Francis Crick	fcrick@mrc.ac.uk	
James Watson	jwat@mrc.ac.uk	

**Sharing Menu** a panel to invite others to conversations, trails, etc.

Pressing enter (or clicking “Add”) adds the selected user to the list of permissions. This grants permissions and sends them a notification.

 **Rosalind Franklin**

 Juan Benet  
juan@benet.ai

 Francis Crick  
fcrick@mrc.ac.uk

 James Watson  
jwat@mrc.ac.uk

 Share ▾

 + Add

 Initiator

 Write ▾



 Read ▾



**Sharing Menu** a panel to invite others to conversations, trails, etc.

Alternative view.

+ invite others to the conversation



Share



Juan Benet  
juan@benet.ai



Initiator



Francis Crick  
fcrick@mrc.ac.uk



Write



James Watson  
jwat@mrc.ac.uk



Read



Rosalind Franklin  
rosalind@mrc.ac.uk



Share



**Sharing Menu** a panel to invite others to conversations, trails, etc.

Once added, the field clears, but sharing selection is remembered

Conversation Title

**B**

*I*

~~S~~

U









Share an insight

+ invite others to the conversation



Juan Benet

juan@benet.ai



Read



Initiator

Start new conversation

New Conversation a blank “new conversation” view

## Re: A Structure for Deoxyribose Nucleic Acid

**B** *I* ~~S~~ U   

This paper is really good because it launched a new field after coming up with the [greatest discovery](#) of all time. This paper is really good because it launched a [new field](#) after coming up with the greatest discovery of all time. This paper is really good. Here is a web link, here is a link [into the paper](#), here is a link to a [@Person](#), here is a link to a [Conversation](#), here is a link to [a figure](#), and i think this paper is [#interesting](#).

+ invite others to the conversation



Read



Juan Benet  
juan@benet.ai



Initiator

**Start new conversation**

**New Conversation** a populated “new conversation” view  
(the title should be seeded with where user came from)



**Juan Benet**



Share an insight

Cancel

Comment

**New (Blank) Comment** at the end of a running conversation



**Juan Benet**

**B** **I** **S** **U** **≡** **≡** **≡** **≡** **≡**

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**Cancel**

**Comment**

**New Comment** at the end of a running conversation. mid-edits.



## Juan Benet

**B** **I** **S** **U** **≡** **≡** **🔍** **🖼️**

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[Cancel](#)

[Comment](#)

alternative view

**Juan Benet**10 minutes ago

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**Posted Comment** in a conversation. if it is current user's, then user can see “edit” and “delete” buttons.

**Juan Benet**

10 minutes ago

**B** **I** **S** **U** **≡** **≡** **🔍** **🖼️**

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**Cancel****Update comment****Editing/Updating Posted Comment**

## Several Comments Together



**Juan Benet**

10 minutes ago



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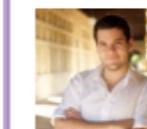


**Juan Benet**

10 minutes ago



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**Juan Benet**



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[Cancel](#)

[Comment](#)

Running Conversation with several comments, and shared with several participants

## Re: A Structure for Deoxyribose Nucleic Acid



**Juan Benet**

10 minutes ago



This paper is really good because it launched a new field after coming up with the [greatest discovery](#) of all time. This paper is really good because it launched a [new field](#) after coming up with the greatest discovery of all time. This paper is really good. Here is a web link, here is a link [into the paper](#), here is a link to a [@Person](#), here is a link to a [Conversation](#), here is a link to [a figure](#), and i think this paper is [#interesting](#).

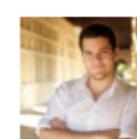


**Juan Benet**

10 minutes ago



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**Juan Benet**

10 minutes ago

This paper is really good because it launched a new field after coming up with the [greatest discovery](#) of all time. This paper is really good because it launched a [new field](#) after coming up with the greatest

Running Conversation after clicking the “Add User” button next to participants, Sharing Menu pops up.

## Re: A Structure for Deoxyribose Nucleic Acid



+ invite others to the conversation

Share ▾

 Juan Benet juan@benet.ai	 Initiator
 Francis Crick fcrick@mrc.ac.uk	 Write ▾
 James Watson jwat@mrc.ac.uk	 Read ▾
 Rosalind Franklin rosalind@mrc.ac.uk	 Share ▾

Close



Juan Benet

10 minutes ago



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## Conversations

### Re: A Structure for Deoxyribose Nucleic Acid



updated 20 minutes ago

12k

### Re: Physical Principles for Scalable Neural Rec...



updated 9 years ago

234

### Re: Millisecond-timescale, genetically targeted ...



updated 9 years ago

1

### Re: A Structure for Deoxyribose Nucleic Acid



updated 20 minutes ago

12k

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updated 9 years ago

234

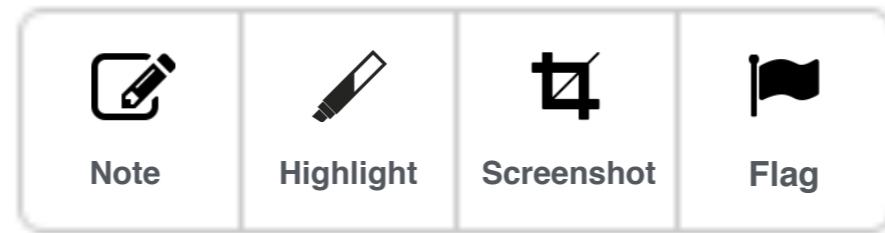
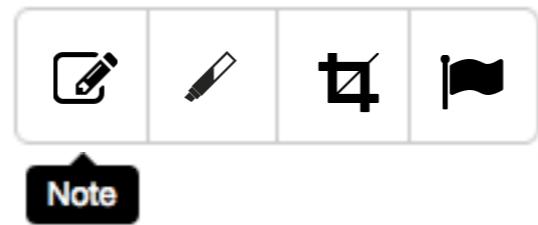
### Re: Millisecond-timescale, genetically targeted ...



updated 9 years ago

1

**Conversations** this view shows a set of conversations.



**Home Toolbar** this are things to do with the current entity.



Note



Edit Highlight



Edit Screenshot

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 Corey<sup>1</sup>. They kindly made their manuscript available to us in advance of publication. Their model consists of three inter-linked 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 three chains are on the outside and the bases on the inside, held together by hydrogen bonds. This structure 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  $\beta$ -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's<sup>2</sup> model No. 1; that is, the bases are on the inside of the helix and the phosphates on



**Annotation Toolbars** this is a toolbar for floating annotations.  
(Edit, Note, Link) — link copies the link to the annotation for use in conversations (smart linking) or anywhere else (link to the annotation only)

# Publication



## A Structure for Deoxyribose Nucleic Acid



Francis Crick



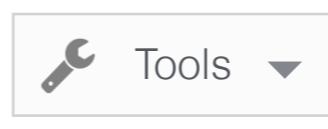
James Watson



234



10634



Tools ▾

**Publication** this view shows publication metadata

# Publication



## A Structure for Deoxyribose Nucleic Acid

Francis Crick James Watson

234  
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Tools ▾



## A Structure for Deoxyribose Nucleic Acid

Francis Crick James Watson

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## A Structure for Deoxyribose Nucleic Acid

Francis Crick James Watson

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## Publication List

# Publication



## A Structure for Deoxyribose Nucleic Acid



Francis Crick



James Watson



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Tools ▾



copy link to beagle page



10.1038/171737a0



search on google scholar



how to cite

**Publication** this view shows publication metadata  
Clicking the tool icon opens a contextual menu with many useful  
tools that we don't want to clutter the UI with.



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.

<sup>1</sup> Young, F. B., Gerrard, H., and Jevons, W., *Phil. Mag.*, **40**, 149 (1920).

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## MOLECULAR STRUCTURE OF NUCLEIC ACIDS

### A Structure for Deoxyribose Nucleic Acid

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is a residue on each chain every 3.4 Å. 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 Å. The distance of a phosphorus atom from the fibre axis is 10 Å. 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<sup>3,4</sup> 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<sup>5,6</sup> 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.



## Publication



A Structure for Deoxyribose Nucleic Acid

Francis Crick

James Watson

234  
10634

Tools ▾

## Conversations

Re: A Structure for Deoxyribose Nucleic Acid



updated 20 minutes ago

12k

Re: Physical Principles for Scalable Neural Rec...



updated 9 years ago

234

Re: Millisecond-timescale, genetically targeted ...



updated 9 years ago

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← Back



Note

## Publication



A Structure for Deoxyribose Nucleic Acid

Francis Crick

James Watson

234

10634

Tools ▾

## Conversations

Re: A Structure for Deoxyribose Nucleic Acid



updated 20 minutes ago

12k

Re: Physical Principles for Scalable Neural Rec...



updated 9 years ago

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Re: Millisecond-timescale, genetically targeted ...



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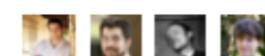
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[← Back](#)

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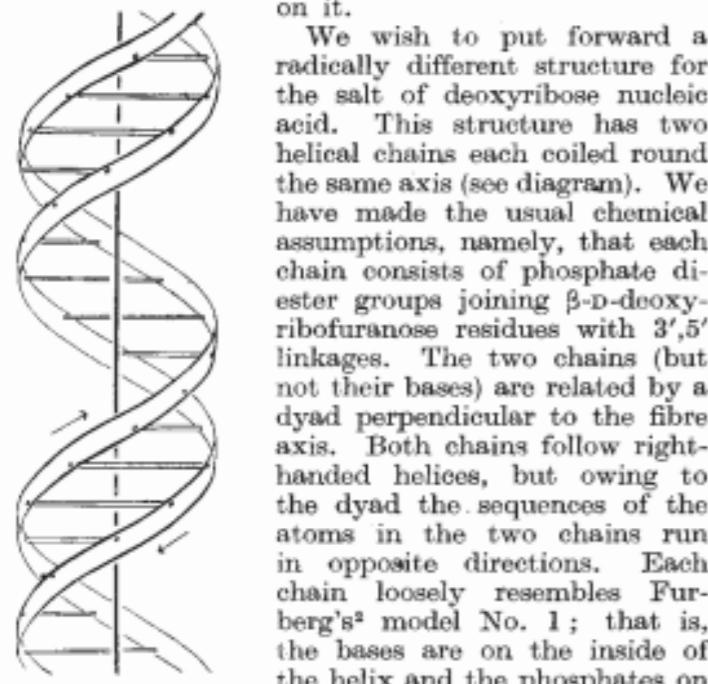
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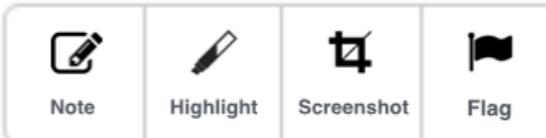
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A Structure for Deoxyribose Nucleic Acid



Francis Crick



James Watson

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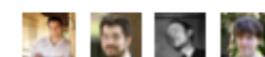
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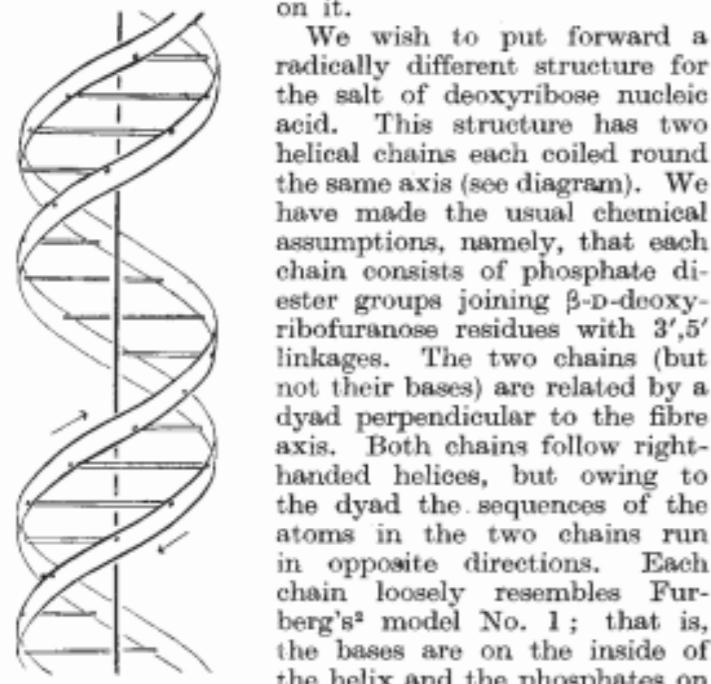
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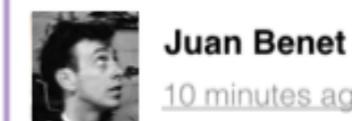
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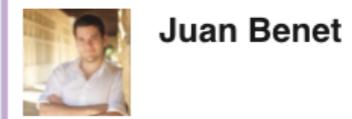
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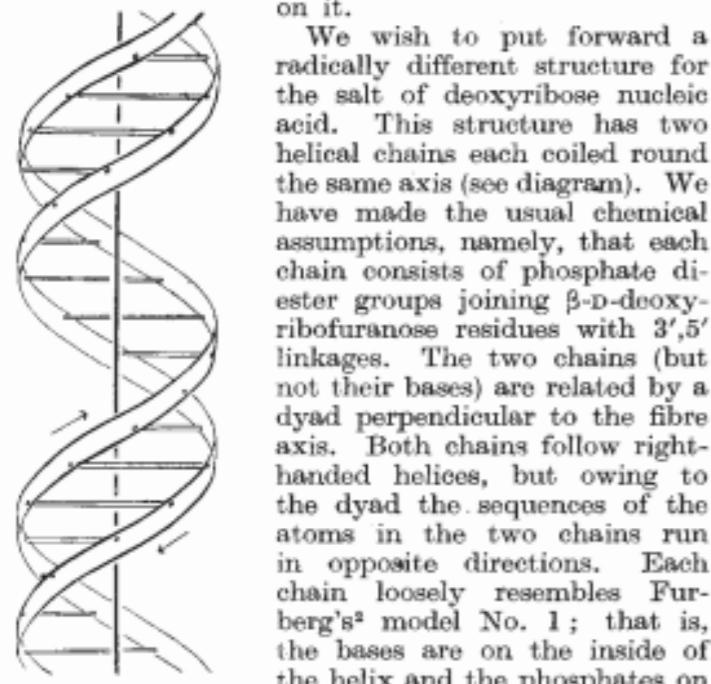
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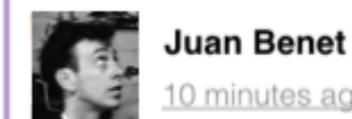
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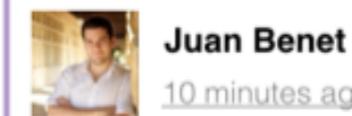
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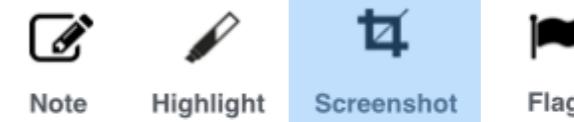
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Francis Crick

James Watson

234  
10634

Tools ▾

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Re: A Structure for Deoxyribose Nucleic Acid



updated 20 minutes ago

12k

Re: Physical Principles for Scalable Neural Rec...



updated 9 years ago

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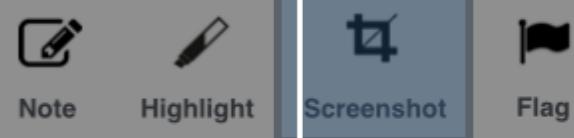
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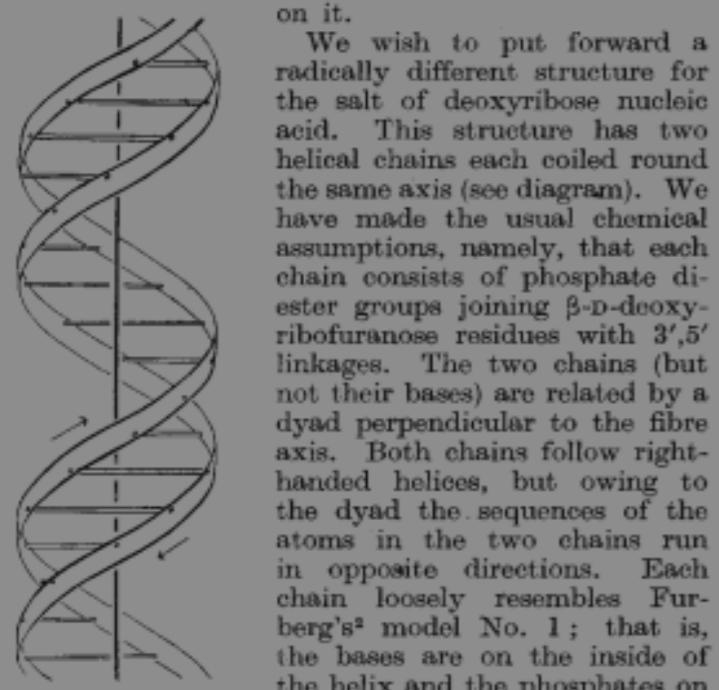
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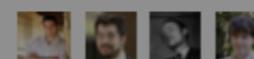
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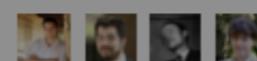
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## Figure from: A Structure for Deoxyribose Nucleic Acid

**B** **I** **S** **U** **≡** **≡** **🔗** **🖼️**

See figure [Fig 1](beagle.io/AT2ggy5okh/Figure-from-A-Structure-for-Deoxyribose-Nucleic-Acid)

Which — embedded — looks like:

![Fig 1](beagle.io/AT2ggy5okh/Figure-from-A-Structure-for-Deoxyribose-Nucleic-Acid)

+ invite others to the conversation



Read



Initiator

Start new conversation



Juan Benet

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**Starting conversation from annotation,**  
including links (pasted and embedded).

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**Juan Benet**

just now



See figure [Fig. 1](#)

Which — embedded — looks like:



[[Figure from A structure for Deoxyribose Nucleic Acid](#)]

#### Comment from annotation,

this is how the links render. Note that the “embed image” markdown embeds a figure with a link, too, for clarity.

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.

<sup>1</sup> Young, F. B., Gerrard, H., and Jevons, W., *Phil. Mag.*, **40**, 149 (1920).

<sup>2</sup> Longuet-Higgins, M. S., *Mon. Not. Roy. Astro. Soc., Geophys. Supp.*, **5**, 285 (1949).

<sup>3</sup> Von Arx, W. S., Woods Hole Papers in Phys. Oceanogr. Meteor., **11** (3) (1950).

<sup>4</sup> 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 Corey<sup>1</sup>. 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 ester groups joining  $\beta$ -D-deoxyribofuranose 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's<sup>2</sup> model No. 1; that is, the bases are on the inside of the helix and the phosphates on

is a residue on each chain every 3.4 Å. 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 Å. The distance of a phosphorus atom from the fibre axis is 10 Å. 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<sup>3,4</sup> 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<sup>5,6</sup> 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.



### Link to annotation,

Takes user to a dedicated page for the annotation (whether or not they have beagle installed). if the pdf is accessible, use it, else use a screenshot.