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
<table>
<thead>
<tr>
<th>Sharing Menu</th>
<th>a panel to invite others to conversations, trails, etc.</th>
</tr>
</thead>
<tbody>
<tr>
<td>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.</td>
<td></td>
</tr>
</tbody>
</table>
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)
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.)
<table>
<thead>
<tr>
<th>Name</th>
<th>Email</th>
<th>Permissions</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rosalind Franklin</td>
<td><a href="mailto:juan@benet.ai">juan@benet.ai</a></td>
<td>Add</td>
<td></td>
</tr>
<tr>
<td>Juan Benet</td>
<td><a href="mailto:juan@benet.ai">juan@benet.ai</a></td>
<td>Share</td>
<td>Initiator</td>
</tr>
<tr>
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<td><a href="mailto:fcrick@mrc.ac.uk">fcrick@mrc.ac.uk</a></td>
<td></td>
<td>Write</td>
</tr>
<tr>
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<td><a href="mailto:jwat@mrc.ac.uk">jwat@mrc.ac.uk</a></td>
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Pressing enter (or clicking “Add”) adds the selected user to the list of permissions. This grants permissions and sends them a notification.
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**Sharing Menu** a panel to invite others to conversations, trails, etc.
Sharing Menu a panel to invite others to conversations, trails, etc.

Once added, the field clears, but sharing selection is remembered
New Conversation a blank “new conversation” view
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.
New (Blank) Comment at the end of a running conversation
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Juan Benet 10 minutes ago

Posted Comment in a conversation. if it is current user’s, then user can see “edit” and “delete” buttons.
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Several Comments Together

Juan Benet
10 minutes ago

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Running Conversation with several comments, and shared with several participants

Re: A Structure for Deoxyribose Nucleic Acid

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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 ...**
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Conversations this view shows a set of conversations.
Home Toolbar: this are things to do with the current entity.
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

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.
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 Corey4. 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 phosphate groups 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.

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If it is assumed that the bases only occur in the structure in the most pleasurable 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 sequences on the other chain is automatically determined.

It has been found experimentally† that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribonucleic acid.

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The previously published X-ray data-stars 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.
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Re: A Structure for Deoxyribose Nucleic Acid

Juan Benet 10 minutes ago

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Share an insight

NO. 4356 April 25, 1953 NATURE

Molecular structure of nucleic acids

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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 diester groups joining β-D-deoxyribofuranoside 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 model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. Each chain 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 pair from one chain being hydrogen-bonded to a single base from the other chain, so that the two sides by side with identical 2'-co-ordinates. One of the pairs 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 configuration) 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).

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It is assumed that the bases only occur in the structure in the most plausible tautomer forms (that is, with the keto rather than the enol configuration) 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).

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The novel feature of the structure is the way 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 co-ordinates. 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 the assumption that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) is made, 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 addition, 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, the sequence on the other chain is automatically determined.

It has been found experimentally,4,5 that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribonucleic acid.

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We believe that the structure we propose resembles that of R.S. Discovery II for their observations.

1. Young, F. E., Cottrell, H., and Jukes, T. W. Phil. Mag., 40, 149 (1929).

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We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled around the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diphosphate groups joining \(\beta\)-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 bases in the two chains run in opposite directions. Each chain loosely resembles Furbank's\(^2\) 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 A. in the z-direction. We have assumed an angle of 36\(^\circ\) 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-co-ordinates. 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.

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\(^3\) 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\(^4\) 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.

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\(^1\) Young, P. B., Gurrard, H. B., and Javavis, W., Phil. Mag., 49, 156 (1929).

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**Conversations**

Re: A Structure for Deoxyribose Nucleic Acid

Re: Physical Principles for Scalable Neural Rec...
MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribonucleic Acid

We wish to suggest a structure for deoxyribonucleic acid, which has novel features of biological interest.

A structure for nucleic acids proposed by Pauling and Corey has certain features in common with the structure we propose. However, the two structures differ in certain respects.

1. We believe that the previously proposed structure is too rigid, whereas the proposed structure is more flexible.
2. The proposed structure has a more favorable water content and a more favorable stability to temperature changes.
3. The proposed structure is more compatible with the known physical and chemical properties of nucleic acids.

Another three-chain structure proposed by Fraser and his co-workers involves the use of intercalators, which are molecules that插入between the base pairs. However, this structure has not been confirmed experimentally.

The proposed structure has the following features:

1. The two chains are held together by hydrogen bonds between the base pairs.
2. The backbone of the chains is composed of alternating phosphates and deoxyribose sugars.
3. The sugar-phosphate backbone is arranged in a helical form, with the bases projecting outward.
4. The proposed structure is capable of adopting a variety of conformations, depending on the conditions.

The proposed structure provides a rationale for the observed physical and chemical properties of nucleic acids, and it offers a framework for understanding the function of these molecules in various biological processes.
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. Doazen and the
chairman and officers of R.R.S. Discovery II for their
part in making the observations.

1 Young, V. E., Gerrard, H., and Jevons, W., Phil. Mag., 49, 149
(1920).
5, 285 (1949).
(1956).

Molecular Structure of Nucleic Acids

A Structure for Deoxyribose Nucleic Acid

We wish to suggest a structure for the salt
of deoxyribose nucleic acid (DNA). 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 inter-
twined 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 sug-
gested 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 is also 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 dis-
ester groups joining β-α-deoxyribonucleic 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 Fur-
berg's1 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 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, sections 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-co-ordinates. 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 config-
urations) it is found that only specific pairs of bases can bond together. These pairs are: adenine
(thymine) and guanine; guanine and cytosine;
pyrimidine and cytosine, tyrosine.

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, guanine or
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 experimentally2 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 data3-6 on deoxy-
ribose 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 unproven 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 stereo-
chemical 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 con-
ditions assumed in building it, together with a set
of co-ordinates for the atoms, will be published else-
where.