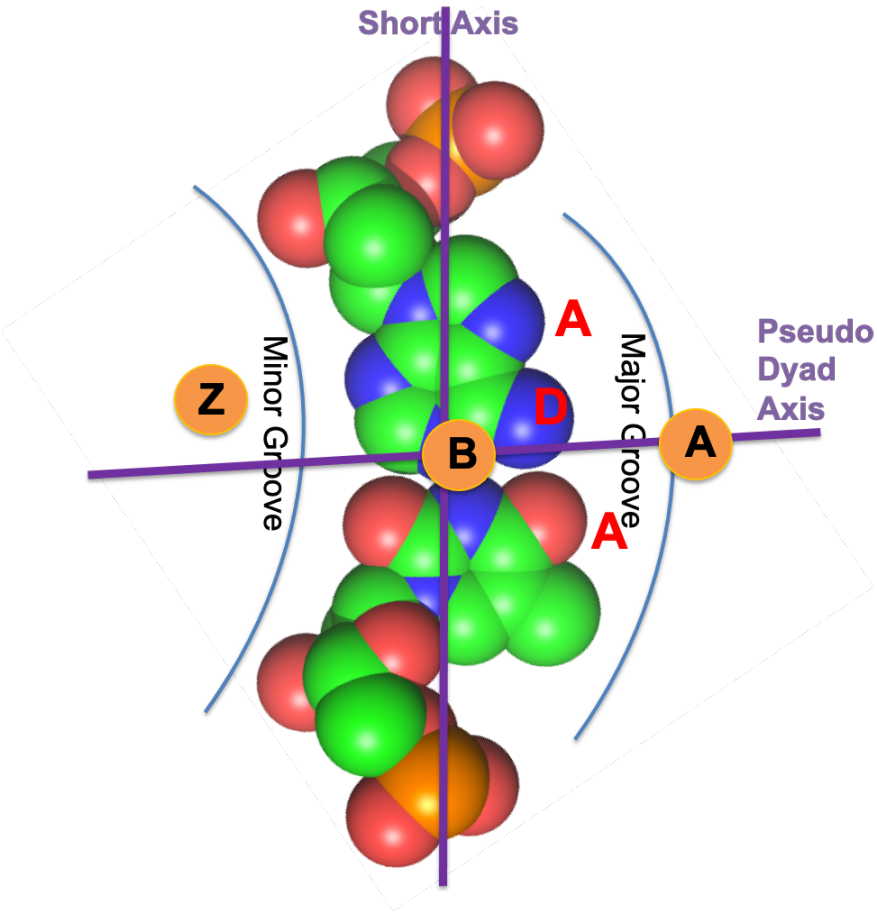
Q1:
This picture shows a base pair in space filling view.

Where would the helical axis be located if this base pair were found in a B, A or Z-DNA form?
See A / B / Z orange marks
Where are the pseudo-dyad axis and the short axis?
See Purple axis
Where are the major and minor grooves?
See Drawing
Identify the H-bonds donors (D) and acceptors (A) in the major groove.
See Drawing



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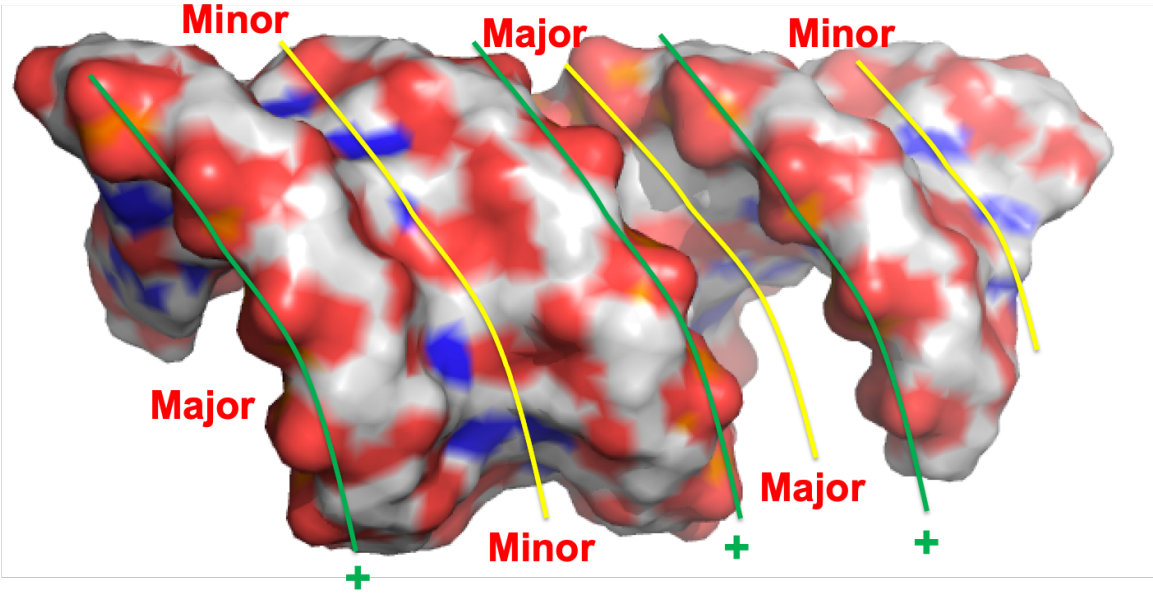
Q2:

The picture below shows the surface representation of a nucleic acid.



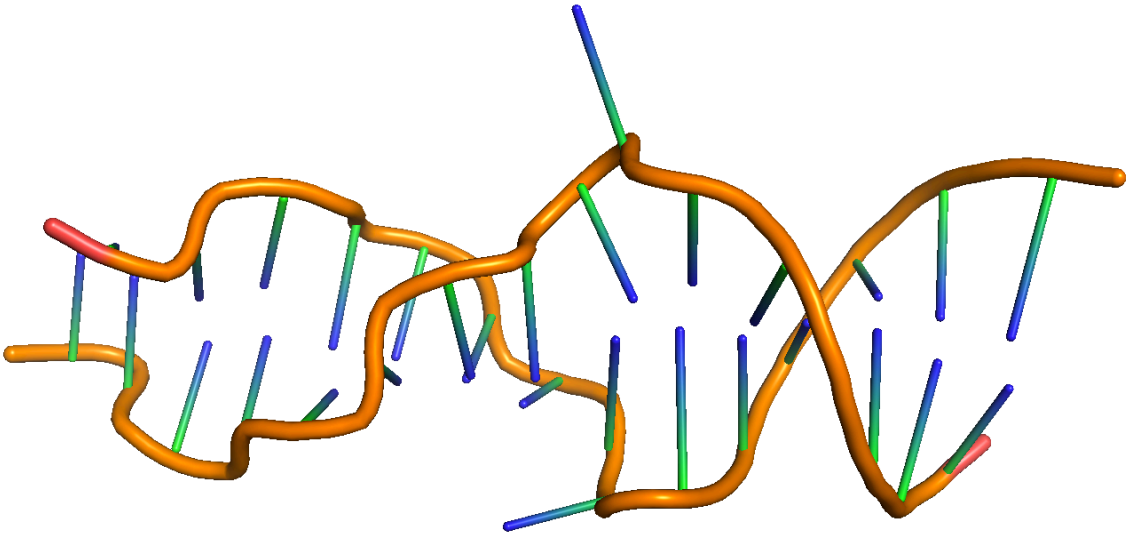
Identify the location of the negative charges on the nucleic acid.
See green marks

Identify all the areas corresponding to the major and minor grooves of the double helix
See yellow marks

What type of structure is formed by this double helix; justify your answer using two independent elements that you can see from the picture.
Smooth double helical form excludes Z double helix.
Deep major groove and narrow minor groove = A form double helix

Based on the representation shown above, what challenge would be encountered by a protein which needs to recognize the sequence of this nucleic acid?
The major groove is very deep, making it difficult for a protein to access H-bond donors and acceptors/Hydrophobic groups that are sequence specific and located primarily in the major groove.

Q3:

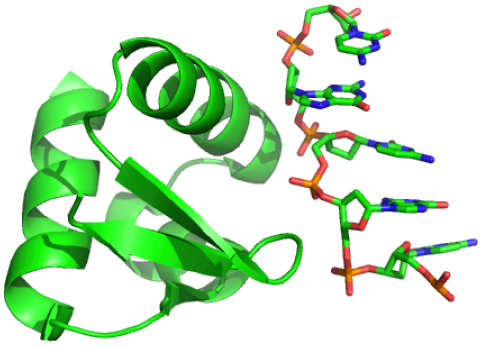


This picture shows the structure of a nucleic acid duplex in cartoon representation.

Is this a right handed or a left handed double helix?
Left half = left handed; Right half = right handed

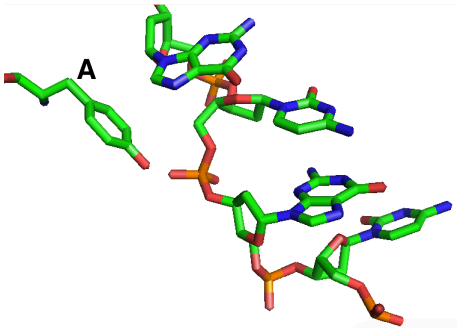
What double helical conformation(s) can you visualize on this nucleic acid?
On the left side the jagged/zig zag trajectory and the left handedness of the helix indicates a Z form. On the right side, the right handed helix, minor base tilting, and equal depth of the major and minor grooves indicate a B conformation.
What specific structural feature is found in this structure which is not observed in A, B or Z forms?
At the junction between the B and Z conformations, the bases are extruded/flipped out of the duplex, which is not seen in A/B/Z forms in which bases are oriented towards the center of the double helices.

Group 4



The structure of a protein that interacts with a double-stranded nucleic acid is shown on the right. Only one strand of the nucleic acid is shown (the other strand shows a complementary sequence). Two amino acids A&B that interact with the nucleic acid are shown below in more detail.

A- based on the structural elements of the nucleic acid chain visible on the three pictures, predict what type of double helical structure is bound by this protein. Justify your answer using at least **two** structural elements of the nucleic acid



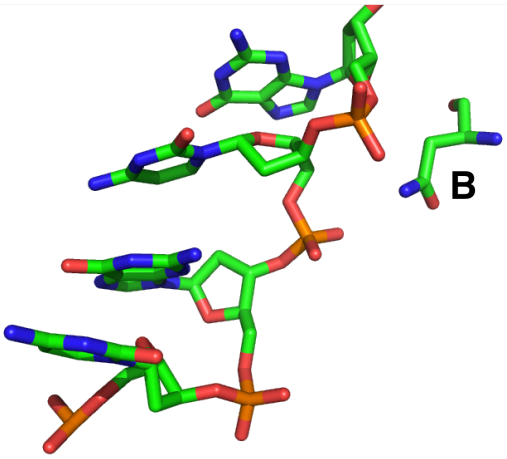
Guanosine nucleotides adopt a syn glycosidic bond conformation

Deoxyriboses show opposite orientation from one nucleotide to the next/zig zag trajectory of the backbone.
=> This is a Z-type DNA double helix

C- Describe briefly what type of interactions amino acids A and B make with the nucleic acid and which chemical groups are involved

A (a Tyrosine – not required) uses the 2'-hydroxyl of its side chain to donate a hydrogen bond to the non-bridging phosphate oxygen
B - an Asparagine – not required) uses the NH2 of its side chain to donate a hydrogen bond to the non-bridging phosphate oxygen

D- Based on the overall picture on the top and on the interactions between the amino acids shown and the nucleic acid, explain how this protein recognizes this nucleic acid specifically



The protein recognizes exclusively the backbone of this DNA duplex by making interactions with the Phosphate oxygens and does not make any interactions with the bases. Since it's a Z-DNA structure it probably recognizes the unique Zig-Zag trajectory of the backbone by making interactions with the phosphate backbone that is geometrically different from A or B conformations.