

Lecture 1: Exercises “Biochemical Building Blocks”

Question 1:

For each statements write whether it is true or false and please explain why:

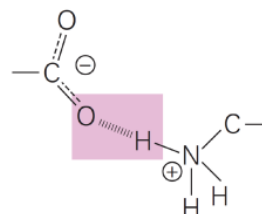
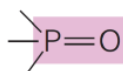
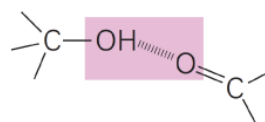
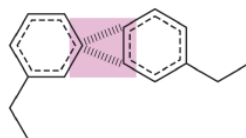
- a) When two atoms come close together, the energy increases due to repulsion between their nuclei.
- b) Ionic interactions are weaker in nonpolar solvents (such as hexane) as compared to polar solvents such as water because polar solvents shield the ions.
- c) DNA can be replicated in both the 5' → 3' direction as well as the 3' → 5' direction
- d) The energy of an $\text{N-H}\cdots\text{O}=\text{C}$ hydrogen bond is at its maximum when the bond is linear.

Question2:

Here we classify bonds in four categories based on their dissociation energy (the change in energy when atoms are moved away from each other).

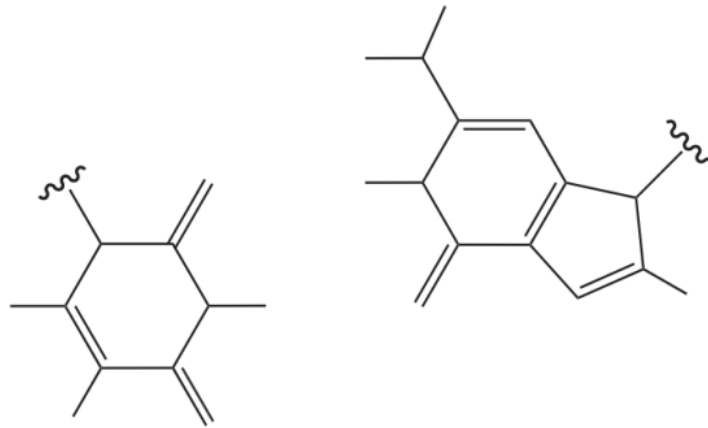
Strong:	>200	kJ/mol
Medium:	20-200	kJ/mol
Weak:	5-20	kJ/mol
Very weak:	0-5	kJ/mol

Below four bond types are shown in purple. (1) Name each bond-type and classify them into the four categories given above (in vacuum). (2) Consider what happens when these molecules are immersed in water (fully solvated). For each bond, indicate whether the bond becomes weaker, stronger, or stays the same. (3) Which of these bonds can be broken by just the thermal fluctuations in water?



Question 3:

Take a look at the two structures below. (1) Can you identify which base pairs are depicted?

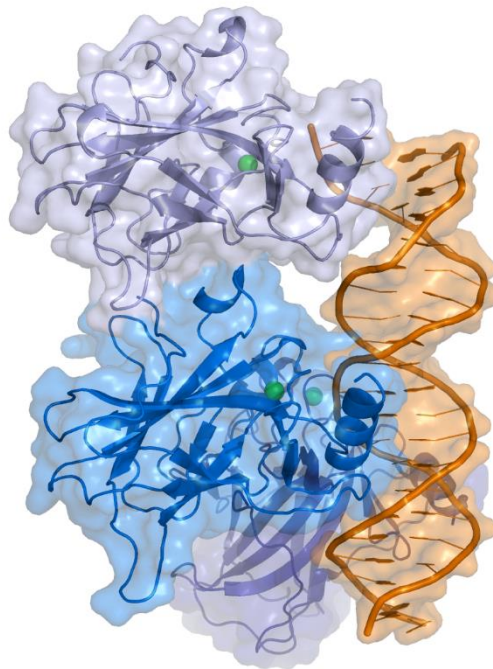


- (1) Can you identify which base pairs are depicted?
- (2) The atom labels are missing in the structure for each atom. Can you label all atoms which correspond to this base pair? If there are hydrogen bonds, please also label them between the base pairs.
- (3) Identify the major and minor grooves of the base pair. Name the interactions along the grooves.
- (4) Is this base pair a standard Watson-Crick pairing?

Question 4:

In the image below you can see a cartoon representation of a complex between DNA and the protein p53. This protein is a well-known tumor suppressor protein that regulates the cell cycle and helps prevent cancer by binding to DNA and activating genes that repair damaged DNA. Many DNA interacting proteins contain cationic domains to bind to DNA.

- (1) Explain why these cationic domains are important for DNA-binding proteins (in terms of electrostatic interactions).
- (2) How do these DNA-binding proteins discriminate between specific DNA sequences? Think about the shape and chemical properties (type of interactions) of the protein and how it relates to specificity.
- (3) DNA-binding proteins can be phosphorylated after translation. Why would the cell phosphorylate these proteins and what does it do to DNA binding?
- (4) Mutations in DNA-binding protein can heavily disrupt their function leading to a disease. Why can a mutation in a DNA-binding protein affect the protein-DNA interaction?



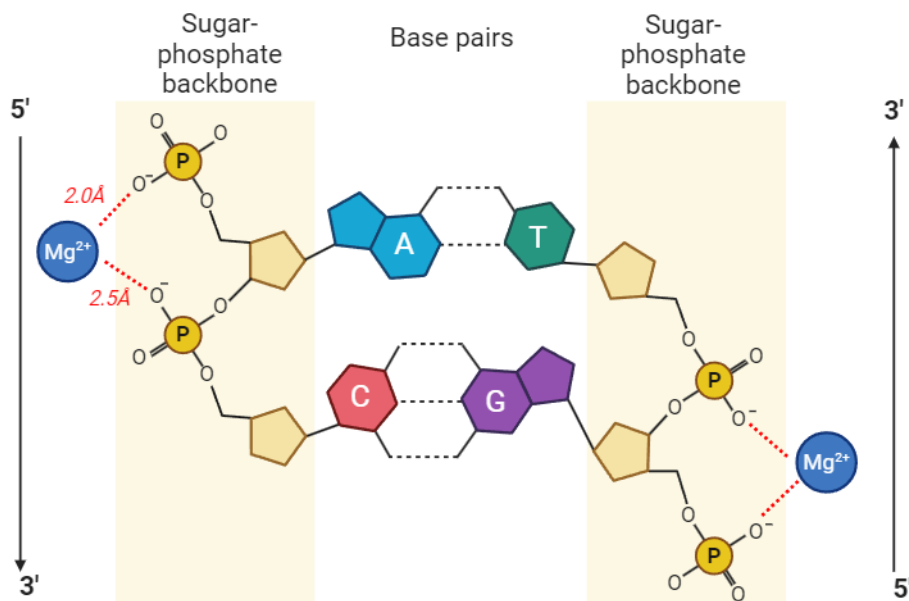
Question 5:

A bacterial DNA polymerase replicates DNA at a rate of approximately 1000 base pairs per second. The polymerase holoenzyme is about 110 Å (angstroms) in length. How many times its own length does the polymerase move forward along the axis of the DNA double helix in 5 seconds? Please show the calculation. We can assume that the DNA remains stationary, and we also ignore the rotational movement of the polymerase around the DNA.

Question 6:

Magnesium ions (Mg^{2+}) play a crucial role in stabilizing DNA structure and are essential cofactors for DNA polymerases during replication. Mg^{2+} binds to the phosphate groups of the DNA backbone to neutralize and stabilize the DNA helix. The positively charged Magnesium is surrounded by two negatively charged phosphate backbones. Assume that all charges lie on the same line. Calculate the ionic energy potential of the system in the following two conditions:

- (1) The stabilization occurs in normal cell conditions in water
- (2) The stabilization occurs in vacuum ($D=1.00$)
- (3) Are the ionic interactions stronger in water or in vacuum? Explain why.



Question 7:

The surface area of *E. coli* is typically calculated based on its shape and dimensions. *E. coli* is usually modeled as a rod-shaped bacterium (a cylinder with hemispherical ends). Both the shape and dry-weight content allow for a rough estimation of its molecular population

- (1) Make a surface area-based estimation of the lipid density in numbers of *E. coli*