

The MOLECULES of LIFE

Physical and Chemical Principles

Solutions Manual

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CHAPTER 1

From Genes to RNA and Proteins

Problems and Solutions

True/False and Multiple Choice

- When two atoms approach each other closely, the energy goes up because the nuclei of the atoms repel each other.
True/False
 - Ionic interactions are stronger in water than in vacuum because water forms strong hydrogen bonds with polar molecules.
True/False
 - An N–H•••O=C hydrogen bond has optimal energy when it:
 - is bent.
 - is linear.**
 - has a donor–acceptor distance of 4 Å.
 - has a donor–acceptor distance of 2 Å.
 - A by-product of forming a peptide bond from two amino acids is water.
True/False
 - Circle all of the polar amino acids in the list below:
 - Phenylalanine
 - Valine
 - Arginine**
 - Proline
 - Leucine
 - Proteins fold with their hydrophobic amino acids on the surface and their hydrophilic amino acids in the core.
True/False
 - Which of the following is not a unit of structure found in proteins?
 - β sheets
 - Loop regions
 - α helices
 - γ arches**
 - The central dogma of molecular biology states that RNA is translated from proteins.
True/False
 - Which of these types of molecules serve as a template for messenger RNA?
 - Protein
 - DNA**
 - Transfer RNA
 - Carbohydrates
 - Ribosomes
 - DNA primase synthesizes DNA molecules.
True/False
- #### Fill in the Blank
- When two atoms approach closer than _____ the interaction energy goes up very sharply.
Answer: their van der Waals radii
 - The van der Waals attraction arises due to _____ induced dipoles in atoms.
Answer: mutually
 - At room temperature, the value of _____ is about 2.5 kJ•mol⁻¹.
Answer: thermal energy
 - _____ is an operational nucleic acid, whereas _____ is strictly an informational nucleic acid.
Answer: RNA, DNA
 - Amino acids are zwitterions: molecules with charged groups but an overall _____ electrical charge.
Answer: neutral
 - The _____ consists of two subunits that assemble around messenger RNA.
Answer: ribosome

Quantitative/Essay

17. Order the following elements from lowest electronegativity to highest: P, C, N, H, O, S. Use your ordering of the atoms to rank the following hydrogen bonds from weakest to strongest:

- SH---O
- NH---O
- OH---O

Answer: $H = P < C = S < N < O$; SH---O < NH---O < OH---O

18. The stabilization energy of a bond or interatomic interaction is the change in energy upon breakage of a bond between two atoms (that is, the change in energy when the atoms are moved away from each other). We can classify bonds into the following categories, based on their dissociation energies:

Strong: $> 200 \text{ kJ}\cdot\text{mol}^{-1}$

Medium: $20\text{--}200 \text{ kJ}\cdot\text{mol}^{-1}$

Weak: $5\text{--}20 \text{ kJ}\cdot\text{mol}^{-1}$

Very weak: $0\text{--}5 \text{ kJ}\cdot\text{mol}^{-1}$

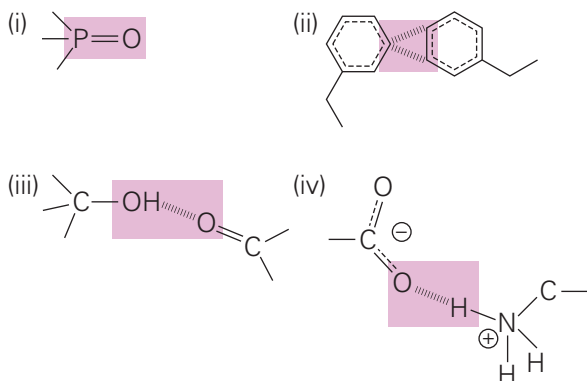
Consider the bonds highlighted in purple in the diagram below.

a. First consider the bonds in molecules isolated from all other molecules (in a vacuum). Classify each of them into the four categories given above, based on your estimation of the bond strength.

b. Which of these bonds could be broken readily by thermal fluctuations?

c. Next, consider what happens when these molecules are immersed in water (fully solvated). For each bond, indicate whether it becomes weaker, stronger, or stays the same in water.

d. Which of these bonds could be broken readily by thermal fluctuations in water?



Answer:

- Strong.
 - Very weak.
 - Weak.
 - Weak.

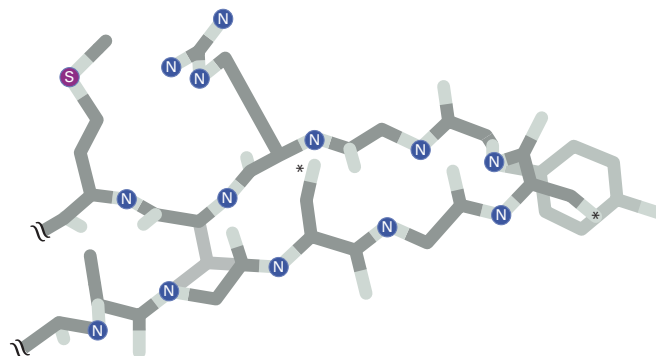
b. Only iv could be broken readily by thermal fluctuation.

- Same.
 - Slightly stronger; the Van der Waals interactions do not change, but the net interaction becomes stronger because of the hydrophobic effect.
 - Weaker.
 - Weaker.
- ii, iii, and iv.

19. The diagram below shows a representation of the structure of a peptide segment (that is, a short portion of a larger protein chain). Hydrogen atoms are not shown. Nitrogen and sulfur atoms are indicated by "N" and "S." Sidechain oxygen atoms are indicated by "*."

a. Identify each of the amino acid residues in the peptides.

b. Draw a linear chemical structure showing the covalent bonding, including the hydrogen atoms, of the entire peptide.



Answer:

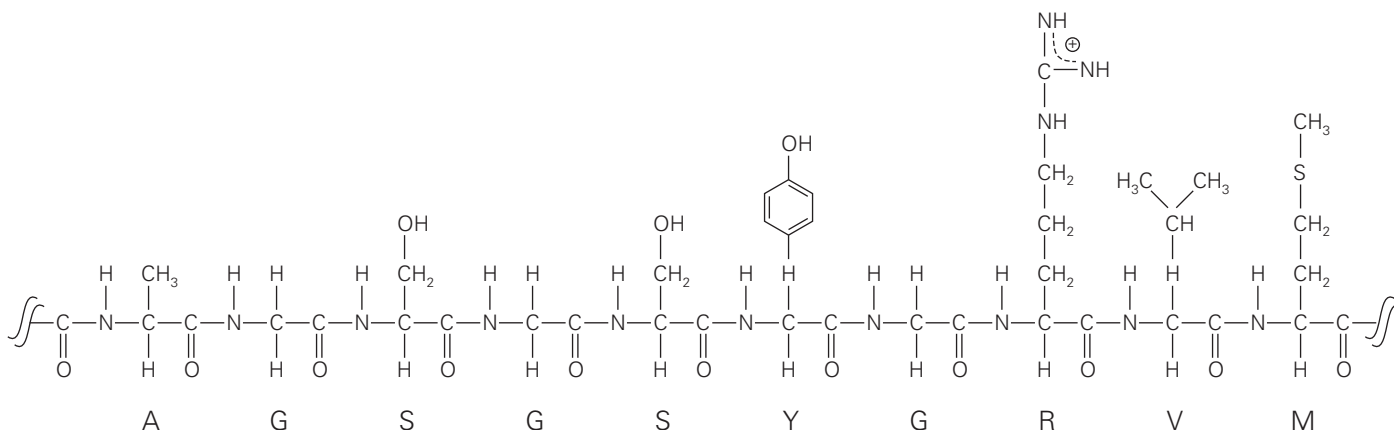
- Ala-Gly-Ser-Gly-Ser-Tyr-Gly-Arg-Val-Met.
- See Figure at the top of the next page.

20. With 64 possible codons and 21 options to code (20 amino acids + stop), (a) what is the average number of codons per amino acid/stop codon? (b) Which amino acids occur more often than expected in the actual codon table?

Answer:

- Average = $64 \text{ codons} / 21 \text{ amino acids} = 3.05 \text{ codons per amino acid}$.
- Leucine (6 codons), valine (4 codons), serine (6 codons), proline (4 codons), threonine (4 codons), alanine (4 codons), arginine (6 codons), glycine (4 codons).

21. There are approximately 3 billion nucleotides in the human genome. If all of the DNA in the entire genome were laid out in a single straight line, how



long would the line be? Express your answer in meters.

Answer:

$$(3 \times 10^9 \text{ bp}) \times (3.4 \times 10^{-10} \text{ m} \cdot \text{bp}^{-1}) = 1.02 \text{ m}$$

22. The human immunodeficiency virus (HIV) is a retrovirus with an RNA genome.
- Assume that each HIV contains two RNA genomes and 50 molecules of the reverse transcriptase enzyme.
 - Assume that each reverse transcriptase molecule acts on each RNA genome 10 times to produce DNA.
 - Assume that an integrase enzyme successfully integrates 1% of the available reverse transcribed HIV genomes into the genome of a human host cell.
 - Assume that each integrated copy of the viral genome is transcribed 500 times/day.

How many HIV RNA genomes are created per day from one infected cell?

Answer:

$$\begin{aligned} &50 \text{ reverse transcriptases} \times 10 \text{ replications} \times \\ &2 \text{ genomes} = 1000 \text{ DNA genomes created.} \\ &1000 \text{ genomes created} \times 0.01 \text{ successfully integrated} \\ &\text{by integrase} = 10 \text{ integrated genomes.} \\ &10 \text{ copies of the genome integrated} \times 500 \\ &\text{transcriptions per day} = 5000 \text{ HIV genomes created} \\ &\text{from one infection per day.} \end{aligned}$$

23. What is a step in RNA processing that occurs in eukaryotes but not in prokaryotes?

Answer:

Eukaryotes have introns, which necessitate splicing. Additionally, eukaryotes add a poly-A tail on the 3' end and a methyl-G cap on the 5' end.

24. What changes to the central dogma were necessary after the discovery of retroviruses?

Answer:

The unidirectional flow from DNA to RNA was no longer true after the discovery of retroviruses. Retroviruses use reverse transcription to create a DNA copy and then generate many RNA copies.

25. What chemical properties have led to DNA being selected through evolution as the information molecule for complex life forms instead of RNA?

Answer:

DNA is inherently more stable. The 2'-OH group in an RNA nucleotide, which DNA lacks, can react to break the backbone just downstream by forming a cyclic 2'-3' phosphodiester bond and breaking the sugar-phosphate backbone. Furthermore, because DNA typically exists as a double-stranded helix, in the event of DNA on one strand being lost or damaged it can be replaced or repaired using the other strand as a template. RNA, typically single-stranded, does not have this capability.

26. How do size considerations forbid G-A base pairs in a double helix?

Answer:

Both G and A are purines and have two rings. The double helix only has enough space for a single purine (two rings) and pyrimidine (one ring), but not enough for four rings total.

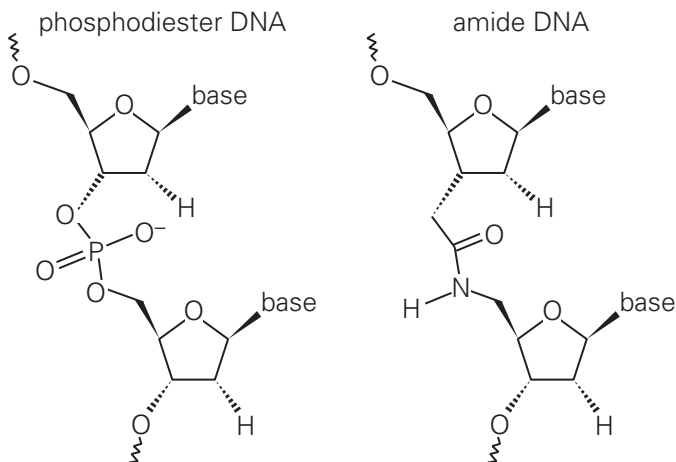
27. Why are DNA chains synthesized only in the 5'-to-3' direction in the cell?

Answer:

Replication proceeds only in the 5' → 3' direction, and not 3' → 5', because only nucleotide

triphosphates with the triphosphate group attached to the 5' carbon of the sugar are present in cells. This is the high-energy, reactive end of the molecule.

28. Chemists are able to synthesize modified oligonucleotides (that is, polymers of nucleotides) in which the phosphate linkage is replaced by a neutral amide linkage, as shown in the diagram below.



(Adapted from M. Nina et al., and S. Wendeborn, *J. Am. Chem. Soc.* 127: 6027–6038, 2005. With permission from the American Chemical Society.)

- Such modified oligonucleotides are able to form double-helical structures similar to those seen for DNA and RNA. Often these double helices are more stable than the natural DNA and RNA double helices with the same sequence of bases. Explain why such helices can form, and why they can be more stable.
- Given the increased stability of such modified nucleotides, why has nature not used them to build the genetic material? Provide two different reasons that could explain why these molecules are not used.

Answer:

- The amide DNA helices lack the unfavorable negative charge concentration present in phosphodiester DNA.
- If the amide DNA double helices were too stable, it wouldn't be possible to unwind them for replication and transcription. Also, without a high-energy phosphate linkage, the amide DNA monomers can't internally store the energy needed for synthesis.

29. Suppose you were told that the two strands of DNA could in fact be readily replicated in opposite directions (that is, one in the 5' → 3' direction, and one in the 3' → 5' direction). Would you have to postulate the existence of a new kind of nucleotide? If so, what would the chemical structure of this compound be?

Answer:

You could postulate a nucleotide triphosphate with the triphosphate attached to the 3' sugar carbon, rather than the 5'. The high energy 3' triphosphate would be susceptible to attack by the 5'-OH group in the growing strand, allowing the chain to grow in the 3' → 5' direction.