1. Write your first name in amino acids (if the letter does not exist, leave it out)
    a. What 3-letter code corresponds with each of the letters?
    b. Give the structure of these amino acids corresponding to each of the letters.
    c. Are there any amino acids, in your name, that could enforce secondary and tertiary structure formation? Could you point them out and in case there are none, could you name two important examples? (Answer: Lysins and Cysteines)

2. You have the following DNA sequence in 5' → 3' direction on the template strand, that serves as template for the transcription: 5'-TTCATTATCTAACAACTCCCA-3'
    a. Please give the sequence of the complementary coding strand of this strand in 5' → 3' direction. (Answer: 5'-TGG GAG TTG TTA GAT AAT GAA-3')
    b. Please give the mRNA-sequence of this strand in 5' → 3' direction. (Answer: 5'-UGG GAG UUG UUA GAU AAU GAA-3')
    c. Please give the corresponding amino acid sequence in single letter code in N-terminal → C-terminal direction (Answer: N-WELLDNE-C)

2. You would like to amplify the following DNA-strand with PCR:
5'- GGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAA-3'
    a. Explain how the PCR technique works.
    b. Design 2 primers for the amplification of this sequence and give their sequence in 5' → 3' direction. (Answer example: Fw: 5'-GGCACCCCAGGCTTTACACT-3'; Rev: 5'-TTCCACACAACATACGAGCC-3')
    c. Please name a potential application for PCR reactions. (Answer: Diagnostics for medical applications)

3. DNA can be used as building material to create nanostructures for many biological applications:
    a. For what application could one use DNA-nanotechnology? (Drug-delivery, Nano-robotics, etc.)
    b. Try to make a scaffold map of the Easter bunny (thus, place your pen on paper and finish the shape without lifting it off and connecting beginning with end).
    c. You have made the green fluorescent protein (GFP) and want to connect it to your Easter bunny DNA scaffold, briefly explain how would you do? (Answer: DNA-handle/anti-handle principle)

Exercise 1.2: Protein structure modeling with AlphaFold3.

Solution 1

1. Homo sapiens
2. α-subunit: 142;

   [MVLSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPT TKTYFPHFDL-SHGSAQVKGHGKKVADALTNAVAHVDDMPN ALSALSDLHAHKLRVDPVN-FKLLSHCLLVTLAAHLPAEFT PAVHASLDKFLASVSTVLTSKYR]

   β-subunit: 147;

   [MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWT QRFFESFGDL-STPDAVMGNPKVKAHGKKVLGAFSDGLAHL DNLKGTFATLSELHCDKLHVD-PENFRLLGNVLVCVLAHHF GKEFTPPVQAAYQKVVAGVANALAHKYH]
3. e.g. 1A00
4. HEMOGLOBIN (VAL BETA1 MET, TRP BETA37 TYR) MUTANT
5. α-helix: yes; β-sheet: no; 4 subunits
6. 4 subunits in total, 2 α-subunits and 2 β-subunits

Solution 2

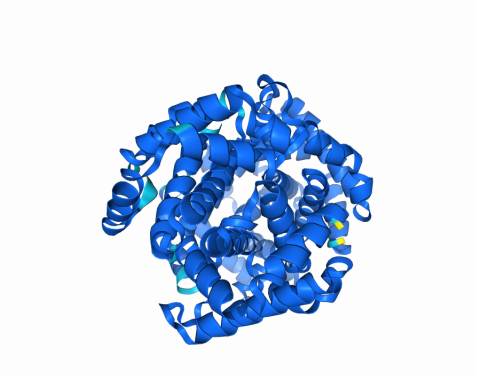
AlphaFold 3 is a machine learning based tool that can be applied to estimate protein structure based on their amino-acid sequence.

Solution 3 and 4

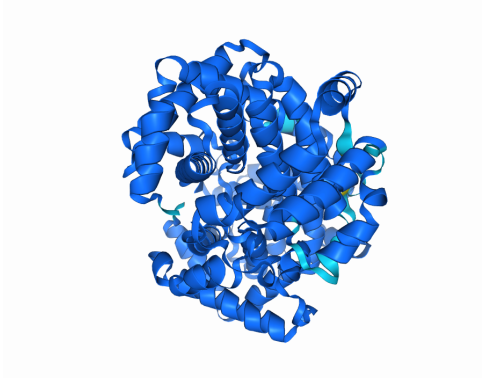
The predominant secondary structure within Hemoglobin is $\alpha-$helix. It is very difficult to find significant differences between the healthy Hemoglobin protein (left) and the one with the mutation in the β-globin subunits (right).

Solution 5

Visualizing the structure of 4 healthy Hemoglobin proteins and comparing it to 4 hemoglobin proteins which exhibit the mutation in the β-globin subunit however, demonstrates rather evidently the vast influence that the single amino acid mutation has on the interaction of multiple hemoglobin proteins. As expected, clustering behavior is observed for the

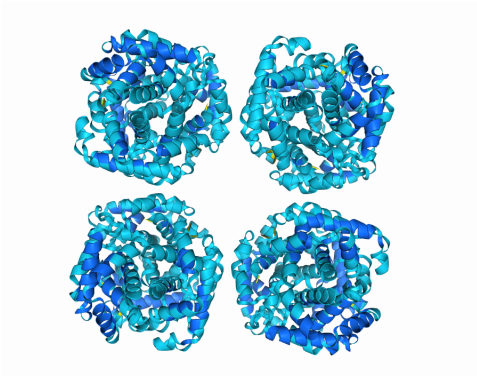


(a) Healthy Hemoglobin

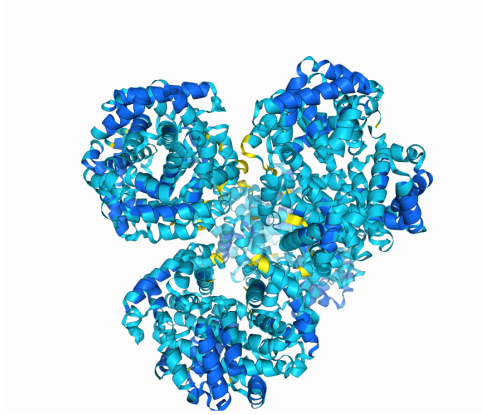


(b) Hemoglobin with mutation in β-globin subunits

mutated proteins, which eventually leads to the name-giving deformation of red blood cells.



(a) 4 healthy Hemoglobin proteins



(b) 4 Hemoglobin proteins with mutation in β-globin subunits