

WGU C785 Biochemistry Unit Exam Questions

Which level of protein structure is disrupted through the hydrolysis of peptide bonds?

Quaternary

Tertiary

Primary

Secondary

Answer- Primary

The primary structure of a protein is the sequence of amino acids held together by peptide bonds. Peptide bonds are formed by dehydration reactions and disrupted by hydrolysis.

A mutation in the beta-hemoglobin gene, which results in the replacement of the amino acid glutamate in position 6 with the amino acid valine, leads to the development of sickle cell anemia. The structures of glutamate and valine are shown below.

If the beta hemoglobin gene in a patient with sickle-cell anemia were to be edited so that the valine in position 6 was replaced with a different amino acid, which replacement for valine would be expected to have the best clinical outcome, in theory, for the patient? (Assume the valine can potentially be replaced with any amino acid other than glutamate.)

Answer- The original amino acid in a healthy patient is glutamate, which is negatively charged. The mutated amino acid is valine, which is non-polar. Valine is causing sickle cell anemia. The best amino acid to replace valine so that the patient is healthy again would be the one most like glutamate, so any negatively charged amino acid.

Secondary, tertiary, and quaternary levels of protein structure can all be impacted by exposing a protein to which treatment?

Change of a hydrophobic amino acid to a different hydrophobic amino acid

Addition of a reducing agent

Placement of the protein in a solution with a low pH

Increase in the concentration of the protein in solution

Answer- Placement of the protein in a solution with a low pH

Changes in pH affect hydrogen bonds and ionic bonds. Hydrogen bonds in the backbone of amino acids occur in secondary structure, and both hydrogen bonds and ionic bonds occur in the side chains of amino acids in tertiary structure.

An increase in beta-pleated sheet structure in some brain proteins can lead to an increase in amyloid deposit formation, characteristic of some neurodegenerative diseases. What is the primary biochemical process that follows the increase in beta-pleated sheet structure that leads to the development of the amyloid deposits?

An increase in glycogen formation in the brain cells

Aggregation of the proteins in the brain

Secretion of glucagon, leading to excessive ketogenesis

An increase in anaerobic metabolism of glucose in the brain

Answer- Aggregation of the proteins in the brain

This question is describing changes in protein structure. Aggregation occurs when proteins clump together inappropriately, causing plaques like amyloid deposits to accumulate.

Which level of protein structure is determined by the sequence of amino acids?

Secondary structure

Quaternary structure

Tertiary structure

Primary structure

Answer- Primary structure

The primary structure of a protein is simply the sequence of amino acids held together by peptide bonds.

Which force is most influential in determining the secondary structure of a protein?

Hydrophobic effect

Disulfide bonding

Hydrogen bonding

Electrostatic interactions

Answer- Hydrogen bonding

The secondary structure of a protein is built by hydrogen bonds between the carboxyl groups and amino groups on the backbones of the amino acids.

Which amino acid would most likely participate in hydrogen bonds?

Answer- Amino Acid structure 4

This is a polar, uncharged amino acid due to the OH group on the side chain. Polar, uncharged amino acids containing oxygen or NH groups make hydrogen bonds.

Which portion of the amino acid is inside the box?

The box is surrounding the section below the Alpha Carbon

Answer- Side Chain

The side chain is the variable group of the amino acid, also called the R group. Every amino acid has the same amino group, carboxylic acid group, and an alpha carbon, but the side chain is different.

Which pair of amino acids will most likely interact through hydrophobic forces between their side chains? Answer- Both of these amino acids are non-polar and therefore can interact together with a hydrophobic interaction. Please note that the "S" in the amino acid on the right is non-polar, while the "SH" group in answer choice D is polar. The S must have an H to be polar and is otherwise non-polar.

Which portion of the amino acid is inside the box?

The box is over the Carbon at the Center of the chain

Answer- Alpha Carbon

The alpha carbon is the central carbon on an amino acid that holds together the other groups of the amino acid. It is always attached to the amino group, the carboxyl group, the side chain, and a single hydrogen. It is part of the backbone of the amino acid and is found in every amino acid.

Given the following amino acid structure, what is the strongest intermolecular force it would participate in to stabilize a protein structure?

Ionic bond

Disulfide bond

Hydrogen bond