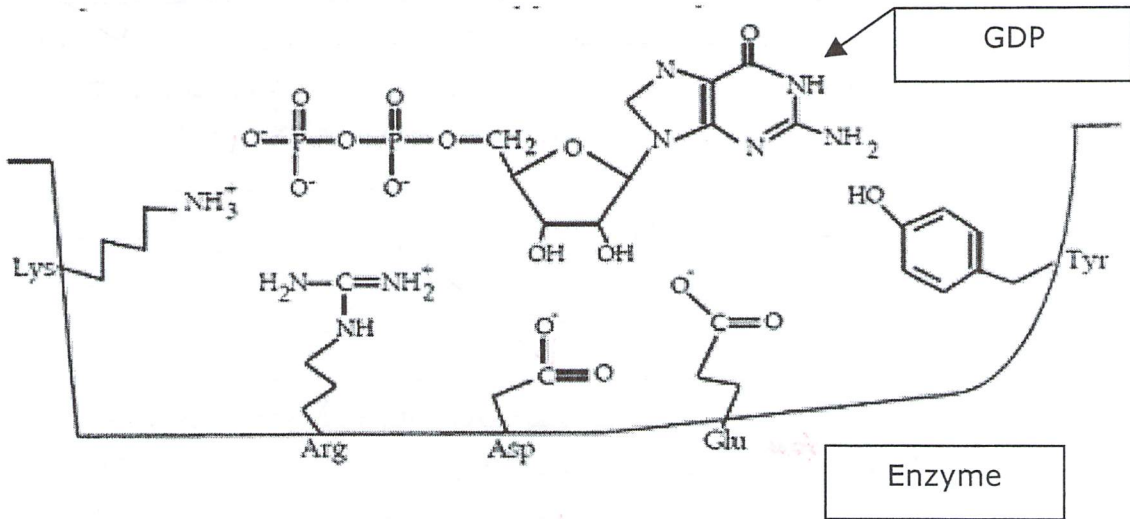


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2. The following diagram shows the active site of an enzyme (G-Protein) with a molecule of GDP in it. Notice the exposed sidechains in the enzyme's active site.

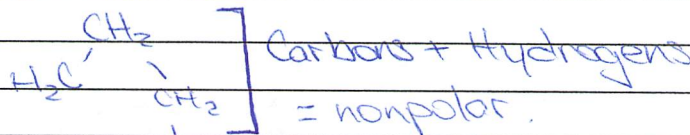


Imagine that you can induce mutations (change the amino acids) in the binding pocket of the G-protein shown above, and hence change the sidechains that line the active site.

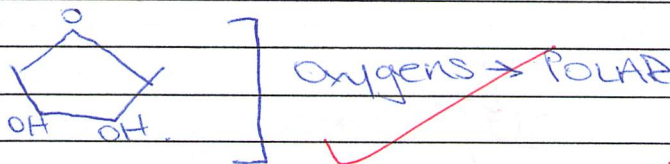
If **Asp** is mutated to a **Pro**, the result is a G protein that cannot bind its substrate, GDP. Explain why. (Hint: You may need the amino acid sheet.)

Include in your discussion ^{explain} how all levels of protein structure may be changed by this mutation.

If Asp is mutated to a Pro, the G protein cannot bind to its substrate GDP for a number of reasons. The structure of Pro is:



The structure ~~is~~ that Asp currently interacts with and Pro will interact with is:



Asp interacts fine with this because Asp itself is a polar molecule, due to its ~~Hydrogens~~ ^{Oxygens}. However, Pro is completely nonpolar. Nonpolar molecules do not interact with polar molecules. Because of this, GDP would no longer be able to bind with the G-protein. ~~Yes!~~

It would be more effective if you showed the P-group for Asp

in P-group

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Another reason why the G-protein will no longer be able to bind to its substrate is because the entire structure of the protein itself will be changed.

- 1) The primary structure will be changed because the sequence of amino acids is now different.
- 2) The secondary structure is different because since Asp is now Pro the backbone might coil in a different way.
- 3) The tertiary structure will be most affected because a hydrophobic amino acid is now in the place of a hydrophilic one. The bonds that Asp originally formed will no longer be present because Pro does not have the same properties as Asp. Pro instead will look for other hydrophobic R-groups, engaging in hydrophobic interactions, resulting in different folding & thus structure.
- 4) The quaternary structure will now be different because due to the changes in the tertiary structure, the active site of the molecule might be completely different. In any case, how this polypeptide bonds with other polypeptides will be affected because now its polarities and structure are different. It might form Hydrogen bonds in different places, or it just might not fit with another molecule.

Excellent Essay

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$$\begin{aligned} MC &= \frac{53}{60} \\ \text{Essay} &= \frac{38}{40} \end{aligned}$$

91/100



38/40