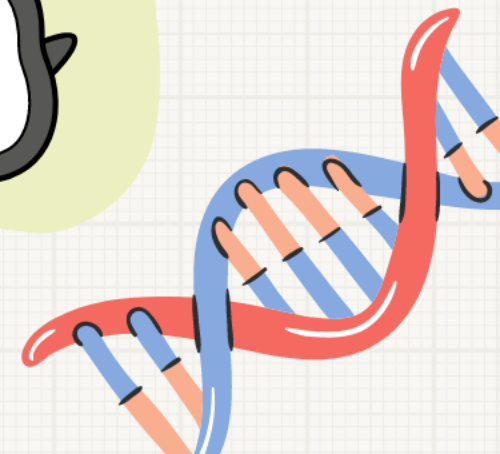
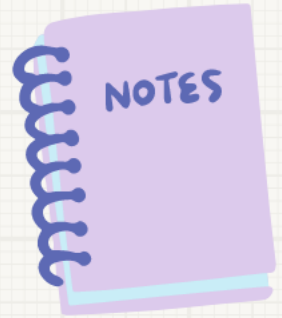
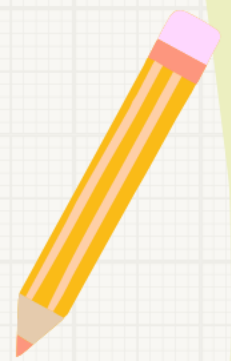


# AP Bio

## FRQ Fridays

2008 #1a  
Protein Structure



# FRQ Friday #2

2008 #1a

The physical structure of a protein often reflects and affects its function.

(a) **Describe** THREE types of chemical bonds/interactions found in proteins. For each type, **describe** its role in determining protein structure.

Bond/interaction	Description	Role associated to bond/interaction
Covalent/ peptide	sharing electrons <b>OR</b> linking amino acids together	amino acid sequence <b>OR</b> primary structure (no credit for chain or polypeptide alone)
Disulfide/ covalent	disulfide, S-S bond (bridges); sulfur-containing R group bonding	tertiary or quaternary structure
Hydrogen	H-O or H-N interactions	$\alpha$ helix, $\beta$ sheet; secondary, tertiary, or quaternary structure
van der Waals	unequal electron clouds in R group; dipole moments	tertiary or quaternary structure
Hydrophobic	nonpolar R groups	tertiary or quaternary structure
Ionic	charged R groups	tertiary or quaternary structure



# FRQ Friday #2

2008 #1a

a) The amino acid cysteine ( $\begin{array}{c} \text{SH} \\ | \\ \text{H} \text{---} \text{N} \text{---} \text{C} \text{---} \text{C} \\ | \quad | \quad | \\ \text{H} \quad \text{H} \quad \text{OH} \end{array}$ ) contains a  $\gamma$  (gamma) sulfur. This sulfur may form a covalent bond with another cysteine to form a disulfide bridge. This has a tremendous stabilizing effect on the conformation because of the strength of a covalent bond. As such, ~~the sulfur~~ disulfide bridge ~~will~~ will cause sulfurs to orient near each other in the tertiary & secondary structures. Disulfide bridges also stabilize protein structure (and can help confer such things as thermal stability).



# FRQ Friday #2

2008 #1a

i) ~~Van der~~ Van der Waals interactions are also a common interaction in proteins. Van der Waals attractions result from the temporary re-alignment of electrons in the orbitals of two nearby atoms. As a result, large molecules w/ many electrons often experience greater van der Waals forces (also called London dispersion forces). This is one reason why amino acids w/ large carbon side chains like Leucine, isoleucine, valine, & Phenylalanine agglomerate near each other, they mutually exert large VDW forces on each other because of this agglomerative tendency (and ~~that~~ their hydrophobicity) - these nonpolar amino acids clump together on the ~~int~~ interior of proteins. The agglomeration also plays a part in the formation of some proteins' ~~secret~~ hydrophobicity.





# FRQ Friday #2

2008 #1a

## Structures

(ii) Hydrogen bonds (H-bonds) are a type of polar bond between oxygen, nitrogen or fluorine & hydrogen & result in a relatively strong bond. H-bonds are critical in the formation of helices as the carbonyl ~~groups~~ groups and the amine groups form hydrogen bonds. Beta sheets are likewise ~~over~~ primarily determined by the presence of H-bonds. Since these two secondary structures are vital to the tertiary structure as a whole, they play a pivotal role in structure.

