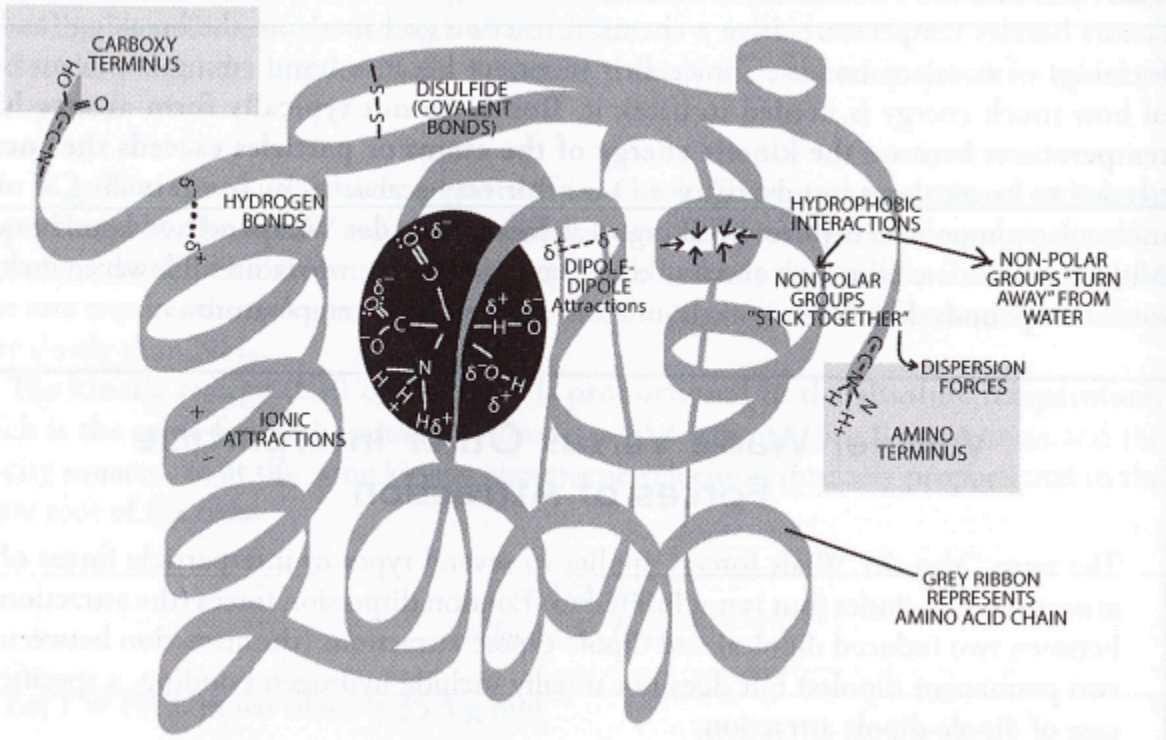
150. Many weak forces can impart stability in large molecules due to their collective action. There are a tremendous number of weak forces acting in a molecule such as a protein, so the cumulative effect can be quite large. Weak forces have a large influence on biological molecules such as proteins and nucleic acids.

151. *The diagram shown below is more complex than what would be expected from you on the AP Chemistry exam.* If you are asked for three types of interactions, only provide three. Below, several are shown, including a covalent interaction (disulfide bridge) that you may not have covered in class. Also shown is a substrate with some functional groups shown to illustrate some types of potential groups that would help a substrate interact with the active site. **The complementary shape and charge distribution between the substrate and the active site are the primary factors determining the affinity of the active site for the substrate.**



152. Structural complementarity and **charge distribution complementarity** are the primary factors determining the affinity of the active site for the substrate. **Weak intermolecular forces are readily reversible because the kinetic energies of the molecules involved are only a few times weaker than the forces of attraction between them.** A substrate fits into an active site due to complementary shapes but is also held in position by forces of attraction such as hydrogen bonds and Van der Waals forces (and others that may not have been mentioned in your AP Chemistry class). Once the substrate has been converted to product, the shape of the molecule as well as the functional groups will be different. That means the product (or products) will most likely have *less* of an attraction (lower affinity) for the active site. **The thermal motion (kinetic energy) of the particles would then be high enough relative to the affinity to release the product from the enzyme.**

153. For this question, it may be helpful to set up a table.

Proteins in solution	Fold only in solution ∴ hydrophilic R-groups in the protein's exterior face the solution while hydrophobic R-groups face the interior.
Peripheral proteins	One surface interacts with the hydrophilic heads of the phospholipid membrane. These R-groups would form weak, reversible interactions such as dipole-dipole attractions, ionic attractions, and hydrogen bonding.
	The surfaces that face the solution would form weak interactions with water, such as dipole-dipole attractions, ionic attractions, and hydrogen bonding.
Integral proteins	The amino acid R-groups on the exterior of the "midsection" of the protein would face outward, forming weak dispersion forces with the phospholipid tails. The hydrophobic environment would also cause hydrophilic amino acid R-groups to face the interior of the protein.
	The hydrophilic R-groups on the surface of the protein face the aqueous intra- and extracellular solutions.

154. *Structural comparison*: Water has a bent molecular geometry while ammonia has a trigonal pyramidal geometry. **This geometry affects the number of hydrogen bonds per molecule that can form.** Water has two hydrogen atoms available for hydrogen bonding and two lone pairs of electrons. In H_2O *(l)* approximately two hydrogen bonds can form per molecule at any one time. Ammonia has three hydrogen atoms available for hydrogen bonding and one lone pair of electrons but will typically form approximately one hydrogen bond per ammonia molecule at any one time.

A mechanism based on intermolecular attractions: **Hydrogen bonds are constantly forming and breaking**. The average lifetime of a hydrogen bond in H_2O *(l)* is on the scale of 10 picoseconds. **The number of hydrogen bonds that form per molecule is dependent on the temperature. Higher temperatures mean higher kinetic energy, which means there is an increased tendency toward molecular dispersal.**