

CBIO 3400 – Week 1 Study Questions

1. What is the endosymbiont hypothesis for the origin of mitochondria? Is there any evidence that supports this hypothesis?

The endosymbiont hypothesis postulates that early eukaryotic cells lacking mitochondria and chloroplasts phagocytosed early aerobic and photosynthetic prokaryotes; rather than digesting these prokaryotes, these early eukaryotes formed a symbiotic relationship with the early prokaryotes, offering them nutrients and shelter while acquiring very efficient energy generating systems in return. Evidence supporting this hypothesis revolves around certain characteristics of mitochondria:

- have circular DNA
- lack histones
- have smaller prokaryote-type ribosomes
- start protein synthesis with formyl-methionine
- protein synthesis inhibited with chloramphenicol, not cycloheximide
- have double membrane

2. Describe the nature of a hydrogen bond and how it affects the structure of molecules in cells.

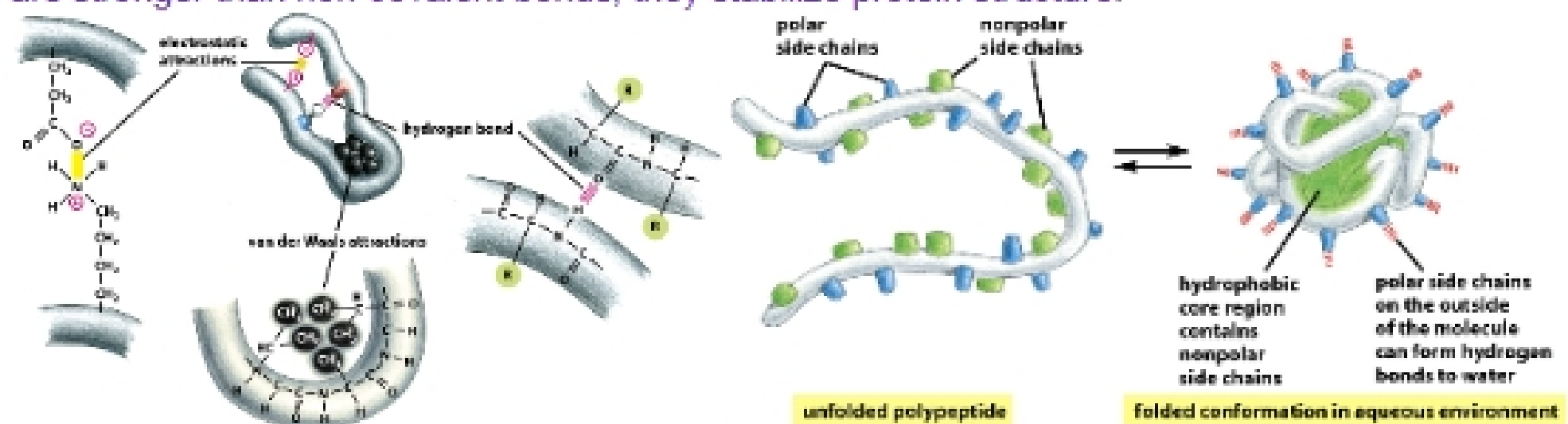
Water H-bonds with 4 other water molecules, creating a tetrahedral orientation. A hydrogen bond's greatest strength is its orientation; hydrogen bonds form in a straight line. Hydrogen bonds are temperature sensitive and very short-lived. For these reasons, hydrogen bonds cause molecules in cells to line up and pack in an orderly fashion.

3. List weak chemical bonds or forces that you can find in proteins, and explain how they affect the conformation of proteins.

Weak chemical bonds or forces found in proteins include:

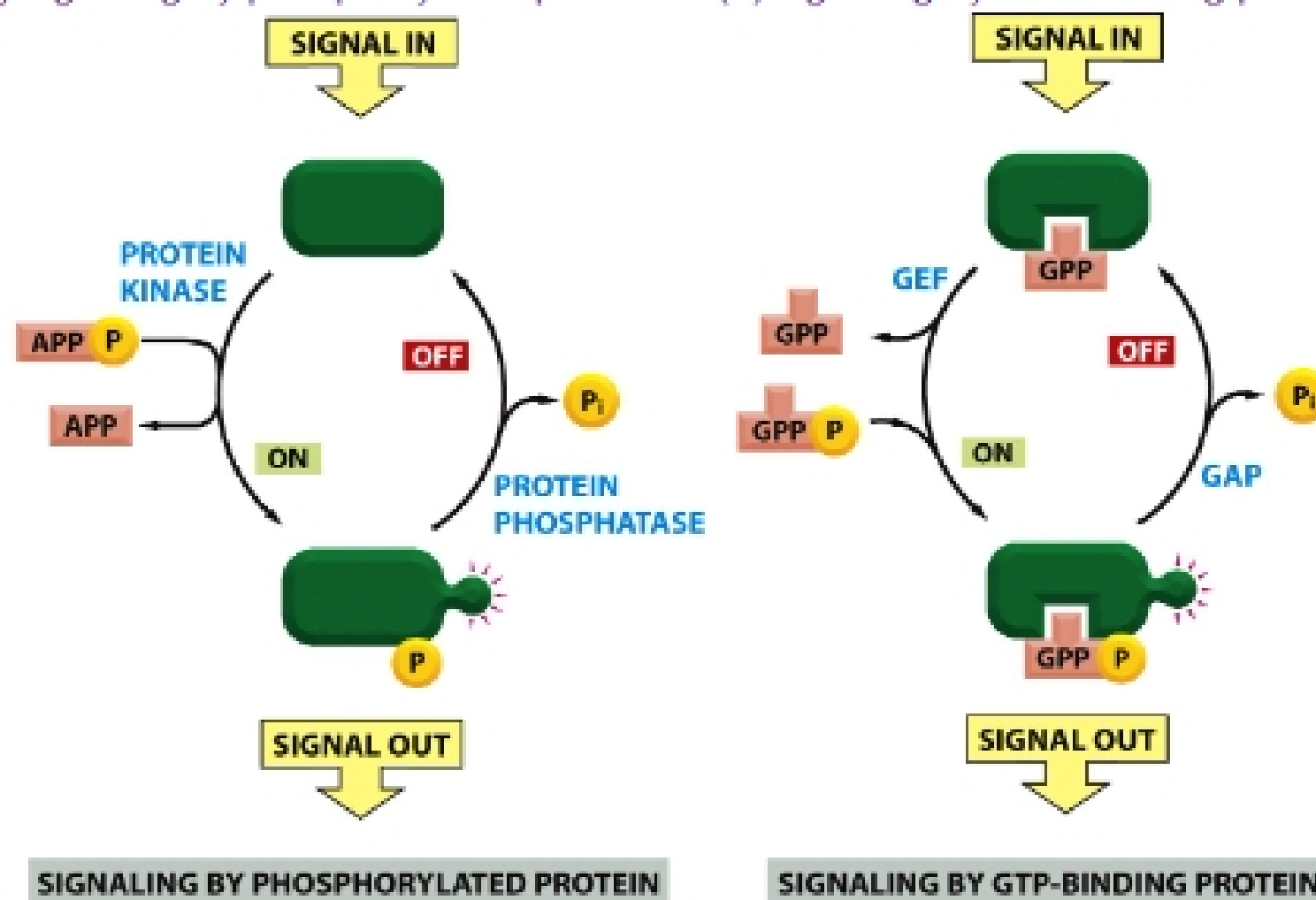
- hydrogen bonds
- hydrophobic interactions
- electrostatic interactions
- dipole interactions

Primary protein folding – that is, the amino acid sequence – is most affected by electrostatic interactions, which are the attraction of positive and negative charges to one another. Secondary protein folding – that is, alpha helices and beta sheets – is most dependent on hydrogen bonds, which determine the helical or sheet shape of a protein. Tertiary protein folding – that is, domains (alpha and beta folds) – is most affected by hydrophobic interactions, which non-polar side chains inward and polar side chains outward. Quaternary protein folding – that is, the assembly of multiple peptides to form the native structure – is most dependent on dipole interactions; since covalent bonds are stronger than non-covalent bonds, they stabilize protein structure.



4. Describe two major methods regarding how cells utilize energy provided by nucleotide triphosphates to control protein conformation.

Cells utilize energy provided by nucleotide triphosphates to control protein conformation via one of two paths: (1) signaling by phosphorylated protein or (2) signaling by GTP-binding protein.



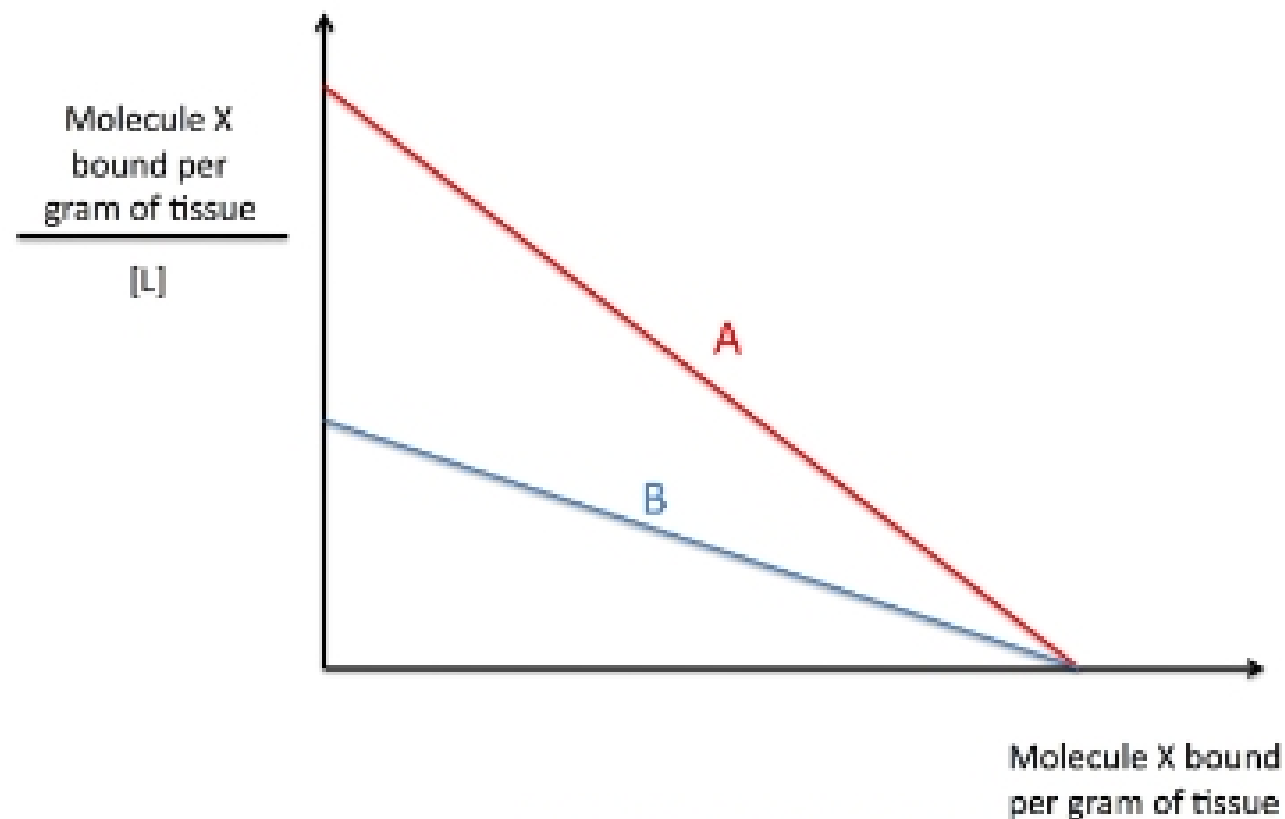
Signaling by a phosphorylated protein goes as follows:

1. Many proteins in a typical eukaryotic cell are modified by the covalent addition of a phosphate group.
2. The general reaction transfers a phosphate group from ATP to an amino acid side chain of the target protein by a protein kinase.
3. Removal of the phosphate group is catalyzed by a second enzyme, a protein phosphatase.
4. The phosphate is added to the -OH group of a serine, threonine, or tyrosine amino acid in the protein.

Signaling by a GTP-binding protein goes as follows:

1. The activity of a GTP-binding protein (also called a GTPase) generally requires the presence of a tightly bound GTP molecule (switch "on").
2. Hydrolysis of this GTP molecule produces GDP and inorganic phosphate (P_i).
3. This causes the protein to convert to a different, usually inactive, conformation (switch "off").
4. Resetting the switch requires the tightly bound GDP to dissociate – a slow step that is greatly accelerated by specific signals.
5. Once the GDP has dissociated, a molecule of GTP is quickly rebound.

5. A scientist tested the binding of molecule X to X receptor in mice and made a Scatchard plot, as shown below. A is the plot from Wild type mice, and B is the plot from mutant mice. Explain the possible defect that mutant mice have by comparing B to A.



Note: $[L]$ is the concentration of ligand free at equilibrium.

Wild-type mice (plot A) must have less ligand free at equilibrium than mutant mice (plot B) because plot A begins with a much larger y-coordinate value than plot B, implying that $[L]$ – the denominator of the y-coordinate unit – must be lower/smaller in wild-type mice than in mutant mice. Mutant mice must, therefore, be experiencing a defect in which there is either not enough ligand – bound or free – in general or too much ligand already bound at equilibrium. Since plot B has a more gradual slope compared to the steep slope of plot A, mutant mice must have a lower affinity for bound ligand than wild-type mice.

6. What kind of lipid can form the lipid bilayer? Why?

Phospholipids can form the lipid bilayer because the hydrophobic tails pack together to exclude water, forming a bilayer with the hydrophilic head of each phospholipid facing the water.

Phospholipids have a polar head group and two hydrophobic hydrocarbon tails, which are usually made up of fatty acids and can vary in length.

