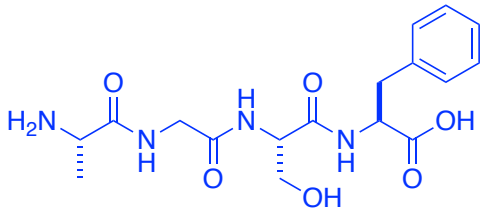
BPS 2110
Assignment 2 Answers

1. What are the 5 major classes of amino acids? Give an example of an amino acid in each class.
   - non-polar (alkyl - alanine, valine, leucine, isoleucine; aromatic – phenylalanine, tyrosine, tryptophan)
   - acidic (aspartic acid, glutamic acid)
   - basic (lysine, arginine, histidine)
   - polar (asparagine, glutamine, serine, cysteine, threonine)
   - special (glycine, proline)

2. 18 of the common amino acids have an S configuration at the α-carbon, however one amino acid exists in the R configuration at this position. Which one and why?
   - cysteine. The sulfur has a higher atomic number than oxygen which reverses the priority for the CIP system

3. Draw the structure of the peptide composed of Alanine-Glycine-Serine-Phenylalanine, including stereochemistry.

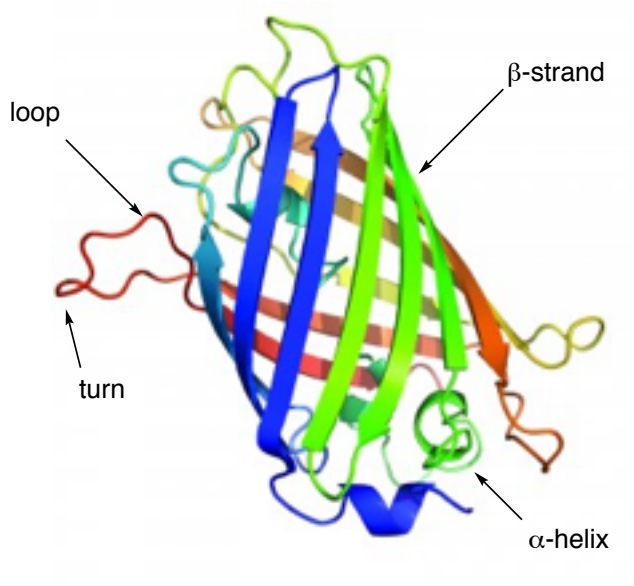


4. Briefly explain what constitutes each of the following with respect to proteins:
   a. Primary structure
      -list of amino acids in a protein in order from the N-terminus towards the C-terminus
   b. Secondary structure
      -areas of local order in the backbone chain. These regions tend to hold a particular shape such as a helix or sheet
   c. Tertiary structure
      -overall three dimensional structure of a protein
   d. Quaternary structure
      -structure of a protein formed by the association of two or more sub-proteins

5. Briefly describe each of the four types of secondary protein structure with respect to overall structure, what causes each structure to form and appearance on a ribbon diagram.

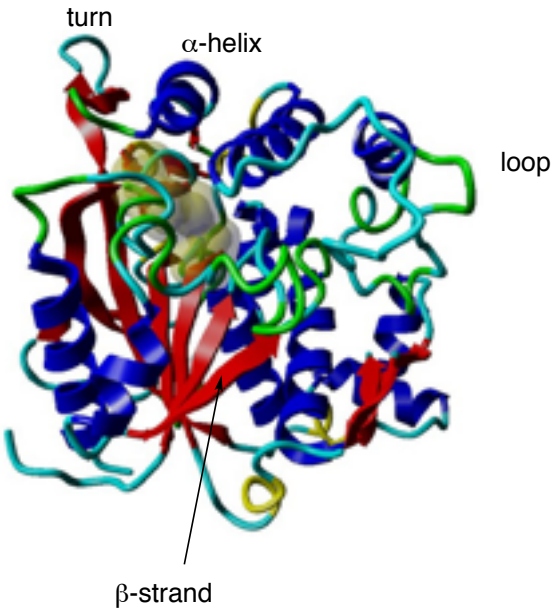
-α-helix is a corkscrew-shaped region. It forms from hydrogen bonds between amide groups approximately 4 amino acids apart. On a ribbon diagram is represented by a coiled, flat ribbon. The plane of the ribbon follows the plane defined by the amide groups in the backbone, and there is an arrow on the ribbon pointing from the N to the C terminus
- β-sheet is a linear strand made up of the chain of atoms in the backbone forming a flat zig-zag structure, which form because amide bonds tend to prefer extended s-trans conformations. Several strands can associate together forming a β-sheet in which the individual strands can be parallel or antiparallel. Large sheets may curl upon themselves to form β-barrels
- turns are areas which change direction by almost 180° within a length of 3 or 4 amino acids. These form because of hydrogen bonding between nearby amide groups, and are favored by amino acids such as glycine or proline. There is no special designation for a turn on a ribbon diagram, but the regions can be identified by their tight-turn shape
- loops are areas of otherwise undefined secondary structure. They are represented by thin tubes

6. Identify one of each type of secondary structure on the following images:

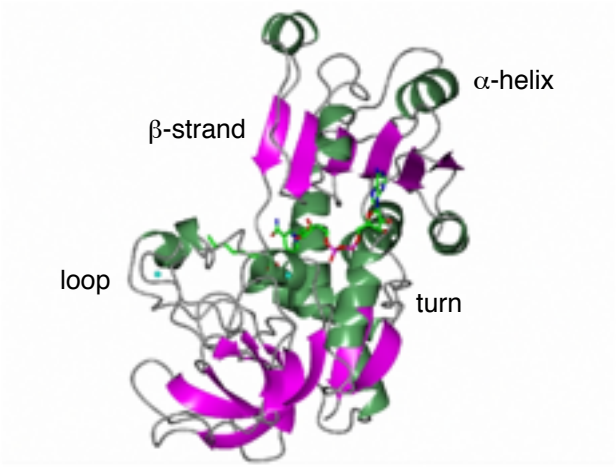


a.

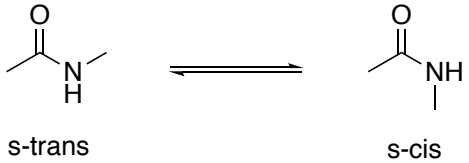
b.



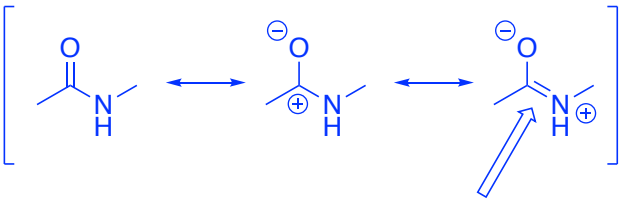
c.



7. The amide bonds in peptides are capable for adopting one of two conformations, called s-cis and s-trans respectively.



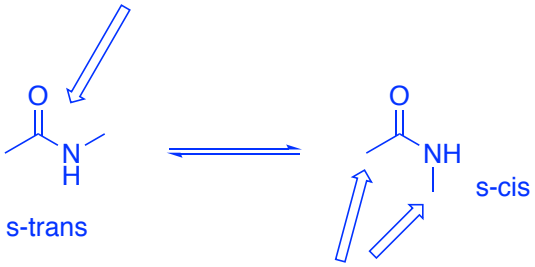
   a. Explain why this functional group usually only adopts one of these conformations.



this form make a large contribution to the overall structure of an amide (all atoms have octets). this gives the C-N bond in this group significant double-bond character, to the degree that the N, C and O are all nearly fully sp^2 hybridized. The double bond character limits rotation about this bond, much like in a C=C bond. this gives cis and trans conformations, just like in a regular double bond. the designations s-cis and s-trans are used because the bond is formally a sigma bond (s=sigma).

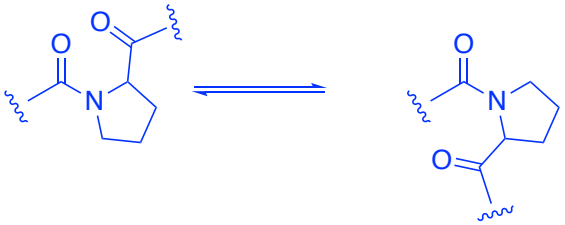
b. Which conformation do you think is most common and why?

Sterics favor the s-trans conformation (large groups far apart)



groups close together - this form is disfavored

c. Explain why proline is the only amino acid that does not show a preference for one amide conformation over the other.



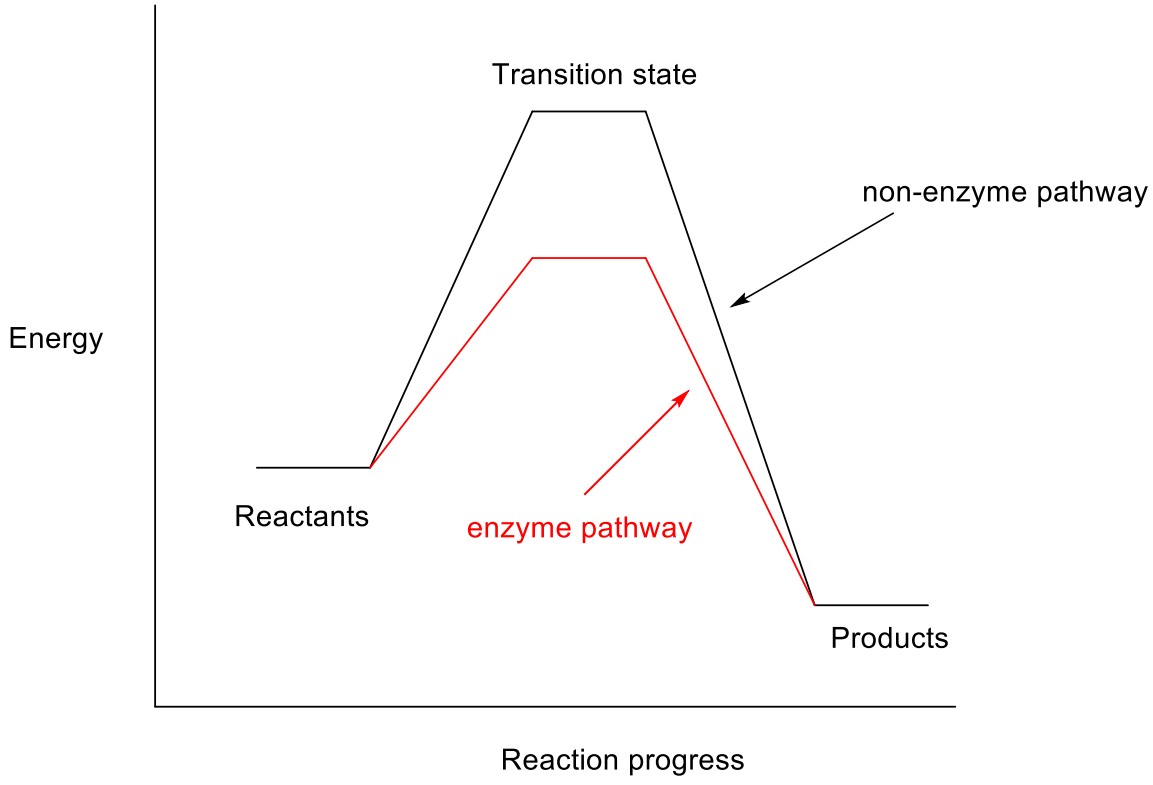
two possible conformations have similar sterics. not a large energy difference between them, so both conformations likely

8. What are the four types of non-bonding interactions responsible for maintaining tertiary structure?
   - electrostatics
   - hydrogen bonding
   -dipole-dipole interactions
   - Van der Waals forces (dispersion forces)

9. One type of interaction, which controls tertiary structure, involves the formation of a covalent bond. What is the name of this interaction and what type of amino acid(s) are involved?
   -disulfide bond, formed between two cysteine side chains

10. Explain why Van der Waals interactions are so important in the maintenance of tertiary structure.
- water tends to be excluded from between two areas that are attracted by VdW interactions. "squeezing" the water out from between the chains helps to hold the chains together and provide structure.
- VdW interactions are found in areas with lots of non-polar side chains. These groups are only capable of interacting using VdW interactions, and cannot participate in other types of non-bonding interactions such as hydrogen bonding. Groups that interact through polar non-bonding interactions (such as hydrogen bonding) experience stronger attractive forces because the attraction between these groups is not "diluted" by interactions with the non-polar groups

11. In general, how do enzymes catalyze reactions? Use an energy diagram in your explanation, and show the key stages in an enzymatic reaction.
- they bind to transition states. This binding lowers the energy of the transition state and accelerates the reaction by reducing the activation energy for enzyme-catalyzed processes.

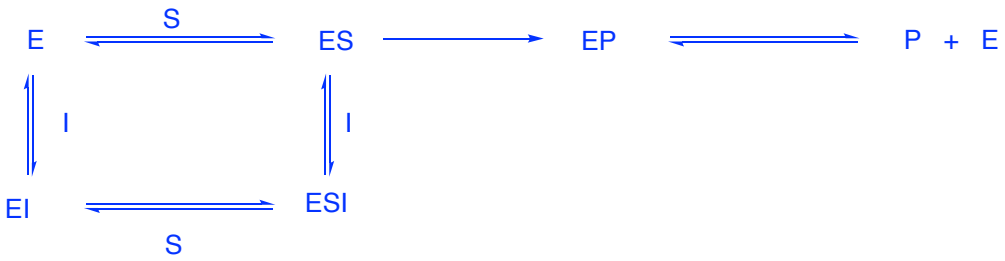


12. Describe the four different types of enzyme inhibitor. Include a simple diagram showing how each mode operates, and briefly explain how each can be identified.
    a. Competitive inhibitor competes with substrate for the same site (active site) on the enzyme. This type of inhibitor alters K_m and k_{cat} but does not affect V_{max}

competitive inhibitor

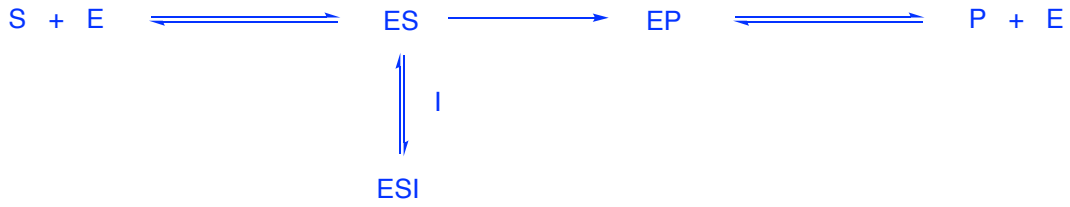
b. Non-competitive inhibitor binds to a different location on the enzyme than the substrate does. Inhibitor binding prevents formation of the ES complex. This type of inhibitor alters k_{cat} and V_{max} but does not affect K_m

non-competitive inhibitor



c. Un-competitive inhibitor binds to the ES complex. Inhibitor binding alters the structure of the ES complex preventing catalysis. This type of inhibitor alters k_{cat} and V_{max} and K_m

un-competitive inhibitor



13. What are the two general modes of signaling through messenger-receptor interactions?

- binding of messenger changes the conformation of the receptor allowing another molecule to bind or be released
- binding of messenger changes the conformation of the receptor creating an enzyme active site on the receptor

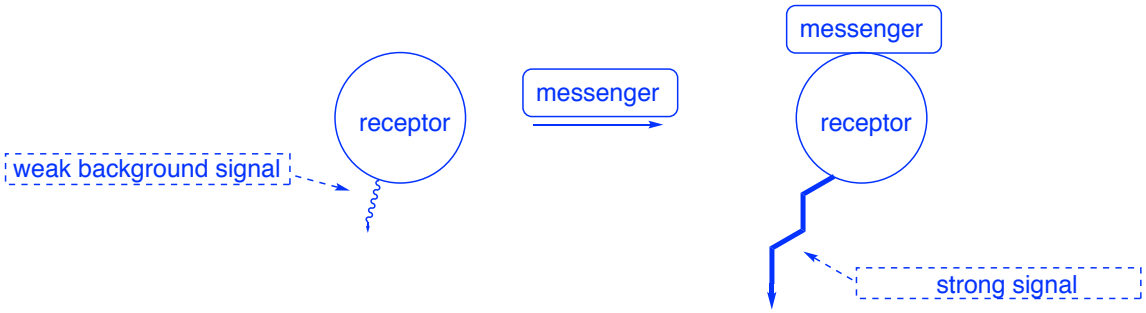
14. What is the difference between an agonist and an allosteric modulator?
    - agonist binds to the "active site" of the receptor, the same location that the messenger normally does.

-allosteric modulator binds to a different location on the receptor, and in doing so alters the active site slightly so that binding of the normal messenger is easier

15. Describe how an inverse agonist works.

An inverse agonist is actually a kind of antagonist that causes an apparent reversal in the way a receptor functions. Inverse agonists can only occur if the receptor involved has a small background function. If a receptor has a small background operation (it produces a signal in the absence of a messenger), adding an antagonist has the effect of shutting off the background signal. This produces a situation in which the receptor now seems to reverse the signal. Because the signal is "reversed", the term inverse agonist is used.

receptor produces a weak background signal



inverse agonist appears to give a reverse effect by blocking the background signal