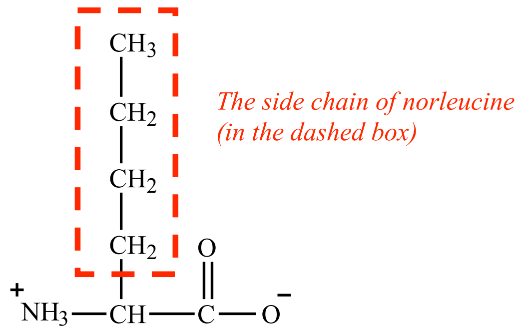
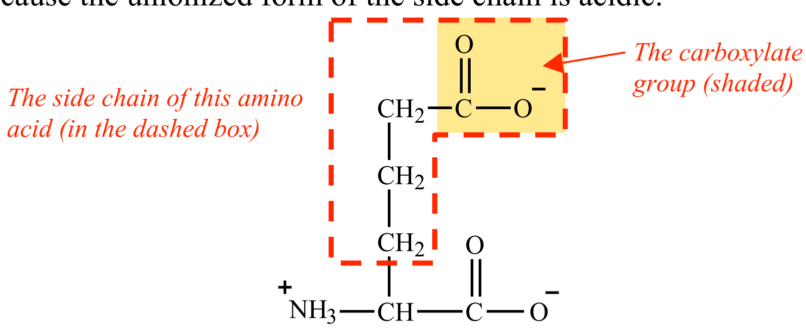
CHAPTER 13: ANSWERS TO SELECTED PROBLEMS

SAMPLE PROBLEMS ("Try it yourself")

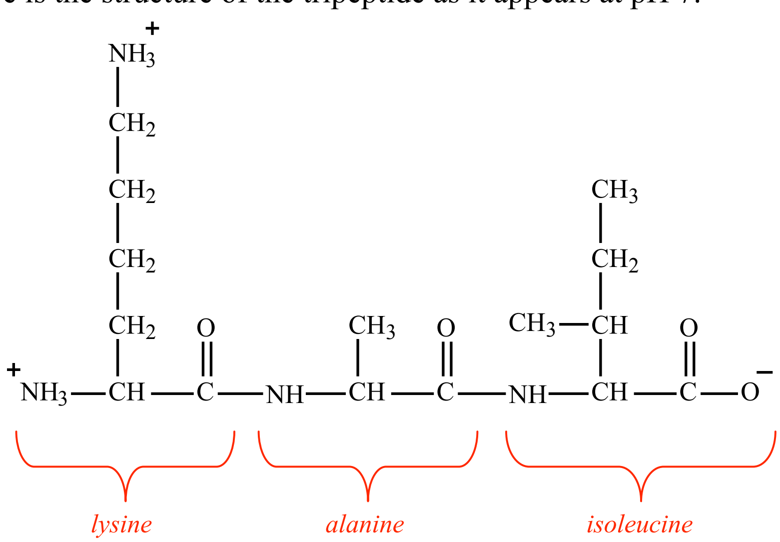
13.1



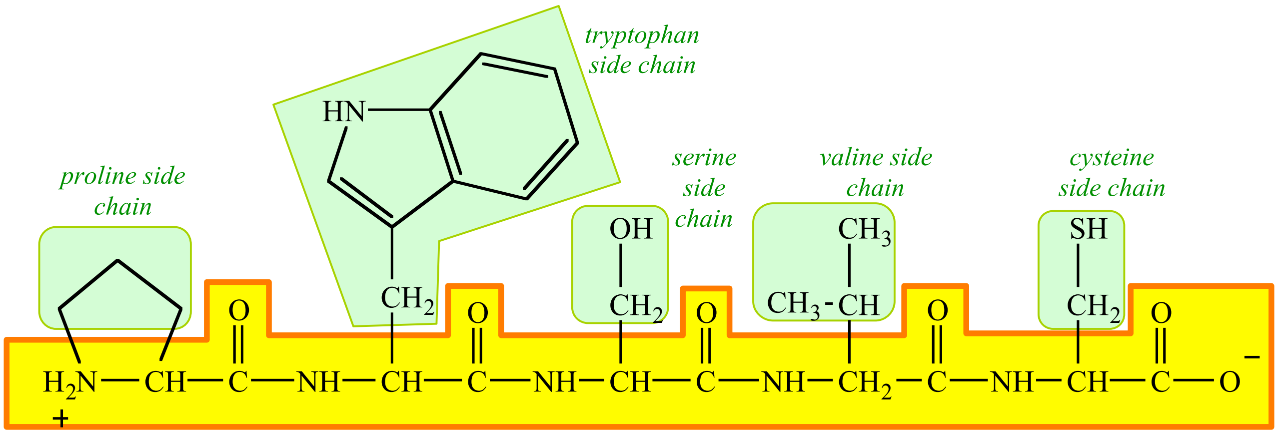
13.2 The side chain of this amino acid contains a carboxylate group (the ionized form of a carboxylic acid). This group is strongly attracted to water, so the amino acid is **hydrophilic**. Amino acids that contain carboxylate groups in their side chains are classified as **acidic** amino acids, because the unionized form of the side chain is acidic.



13.3 Here is the structure of the tripeptide as it appears at pH 7.



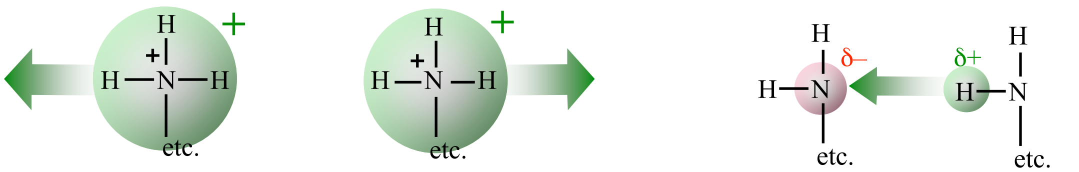
13.4 The primary structure of the polypeptide is Pro-Trp-Ser-Val-Cys. The backbone of this polypeptide is shaded yellow in the structure below, and the side chains are shaded in green.



13.5 Aspartic acid and arginine are most likely to be found on the surface of a polypeptide, because they have charged side chains that are strongly attracted to water. (Methionine and tryptophan have hydrophobic side chains.)

13.6 a) Two cysteine side chains normally form a disulfide bridge.
b) The side chains of threonine and asparagine form hydrogen bonds with one another (side-chain hydrogen bonding).

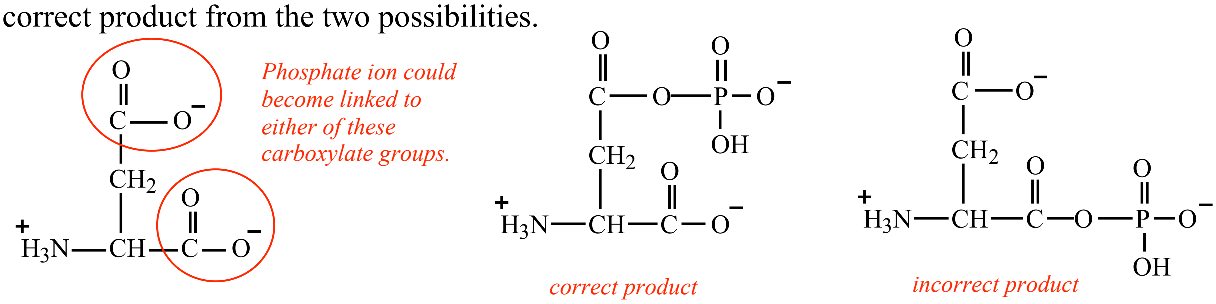
13.7 At pH 7, the amino group on the side chain of lysine is positively charged, so the two lysine side chains repel one another. If the pH is raised to 12, the side chains lose H^+, so the amino groups on the side chains now attract one another (they form a hydrogen bond).



At pH 7, the amino groups are positively charged and repel one another strongly.

At pH 7, the amino groups have no net charge, so they can form a hydrogen bond.

13.8 The reaction condenses one of the carboxylate groups of aspartic acid with a phosphate group. Aspartic acid contains two carboxylate groups, and phosphate group could become linked to either of these. Therefore, the enzyme (aspartate kinase) must be able to select the correct product from the two possibilities.



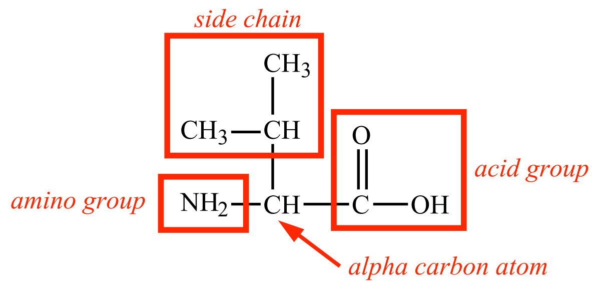
13.9 ATP is a positive effector. It does not bind to the active site, so it is an effector rather than a competitive inhibitor. Since ATP makes the enzyme more active, it is a positive effector.

13.10 Susan is not eating enough carbohydrate and fat to supply her Calorie needs, so her body is using a substantial amount of the protein she eats to provide additional energy. When our bodies use protein as an energy source, we (in effect) burn the amino acids, destroying them so they are not available to build proteins. The remaining amino acids are evidently not sufficient to meet Susan's needs.

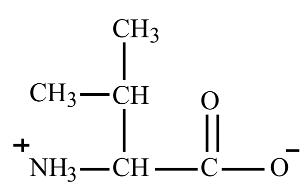
SECTION PROBLEMS

Section 13.1

13.1



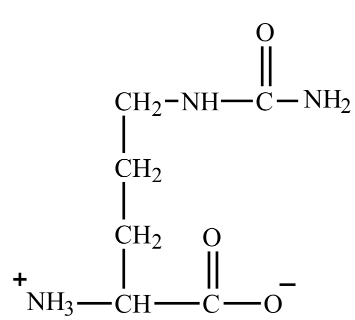
13.2 a) To make the zwitterion structure, move H^+ from the acid group to the amino group:



b) Although both forms of valine are present under physiological conditions, the overwhelming majority of the molecules are in the zwitterion form.

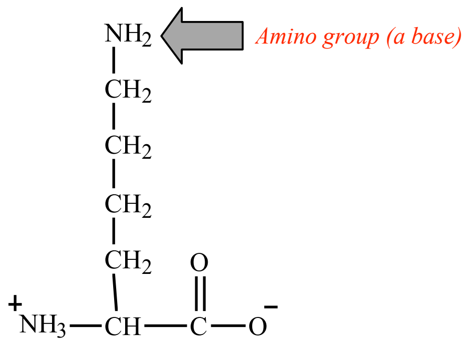
13.3 The side chain of valine contains no groups that can form hydrogen bonds, so valine is a hydrophobic amino acid.

13.4



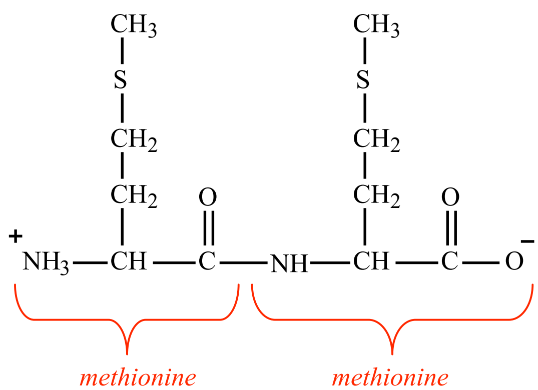
13.5 The side chain of citrulline contains oxygen and nitrogen atoms, so it can participate in hydrogen bonds. Therefore, citrulline is a **hydrophilic** amino acid. However, citrulline does not lose or gain H^+ at pH 7, so citrulline is **neutral**. (The nitrogen atoms in citrulline are part of an amide group, which is not basic.)

13.6 Acidic and basic amino acids are classified based on the unionized form of their side chains. For lysine, the unionized form of the side chain contains an amino group, which is basic. Therefore, lysine is classified as a basic amino acid.



Section 13.2

13.7 a)



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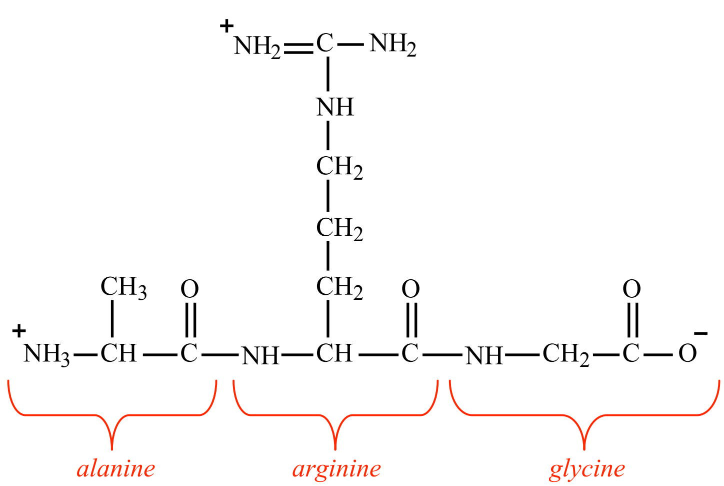
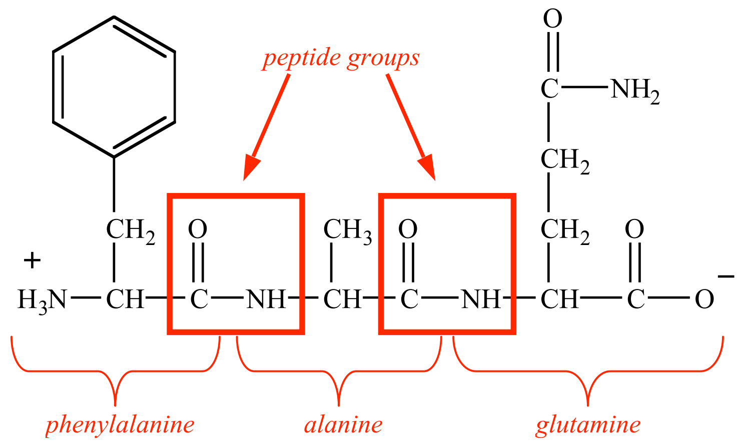


13.8 The primary structure of a protein is the sequence of amino acids in the protein.

13.9 a) This tripeptide contains phenylalanine, alanine, and glutamine.
b) There are two peptide groups, as shown below.
c) The C-terminal amino acid is glutamine.
d) The N-terminal amino acid is phenylalanine.

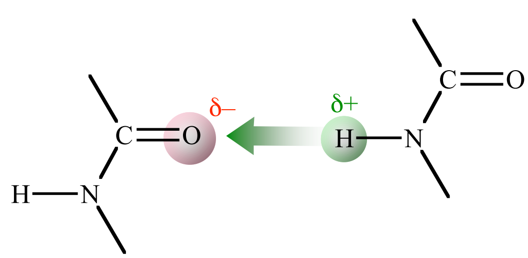


13.10 The two common secondary structures are the alpha-helix and the beta-sheet. In the alpha-helix, the polypeptide coils like a spring, with the side chains pointing outward. In the beta-sheet, the polypeptide forms parallel rows, running back and forth, with the side chains projecting above and below the sheet.

13.11 A beta turn is an abrupt bend in a polypeptide that connects two strands within a beta sheet. Proline often appears at a beta turn because it cannot participate in the hydrogen bonds that form alpha helices and beta sheets, and its shape naturally produces a bend in the chain.

13.12 A triple helix contains three polypeptide chains, wound around one another like braided hair. Collagen contains this type of structure.

13.13



Section 13.3

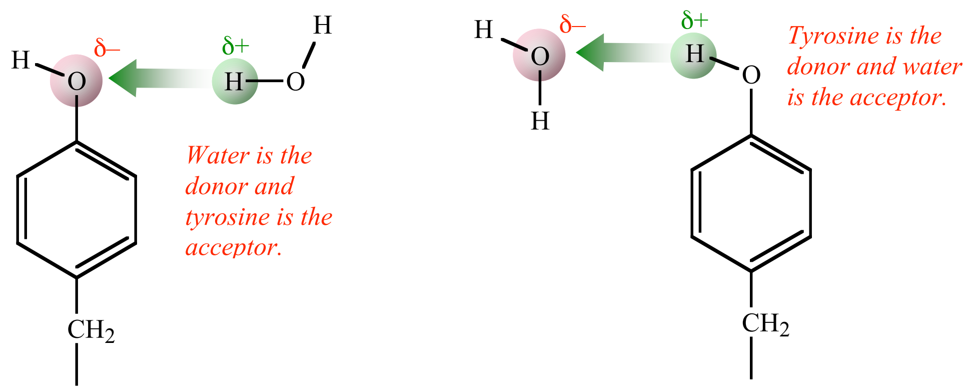
13.14 The hydrophobic interaction is important for leucine and phenylalanine, because their side chains cannot form hydrogen bonds and have little attraction for water.

13.15 The hydrophilic interaction is important for lysine, threonine, and glutamic acid. These amino acids contain oxygen or nitrogen atoms that can participate in hydrogen bonds and are attracted to water molecules.

13.16 Lysine and glutamic acid can form an ion pair. The side chain of lysine is a +1 ion at pH 7, and the side chain of glutamic acid is a –1 ion at pH 7.

13.17 Leucine and phenylalanine are most likely to be in the interior of a protein, because their side chains cannot form hydrogen bonds with water molecules.

13.18



13.19 Only cysteine can form a disulfide bridge.

13.20 The secondary structure is the folding or coiling of short regions of a polypeptide, and is produced by hydrogen bonds between peptide groups within the polypeptide. The tertiary structure is the way the entire polypeptide folds into its final shape, and is produced by interactions between the amino acid side chains.

13.21 All membranes are primarily nonpolar. The hydrophobic amino acids in a membrane protein allow the protein to remain embedded in the membrane, because they are not attracted to the surrounding water molecules.

13.22 This is a description of the quaternary structure of the enzyme, because it involves an interaction between two separate polypeptide chains.

13.23 This is a (partial) description of the secondary structure of the enzyme, because the alpha helix is produced by hydrogen bonds between peptide groups.

13.24 This is a (partial) description of the tertiary structure of the enzyme, because it involves an interaction between side chains.

Section 13.4

13.25 When a protein is denatured, the secondary and tertiary structures of the protein are disrupted, so the protein folds into a different shape (or unfolds completely).

13.26 a) HCl is a strong acid, so it makes the solution very acidic. This disrupts the ion pairs within the protein, because it converts the acidic side chains from their conjugate base form (which is negatively charged and can form an ion pair) into their acid form (which has no net charge).

b) Hg^{2+} bonds to sulfur atoms, breaking the disulfide bridges in the protein.

c) Heating the protein disrupts the weak hydrogen-bonding interactions within the protein (and between the protein and water), allowing the protein to unfold.

13.27 Ethanol is an organic liquid that forms hydrogen bonds less effectively than water. As a result, adding ethanol disrupts the hydrophilic attraction that keeps the polar amino acids on the exterior of the protein. The protein denatures, making it inactive.

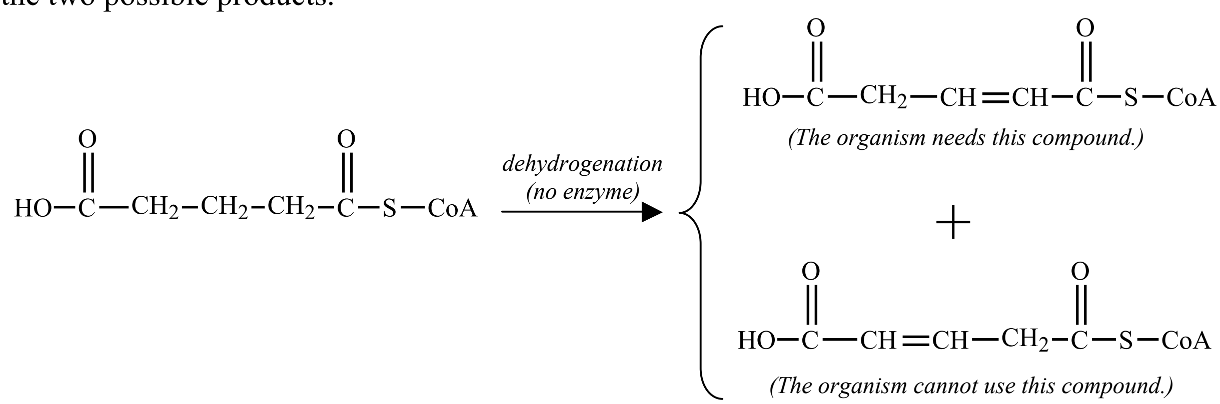
13.28 The secondary, tertiary, and quaternary structures of a protein are disrupted when the protein is denatured, but the primary structure is not.

13.29 When the concentration of NaCl is high, the ionized amino acids form ion pairs with Na^+ and Cl^-, rather than with each other. When we disrupt the original ion pairs, the protein denatures.

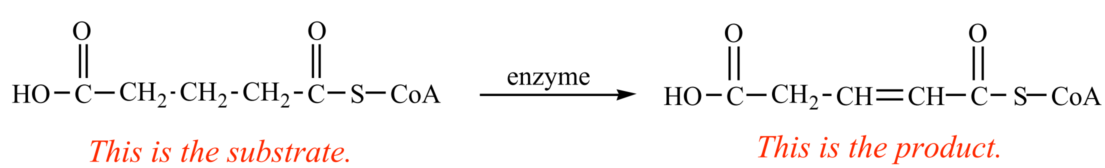
Section 13.5

13.30 Enzymes are proteins that act as catalysts; they speed up reactions in living organisms, and they control which of the possible products is actually formed. Organisms need enzymes because most reactions do not occur rapidly enough to be of use to the organism without a catalyst. Also, many reactions can form two or more products, only one of which is useful to the organism, so the enzyme keeps the organism from wasting its nutrients.

13.31 This dehydrogenation reaction has two possible products. The enzyme forms only one of the two possible products.



13.32

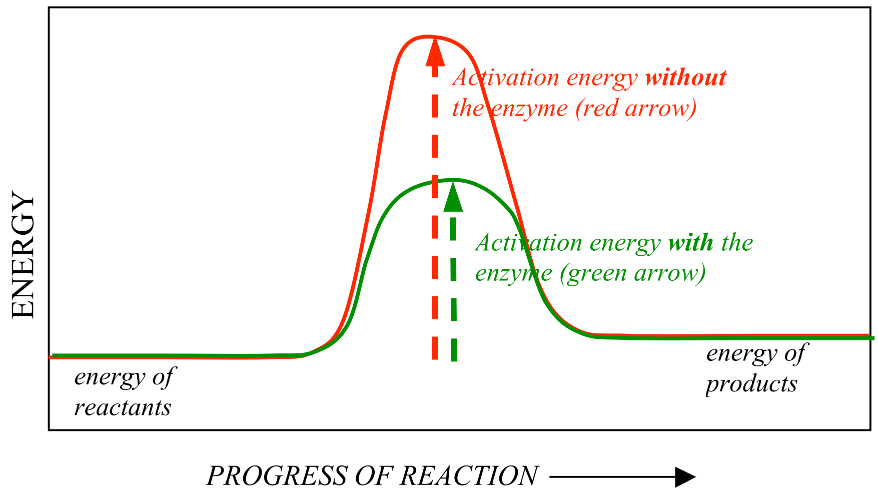


13.33 a) The active site is a cavity in the surface of the enzyme where the substrate binds and where the reaction occurs.

b) The enzyme-substrate complex is a cluster containing the enzyme and the substrates. The substrates sit in the active site of the enzyme.

c) The enzyme-product complex is a cluster containing the enzyme and the products. The products sit in the active site of the enzyme.

13.34



13.35 First, the substrate binds to the active site of the enzyme, forming the enzyme-substrate complex. Second, the reaction occurs within the active site, forming the enzyme-product complex. Third, the products leave the active site.

13.36 The side chain of arginine is basic and is positively charged at pH 7. This side chain is strongly hydrophilic and does not enter the hydrophilic pocket in the active site.

13.37 The activity of an enzyme is the number of reaction cycles that the enzyme can catalyze in a second, and is generally between 10 and 1000 reaction cycles per second.

13.38 Chymotrypsin does not function in the stomach, because the digestive fluids in the stomach are very acidic. The pH of the stomach contents is far below the active range for chymotrypsin (pH 7 to 8).

13.39 Most enzymes become denatured in this temperature range. The denatured form of the enzyme is not active.

13.40 A substrate is a molecule that is converted into a different substance by the enzyme. Substrates are the reactants in the balanced equation. An effector is a molecule that binds to an enzyme and makes the enzyme more or less active. The enzyme does not change the effector into another molecule, so effectors do not appear in the balanced equation.

13.41 Competitive inhibitors fit into the active site of the enzyme and prevent the substrate from entering the active site. Negative effectors bind to the enzyme outside the active site, so they do not block the substrate. Instead, negative effectors force the enzyme to change the shape of the active site, so the substrate does not fit into the active site. The structure of a competitive inhibitor resembles that of the substrate, while the structure of a negative effector normally does not.

Section 13.6

13.42 The two categories are the metal ions (such as Zn^{2+}, Cu^{2+}, and Mg^{2+}) and the coenzymes (organic compounds such as NAD^+ and FAD).

13.43 A cofactor is a substance that an enzyme requires in order to catalyze its reaction.

13.44 FAD is permanently bonded to all of the enzymes that require it, so there is no FAD in intracellular fluid. In contrast, NAD^+ binds reversibly to the enzymes that require it, so there is always some NAD^+ in the surrounding solution.

13.45 We obtain all of the metallic cofactors we need from our diet.

13.46 Our bodies use vitamins to build coenzymes. Each coenzyme contains a vitamin attached to some other substance that our bodies can make. Table 13.3 lists some specific examples.

13.47 Plants make riboflavin from other substances, and we obtain riboflavin by eating the plants (or by eating animals that have eaten plants, or by eating animals that have eaten other animals that have eaten plants, etc.).

Section 13.7

13.48 The enzyme would be broken down into amino acids in our digestive tract, so none of it would be available to our bodies.

13.49 Our bodies cannot make the essential amino acids from other nutrients, so we must have a dietary source of these amino acids. However, we can make the other amino acids from other nutrients, so we do not need a dietary source of the non-essential amino acids.

13.50 Humans can make arginine from other nutrients, but children and some adults cannot make enough arginine to meet their needs, so they need a dietary source of arginine.

13.51 The nitrogen atoms come from other amino acids. The other three elements can come from amino acids or from other nutrients, primarily carbohydrates.

13.52 Our diet must include all of the essential amino acids, and it must include enough protein to supply the nitrogen we need to make the non-essential amino acids and other nitrogen-containing compounds.

13.53 We also use amino acids as an energy source, burning them to obtain energy for our bodies. If our diet does not include enough carbohydrate and fat, we break down most of the amino acids in our diet, because our very survival requires energy. As a result, we do not have enough amino acids to build proteins.

13.54 a) Nitrogen fixation is the reaction that converts atmospheric nitrogen (N_2) into ammonium ions (NH_4^+).

b) Nitrification is the set of reactions that convert ammonium ions into nitrite and nitrate ions (NO_2^- and NO_3^-).

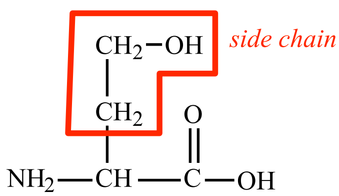
c) Denitrification is the set of reactions that convert nitrite and nitrate ions back into N_2.

13.55 All of the reactions in Problem 13.54 can be carried out by bacteria (although only some bacteria can do so). None of these reactions can be carried out by plants. (Plants can convert nitrite and nitrate ions into ammonium ions, but not the reverse.)

13.56 We do not excrete wastes continuously, so we must store our waste products for a while before we excrete them. Ammonium ions are toxic, so our bodies cannot store significant amounts of ammonium ions. Therefore, our bodies convert ammonium ions into urea, which is relatively non-toxic, and we excrete the urea when we need to get rid of excess nitrogen.

CUMULATIVE PROBLEMS (Odd-numbered problems only)

13.57 a)



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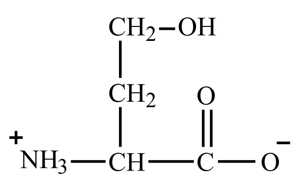
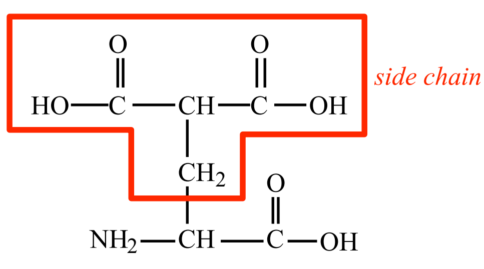
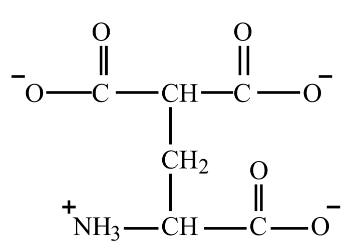


c) Homoserine is a hydrophilic (polar) amino acid, because it contains an alcohol group in its side chain. It is not acidic or basic.

13.59 a) Gamma-carboxyglutamic acid is an acidic amino acid, because it contains two acidic groups in its side chain.

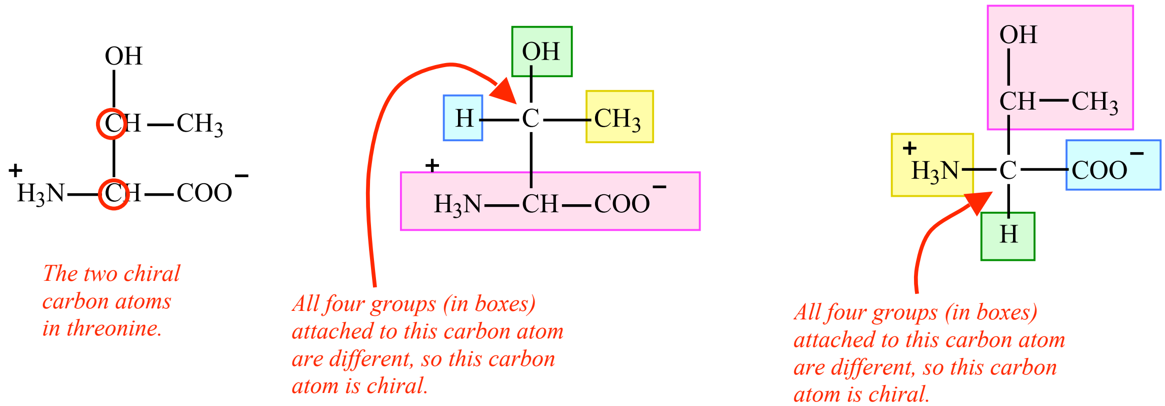


b) At pH 7, the amino group gains H^+ and all three carboxylic acid groups lose H^+.

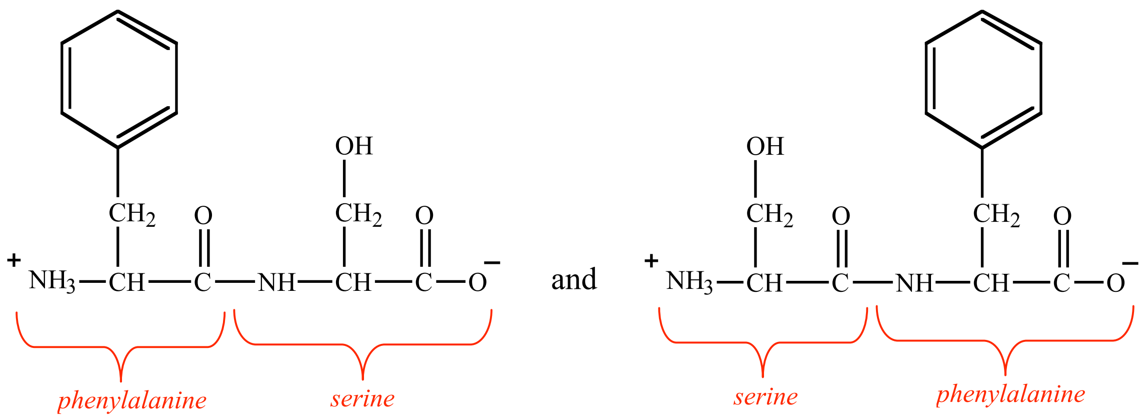


13.61 Glycine is not chiral because it does not contain a carbon atom that is attached to four different groups. The alpha carbon atom of glycine is attached to two hydrogen atoms, as well as the amino group and the carboxylate group. (The alpha carbon atom of all other amino acids is attached to four different groups, so all of the other amino acids are chiral.)

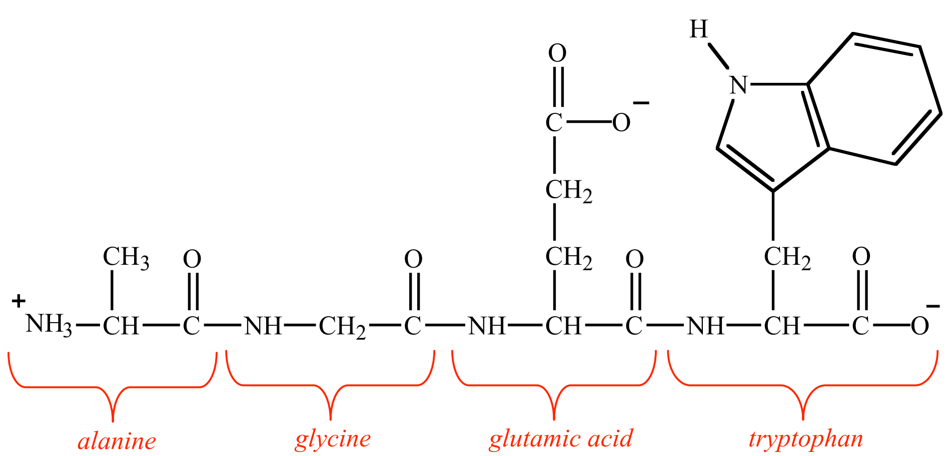
13.63 The two carbon atoms circled below are chiral.



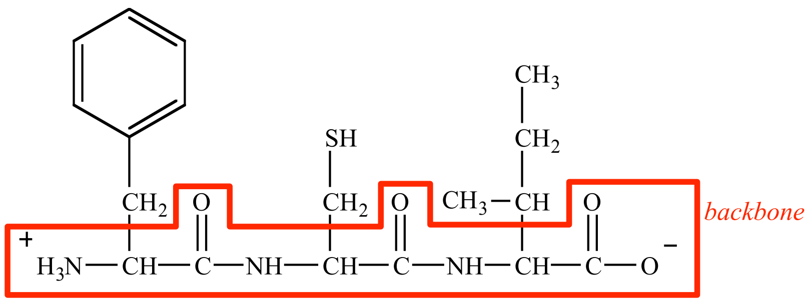
13.65



13.67



13.69 a)



b) This tripeptide contains phenylalanine, cysteine, and isoleucine (Phe-Cys-Ile).
c) The N-terminal amino acid is phenylalanine.

13.71 You can make six different tripeptides. Here are their primary structures:

Arg-Ile-Val	Ile-Arg-Val	Val-Arg-Ile
Arg-Val-Ile	Ile-Val-Arg	Val-Ile-Arg

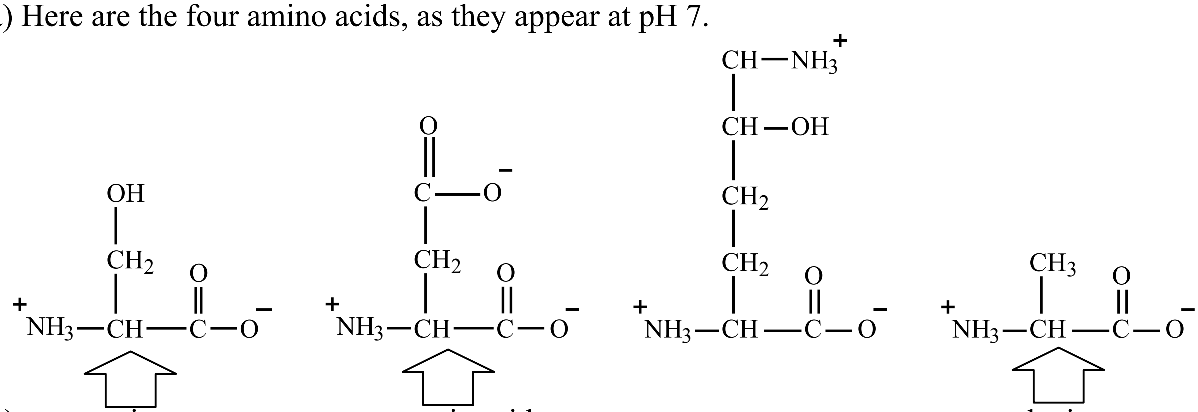
13.73 a) There are 73 hydrophilic and 62 hydrophobic amino acids in histone H3. See Table 13.1 for the list of hydrophilic and hydrophobic amino acids.

b) There are 29 polar neutral amino acids (asparagine, cysteine, glutamine, serine, threonine, and tyrosine). There are 11 acidic amino acids (aspartic acid and glutamic acid). There are 33 basic amino acids (arginine, histidine, and lysine).

c) Histone H3 is positively charged, because it contains more basic amino acids than acidic amino acids. Remember that the basic amino acids have a +1 charge at pH 7, and the acidic amino acids have a –1 charge at pH 7.

d) Opposite charges attract one another. Since histone H3 is positively charged, DNA must be negatively charged.

13.75 a) Here are the four amino acids, as they appear at pH 7.



b) serine aspartic acid alanine

c) The other amino acid is basic, because its side chain contains an amino group. Note that at pH 7, the amino group in the side chain of this amino acid has bonded to H^+.

13.77 Proline cannot form an alpha helix because there is no hydrogen atom bonded to the amine nitrogen when proline is incorporated into a polypeptide. (See Figure 13.7.) The alpha helix structure requires this hydrogen atom to form the hydrogen bond between peptide groups.

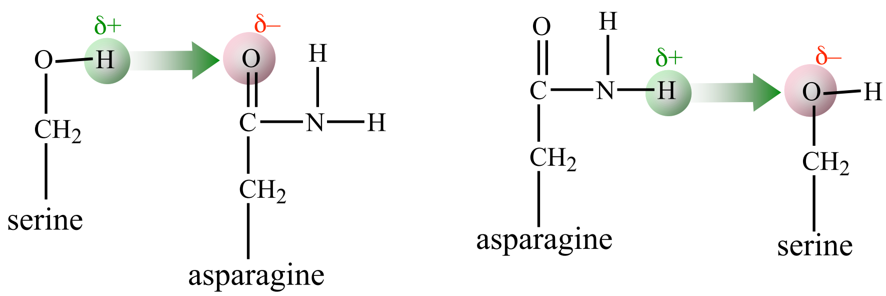
Collagen contains a high percentage of proline, allowing collagen to form the triple helix structure instead of an alpha helix.

13.79 The hydrogen atom has a positive charge, and the oxygen atom has a negative charge. (See Figure 13.6.)

13.81 In an alpha helix, the polypeptide backbone forms a tight coil, with the side chains pointing outward from the coil.

13.83 Phenylalanine is the most likely to be found in the interior, because its large hydrocarbon side chain cannot form hydrogen bonds. Glycine does not have a hydrophilic side chain, but its side chain is so small (just a hydrogen atom) that glycine does not have a strong preference for the interior of a polypeptide.

13.85



Here, serine is the donor and asparagine is the acceptor.

Here, asparagine is the donor and serine is the acceptor.

(You can also form a hydrogen bond between the serine hydrogen and the asparagine nitrogen.)

13.87 Aspartic acid can form an ion pair with lysine. Lysine is a basic amino acid and is positively charged at pH 7. Only acidic amino acids (which are negatively charged at pH 7) can form an ion pair with lysine.

13.89 Lysine, threonine, and tyrosine can form hydrogen bonds with water. Their side chains contain nitrogen or oxygen atoms that can function as hydrogen bond acceptors.

13.91 To form a disulfide bridge, the amino acid must have a thiol group (–SH) in its side chain. Cysteine contains a thiol group, but methionine does not, so methionine cannot form a disulfide bridge.

13.93 This sequence contains eleven amino acids. Nine of these eleven have nonpolar side chains, and the other two (serine and asparagine) are polar but are not ionized. Therefore, this section of the polypeptide is not attracted to water to any significant extent, so it is probably in the interior of the protein.

13.95 a) This statement describes the quaternary structure of the protein, because it involves more than one polypeptide chain.

b) This statement describes the tertiary structure of the protein. Aspartic acid prefers to be on the exterior of the protein because of its charged side chain. Interactions involving side chains contribute to the tertiary structure of a protein.

c) This statement describes the secondary structure of the protein.

13.97 Ethanol disrupts the hydrophilic interaction between polar amino acids and the surrounding solvent (which is normally water). The hydrophilic side chain are not attracted to the surrounding ethanol molecules as strongly as they are to water molecules, so they move into the interior of the protein. As a result, the protein becomes denatured.

13.99 Some possibilities are Mg^{2+}, Zn^{2+}, Fe^{2+}, Fe^{3+}, Cu^{2+}, and Mn^{2+}.

13.101 a) Lysine is not a cofactor; it is one of the amino acids in the polypeptide chain. Cofactors are substances that are required by an enzyme, but are not amino acids. Lysine is not a coenzyme, because a coenzyme is simply an organic cofactor.

b) Biotin is a cofactor, since it is required by the enzyme but is not an amino acid. Since biotin is an organic compound, it is also a coenzyme.

13.103 The substrates are sucrose and water, the products are glucose and fructose, and the enzyme is sucrase.

13.105 Enzymes speed up reactions, and they select the correct product when more than one product is possible.

13.107 Magnesium ion is positively charged and phosphate is negatively charged, so the magnesium attracts the phosphate ion and holds it in the active site of the enzyme.

13.109 Enzymes make the activation energy smaller. Remember that the activation energy is not the energy that the reactants actually have; it is the minimum energy that the reactants need in order to react. If the activation energy becomes smaller, more molecules will have enough energy to react.

13.111 Enzyme A has the higher activity. Enzyme carries out 100 reaction cycles in a second, while enzyme B carries out only 10 reaction cycles in a second (100 cycles in 10 seconds).

13.113 Papain has the highest activity around pH 6, and catalase has the highest activity around pH 8.

13.115 The pH-activity curve of an enzyme normally peaks at the pH of the enzyme's surroundings. (If it didn't, the enzyme wouldn't work!) Therefore, it reasonable to conclude that the typical pH inside a cell is around 7 to 8 (corresponding to the pH peak for trypsin).

13.117 The enzyme's activity increases as it is heated from 20ºC to 40ºC. As long as the temperature isn't high enough to denature the enzyme, enzymes work faster as the temperature increases. In this case, 40ºC is not hot enough to denature enzymes (40ºC is barely above body temperature).

13.119 This organism must live in an extremely hot environment, probably above 80ºC. The activity of the enzyme is essentially zero at "normal" temperatures (20 to 40ºC), so this enzyme will not function effectively in this temperature range. The peak activity for this enzyme is around 90ºC.

13.121 NADH is a negative effector, because it makes the enzyme less active.

13.123 Since atorvastatin is a competitive inhibitor, it must fit into the active site of the enzyme. Therefore, it must resemble the substrate.

13.125 Oxaloacetate is a competitive inhibitor of succinate dehydrogenase. The structure of oxaloacetate ion is quite similar to the structure of succinate ion. Therefore, oxaloacetate probably fits nicely into the active site of succinate dehydrogenase, blocking succinate ions from entering the active site. This behavior is characteristic of a competitive inhibitor.

13.127 Antibodies are proteins, so they are broken down into amino acids in the digestive tract. As a result, none of the antibodies would reach the rabies viruses.

13.129 a) This diet would not be able to meet the person's protein needs, because the total amount of amino acids is so low that it would not satisfy the person's need for nitrogen to make the nonessential amino acids.

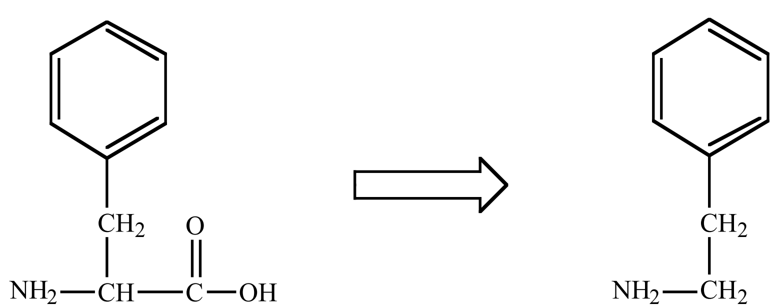
b) This diet might satisfy the person's protein needs. However, if this diet does not contain enough of each individual essential amino acid, it could still be deficient.

13.131 Plants and microorganisms can make proteins using inorganic sources of nitrogen.

13.133 Nitrogen fixation is a series of reactions that convert gaseous nitrogen (N_2) into ammonium ions (NH_4^+). Only a few microorganisms can carry out these reactions. Most organisms cannot use N_2 to make organic compounds such as amino acids, so nitrogen fixation converts atmospheric nitrogen into a form that can be used by plants and other microorganisms.

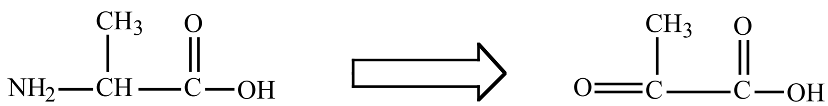
13.135 When our bodies make asparagine from other substances, the nitrogen atoms come from other amino acids in our diet.

13.137 a) We make phenethylamine by removing CO_2 from phenylalanine.



phenylalanine *phenethylamine*

b) We make pyruvic acid by removing NH_3 (and adding oxygen to) alanine.



alanine *pyruvic acid*

13.139 A complete protein is a protein source that contains all of the essential amino acids. Meat, milk (and other dairy products), and eggs are sources of complete protein.