

Chapter 13 Review Problems

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13.1) **Peptides** are a linear (non branched) polymer made from amino acid residues. A **protein** consists of *one or more large peptides* and has *a specific biological function*. In order to best understand how proteins function, you first learned about their building blocks: **amino acids**.

At $\text{pH} = 7$, the predominant forms of **amino acids** contain a *quaternary ammonium group* and a *carboxylate functional group*.

- When carboxylate ions are in an aqueous solution, the carboxylate ion (base form) and carboxylic acid (acid form) conjugates are both present because they are in equilibrium.
- Likewise, when quaternary ammonium compounds are in an aqueous solution, the quaternary ammonium ion (acid form) and amine (base form) conjugates are both present.
- We can predict whether the acid form or the base form of these functional groups is predominant using the implications of the *Henderson-Hasselbalch* relation; we compare the pH of the solution to the pK_a of the group.

i) What is the pK_a range of the carboxyl groups in amino acids? _____

ii) What is the approximate pK_a of the quaternary ammonium group in amino acids? _____



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13.1) **Peptides** are a linear (non branched) polymer made from amino acid residues. A **protein** consists of *one or more large peptides* and has *a specific biological function*. In order to best understand how proteins function, you first learned about their building blocks: **amino acids**.

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- When carboxylate ions are in an aqueous solution, the carboxylate ion (base form) and carboxylic acid (acid form) conjugates are both present because they are in equilibrium.
- Likewise, when quaternary ammonium compounds are in an aqueous solution, the quaternary ammonium ion (acid form) and amine (base form) conjugates are both present.
- We can predict whether the acid form or the base form of these functional groups is predominant using the implications of the *Henderson-Hasselbalch* relation; we compare the pH of the solution to the pK_a of the group.

i) What is the pK_a range of the carboxyl groups in amino acids? _____

ii) What is the approximate pK_a of the quaternary ammonium group in amino acids? _____

HINT:

You can find the information needed for this problem in the “amino acids” section of your lecture notes or the textbook.

For more help: See [chapter 13 part 1 video](#) or chapter 13 section 2 in the textbook.

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13.1) **Peptides** are a linear (non branched) polymer made from amino acid residues. A **protein** consists of *one or more large peptides* and has *a specific biological function*. In order to best understand how proteins function, you first learned about their building blocks: **amino acids**.

At pH = 7, the predominant forms of **amino acids** contain a *quaternary ammonium group* and a *carboxylate functional group*.

- When carboxylate ions are in an aqueous solution, the carboxylate ion (base form) and carboxylic acid (acid form) conjugates are both present because they are in equilibrium.
- Likewise, when quaternary ammonium compounds are in an aqueous solution, the quaternary ammonium ion (acid form) and amine (base form) conjugates are both present.
- We can predict whether the acid form or the base form of these functional groups is predominant using the implications of the *Henderson-Hasselbalch* relation; we compare the pH of the solution to the pK_a of the group.

i) What is the pK_a range of the carboxyl groups in amino acids? 2 to 5

ii) What is the approximate pK_a of the quaternary ammonium group in amino acids? ~9.5

For more details: See [chapter 13 part 1 video](#) or chapter 13 section 2 in the textbook.

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13.2) Draw the line bond structure for the general form of an amino acid using “R” to represent the side chain. Draw the N- and C-terminus groups using the forms that are predominant at physiological pH (pH = 7.4). Include lone pairs in your drawing.



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13.2) Draw the line bond structure for the general form of an amino acid using "R" to represent the side chain. Draw the N- and C-terminus groups using the forms that are predominant at physiological pH (pH = 7.4). Include lone pairs in your drawing.

HINT:

The structure of the predominant form of an amino acid will depend on the pH because amino acids involve the carboxyl group/carboxylate group conjugate pair and the quaternary ammonium group/amine group conjugate pair. Using the implications of the the *Henderson-Hasselbalch* relation, summarized in the table below, it is possible to predict the predominant form of these groups at a particular pH.

Solution Condition	Relative Amounts of Acid and Base Forms
pH < pK _a	[HA] > [A ⁻]
pH > pK _a	[A ⁻] > [HA]
pH = pK _a	[HA] = [A ⁻]

The pK_a values of amino acid *carboxyl groups* are between **2** and **5** (depending on which amino acid), therefore, at pH = 7.4, the base form (carboxylate ion) is predominant.

Quaternary ammonium groups that are attached to the α-carbons of amino acids have pK_a values of about **9.5**, therefore, at pH = 7.4, the acid form (quaternary ammonium group) is predominant.

For more help: See [chapter 13 part 1 video](#) or chapter 13 section 2 in the textbook.

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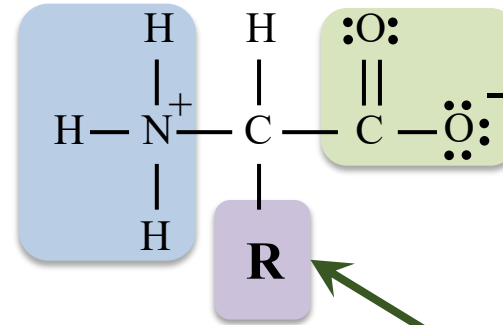
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13.2) Draw the line bond structure for the general form of an amino acid using "R" to represent the side chain. Draw the N- and C-terminus groups using the forms that are predominant at physiological pH (pH = 7.4). Include lone pairs in your drawing.

quaternary ammonium group

Quaternary ammonium groups that are attached to the α -carbons of amino acids have pK_a values of about **9.5**, therefore, at **pH = 7.4**, the acid form (quaternary ammonium group) is predominant.

ANSWER:



carboxylate group

The pK_a values of amino acid *carboxyl groups* are between **2** and **5** (depending on which amino acid), therefore, at **pH = 7.4**, the base form (carboxylate ion) is predominant.

R-group
(called "side-chain")

For more details: See [chapter 13 part 1 video](#) or chapter 13 section 2 in the textbook.

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13.3) Leucine is an *essential amino acid*; the body cannot produce it from other compounds, so it must be present in the diet.

Draw the predominant form of *leucine* when the pH = 1.0, pH = 7.4, and pH = 12.0 (include lone pairs).

pH = 1.0

physiological pH (pH = 7.4)

pH = 12.0

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Draw the predominant form of *leucine* when the pH = 1.0, pH = 7.4, and pH = 12.0 (include lone pairs).

pH = 1.0

physiological pH (pH = 7.4)

pH = 12.0

HINT: The structures of the amino acids that are drawn in your amino acids table are the predominant forms at **pH = 7.4**. The structure of the predominant form of an amino acid will depend on the pH because amino acids involve the carboxyl group/carboxylate group conjugate pair and the quaternary ammonium group/amine group conjugate pair. Using the implications of the *Henderson-Hasselbalch* relation, summarized in the table below, it is possible to predict the predominant form of these groups at a particular **pH**.

- The **pK_a** values of amino acid *carboxyl groups* are between **2** and **5** (depending on which amino acid).
- *Quaternary ammonium groups* that are attached to the **α**-carbons of amino acids have **pK_a** values of about **9.5**.
- The **side-chain** of leucine is **not polar acidic** or **polar basic**, so it is **not** affected by pH.

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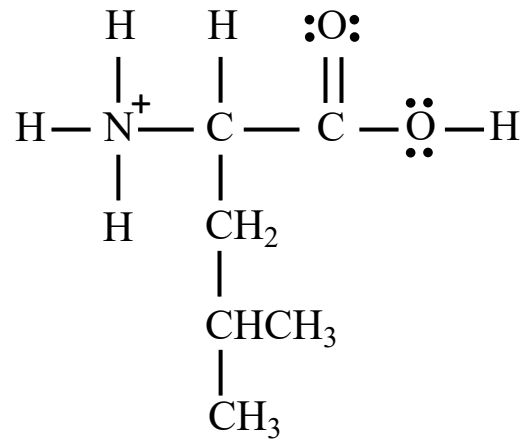
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13.3) Leucine is an *essential amino acid*; the body cannot produce it from other compounds, so it must be present in the diet.

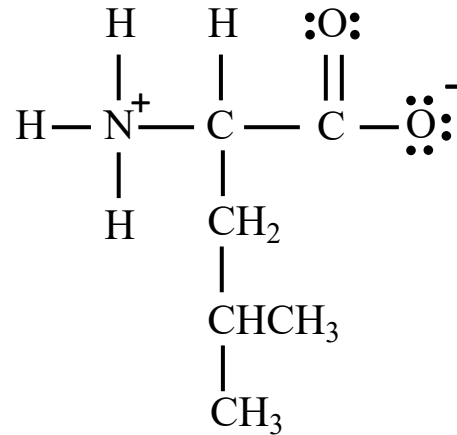
Draw the predominant form of *leucine* when the pH = 1.0, pH = 7.4, and pH = 12.0 (include lone pairs).

pH = 1.0



At **pH = 1.0** (an extremely acidic solution) the **pH** is less than the **pK_a** of both the carboxyl group and the quaternary ammonium group, therefore **both groups** exist in their **acid forms**, as shown above.

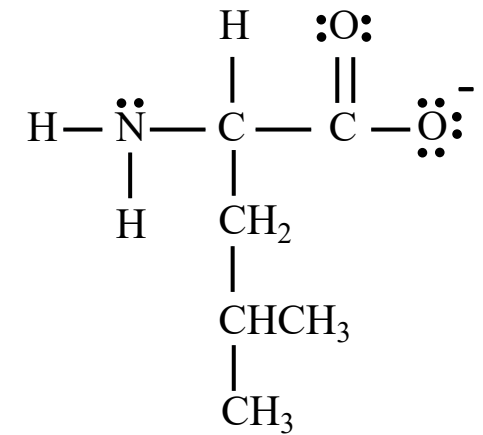
physiological pH (pH = 7.4)



Quaternary ammonium groups have **pK_a** values of about **9.5**, therefore, at **pH = 7.4**, the acid form (quaternary ammonium group) is predominant.

The **pK_a** values of *carboxyl groups* are between **2** and **5** (depending on which amino acid), therefore, at **pH = 7.4**, the base form (carboxylate ion) is predominant.

pH = 12.0



At **pH = 12.0** (an extremely basic solution) the **pH** is greater than the **pK_a** of both the carboxyl group and the quaternary ammonium group, therefore **both groups** exist in their **base forms**, as shown above.

The side-chain of leucine is **not polar acidic** or *polar basic*, so it is **not** affected by pH.

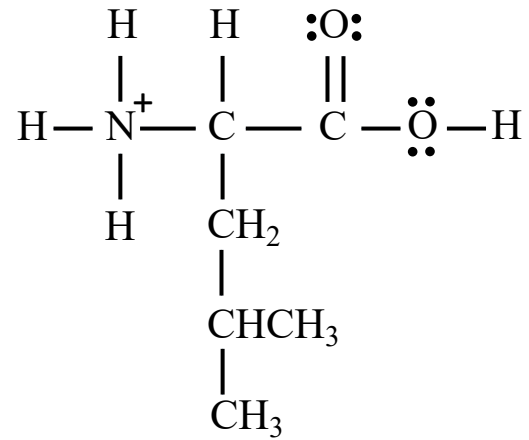
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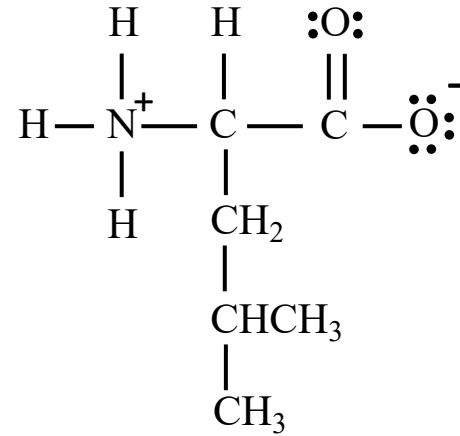
13.4) In the previous problem, you drew the predominant form of leucine at pH = 1.0, pH = 7.4, and pH = 12.0. These structures are shown below. What is the **total charge** of leucine at pH = 1.0, pH = 7.4, and pH = 12.0?

pH = 1.0



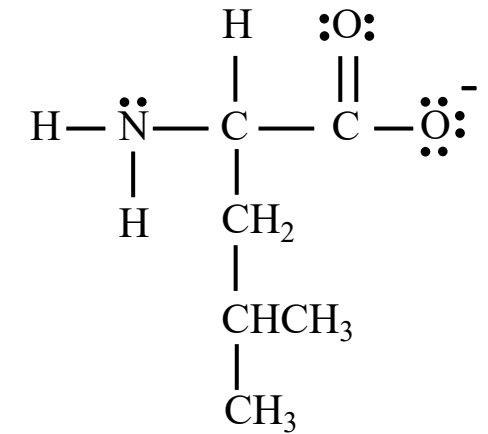
total charge = ?

physiological pH (pH = 7.4)



total charge = ?

pH = 12.0



total charge = ?

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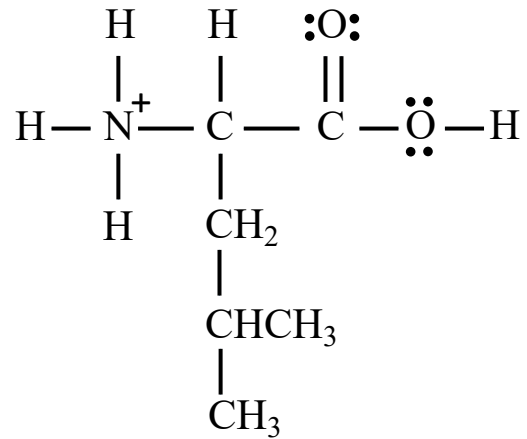
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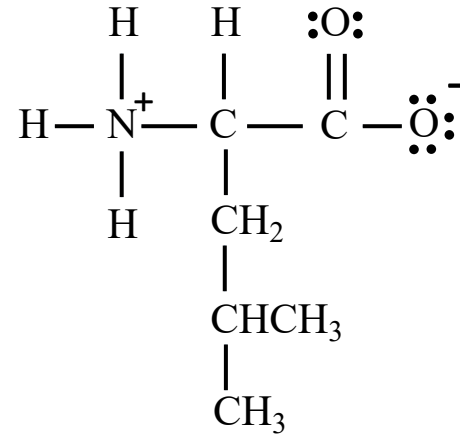
13.4) In the previous problem, you drew the predominant form of leucine at pH = 1.0, pH = 7.4, and pH = 12.0. These structures are shown below. What is the **total charge** of leucine at pH = 1.0, pH = 7.4, and pH = 12.0?

pH = 1.0



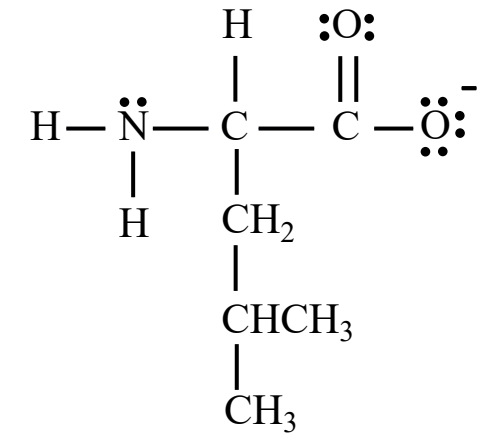
total charge = ?

physiological pH (pH = 7.4)



total charge = ?

pH = 12.0



total charge = ?

HINT: The **total charge** is equal to the sum of the *formal charges* that are present.

For more help: See [chapter 13 part 1 video](#) or chapter 13 section 2 in the textbook.

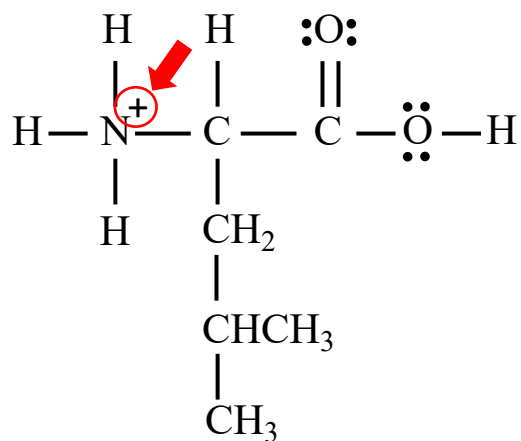
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13.4) In the previous problem, you drew the predominant form of leucine at pH = 1.0, pH = 7.4, and pH = 12.0. These structures are shown below. What is the **total charge** of leucine at pH = 1.0, pH = 7.4, and pH = 12.0?

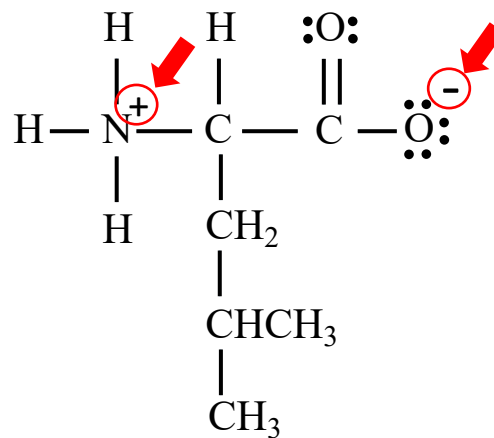
pH = 1.0



total charge = 1+

There is a formal charge of 1+ on the nitrogen.

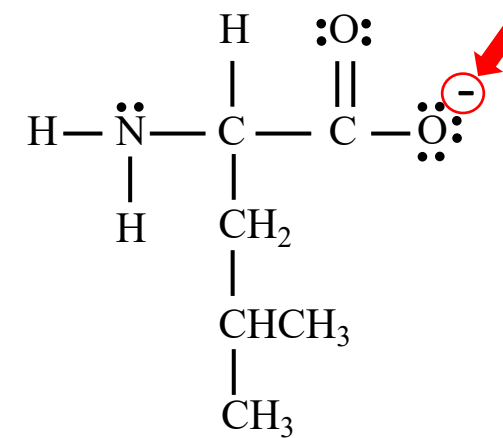
physiological pH (pH = 7.4)



total charge = 0

There is a formal charge of 1+ on the nitrogen, and a formal charge of 1- on the oxygen. Adding these charges give a total charge = 0.

pH = 12.0



total charge = 1-

There is a formal charge of 1- on the oxygen.

For more details: See [chapter 13 part 1 video](#) or chapter 13 section 2 in the textbook.

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13.5) The amino acid called *aspartic acid* was discovered in 1827 from an asparagus juice extract.

a) Draw the predominant form of *aspartic acid* when the $\text{pH} = 7.4$. Include lone pairs in your drawing.

b) What is the total charge of the *aspartic acid* structure that you drew in part (a)?



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13.5) The amino acid called *aspartic acid* was discovered in 1827 from an asparagus juice extract.

a) Draw the predominant form of *aspartic acid* when the $\text{pH} = 7.4$. Include lone pairs in your drawing.

HINT:

The structures of the amino acids that are drawn in your amino acids table are the predominant forms at $\text{pH} = 7.4$

b) What is the total charge of the *aspartic acid* structure that you drew in part (a)?

HINT:

The **total charge** is equal to the sum of the *formal charges* that are present.

For more help: See [chapter 13 part 1 video](#) or chapter 13 section 2 in the textbook.

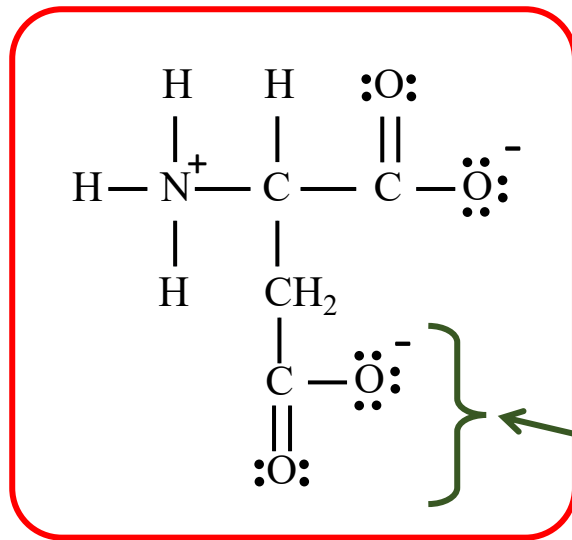
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13.5) The amino acid called *aspartic acid* was discovered in 1827 from an asparagus juice extract.

a) Draw the predominant form of *aspartic acid* when the pH = 7.4. Include lone pairs in your drawing.



EXPLANATION:

The structures of the amino acids that are drawn in your amino acids table are the predominant forms at **pH = 7.4**

Not *all* predominant forms of amino acids have *uncharged side-chains* at physiological **pH**. **Polar acidic amino acids** have *polar (hydrophilic) side-chains* and, at physiological **pH**, their predominant forms have side-chains with **negative (1-) formal charge**.

This formal charge in the side-chain is from a *carboxylate group*.

- Note that the pH dependence of the carboxyl groups in side chains is the same as that of the other carboxyl groups; the **pK_a** values are between **2** and **5** (depending on which amino acid), therefore, at **pH = 7.4**, the *base form* (carboxylate ion) is predominant.

b) What is the total charge of the *aspartic acid* structure that you drew in part (a)? **total charge = 1-**

EXPLANATION:

The **total charge** is equal to the sum of the *formal charges* that are present.

There is a formal charge of **1+** on the nitrogen, and a TWO formal charges of **1-** (on the oxygens in the carboxylate groups). Adding these charges give a **total charge = 1-**.

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13.6) Lysine is an amino acid that plays several roles in humans, primarily it is used for the production of proteins. It also plays a part in collagen structure, the uptake of essential mineral nutrients, and in the production of fatty acids.

a) Draw the predominant form of *lysine* when the $\text{pH} = 7.4$. Lone pairs are optional.

b) What is the total charge of the *lysine* structure that you drew in part (a)?



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a) Draw the predominant form of *lysine* when the $\text{pH} = 7.4$. Lone pairs are optional.

HINT:

The structures of the amino acids that are drawn in your amino acids table are the predominant forms at $\text{pH} = 7.4$

b) What is the total charge of the *lysine* structure that you drew in part (a)?

HINT:

The **total charge** is equal to the sum of the *formal charges* that are present.



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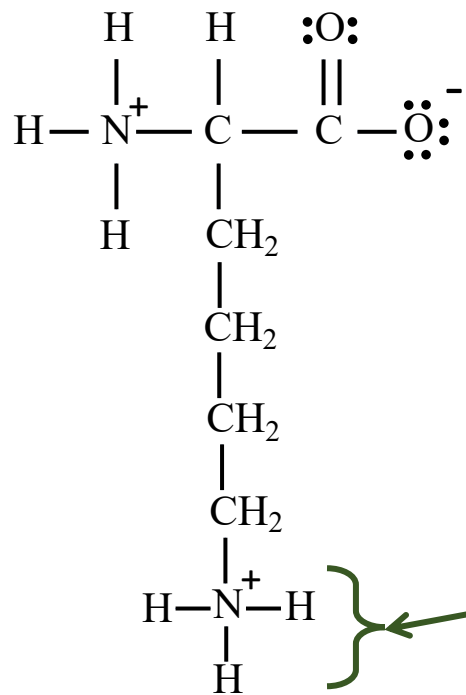
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13.6) Lysine is an amino acid that plays several roles in humans, primarily it is used for the production of proteins. It also plays a part in collagen structure, the uptake of essential mineral nutrients, and in the production of fatty acids.

a) Draw the predominant form of *lysine* when the $\text{pH} = 7.4$. Lone pairs are optional.



EXPLANATION:

The structures of the amino acids that are drawn in your amino acids table are the predominant forms at $\text{pH} = 7.4$

Not *all* predominant forms of amino acids have *uncharged side-chains* at physiological pH . **Polar basic amino acids** have *polar (hydrophilic) side-chains* and, except for *histidine*, their predominant forms have side-chains with **positive (1+) formal charge** at physiological pH .

This formal charge in the side-chain is from a *quaternary ammonium group*.

b) What is the total charge of the *lysine* structure that you drew in part (a)? **total charge = 1+**

EXPLANATION:

The **total charge** is equal to the sum of the *formal charges* that are present.

There is a formal charge of **1-** on an oxygen, and a TWO formal charges of **1+** (on the nitrogen in the quaternary ammonium groups). Adding these charges give a **total charge = 1+**.

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For more details: See [chapter 13 part 1 video](#) or chapter 13 section 2 in the textbook.

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13.7) Peptides (sometimes called polypeptides) are composed of amino acid residues bonded to each other in a linear (non branched) pattern. A dipeptide contains two amino acid residues. Draw the *dipeptide* that contains *two alanine* amino acid residues. Use the structure that is predominate at $\text{pH} = 7.4$ in your drawing. Lone pairs are optional.



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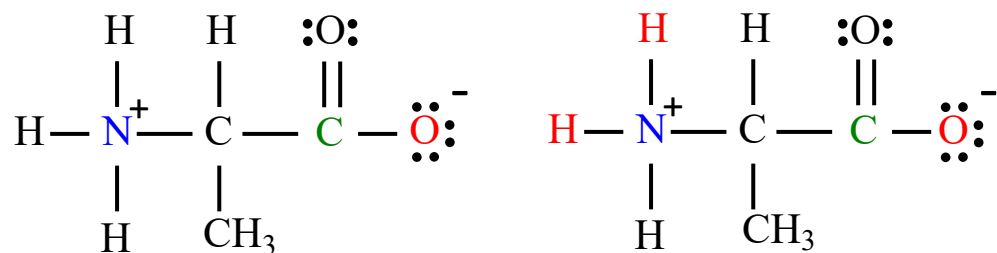
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13.7) Peptides (sometimes called polypeptides) are composed of amino acid residues bonded to each other in a linear (non branched) pattern. A dipeptide contains two amino acid residues. Draw the **dipeptide** that contains *two alanine* amino acid residues. Use the structure that is predominate at pH = 7.4 in your drawing. Lone pairs are optional.



HINT: Formation of a Peptide Bond

Step 1: The two amino acids are drawn side-by-side.

- To obtain the dipeptide structure that is predominant at pH = 7.4, begin with the structure of each amino acid that is predominant at pH = 7.4.

The single-bonded *oxygen atom* is removed from the *carboxylate group* on the *left-most* amino acid. *Two hydrogen atoms* are removed from the *quaternary ammonium group* on the *right-most* amino acid. The *oxygen atom* and the *two hydrogen atoms* combine to form a water molecule.

Step 2: A *new bond* is made between the carbonyl carbon and the nitrogen

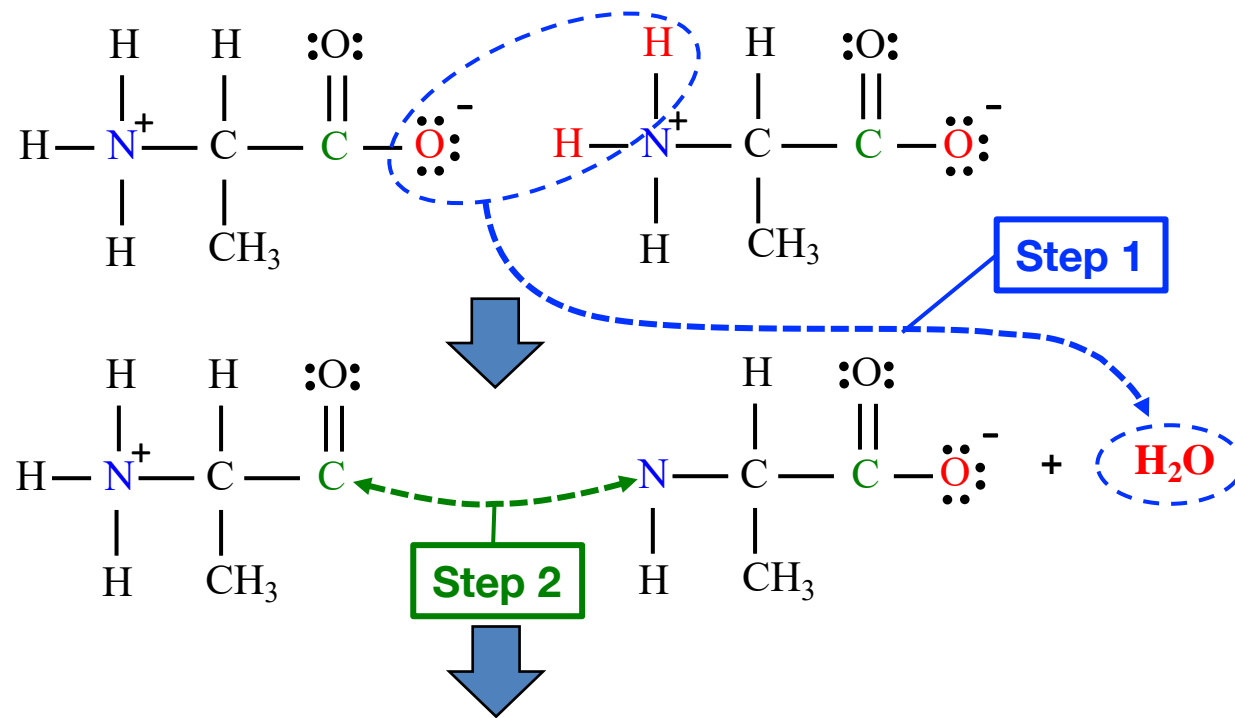
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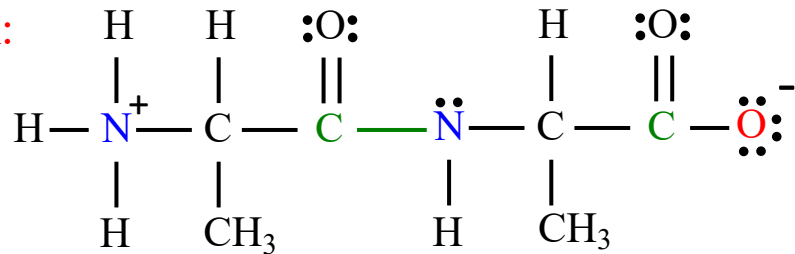
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ANSWER:



EXPLANATION: Formation of a Peptide Bond

Step 1: The two amino acids are drawn side-by-side.

- To obtain the dipeptide structure that is predominant at pH = 7.4, begin with the structure of each amino acid that is predominant at pH = 7.4.

The single-bonded *oxygen atom* is removed from the *carboxylate group* on the *left-most* amino acid. *Two hydrogen atoms* are removed from the *quaternary ammonium group* on the *right-most* amino acid. The *oxygen atom* and the *two hydrogen atoms* combine to form a *water molecule*.

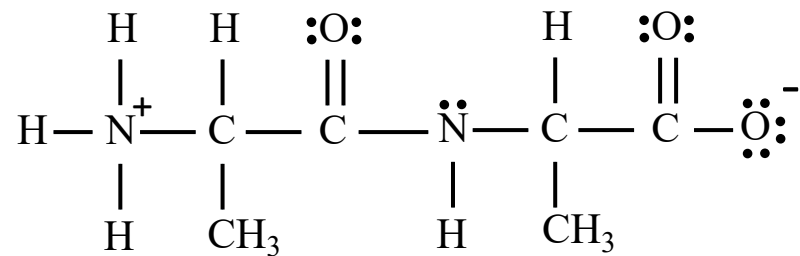
Step 2: A *new bond* is made between the carbonyl carbon and the nitrogen

For more details: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

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13.8) In the previous problem, you drew the *dipeptide* that contains *two alanine* amino acid residues (it is shown below). Identify and label the peptide bond in your drawing of that dipeptide.



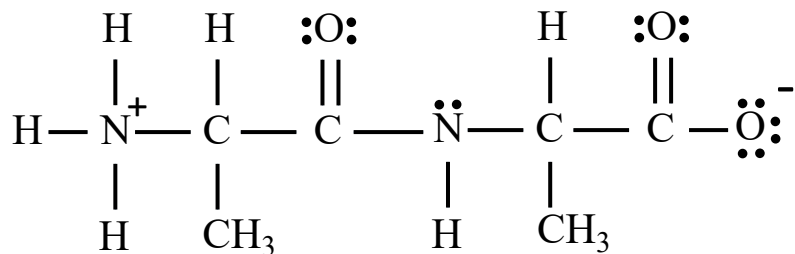
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13.8) In the previous problem, you drew the *dipeptide* that contains *two alanine* amino acid residues (it is shown below). Identify and label the peptide bond in your drawing of that dipeptide.



HINT:

The *new bond* between the two amino acid residues is called a **peptide bond**.

For more help: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

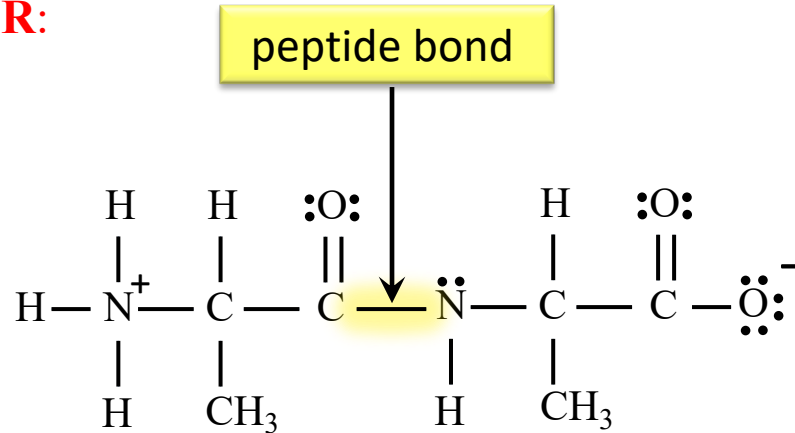
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13.8) In the previous problem, you drew the *dipeptide* that contains *two alanine* amino acid residues (it is shown below). Identify and label the peptide bond in your drawing of that dipeptide.

ANSWER:



EXPLANATION:

The *new bond* between the two amino acid residues is called a **peptide bond**.

For more details: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

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13.9) The peptide bond that connects amino acids in proteins is part of an _____ bonding pattern.

- a) ether
- b) ester
- c) amide
- d) amine



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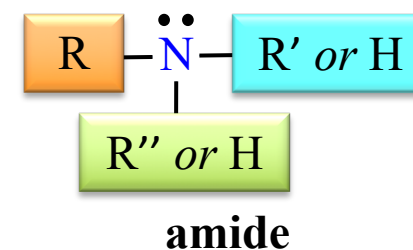
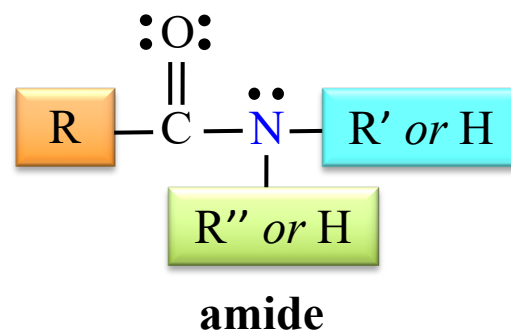
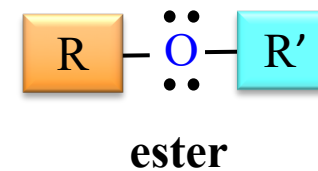
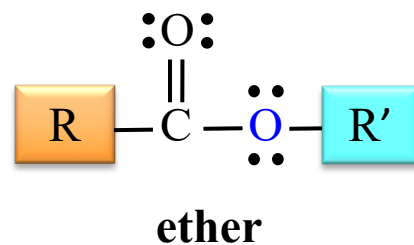
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13.9) The peptide bond that connects amino acids in proteins is part of an _____ bonding pattern.

- a) ether
- b) ester
- c) amide
- d) amine

HINT:

The general forms of these organic families of compounds are shown below.



For more help: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

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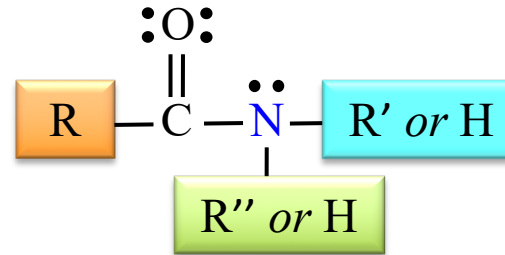
13.9) The peptide bond that connects amino acids in proteins is part of an _____ bonding pattern.

- a) ether
- b) ester
- c) amide
- d) amine

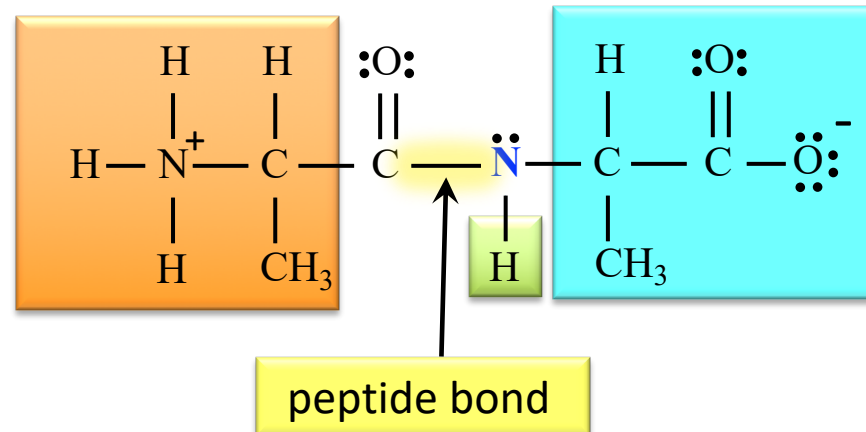
EXPLANATION:

Amides contain both a *carbonyl group* (C=O), and a nitrogen (N), with the nitrogen bonded to the *carbonyl* carbon.

The general form of an amide is shown below.



This *amide bonding pattern* occurs in amines; the *peptide bond* connects the *carbonyl group* (C=O), and a nitrogen (N).

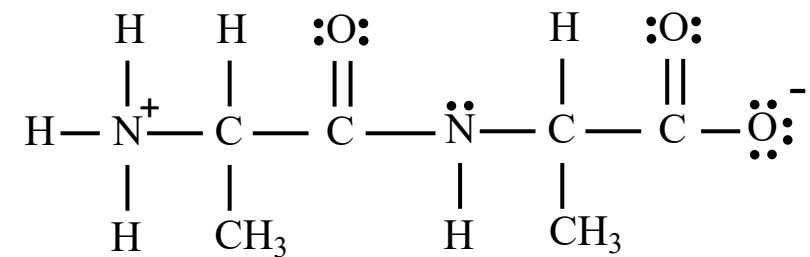


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13.10) Identify and label the N-terminus and the C-terminus in the dipeptide shown here.



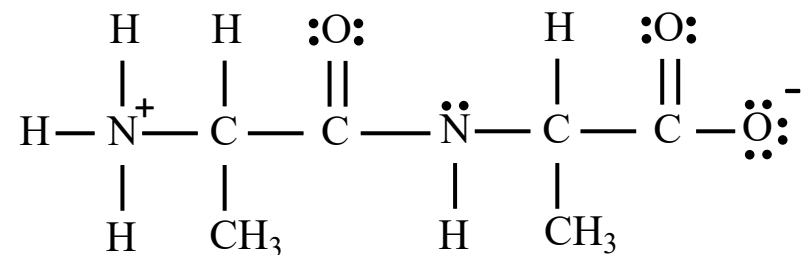
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13.10) Identify and label the N-terminus and the C-terminus in the dipeptide shown here.



HINT:

The end of the peptide structural formula that has a *quaternary ammonium group* is called the **N-terminus**, and the end that has a *carboxylate group* is called the **C-terminus**.

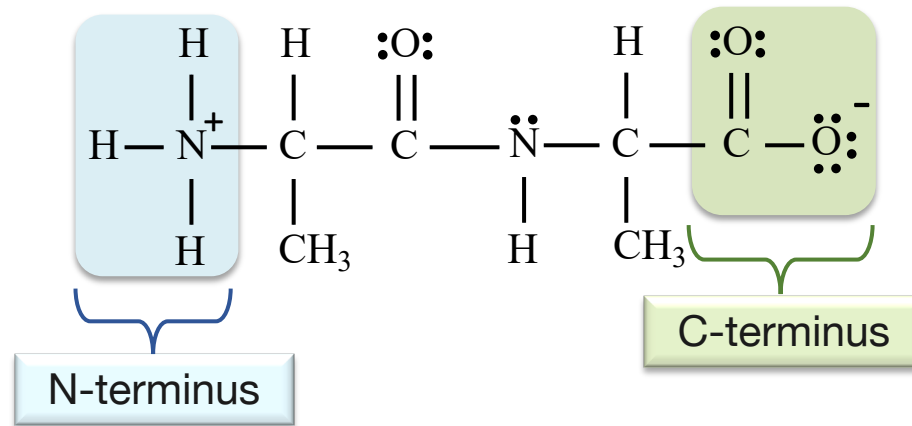
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13.10) Identify and label the N-terminus and the C-terminus in the dipeptide shown here.



EXPLANATION:

The end of the peptide structural formula that has a *quaternary ammonium group* is called the **N-terminus**, and the end that has a *carboxylate group* is called the **C-terminus**.

For more details: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

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13.11) Draw the structural formula for the predominant form of **Asp-Gly-Lys-Ala** at physiological **pH**. Lone pairs are optional.



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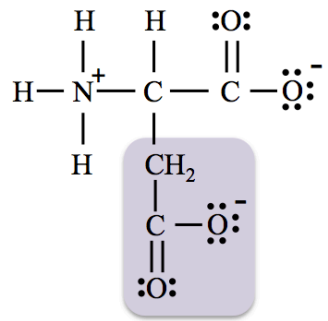
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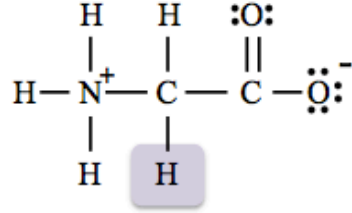


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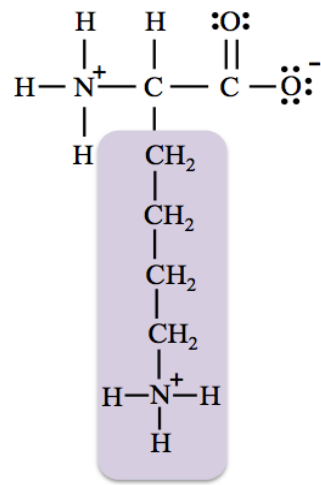
13.11) Draw the structural formula for the predominant form of **Asp-Gly-Lys-Ala** at physiological **pH**. Lone pairs are optional.



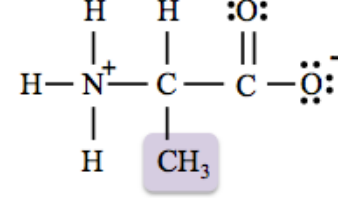
aspartic acid



glycine



lysine



alanine

HINT:

Peptides are often identified by listing its amino acid residues' *three-letter abbreviations in order from N-terminus to C-terminus*.

To begin, draw the four amino acids side-by-side (as shown on the right) and then connect them in the same manner that was used for the dipeptide in problem 13.7

- Because the structures in your table of amino acids are the predominant forms at physiological pH, if you correctly connect the amino acid structures from the amino acid table, then the peptide that you draw will be the predominant form at physiological **pH**.

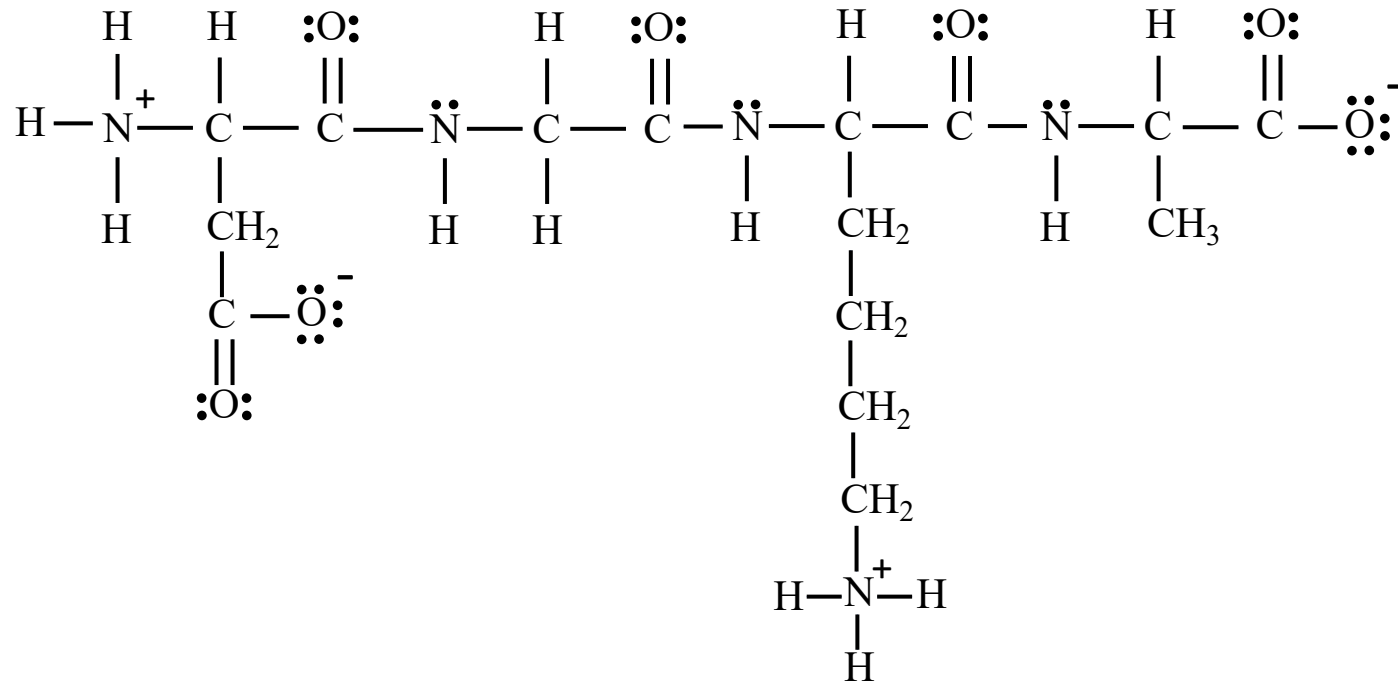
For more help: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

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13.11) Draw the structural formula for the predominant form of **Asp-Gly-Lys-Ala** at physiological **pH**. Lone pairs are optional.



Asp-Gly-Lys-Ala

EXPLANATION:

Peptides are often identified by listing its amino acid residues' *three-letter abbreviations* in **order from N-terminus to C-terminus**.

The four amino acids can be drawn side-by-side and then connected in the same manner that was used for the dipeptide in problem 13.7.

- Because the structures in your table of amino acids are the predominant forms at physiological pH, if you correctly connect the amino acid structures from the amino acid table, then the peptide that you draw will be the predominant form at physiological **pH**.

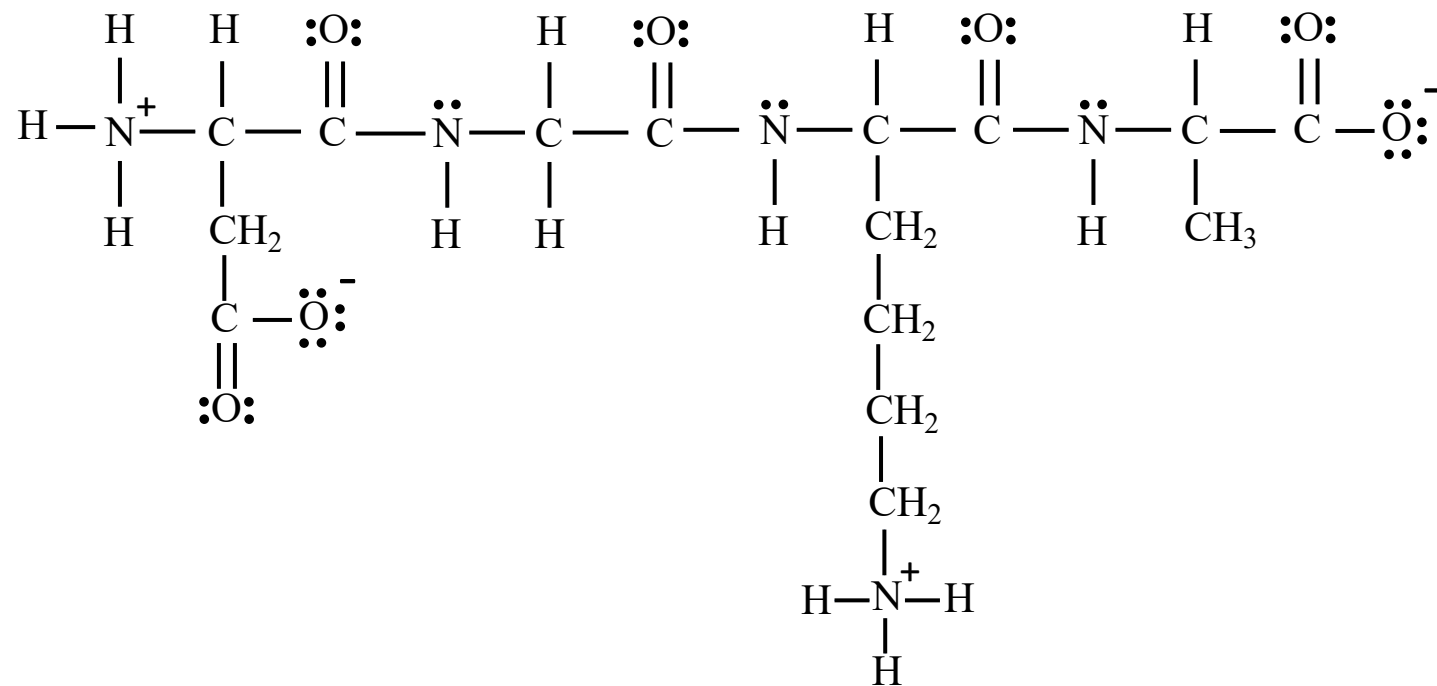
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13.12) In the previous problem, you drew the structural for **Asp-Gly-Lys-Ala** (it is shown below).

- Identify and label the **peptide bonds** in your drawing.
- Identify and label the **peptide groups** in your drawing.
- Identify and label the **C-terminus** in your drawing.
- Identify and label the **N-terminus** in your drawing.
- What is the **total charge** of the this peptide?



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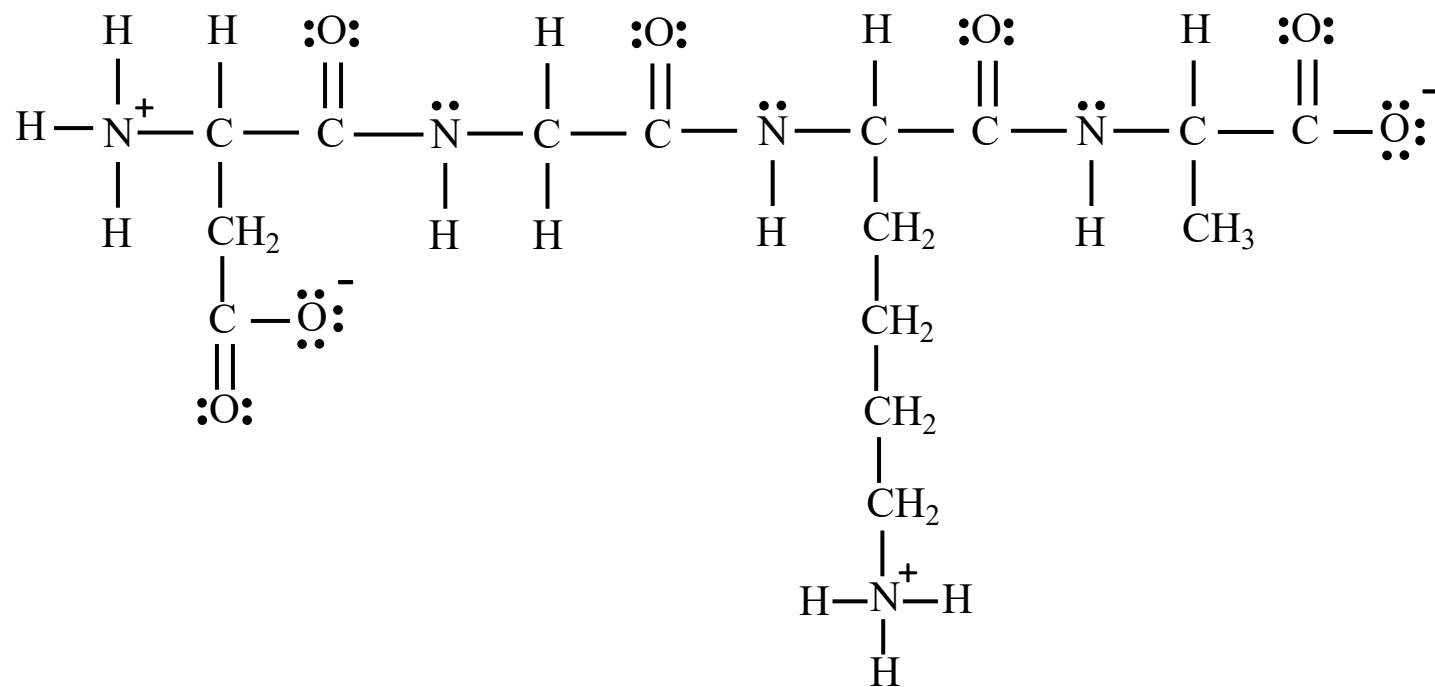
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13.12) In the previous problem, you drew the structural for **Asp-Gly-Lys-Ala** (it is shown below).

- Identify and label the **peptide bonds** in your drawing.
- Identify and label the **peptide groups** in your drawing.
- Identify and label the **C-terminus** in your drawing.
- Identify and label the **N-terminus** in your drawing.
- What is the **total charge** of the this peptide?



HINTS:

1) The bonding pattern around a *peptide bond* is called the **peptide group**.

2) The **total charge** is equal to the sum of the *formal charges* that are present.

Note that in this peptide, there are formal charges present in the C-terminus and N-terminus. There are also formal charges present in some of the side-chains.

For more help: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

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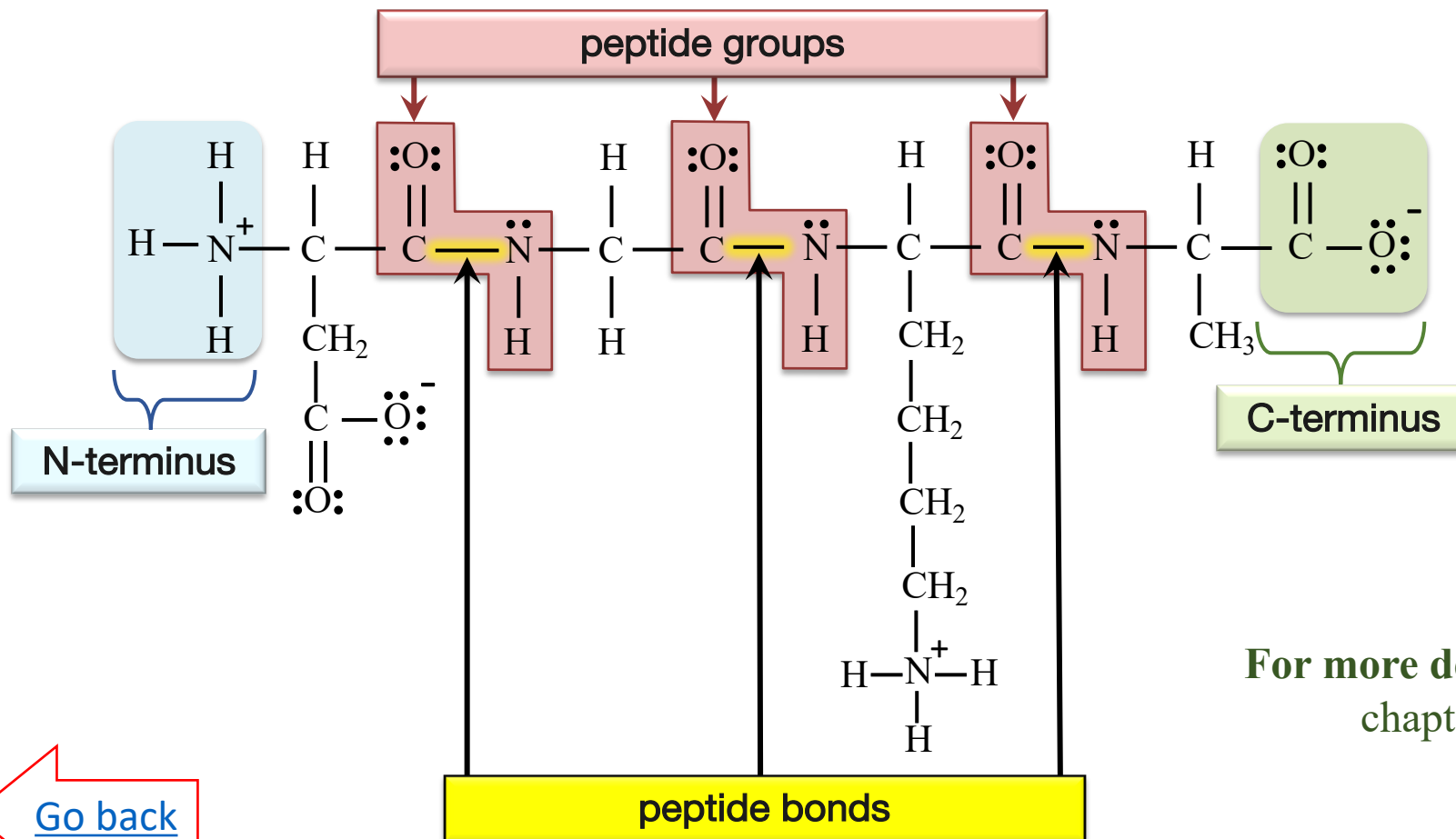
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13.12) In the previous problem, you drew the structural for **Asp-Gly-Lys-Ala** (it is shown below).

- Identify and label the **peptide bonds** in your drawing.
- Identify and label the **peptide groups** in your drawing.
- Identify and label the **C-terminus** in your drawing.
- Identify and label the **N-terminus** in your drawing.
- What is the **total charge** of the this peptide? **total charge = 0**

The bonding pattern around a *peptide bond* is called the **peptide group**. The atoms of the peptide groups in the peptide are **highlighted** and labeled.



TOTAL CHARGE :
The **total charge** is equal to the sum of the *formal charges* that are present. There is a formal charge of **1-** on an oxygen in the C-terminus **and** on an oxygen in aspartic acid's side-chain. There is a formal charge of **1+** on a nitrogen in the N-terminus **and** on a nitrogen in lysine's side-chain. Adding these charges give a **total charge = 0**.

For more details: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

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- 13.13) Write the names (using the three letter abbreviation method) of **all** of the tripeptides that can be made by combining one lysine (Lys), one asparagine (Asn), and one glutamic acid (Glu) residue.
- For example, one of the tripeptides is **Lys-Asn-Glu**.



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- 13.13) Write the names (using the three letter abbreviation method) of **all** of the tripeptides that can be made by combining one lysine (Lys), one asparagine (Asn), and one glutamic acid (Glu) residue.
- For example, one of the tripeptides is **Lys-Asn-Glu**.

HINT:

List of all the distinct ways that *one* Lys, *one* Asn and *one* Glu can be combined into a tripeptide.

- Here are three of the ways to do so:

{	Lys-Asn-Glu
	Lys-Glu-Asn
	Asn-Lys-Glu
- There are several more possible.

For more help: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

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13.13) Write the names (using the three letter abbreviation method) of **all** of the tripeptides that can be made by combining one lysine (Lys), one asparagine (Asn), and one glutamic acid (Glu) residue.

EXPLANATION:

List of all the distinct ways that *one* Lys, *one* Asn and *one* Glu can be combined into a tripeptide.

ANSWER:

Lys-Asn-Glu
Lys-Glu-Asn
Asn-Lys-Glu
Asn-Glu-Lys
Glu-Lys-Asn
Glu-Asn-Lys

For more details: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

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13.14) How many distinct *tripeptides* can be made from Glycine (Gly) **and/or** Alanine (Ala)?



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13.14) How many distinct *tripeptides* can be made from Glycine (Gly) **and/or** Alanine (Ala)?

HINT:

List of all the distinct ways that Gly and Ala can be combined into a tripeptide.

- Here are two of the ways to do so:  Gly-Gly-Gly
Gly-Gly-Ala
- There are several more possible.

For more help: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.



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13.14) How many distinct *tripeptides* can be made from Glycine (Gly) **and/or** Alanine (Ala)? **ANSWER: eight**

EXPLANATION:

List of all the distinct ways that Gly and Ala can be combined into a tripeptide.

Gly-Gly-Gly
Gly-Gly-Ala
Gly-Ala-Ala
Gly-Ala-Gly
Ala-Ala-Ala
Ala-Ala-Gly
Ala-Gly-Gly
Ala-Gly-Ala

For more details: See [chapter 13 part 3 video](#) or chapter 13 section 3 in the textbook.

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13.15) It is very important to understand the chemical bonding patterns and shapes of proteins in order to better understand how proteins are able to perform their biological functions. The bonding pattern and shape of a protein is referred to as “**protein structure.**” To describe a protein’s structure, we use four “levels,” which we call **primary, secondary, tertiary, and quaternary structure.** Using complete sentences, write a definition for each of these terms.

a) **primary structure:**

b) **secondary structure:**

c) **tertiary structure:**

d) **quaternary structure:**



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13.15) It is very important to understand the chemical bonding patterns and shapes of proteins in order to better understand how proteins are able to perform their biological functions. The bonding pattern and shape of a protein is referred to as “**protein structure.**” To describe a protein’s structure, we use four “levels,” which we call **primary, secondary, tertiary, and quaternary structure.** Using complete sentences, write a definition for each of these terms.

a) **primary structure:**

b) **secondary structure:**

c) **tertiary structure:**

d) **quaternary structure:**

HINT:

The **four levels of protein structure** are defined and discussed in your lecture notes and the textbook.

For more help, you may wish to review chapter 13 [part 4](#) and [part 5](#) videos.

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13.15) It is very important to understand the chemical bonding patterns and shapes of proteins in order to better understand how proteins are able to perform their biological functions. The bonding pattern and shape of a protein is referred to as “**protein structure.**” To describe a protein’s structure, we use four “levels,” which we call **primary, secondary, tertiary, and quaternary structure.** Using complete sentences, write a definition for each of these terms.

- a) **primary structure:** **The primary structure** of a protein is the *sequence of amino acid residues* in its peptide chain(s).

- b) **secondary structure:** **Secondary structure** describes the geometric patterns that occur when individual peptide chains “fold” back on themselves, more specifically, the patterns that result from **hydrogen bonding** interactions between *peptide groups* within an individual peptide.

- c) **tertiary structure:** **Tertiary structure** describes the *compacted shape* of a *peptide*.

- d) **quaternary structure:** **Quaternary structure** describes the overall shape that occurs when *two or more individual peptide chains* assemble to make a protein.

For more details: See chapter 13 [part 4](#) and [part 5](#) videos or chapter 13 section 4 in the textbook.

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13.16) Match the *level of protein structure* with the *type(s) of attractive forces* that they involve.

- Note that *some* of the levels of protein structures involve *more than one type of attractive force*.

Levels of protein structure:

i) primary structure:

ii) secondary structure:

iii) tertiary structure:

iv) quaternary structure:

Type of attractive force choices:

- a) covalent bonding *only*
- b) hydrogen bonding
- c) dipole-dipole
- d) ion-dipole
- e) hydrophobic interactions
- f) salt bridges
- g) disulfide bridges

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Levels of protein structure:

i) primary structure:

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Type of attractive force choices:

- a) covalent bonding *only*
- b) hydrogen bonding
- c) dipole-dipole
- d) ion-dipole
- e) hydrophobic interactions
- f) salt bridges
- g) disulfide bridges

HINT:

See the discussion of **protein structure** in your lecture notes or the textbook.

For more help, you may wish to review chapter 13 [part 4](#) and [part 5](#) videos.

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13.16) Match the *level of protein structure* with the *type(s) of attractive forces* that they involve.

- Note that *some* of the levels of protein structures involve *more than one type of attractive force*.

Levels of protein structure:

i) primary structure: (a)

ii) secondary structure: (b)

iii) tertiary structure: (b, c, d, e, f, and g)

iv) quaternary structure: (b, c, d, e, f, and g)

Type of attractive force choices:

- a) covalent bonding *only*
- b) hydrogen bonding
- c) dipole-dipole
- d) ion-dipole
- e) hydrophobic interactions
- f) salt bridges
- g) disulfide bridges

For more details: See chapter 13 [part 4](#) and [part 5](#) videos or chapter 13 section 4 in the textbook.

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13.17) Determine whether a salt bridge interaction can occur between the side-chains of each of the amino acid residue pairs listed below. Assume that the protein is at physiological pH.

a) aspartic acid and lysine

b) aspartic acid and glutamic acid

c) aspartic acid and arginine

d) aspartic acid and alanine



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13.17) Determine whether a salt bridge interaction can occur between the side-chains of each of the amino acid residue pairs listed below. Assume that the protein is at physiological pH.

- a) aspartic acid and lysine

- b) aspartic acid and glutamic acid

- c) aspartic acid and arginine

- d) aspartic acid and alanine

HINT:

A **salt bridge** is an attractive force between the *positive* formal charge on a *polar basic* amino acid residue's side-chain and a *negative* formal charge on a *polar acidic* residue's side-chain.

For more help: See chapter 13 [part 4](#) and [part 5](#) videos or chapter 13 section 4 in the textbook.

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13.17) Determine whether a salt bridge interaction can occur between the side-chains of each of the amino acid residue pairs listed below. Assume that the protein is at physiological pH.

a) aspartic acid and lysine

a salt bridge interaction can occur - Aspartic acid's side-chain has a negative formal charge and lysine's side-chain has a positive formal charge.

b) aspartic acid and glutamic acid

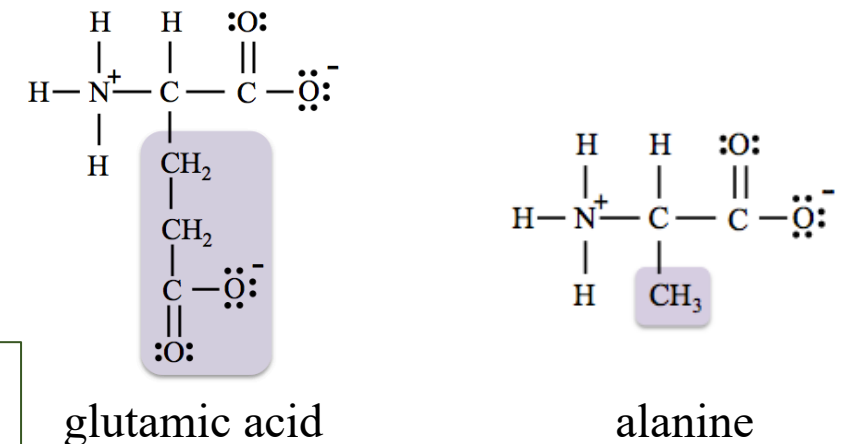
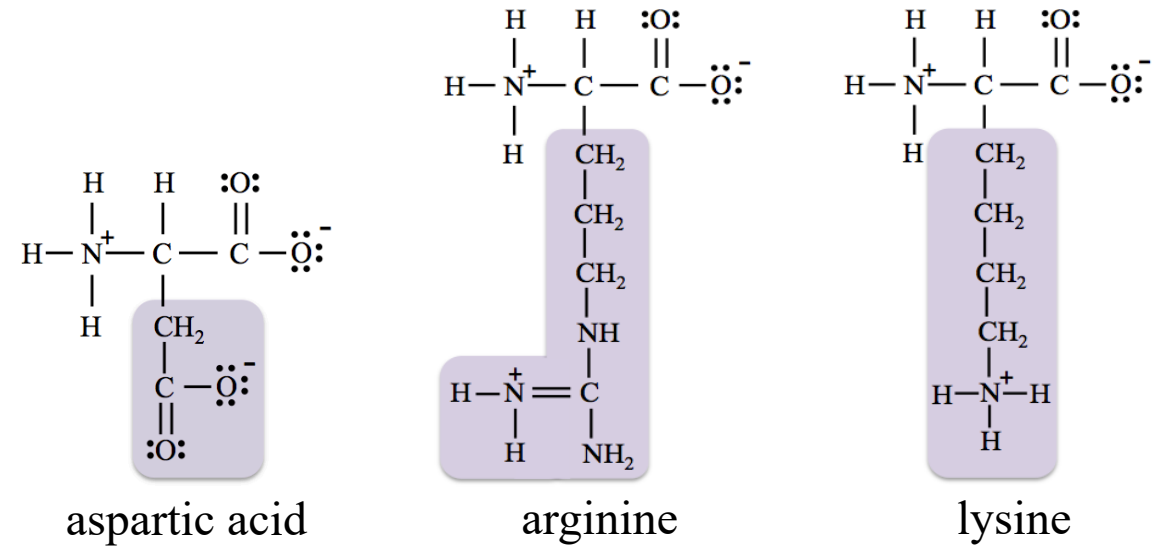
a salt bridge interaction cannot occur - Both residues' side-chains have a negative formal charge; salt bridges occur between a negative **and** a positive formal charge.

c) aspartic acid and arginine

a salt bridge interaction can occur - Aspartic acid's side-chain has a negative formal charge and arginine's side-chain has a positive formal charge.

d) aspartic acid and alanine

a salt bridge interaction cannot occur - Although aspartic acid's side-chain has a negative formal charge, alanine's side chain is *uncharged*.



EXPLANATION: A **salt bridge** is an attractive force between the *positive* formal charge on a *polar basic* amino acid residue's side-chain and a *negative* formal charge on a *polar acidic* residue's side-chain.

For more details: See chapter 13 [part 4](#) and [part 5](#) videos or chapter 13 section 4 in the textbook.

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13.18) Proteins are sometimes classified as being **globular proteins** *or* **fibrous proteins** based on their three-dimensional shape. Determine whether the properties and examples listed below refer to **globular proteins** or **fibrous proteins**.

- a) peptide chains are highly-folded into compacted shapes
- b) have long and narrow “string-like” shapes
- c) collagen
- d) hemoglobin
- e) enzymes
- f) transport proteins
- g) generally water soluble
- h) generally water insoluble
- i) function as structural proteins
- j) involved in chemical signaling
- k) transport proteins
- l) antibodies
- m) myosin



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- e) enzymes
- f) transport proteins
- g) generally water soluble
- h) generally water insoluble
- i) function as structural proteins
- j) involved in chemical signaling
- k) transport proteins
- l) antibodies
- m) myosin

HINT:

See the discussion of **globular proteins** and **fibrous proteins** in your lecture notes or the textbook.

For more help, you may wish to review [chapter 13 part 6 video](#).

For more details: See [chapter 13 part 6 video](#) or chapter 13 section 4 in the textbook.

For more help: See [chapter 13 part 6 video](#) or chapter 13 section 4 in the textbook.

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- a) peptide chains are highly-folded into compacted shapes **globular proteins**
- b) have long and narrow “string-like” shapes **fibrous proteins**
- c) collagen **fibrous proteins**
- d) hemoglobin **globular proteins**
- e) enzymes **globular proteins**
- f) transport proteins **globular proteins**
- g) generally water soluble **globular proteins**
- h) generally water insoluble **fibrous proteins**
- i) function as structural proteins **fibrous proteins**
- j) involved in chemical signaling **globular proteins**
- k) transport proteins **globular proteins**
- l) antibodies **globular proteins**
- m) myosin **fibrous proteins**

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For more details: See [chapter 13 part 6 video](#) or chapter 13 section 4 in the textbook.

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13.19)

i) Proteins, such as antibodies, that contain carbohydrates are called _____.

- a) simple proteins
- b) sugar proteins
- c) immunoproteins
- d) glycoproteins

ii) An antibody's antigen binding site binds to a particular part of an antigen called the _____.

- a) epitope
- b) paratope
- c) active site
- d) immunoglobulin

iii) Proteins that contain *non amino acid* components are called **conjugated proteins**. The non amino acid components of these proteins are called _____ groups.

- a) essential
- b) prosthetic
- c) paratope
- d) hemoglobin

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i) Proteins, such as antibodies, that contain carbohydrates are called _____.

- HINT:**
- a) simple proteins
 - b) sugar proteins
 - ~~c) immunoproteins~~
 - d) glycoproteins

ii) An antibody's antigen binding site binds to a particular part of an antigen called the _____.

- HINT:**
- a) epitope
 - b) paratope
 - ~~c) active site~~
 - d) immunoglobulin

iii) Proteins that contain *non amino acid* components are called **conjugated proteins**. The non amino acid components of these proteins are called _____ groups.

- HINT:**
- a) essential
 - b) prosthetic
 - c) paratope
 - ~~d) hemoglobin~~

For more help: See [chapter 13 part 6 video](#) or [chapter 13 section 4](#) in the textbook.

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13.19)

i) Proteins, such as antibodies, that contain carbohydrates are called _____.

- a) simple proteins
- b) sugar proteins
- c) immunoproteins
- d) glycoproteins**

Antibodies are **glycoproteins** because they have carbohydrates (oligosaccharides) that are covalently bound to some of their amino acid residue side-chains.

ii) An antibody's antigen binding site binds to a particular part of an antigen called the _____.

- a) epitope**
- b) paratope
- c) active site
- d) immunoglobulin

An antigen binding site, called the *paratope*, binds to a particular part of an antigen called the **epitope**. The binding between antigen and antibody occurs because of noncovalent attractive forces, which are maximized due to the complementary shapes of the paratope and epitope. You can think of this as analogous to a lock-and-key system.

iii) Proteins that contain *non amino acid* components are called **conjugated proteins**. The non amino acid components of these proteins are called _____ groups.

- a) essential
- b) prosthetic**
- c) paratope
- d) hemoglobin

An example of a **prosthetic group** is the *heme group*, which is present in hemoglobin. The main role of hemoglobin is to transport oxygen (O₂) molecules. Heme groups contain an iron ion, to which an oxygen molecule can be quite strongly attached. Hemoglobin contains four heme groups. Each heme group is capable of binding one oxygen molecule. Heme prosthetic groups are also found in myoglobin, catalase, and other proteins.

For more details: See [chapter 13 part 6 video](#) or chapter 13 section 4 in the textbook.

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13.20) The shape of a protein is the key factor in its ability to perform its biological role. It is therefore critical that an organism's proteins maintain their shapes. Protein shape is maintained by the attractive forces involved in secondary, tertiary, and quaternary structures. When these attractive forces are disrupted, the native shape of proteins can be changed enough that a partial or complete loss of bioactivity (function) occurs. When a protein loses some or all of its biological activity in such a manner, this is referred to as “**protein denaturation.**” In most cases, unless the shape change is very minor, the denaturation is *irreversible*. Any mechanical or chemical agent that causes the denaturation of a protein is called a **denaturing agent**.

List five types of denaturing agents:

i) _____

ii) _____

iii) _____

iv) _____

v) _____



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List five types of denaturing agents:

i) _____

ii) _____

iii) _____

iv) _____

v) _____

HINT:

Five types of **denaturing agents** are listed and discussed in your lecture notes and the textbook.

For more help, you may wish to review [chapter 13 part 6 video](#).

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13.20) The shape of a protein is the key factor in its ability to perform its biological role. It is therefore critical that an organism's proteins maintain their shapes. Protein shape is maintained by the attractive forces involved in secondary, tertiary, and quaternary structures. When these attractive forces are disrupted, the native shape of proteins can be changed enough that a partial or complete loss of bioactivity (function) occurs. When a protein loses some or all of its biological activity in such a manner, this is referred to as “**protein denaturation.**” In most cases, unless the shape change is very minor, the denaturation is *irreversible*. Any mechanical or chemical agent that causes the denaturation of a protein is called a **denaturing agent**.

List five types of denaturing agents:

- i) **heating** _____
- ii) **mechanical agitation** _____
- iii) **amphipathic compounds** _____
- iv) **polar solvents** _____
- v) **pH changes** _____

For more details: See [chapter 13 part 6 video](#) or chapter 13 section 4 in the textbook.

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13.21) Using complete sentences, explain how pH changes can denature a protein.



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13.21) Using complete sentences, explain how pH changes can denature a protein.

HINT:

Formal charges on side-chains are necessary for salt bridges and ion-dipole interactions. How would changes in pH affect side-chain formal charge?

For more help: See [chapter 13 part 6 video](#) or chapter 13 section 4 in the textbook.



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13.21) Using complete sentences, explain how pH changes can denature a protein.

YOUR ANSWER SHOULD BE SOMETHING LIKE THIS:

pH changes can disrupt a protein's salt bridges and ion-dipole interactions. Near physiological pH, the predominant form of polar acidic side-chains and polar basic side-chains (except for histidine) have a formal charge. These **charged side-chains are necessary for salt bridges and ion-dipole interactions.**

- If the pH is changed to a value greater than the pK_a of a polar basic side-chain's quaternary ammonium group, then its *uncharged base form* becomes predominant.
- If the pH is changed to a value less than the pK_a of a polar acidic side-chain's carboxyl group, its *uncharged acid form* becomes predominant.

Either of these pH changes will disrupt a protein's salt bridges and ion-dipole interactions because of the loss of the formal charge that is necessary for salt bridge and ion dipole attractions.

For more details: See [chapter 13 part 6 video](#) or chapter 13 section 4 in the textbook.

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13.22) Explain the difference between **complete proteins** and **incomplete proteins**.



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13.22) Explain the difference between **complete proteins** and **incomplete proteins**.

HINT: See the discussion of **complete proteins** and **incomplete proteins** in your lecture notes or the textbook.

For more help, you may wish to review [chapter 13 part 7 video](#).



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13.22) Explain the difference between **complete proteins** and **incomplete proteins**.

Organisms produce (synthesize) protein from dietary amino acids. Our bodies are capable of producing eleven of the twenty common amino acids (from other amino acids or certain other compounds), therefore we do not necessarily need to obtain these eleven amino acids in our diet. However, the other nine amino acids can only be obtained by eating proteins that contain them. These nine amino acids are called *essential amino acids*.

YOUR ANSWER SHOULD BE SOMETHING LIKE THIS:

Foods that contain *all of the essential amino acids* are called **complete proteins** (although they are not actually true proteins, a more accurate name would be “complete protein foods”).

Foods that contain proteins but do not contain all of the essential amino acids are called **incomplete proteins**.

For more details: See [chapter 13 part 7 video](#) or chapter 13 section 4 in the textbook.



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13.23) Foods that contain all of the essential amino acids are called **complete proteins**. Most animal products are complete proteins. Foods that contain proteins but do not contain all of the essential amino acids are called **incomplete proteins**. These include most plant proteins. Examples of *incomplete proteins* and their missing essential amino acids are listed in the table below:

Food	Amino Acid Deficiency
rice, wheat, oats	lysine
beans	methionine, tryptophan
peas	methionine
soy	low in methionine
corn	lysine, tryptophan
almonds, walnuts	lysine, tryptophan

A combining of two or more incomplete proteins that are deficient in different amino acids is a dietary strategy used to ensure the intake of all nine essential amino acids. When proteins are combined in this way, they are called **complementary proteins**.

QUESTION: Which *three* foods (from the table above) could *each* be eaten with **rice** as a **complementary protein**?

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13.23) Foods that contain all of the essential amino acids are called **complete proteins**. Most animal products are complete proteins. Foods that contain proteins but do not contain all of the essential amino acids are called **incomplete proteins**. These include most plant proteins. Examples of *incomplete proteins* and their missing essential amino acids are listed in the table below:

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A combining of two or more incomplete proteins that are deficient in different amino acids is a dietary strategy used to ensure the intake of all nine essential amino acids. When proteins are combined in this way, they are called **complementary proteins**.

QUESTION: Which *three* foods (from the table above) could *each* be eaten with **rice** as a **complementary protein**?

HINT: Rice is deficient in *lysine*. Foods that *are not deficient in lysine*, would complement rice.

For more help: See [chapter 13 part 7 video](#) or chapter 13 section 4 in the textbook.

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13.23) Foods that contain all of the essential amino acids are called **complete proteins**. Most animal products are complete proteins. Foods that contain proteins but do not contain all of the essential amino acids are called **incomplete proteins**. These include most plant proteins. Examples of *incomplete proteins* and their missing essential amino acids are listed in the table below:

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almonds, walnuts	lysine, tryptophan

A combining of two or more incomplete proteins that are deficient in different amino acids is a dietary strategy used to ensure the intake of all nine essential amino acids. When proteins are combined in this way, they are called **complementary proteins**.

QUESTION: Which *three* foods (from the table above) could *each* be eaten with **rice** as a **complementary protein**?

ANSWER: beans, peas, and soy

EXPLANATION: Rice is deficient in *lysine*. Beans, peas, and soy ARE NOT deficient in *lysine*, so they would *complement* rice. Corn, almonds, and walnuts ARE deficient in *lysine*, so they **would not** complement rice.

For more details: See [chapter 13 part 7 video](#) or chapter 13 section 4 in the textbook.

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13.24) Catalysts are substances that increase the rates of chemical reactions. Life requires that many chemical reactions occur within organisms. The human body employs over a thousand chemical reactions. Many of these reactions would occur too slowly to be useful in the absence of a catalyst. Nature provides humans and other biological organisms with proteins that are capable of catalyzing reactions.

i) Catalysts _____ the activation energy of a reaction and thereby increase the reaction rate.

- a) lower
- b) increase
- c) eliminate

ii) Protein catalysts are called _____.

- a) cataproteins
- b) membrane proteins
- c) enzymes
- d) transition proteins

iii) Enzymologists (scientists who specialize in studying enzymes) refer to the *reactants* of catalyzed reactions as

_____.

- a) precursors
- b) substrates
- c) active sites
- d) enzymes



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b) increase
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- HINT:** ~~a) cataproteins~~
b) membrane proteins
c) enzymes
d) transition proteins

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- _____.
- HINT:** a) precursors
b) substrates
c) active sites
~~d) enzymes~~



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i) Catalysts _____ the activation energy of a reaction and thereby increase the reaction rate.

a) lower

b) increase

c) eliminate

When substrates bind to an enzyme's active site, interactions with the enzyme change the shape of the substrates (and enzyme) to a configuration that lowers the energy of the transition state (relative to an un-catalyzed reaction).

ii) Protein catalysts are called _____.

a) cataproteins

b) membrane proteins

c) enzymes

d) transition proteins

Among all plants and animal species, over 5,000 chemical reactions are catalyzed by enzymes. Enzymes are capable of increasing the rate of a chemical reaction by up to *a factor of one thousand*.

iii) Enzymologists (scientists who specialize in studying enzymes) refer to the *reactants* of catalyzed reactions as _____.

a) precursors

b) substrates

c) active sites

d) enzymes

Most enzymes are composed of hundreds or thousands of amino acid residues, however only a small region of the enzyme makes contact with the **substrates**. The part of the enzyme that makes contact with substrates is called the "**active site**."

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13.25) Match each **description** with the *type of enzyme specificity* that it implies.

Descriptions:

- i)* enzyme catalyzes the lysis (breaking) of peptide bonds

- ii)* enzyme catalyzes the conversion of lactose to glucose and galactose

- iii)* enzyme accepts only cis substrates

- iv)* enzyme catalyzes the conversion of alcohols to aldehydes

Enzyme specificity choices:

- a) absolute specificity
- b) relative specificity
- c) stereospecificity

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Enzyme specificity choices:

- a) absolute specificity
- b) relative specificity
- c) stereospecificity

HINT:

Some enzymes will only catalyze the reaction of a *particular substrate*; this is called **absolute specificity**.

Some enzymes are less specific, and will catalyze reactions for a *particular family of substrates*; this is called **relative specificity**.

Some enzymes will only catalyze the reaction of, or production of, *one particular stereoisomer*; this is called **stereospecificity**.

For more help: See [chapter 13 part 8 video](#) or chapter 13 section 5 in the textbook.

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13.25) Match each **description** with the *type of enzyme specificity* that it implies.

Descriptions:

- i) enzyme catalyzes the lysis (breaking) of peptide bonds
(b) relative specificity – This enzyme catalyzes reactions for a *particular family of substrates* (peptides/proteins).
- ii) enzyme catalyzes the conversion of lactose to glucose and galactose
(a) absolute specificity – This enzyme will only catalyze the reaction of a particular substrate (lactose).
- iii) enzyme accepts only cis substrates
(c) stereospecificity – This enzyme will only catalyze the reaction of one particular stereoisomer (cis isomer).
- iv) enzyme catalyzes the conversion of alcohols to aldehydes
(b) relative specificity – This enzyme catalyzes reactions for a *particular family of substrates* (alcohols).

Enzyme specificity choices:

- a) absolute specificity
- b) relative specificity
- c) stereospecificity

EXPLANATION:

Some enzymes will only catalyze the reaction of a *particular substrate*; this is called **absolute specificity**.

Some enzymes are less specific, and will catalyze reactions for a *particular family of substrates*; this is called **relative specificity**.

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For more details: See [chapter 13 part 8 video](#) or chapter 13 section 5 in the textbook.

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13.26) Describe how temperature affects the rate of an enzymatically catalyzed reaction.



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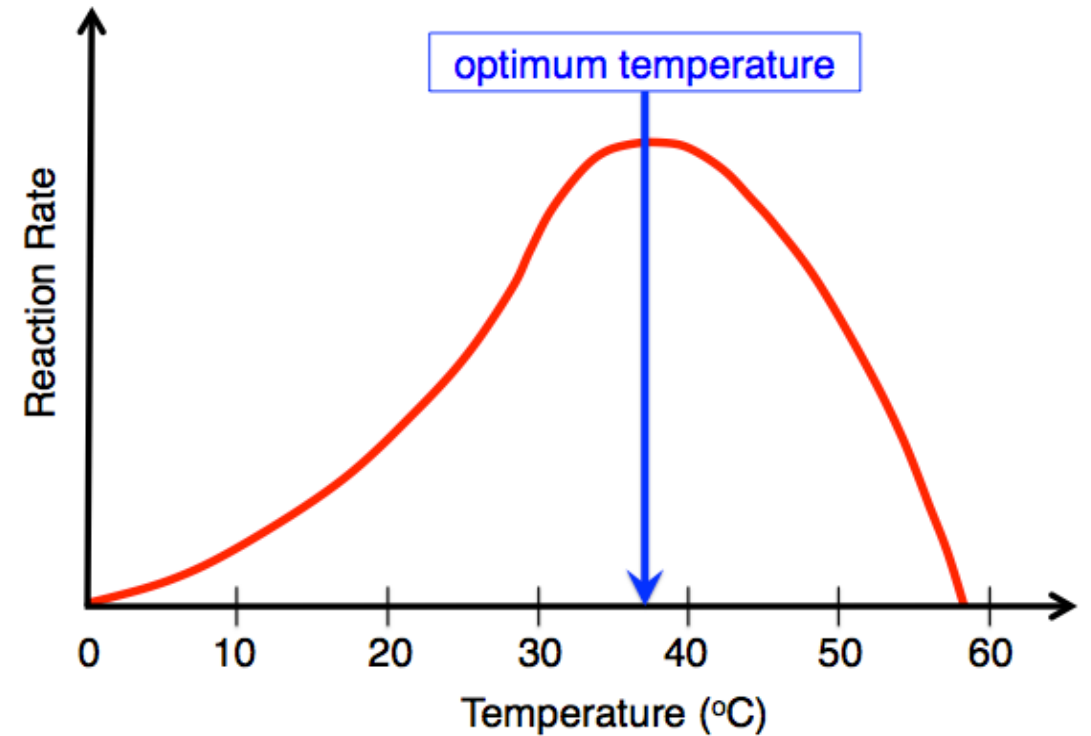
13.26) Describe how temperature affects the rate of an enzymatically catalyzed reaction.

HINT:

A typical graph of the rate of an enzymatically catalyzed reaction vs. temperature is shown on the right.

Starting at a relatively low temperature, describe what happens to the reaction rate *as the temperature increases*.

For more help: See [chapter 13 part 9 video](#) or chapter 13 section 5 in the textbook.



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13.26) Describe how temperature affects the rate of an enzymatically catalyzed reaction.

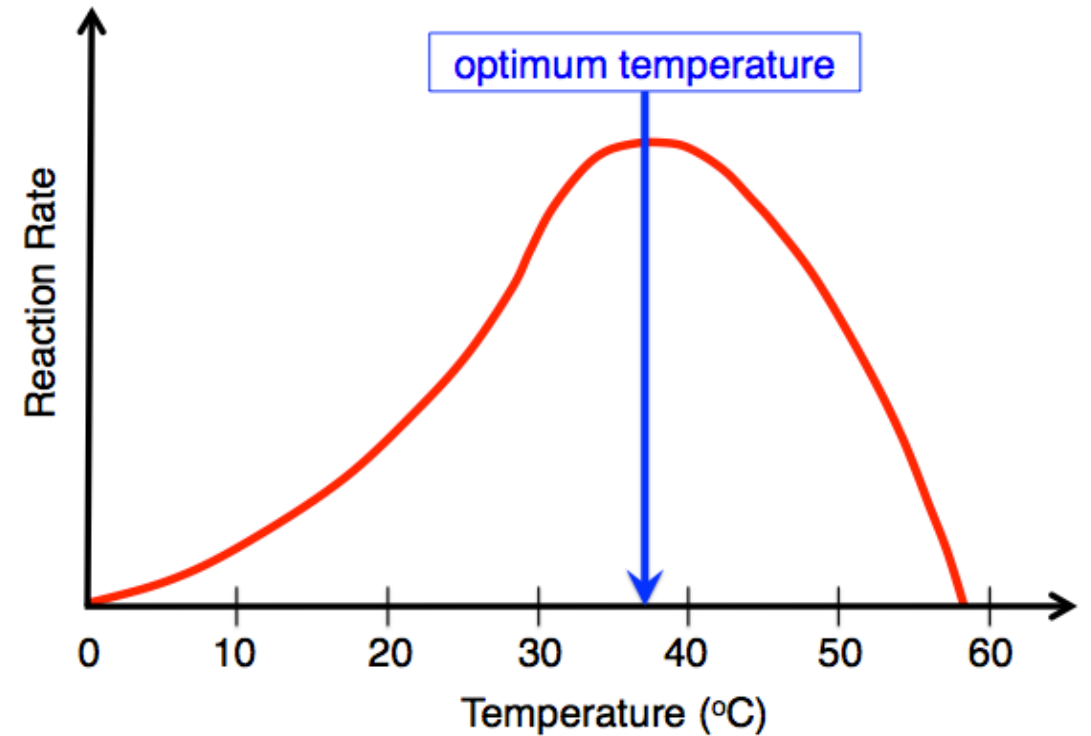
A typical graph of the rate of an enzymatically catalyzed reaction vs. temperature is shown on the right. Starting at a relatively low temperature, as the temperature begins to increase there is an *initial increase* in the rate of the reaction.

- This is the case for both catalyzed and uncatalyzed reactions; the elevated temperatures provide more energy for reactants to overcome the *activation energy*.

As the temperature continues to increase, the reaction rate of an enzymatically catalyzed reaction reaches a maximum value (the peak of the graph's curve).

- The temperature at which the rate of the reaction is greatest is called the enzyme's **optimum temperature**. The reason that the reaction rate does not continue to increase after reaching the optimum temperature is that the enzyme begins to denature at the higher temperature.

As the temperature increases *past the optimum temperature*, the rate of the reaction quickly decreases.

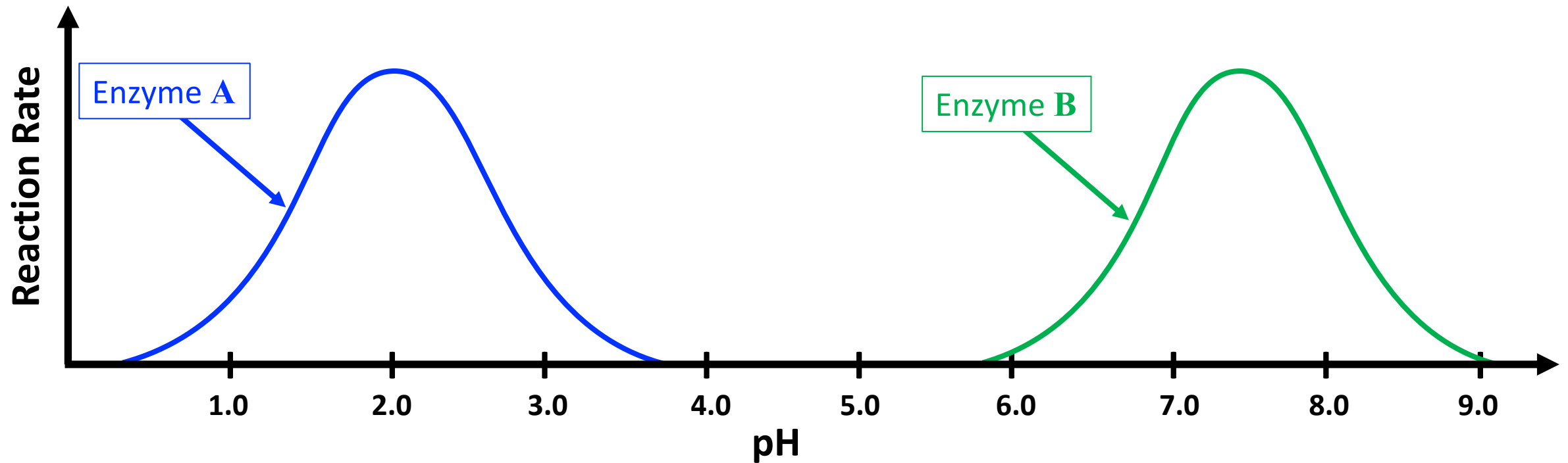


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13.27) The rate of an enzymatically catalyzed reaction depends on the pH. A graph of the rates of enzymatically catalyzed reactions vs. pH is shown for two hypothetical enzymes (**enzyme A** and **enzyme B**).



- What is the *approximate* value of the **pH optimum** for enzyme A?
- What is the *approximate* value of **pH optimum** for enzyme B?
- Which enzyme, A or B, would best catalyze a digestion reaction that occurs in the stomach?

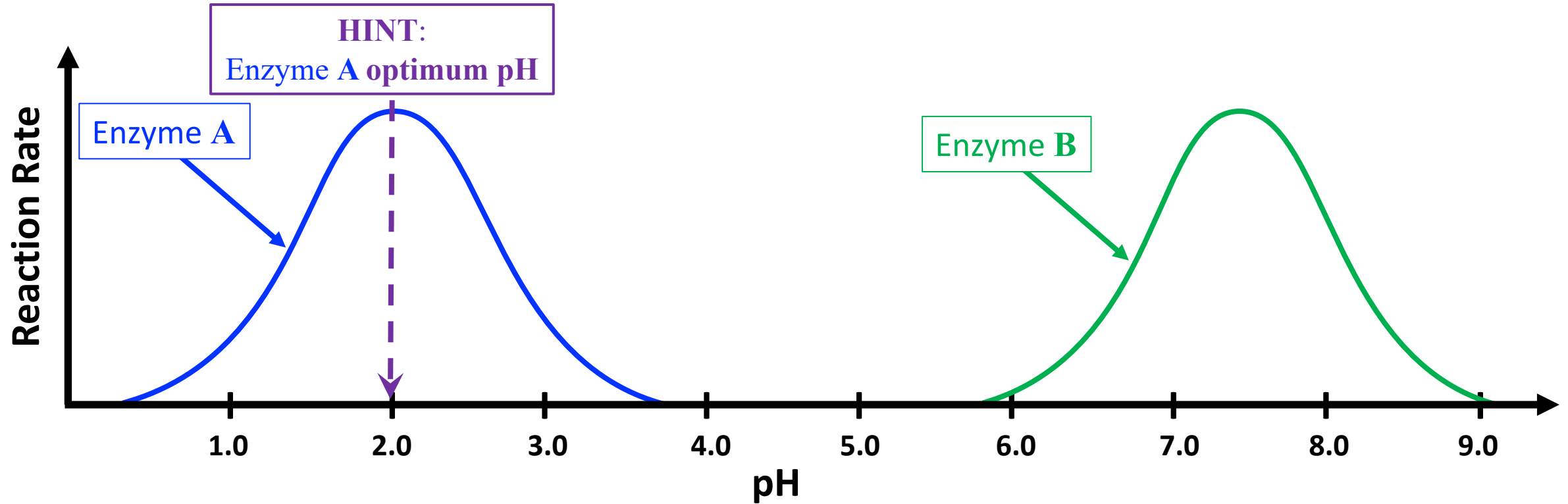
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- What is the *approximate* value of **pH optimum** for enzyme B?
- Which enzyme, A or B, would best catalyze a digestion reaction that occurs in the stomach?

HINT: The enzyme that would best catalyze a digestion reaction has an **optimum pH that is *closest*** to the pH range in the stomach.

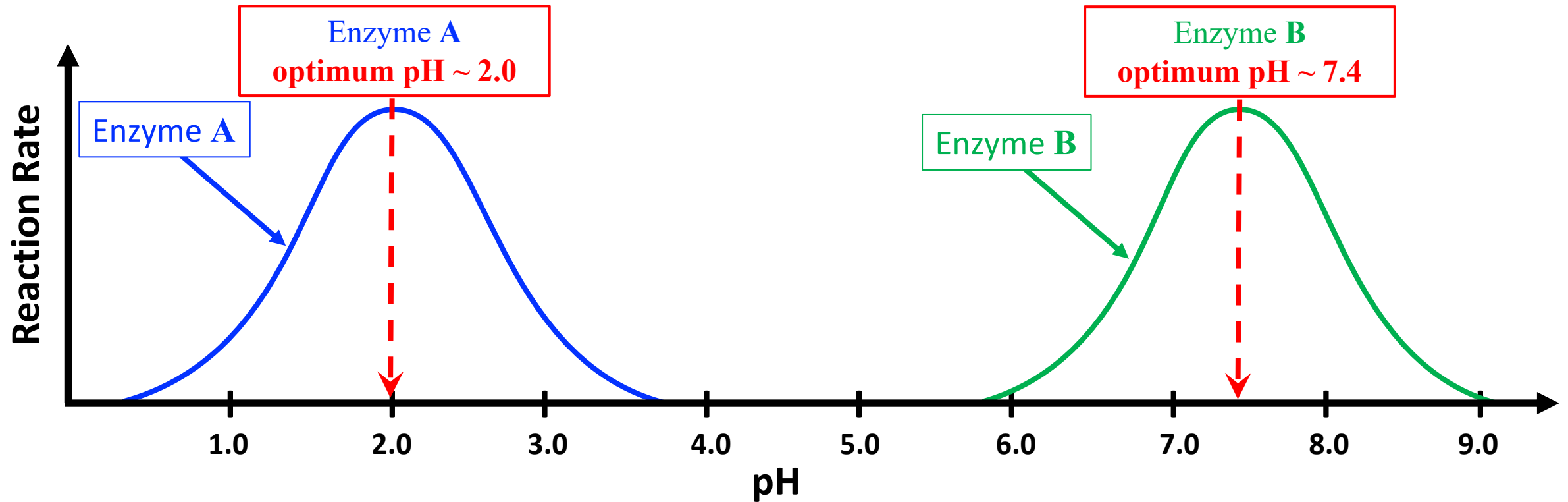
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13.27) The rate of an enzymatically catalyzed reaction depends on the pH. A graph of the rates of enzymatically catalyzed reactions vs. pH is shown for two hypothetical enzymes (**enzyme A** and **enzyme B**).



- What is the *approximate* value of the **pH optimum** for enzyme A? **~ 2.0**
- What is the *approximate* value of **pH optimum** for enzyme B? **~ 7.4**
- Which enzyme, A or B, would best catalyze a digestion reaction that occurs in the stomach? **Enzyme A**

EXPLANATION: **Enzyme A** would best catalyze a digestion reaction because its **optimum pH (~ 2.0)** is *closest* to the pH range in the stomach (**pH ~ 1 to 3**).

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13.28) Determine whether each of the inhibitors (or inhibitor characteristics) are involved in **reversible inhibition** *or* **irreversible inhibition**.

- a) inhibitor structure often resembles the substrate structure
- b) inhibitor forms a new and permanent covalent bond to the enzyme's active site
- c) sulfanilamide
- d) aspirin
- e) inhibitor binds weakly and noncovalently to an enzyme's active site and decreases its activity
- f) penicillin V
- g) inhibitor binds weakly and noncovalently to the enzyme at a region other than the active site
- h) inhibitors repeatedly attach to and detach from enzyme
- i) inhibitor is used in a pathway that is regulated by feedback inhibition



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13.28) Determine whether each of the inhibitors (or inhibitor characteristics) are involved in **reversible inhibition** *or* **irreversible inhibition**.

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- h) inhibitors repeatedly attach to and detach from enzyme
- i) inhibitor is used in a pathway that is regulated by feedback inhibition

HINT: Irreversible inhibition occurs when an inhibitor reacts with an enzyme, forming a new and permanent covalent bond to the enzyme. In almost all cases of irreversible inhibition, the new bond is made to the enzyme's active site, which results in complete and permanent loss of the enzyme's activity.

Reversible inhibition occurs when an inhibitor is weakly bound to an enzyme and decreases its activity. Like the substrates, reversible inhibitors are specific for particular enzymes. Reversible inhibitors do not form covalent bonds to the enzyme, therefore they repeatedly attach to and detach from enzymes.

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13.28) Determine whether each of the inhibitors (or inhibitor characteristics) are involved in **reversible inhibition** or **irreversible inhibition**.

- a) inhibitor structure often resembles the substrate structure **reversible inhibition**
- b) inhibitor forms a new and permanent covalent bond to the enzyme's active site **irreversible inhibition**
- c) sulfanilamide **reversible inhibition**
- d) aspirin **irreversible inhibition**
- e) inhibitor binds weakly and noncovalently to an enzyme's active site and decreases its activity **reversible inhibition**
- f) penicillin V **irreversible inhibition**
- g) inhibitor binds weakly and noncovalently to the enzyme at a region other than the active site **reversible inhibition**
- h) inhibitors repeatedly attach to and detach from enzyme **reversible inhibition**
- i) inhibitor is used in a pathway that is regulated by feedback inhibition **reversible inhibition**

EXPLANATION: **Irreversible inhibition** occurs when an inhibitor reacts with an enzyme, forming a new and permanent covalent bond to the enzyme. In almost all cases of irreversible inhibition, the new bond is made to the enzyme's active site, which results in complete and permanent loss of the enzyme's activity.

Reversible inhibition occurs when an inhibitor is weakly bound to an enzyme and decreases its activity. Like the substrates, reversible inhibitors are specific for particular enzymes. Reversible inhibitors do not form covalent bonds to the enzyme, therefore they repeatedly attach to and detach from enzymes.

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For more details: See [chapter 13 part 9 video](#) or chapter 13 section 5 in the textbook.

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13.29) The function of feedback inhibition is to _____.

- a) provide a way of keeping the wrong substrate from coming in contact with an enzyme
- b) control a reaction pathway so that there isn't an overproduction of the pathway's product(s)
- c) provide a stimulus to the enzyme that makes it active during a reaction
- d) affect the polarity of a substrate so that it will not be picked up by an enzyme



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This is the last question.

13.29) The function of feedback inhibition is to _____.

- HINT:**
- a) provide a way of keeping the wrong substrate from coming in contact with an enzyme
 - b) control a reaction pathway so that there isn't an overproduction of the pathway's product(s)
 - ~~c) provide a stimulus to the enzyme that makes it active during a reaction~~
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This is the last question.

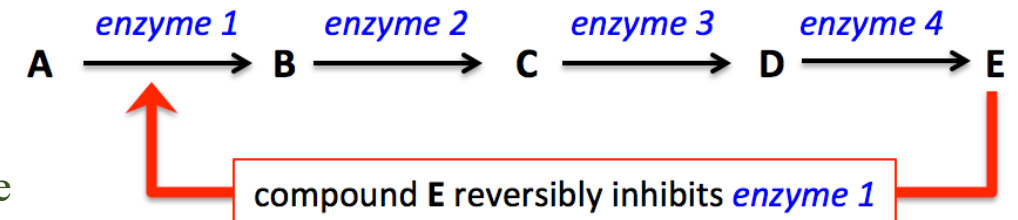
13.29) The function of feedback inhibition is to _____.

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- b) control a reaction pathway so that there isn't an overproduction of the pathway's product(s)
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- d) affect the polarity of a substrate so that it will not be picked up by an enzyme

EXPLANATION: Organisms often use several reactions in series (one after another) in order to carry out the chemical changes they require to meet their physiological needs. These reaction series are referred to as metabolic pathways. Many of the reactions in metabolic pathways require enzymes, therefore organisms can regulate (slow down) a metabolic process, according to their needs, by inhibiting one (or more) of the enzymes involved in the metabolic pathway. The product of a reaction in a metabolic pathway often acts as a *reversible inhibitor* for one (or more) of the reactions in the pathway. This biological strategy makes sense because when there is a relatively high concentration of a product in a metabolic pathway, it would be inefficient, and in some cases harmful, to continue its production.

For example, consider the hypothetical metabolic pathway (shown on the right)

involving four enzymatically-catalyzed reactions that eventually converts compound "A" into compound "E," where compound E reversibly inhibits *enzyme 1*.



- If compound E is not present, or is present in relatively low concentration, the reactions proceed, and therefore compound E is produced at a significant rate.
- If compound E is produced at a greater rate than the organism uses it, its concentration will increase. As the concentration of E increases, more E is available to bind to and inhibit, *enzyme 1*, and this results in a decrease in the production of B, C, D, and, ultimately, a decrease in the production of E. The *regulation* of a metabolic pathway by *the inhibition of an enzyme by products of any of the reactions* in the pathway is called **feedback inhibition**.

For more details: See [chapter 13 part 9 video](#) or chapter 13 section 5 in the textbook.

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