

Chem 464
Biochemistry

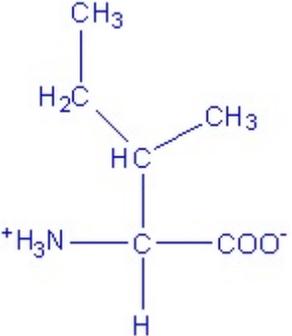
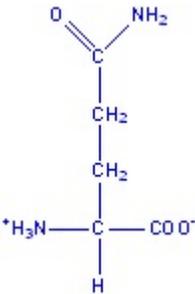
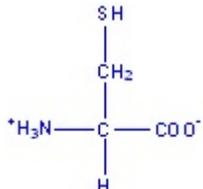
Multiple choice (4 points apiece):

- The pH of a sample of blood is 7.4, while gastric juice is pH 1.4. The blood sample has:
 - 0.189 times the $[H^+]$ as the gastric juice.
 - 5.29 times lower $[H^+]$ than the gastric juice.
 - 6 times lower $[H^+]$ than the gastric juice.
 - 6,000 times lower $[H^+]$ than the gastric juice.
 - a million times lower $[H^+]$ than the gastric juice.
- Which of the following properties of water does not contribute to the fitness of the aqueous environment for living organisms?
 - Cohesion of liquid water due to hydrogen bonding.
 - High heat of vaporization.
 - High specific heat.
 - The density of water is greater than the density of ice.
 - The very low molecular weight of water.
- The chirality of an amino acid results from the fact that its α -carbon:
 - has no net charge.
 - is a carboxylic acid.
 - is bonded to four different chemical groups.
 - is in the L absolute configuration in naturally occurring proteins.
 - is symmetric.
- At the isoelectric pH of a tetrapeptide:
 - only the amino and carboxyl termini contribute charge.
 - the amino and carboxyl termini are not charged.
 - the total net charge is zero.
 - there are four ionic charges.
 - two internal amino acids of the tetrapeptide cannot have ionizable R groups.
- Pauling and Corey's studies of the peptide bond showed that:
 - at pH 7, many different peptide bond conformations are equally probable.
 - peptide bonds are essentially planar, with no rotation about the C-N axis.
 - peptide bonds in proteins are unusual, and unlike those in small model compounds.
 - peptide bond structure is extraordinarily complex.
 - primary structure of all proteins is similar, although the secondary and tertiary structure may differ greatly.
- A sequence of amino acids in a certain protein is found to be -Ser-Gly-Pro-Gly-. The sequence is most probably part of a(n):
 - antiparallel sheet.
 - parallel sheet.
 - helix.
 - sheet.
 - turn.

7. An average protein will not be denatured by:
- A) a detergent such as sodium dodecyl sulfate.
 - B) heating to 90°C.
 - C) iodoacetic acid.
 - D) pH 10.
 - E) urea.

Longer questions (70 points total)

7. (20 points) Fill in the following table:

Name	Isoleucine	Glutamine	Cysteine
3 letter abbreviation	Ile	Gln	Cys
1 letter abbreviation	I	Q	C
Structure			
side chain pK _a (if ionizable)	-	-	8.18
General classification (nonpolar, polar, etc)	Nonpolar	Polar	Polar - uncharged

These questions go in the blue book

8. (10 points) The pH of blood is 7.4. The pK_a of $H_2PO_4^-$ is 6.86. What is the ratio $HPO_4^{2-}/H_2PO_4^-$ in blood? The normal level for phosphorous is 3 mg/dL (I know the units are funky) What is the concentration of HPO_4^{2-} & $H_2PO_4^-$ in normal blood. (You may express this concentration in either mg/dL or Molarity)

$$\begin{aligned} pH &= pK_a + \log \left(\frac{HPO_4^{2-}}{H_2PO_4^-} \right) \\ 7.4 &= 6.86 + \log \left(\frac{HPO_4^{2-}}{H_2PO_4^-} \right) \\ 7.4 - 6.86 &= \log \left(\frac{HPO_4^{2-}}{H_2PO_4^-} \right) \\ .54 &= \log \left(\frac{HPO_4^{2-}}{H_2PO_4^-} \right) \\ 10^{.54} &= \left(\frac{HPO_4^{2-}}{H_2PO_4^-} \right) \\ HPO_4^{2-}/H_2PO_4^- &= 3.467 \end{aligned}$$

$$3 \text{ mg/dL} = [HPO_4^{2-}] + [H_2PO_4^-] \text{ (total concentration of both forms)}$$

$$[HPO_4^{2-}] = 3 \text{ mg/dL} - [H_2PO_4^-]$$

Plugging above equation into ratio equation:

$$3.467 = \frac{HPO_4^{2-}}{H_2PO_4^-} = \frac{(3 \text{ mg/dL} - [H_2PO_4^-])}{[H_2PO_4^-]}$$

$$[H_2PO_4^-] 3.467 = (3 \text{ mg/dL} - [H_2PO_4^-])$$

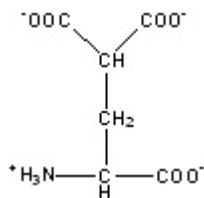
$$[H_2PO_4^-] + 3.467[H_2PO_4^-] = 3 \text{ mg/dL}$$

$$4.467 [H_2PO_4^-] = 3 \text{ mg/dL}$$

$$[H_2PO_4^-] = 3 \text{ mg/dL} / 4.467 = .671 \text{ mg/dL}$$

$$[HPO_4^{2-}] = 3 - .671 = 2.329 \text{ mg/dL}$$

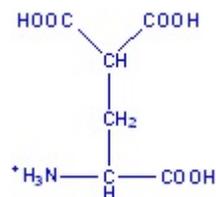
9. (10 points) One of the non-standard amino acid, γ -carboxyglutamic acid has the following structure at pH 7



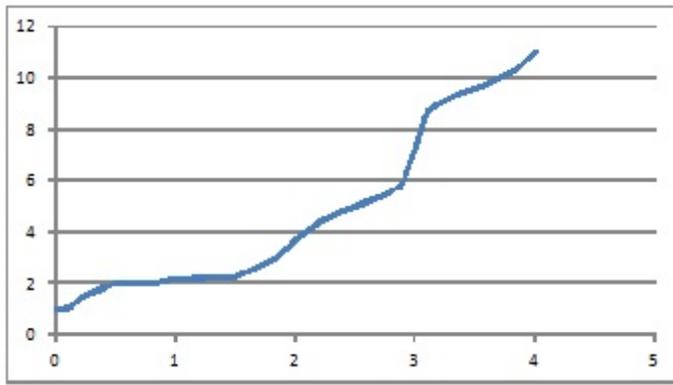
If the main chain has pK_a 's of 2.3 and 9.6, and the side chain has pK_a 's of 2 and 5,

A. What is the structure of this amino acid at pH 1?

At pH 1 we have high $[H^+]$ so it will be fully protonated



B. Draw a titration curve for this amino acid



C. Predict the pI of this amino acid

From A we know is +1 initial

So at first equivalence point it will be zero

First equivalence point is $(2+2.3)/2 = 2.15$

10. (10 points) Histones are proteins found in eukariotic cell nuclei, tightly bound to DNA which has many negatively charged phosphate groups. The pI of histones is very high, about 10.8, What amino acid residues must be present in relatively large numbers in histones? In what way do these residues contribute to the strong binding of histones to DNA?

If the histones have a high pI, they must be composed of mostly + charged residues, so this would be his, arg, and lys. Having a high pI would mean that the protein would have a + net charge at pH 7, and this would be what would bind the negatively charged DNA

11. (10 points) When discussing protein secondary structure everybody usually focuses on helices and sheets. Just to be different, tell me about turns. What are they, how many types of turns are there, and what can you tell me about the Amino acids that are usually found in turns.

In globular proteins about 1/3 of the residues are involved in turns or loops where the protein structure reverses course at the protein's surface. The most common structure observed here is the β -turn, where the protein structure does a 180° turn in 4 residues, and the first residue of the turn is hydrogen bonded to the 4th residue. In lecture I said that there are 6 types of β -turns, and the book shows pictures of two of these, the type I and type II turns. The residues observed in turns are generally small and polar. Glycine is often seen because it is very flexible. Proline is also often seen in turns because it can adopt a cis peptide bond.

In class I also mentioned Ω loops, these structures are larger than 4 residues and have a more random structure so it is hard to describe them in any consistent form.

12. (10 points) There was a key experiment that proved that proteins can fold up all by themselves, and they don't need to have any of the cellular machinery to help them fold. Tell me about that experiment.

This now classic experiment was performed by Anfinsen in the 1950's. In this experiment a protein, Ribonuclease A was exposed to both urea and mercaptoethanol to denature the protein by completely destroying the protein's three dimensional structure. Mercaptoethanol removed stabilizing disulfide bonds, and urea interfered with hydrogen bonds to remove all secondary structure. In this state the enzyme had absolutely no enzymatic activity.

The protein was then renatured by simple dialysis to remove the urea and mercaptoethanol. After dialysis the protein reformed its original structure so completely that all proper disulfides were formed and then enzyme recovered full activity. This experiment proved that the structure of the enzyme is coded into its primary sequence, and that no cellular machinery was required for folding.