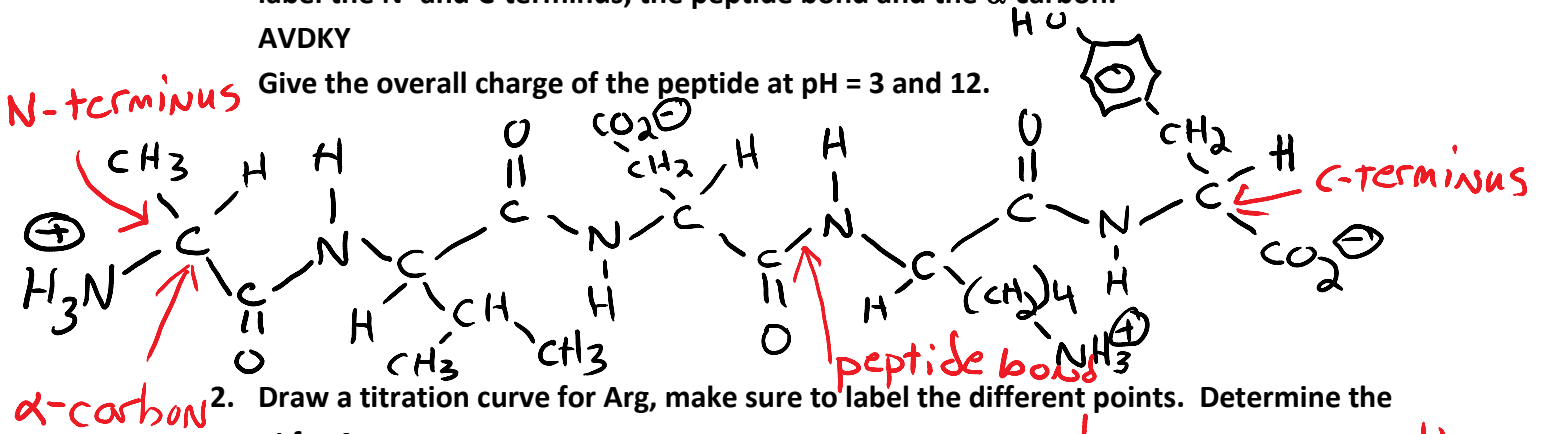


Workshop 1 – Biochemistry (Chem 160)

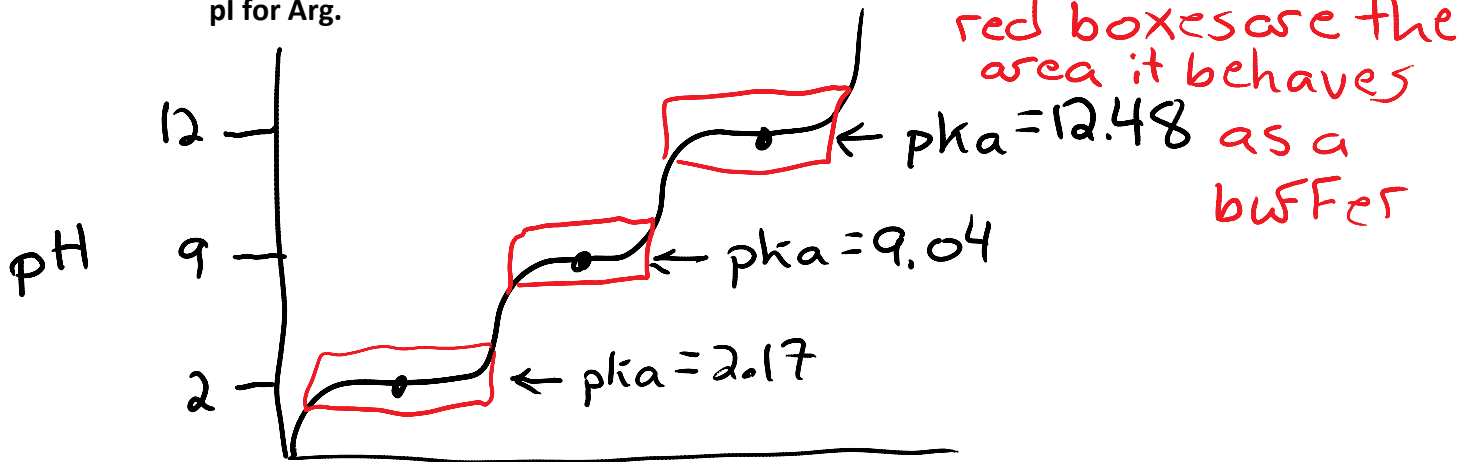
1. Draw the following peptide at pH = 7 and make sure to include the overall charge, label the N- and C-terminus, the peptide bond and the α -carbon.

AVDKY

Give the overall charge of the peptide at pH = 3 and 12.



2. Draw a titration curve for Arg, make sure to label the different points. Determine the pI for Arg.



3. Nonpolar solute + water = solution

a. What is the ΔS of the universe, system and surroundings?

The S of the universe would decrease this is why it is not spontaneous, the S of the system would increase but to a lesser extent to which the S of the surrounding would decrease

$$S_{\text{universe}} = S_{\text{system}} + S_{\text{surroundings}}$$

4. What is the hydrophobic effect and explain why it is thermodynamically favorable.

The hydrophobic effect is when hydrophobic molecules tend to clump together burying them and placing hydrophilic molecules on the outside. The reason this is thermodynamically favorable is because it frees caged water molecules when burying clumping the hydrophobic molecules together.

5. Urea dissolves very readily in water, but the solution becomes very cold as the urea dissolves. How is this possible?

Urea dissolves in water because when dissolving there is a net increase in entropy of the universe. The heat exchange, getting colder only reflects the enthalpy (ΔH) component of the total energy change. The entropy change is high enough to offset the enthalpy component and to add up to an overall $-\Delta G$

6. A mutation that changes an alanine residue in the interior of a protein to valine is found to lead to a loss of activity. However, activity is regained when a second mutation at a different position changes an isoleucine residue to glycine. How might this second mutation lead to restoration of activity? (4 points)

A mutation to alanine to a valine could cause loss of function because valine is a much larger hydrophobic R group than Alanine which may have caused steric hindrance causing the protein to misfold. When another residue was mutated from Isoleucine to glycine it restored function by allowing room for the valine restoring the proper fold of the protein.

7. Determine the sequence of the peptide given the following pieces of information (the following are just a list of the amino acids present after each digestion not the sequence).
- a) amino acid composition: (A, F, G, K, R, S, Y)
 - b) N-terminal analysis: A
 - c) Carboxypeptidase digestion: G
 - d) trypsin digestion: (A, R, Y) (K, S) (F, G)
 - e) chymotrypsin digestion: (A, Y) (G) (F, K, R, S)

AYRSKFG