03-231 Biochemistry SI
Thursday, September 15, 2005

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Study Tip – Take advantage of the practice problems on the course website. If you're still shaky with titration (hopefully you won't after this SI session), make sure you give them a try! ☺

Review: Draw the structures of glycine (Gly), valine (Val), phenylalanine (Phe), aspartic acid (Asp), glutamic acid(Glu). Also list the pKa, if the amino acid has one.

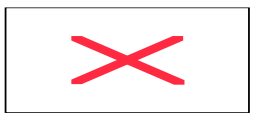
Please use the back of this page ☺

New Amino acids: Asparagine (Asn), glutamine (Gln), Tyrosine (Tyr) pKa = 10, Alanine (Ala), Lysine (Lys) pKa = 10.5. Try drawing a tripeptide: Asp-Tyr-Ala; what's the net charge? Draw another animo acid you know that can hydrogen bond with any of the side chains on this tripeptide.

More Review

How do you prepare a buffer solution made from 500 mL of 0.5 M malonate salt solution? (pKa_1 = 2.9, pKa_2 = 6.1)

a) Pick a titrant: (NaOH, HCl, H_2SO_4, KOH)



b) How much of your titrant should be added to obtain a pH of 2.9

c) How much of your titrant should be added to obtain a pH of 7? What the conjugate acid? What's the conjugate base? What is the ratio of $[A^-]/[HA]$?

Protein Sequencing

Cyanogen bromide (CNBr) cleaves peptides after _____ (what kind of residue?)
Trypsin cleaves peptides after _____
Chymotrpsin cleaves peptide after _____

A sample of an unknown peptide was divided into two portions. One portion was treated with trypsin and the other with cyanogen bromide (CNBr). Given the following sequences (N->C terminal) of the resulting fragments, deduce the sequence of the original peptide.

Trypsin treatment:
- Gly-Tyr-Met-Cys-Phe
- Ala-Ile-Glu-Met-Ser-Lys
- Asp-Thr-Trp-Met-Leu-Arg

Cyanogen bromide treatment:
- Cys-Phe
- Ala-Ile-Glu-Met
- Leu-Arg-Gly-Tyr-Met
- Ser-Lys-Asp-Thr-Trp-Met

a) Write your sequence here:

b) What is the net charge of the original peptide at pH 7?

Protein Structure

List three characteristics of the peptide bond that are important for protein structure. Why are they important?

In _-pleated sheet structures

a) neighboring chains lie in a flat plane.
b) neighboring residues are hydrogen bonded.
c) neighboring residues have _ and _ angles of about 90°.
d) neighboring chains are hydrogen bonded.

_-helix with 11 residues completes three turns. The length of this helix is about

a) 10 Å
b) 15 Å
c) 20 Å
d) 25 Å