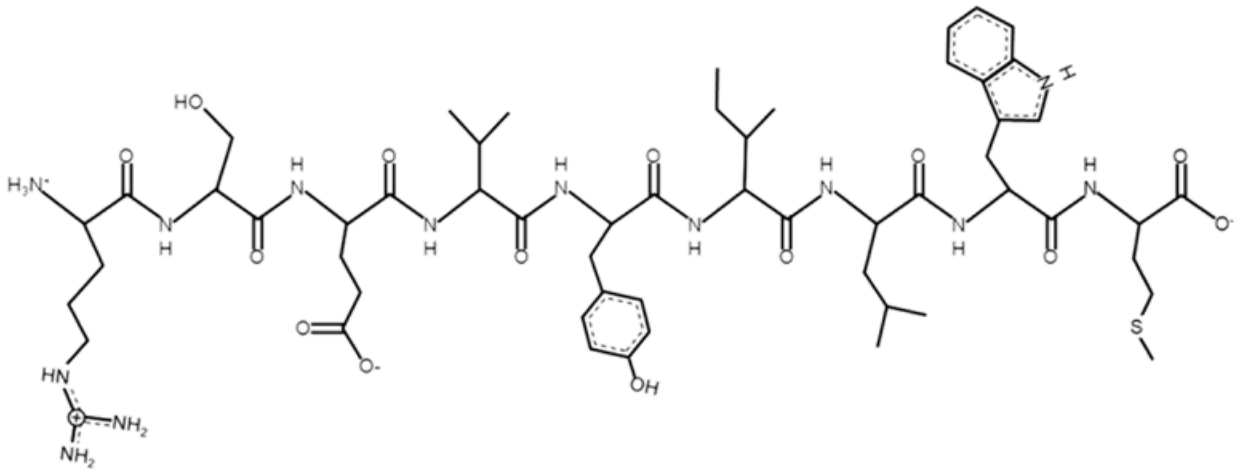
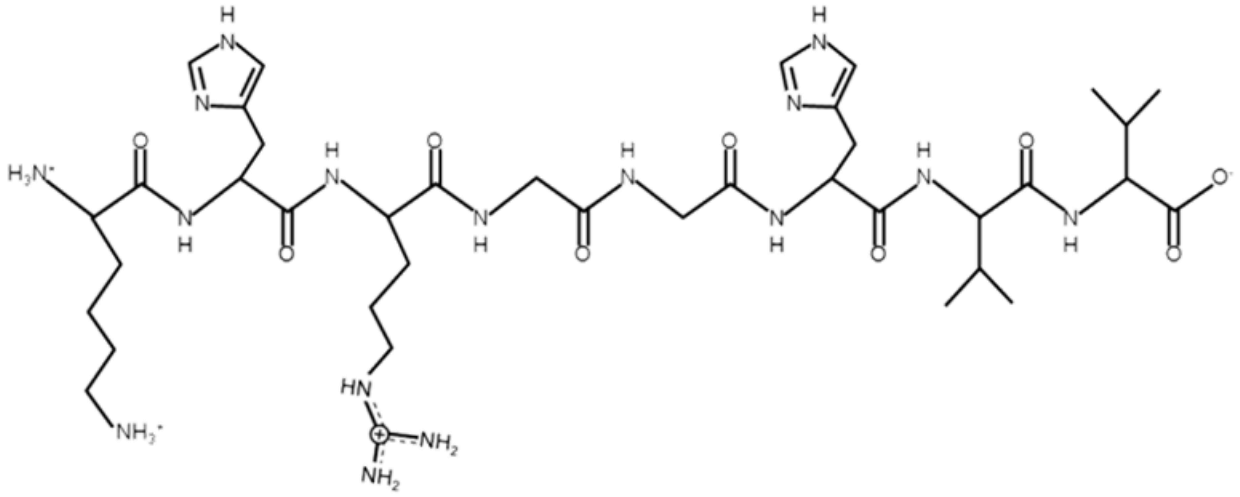
27. What is the sequence of the following peptide?



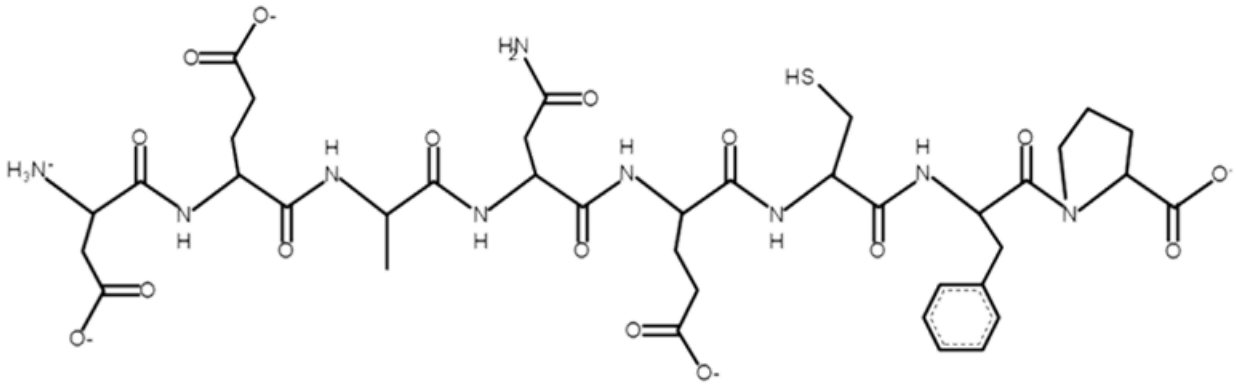
A) LSDVYILFC B) RTEVYLIWC C) RSEVYILWM D) LSEVYILWM E) RSDVYILWM

28. Based on what we have learned in class on the properties of the N and C termini and the side chains, what is the nearest estimate to the pI of the following peptide?



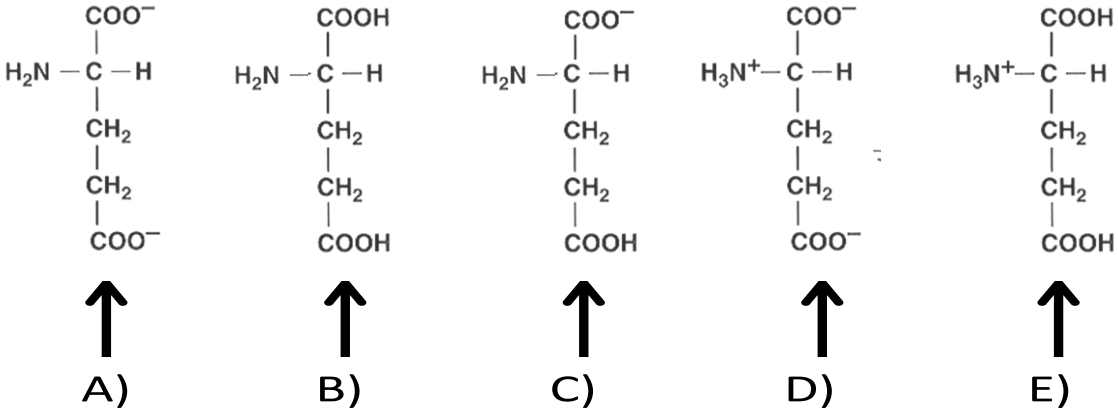
A) 4.0 B) 11.5 C) 7.2 D) 2.5 E) 8.0

29. Based on what we have learned in class on the properties of the N and C termini and the properties of the side chains, what is the nearest estimate to the pI of the following peptide?



A) 12.5 B) 9.5 C) 8.3 D) 6.0 E) 2.7

30. Which of the following structures correspond to glutamic acid at pH 7.0?



31. Which of the following statements is true?

A) Phosphorylation on tyrosine is irreversible.

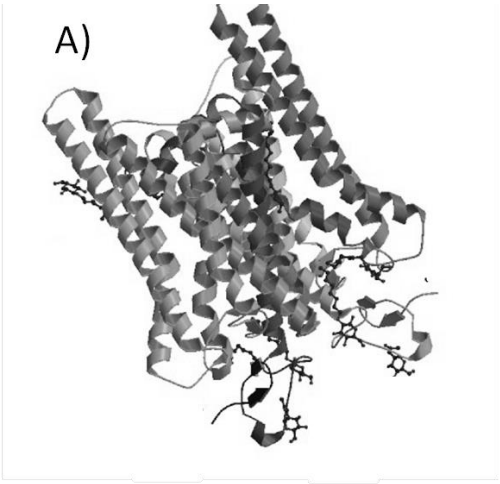
B) Arginine can have asymmetric trimethylation.

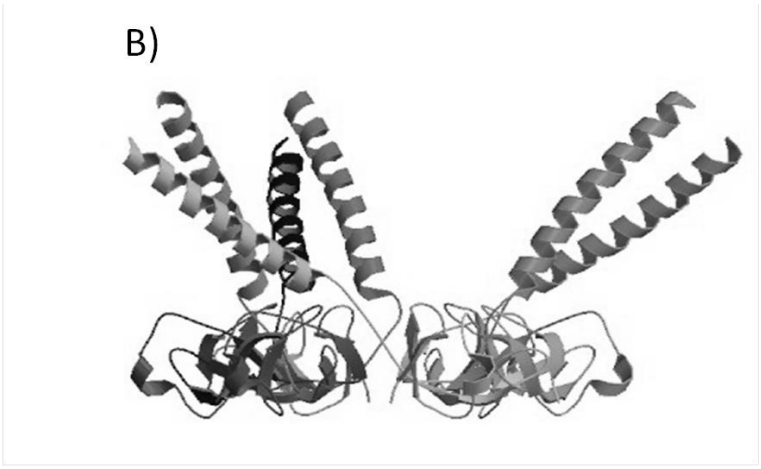
C) Monomethylated lysine is protonated on the ε-amino group at physiological pH.

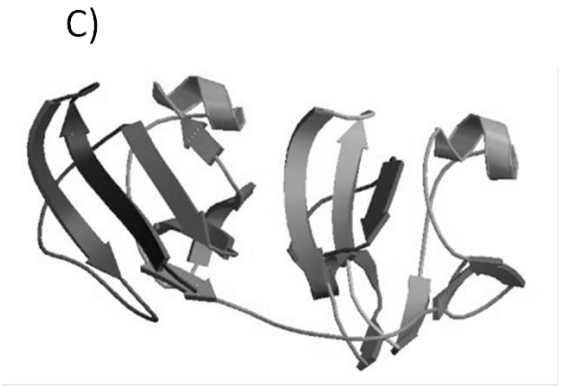
D) In protein structures, phenylalanine prefers to be exposed to water.

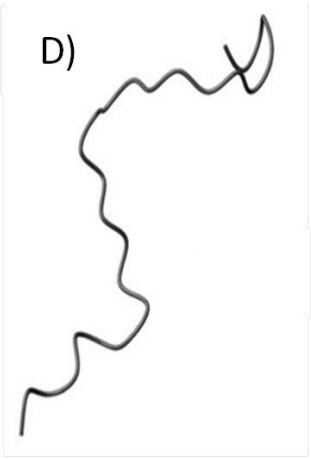
E) Glycine cannot form a Zwitterion.

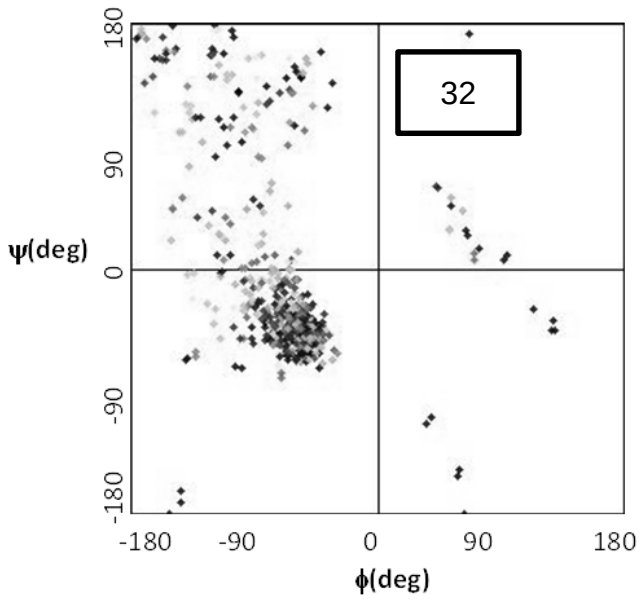
32-33. Which of the following proteins best correspond to the following Ramachandran diagrams?

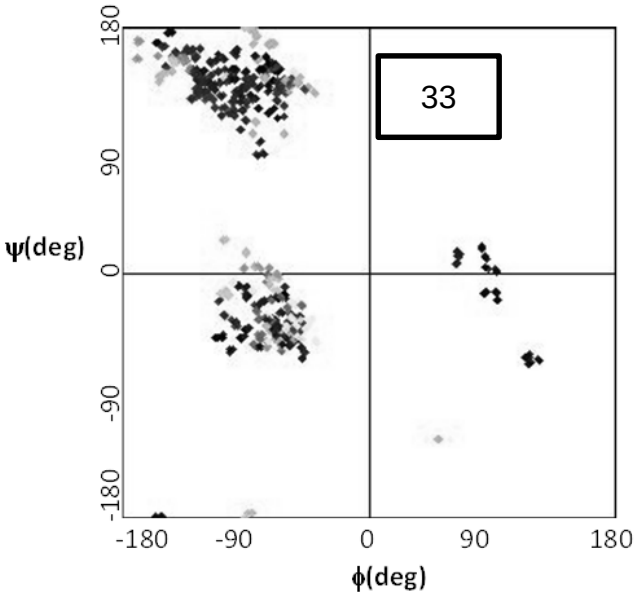




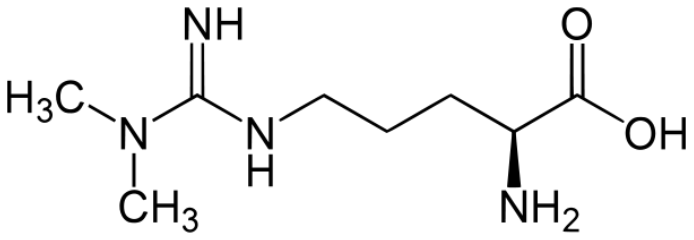








34. Which amino acid has the following structure?



A) dimethyl lysine
B) monomethyl lysine
C) monomethyl arginine
D) symmetrical dimethyl arginine
E) asymmetrical dimethyl arginine

35. The normal form of the protein illustrated below is composed of two β-strands and one β -turn. In this protein a proline is normally present at the entry of the β-turn followed by two glycines. However, in a mutated form of the protein they are replaced by valine, phenylalanine and isoleucine. What is the most likely impact of these mutations on the structure of the protein?

A) No changes the turn will remain.
B) The β-turn will disappear and a single β-strand will be formed.
C) The β-turn will disappear from the protein structure but the antiparallel β-strand will still interact.
D) The β-turn will be inverted.
E) The β-turn will disappear from the protein structure but the parallel b-strand will still interact.

36. Which of the following statements is false?

A) β-sheets consist of 3 or more polypeptide strands.
B) β-sheets repeat distance between residues is 7 Å
C) The polypeptide chains in β-sheets are on average 6 residue long
D) Parallel β-sheets are less stable than antiparallel β-sheets
E) β-sheets are common in protein structure.

37. Which of the following statements is false?

A) Increasing the temperature can denature proteins.
B) Ammonium sulfate can stabilize proteins.
C) Protein can denature at low pH.
D) Lithium chloride can denature proteins.
E) Urea denatures proteins by increasing the penalty for exposing nonpolar groups to solvent relative to pure water.

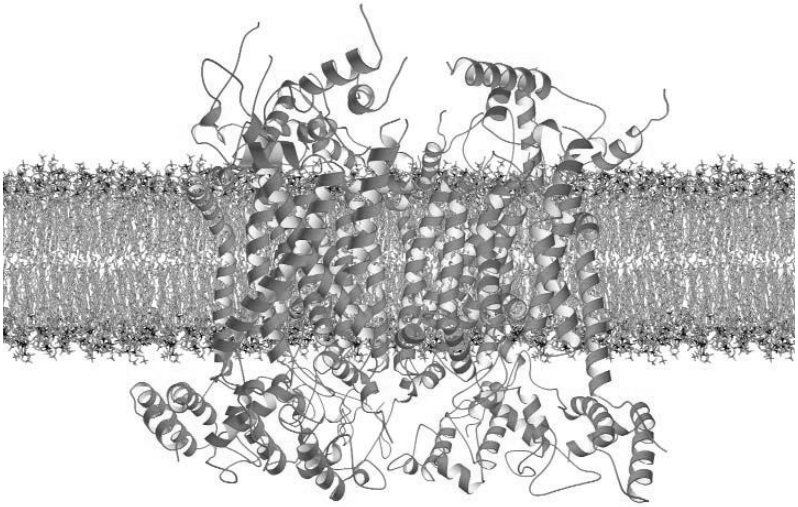
38. Which of the following statements is false?

A) The entropy favors the unfolded form of a protein.
B) When the polypeptide backbone is buried in a hydrophobic environment within a protein structure it has a stabilizing effect on the protein structure.
C) When hydrophobic side chains are buried in a hydrophobic environment within a protein structure it has a stabilizing effect on the protein structure.
D) The formation of hydrogen bonds within a protein structure is a stabilizing force.
E) Formation of intramolecular cysteine bridges stabilizes protein structures.

39. Which of the following statements is false about domains?

A) Domains have different sequence length from 25 to 500 amino acids.
B) Domains are usually structured subregions of a protein.
C) Domains are discrete structural units.
D) Domains are exclusively defined by sequence.
E) An independent unit of function.

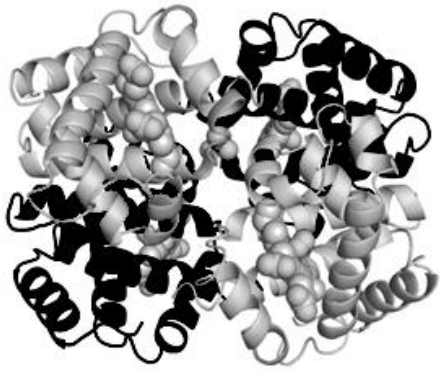
40. The following protein is a transmembrane protein receptor that crosses a bilayer of lipid molecules. Which of the following statements is false.



A) Upon binding of the ligand to the receptor, the intracellular portion of the receptor will be involved in signal transduction.
B) Amino acids with hydrophobic side chains will be in the transmembrane section of the protein and interact with the hydrophobic tails of lipids.
C) The extracellular portion of the protein is responsible for binding the ligand.
D) Transmembrane protein receptors are generally non-specific and will bind any ligands available leading to signal transduction.
E) In many instances, upon binding of the ligand to the receptor, kinases will phosphorylate specific serine threonine, or tyrosine present on the intracellular portion of the receptor.

41. Which of the following statements is true about hemoglobin?

A) It is a homotetramer composed of four identical units.
B) It is a heterotetramer composed of four different units.
C) It is a heterotetramer composed of two alpha and two beta units.
D) It is a homotetramer composed of two alpha and two beta units.
E) it does not have a quaternary structure.



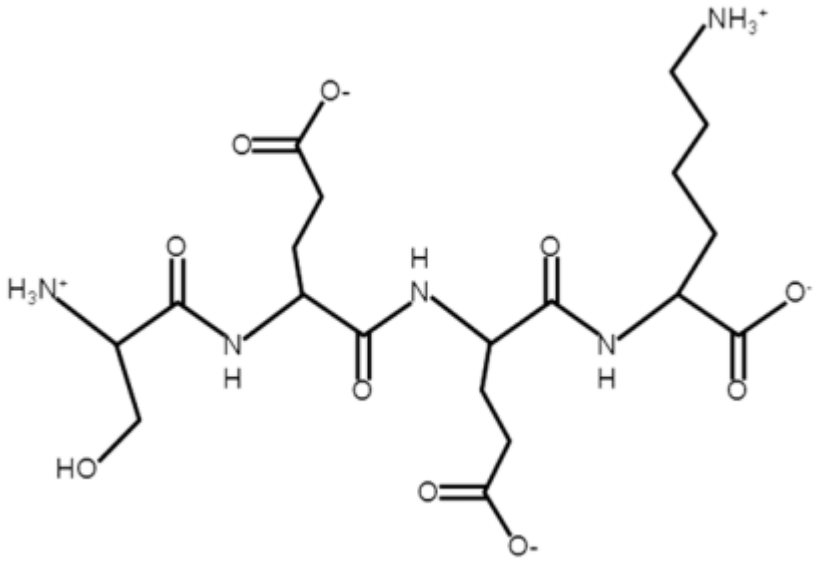
42. From chapter 6: silkworm fibroin is primarily composed of?

A) proline and valine.
B) glycine and isoleucine.
C) leucine and tyrosine.
D) glycine and alanine.
E) valine and leucine.

Answer three of these four questions directly on the exam

1) Please i) draw the titration curve (pH vs equivalent of NaOH added) for the following peptide, ii) draw all possible charge states of the peptide at corresponding pHs, iii) indicate when the pH is equal to the pK's and iv) calculate the pI.

Amino acids	Side chain pKa
Lysine	10.5
Arginine	12.5
Aspartic acid	3.9
Glutamic acid	4.1



2) **The STAT5b protein is important in signaling in breast cancer and leads to the activations of the transcription of many genes. Describe, using all the information below, a model of gene expression activation and inactivation in response to growth factors (GF) binding to the endothelial growth factor receptor (EGFR). Explain the roles of the different proteins, domains and phosphorylation sites in this process.**

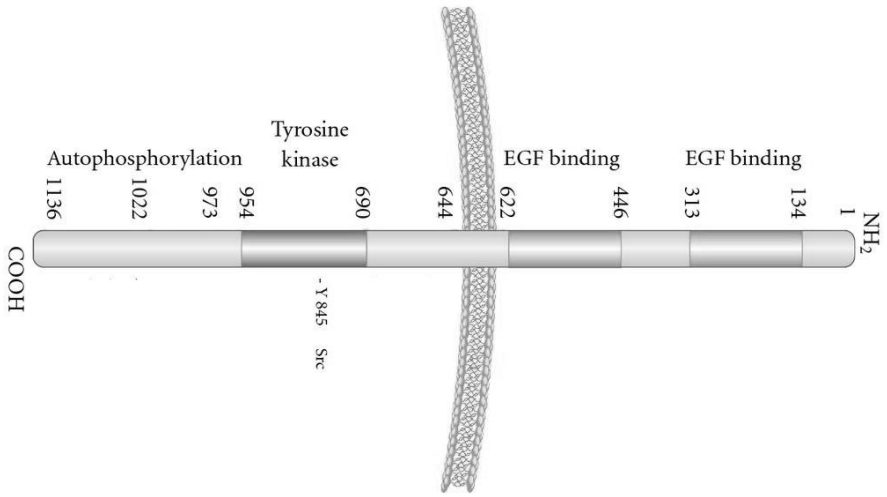
c-SRC:

Y Kinase: is a domain involved in the phosphorylation of tyrosine. It can phosphorylate Y845 of EGFR upon GF stimulation of EGFR. Once in complex with EGFR it can recruit and phosphorylate STAT5b.

STAT5b: The Stat proteins(including STAT5b) have the generic structure in which a DNA BD domain is present for binding to DNA, an SH2 domain and a TA domain for protein-protein interactions.

The activation of STAT5b requires it phosphorylation at Y699 by c-SRC.
STAT5b can also be phosphorylated at Y725, Y740,and Y743 by EGFR. However, in the presence of c-Src kinase activity, Y740 and Y743 phosphorylation will be reduced or not detected. The phosphorylation of STAT5b at Y699 and Y725 lead to its ability to activate gene expression. In contrast the phosphorylation of STAT5b at Y740 and Y743 eliminate its ability to activate gene expression.
STAT5b must forms a homodimers in the nucleus in order to be able to activate DNA.
Phosphorylated STAT5b can migrate from the cytosol to the nucleus.
STAT5b must be phosphorylated by the EGFR and c-SRC for the homodimer to form.

EGFR: EGFR is present on the cell surface and form a homodimers upon binding of the GF (such as EGF). When c-Src is present it mediates the phosphorylation of tyrosine 845 (Y845) of the EGFR upon binding of the GF to the EGFR. This phosphorylation site is not required for EGFR kinase activity. Phosphorylation of Y845 on the EGFR is required for GF stimulation to lead to STAT5b activation of gene expression, whereas in the absence of Y845 phosphorylation on the EGFR, STAT5b is not able to activate gene expression.


Autophosphorylation
Tyrosine kinase
EGF binding
EGF binding
1136
1022
973
954
690
644
622
446
313
134
1
NH2
COOH
- Y 845 Src