beta-glucose   beta-glucose   beta-galactose

1) Consider the diagrams of the chair form of beta-glucose and the Haworth projection of beta-glucose and beta galactose
a) In alpha-galactose, the hydroxyl on the anomeric carbon is
(equatorial) (axial) (both) (neither). No explanation required

b) In glucose (beta 1,4) galactose, the glycosidic bond is (no explanation required) :
(axial-axial) (axial-equatorial) (equatorial-axial) (equatorial-equatorial) (none of these)

c) Which of the following disaccharides contains an axial-axial glycosidic bond? Circle as many as apply.
No explanation required.
a) glucose (alpha1,4)-glucose
b) galactose (alpha 1,4)-glucose
c) glucose (alpha1,4)-galactose
d) galactose (alpha1,4)-galactose
e) none of these

2) Which of the following types of bonds is likely to contribute to holding individual polymers of cellulose together in a strand of cotton ? Circle as many as apply. No explanation necessary.
a) covalent   b) ionic   c) hydrogen   d) Van der Waals   e) hydrophobic forces

3) Which of the following molecules has more hydrogen atoms?
Circle one answer in each case and explain in one sentence.

a) (2 separate glucose molecules) (lactose, a disaccharide made up of glucose and galactose) (both the same)

b) (a saturated fatty acid) (a trans-unsaturated fatty acid with the same number of carbons) (both the same)

c) at pH7: (glutamate [=glutamic acid)]) (asparagine) (both the same)

d) (a fat containing saturated fatty acids 16 carbons in length)
    (a phospholipid containing saturated fatty acids 16 carbons in length) (both the same)

e) (a single molecule of glycogen with a 100 glucose residues)
(a single molecule of cellulose with 100 glucose residues) (both the same)

4) The protein GDNF exists as a dimer in solution, with the 15000 molecular weight monomers linked by an interchain disulfide bond through the cys101 residues. Suppose a variant of GDNF exists (variant 1) in which the cys 101 has been replaced by a serine residue. Ultracentrifugation experiments under mild conditions demonstrated that the molecular weight of the variant GDNF is 30,000.

a) Fill in the table below with the expected molecular weights as measured by the indicated method (PAGE= polyacrylamide gel electrophoresis) :

	gel filtration	gel filtration	SDS PAGE	SDS PAGE
	Normal GDNF	Variant 1 GDNF	Normal GDNF	Variant 1 GDNF
Without mercaptoethanol				
With mercaptoethanol	*			

You need explain only the answer in the box with the asterisk.

b) Suppose there is a second variant of GDNF (variant 2) which differs form normal in that it lacks the 8 amino acid residues normally at the amino terminus (and still has the cys that forms the disulfide in the normal protein). The molecular weight of the variant 2 is 28000. Suppose you carry out an Anfinsen type experiment on a mixture of equal parts of the the normal and variant 2 GDNF proteins: reduce all disulfides, subject the proteins to urea denaturation and then renaturation and then re-oxidize the disulfides.
i.)How many bands would you expect after SDS-PAGE WITH mercaptoethanol of this mixture?
 (0) (1) (2) (3) (4) (5) (>5). For an explanation you need only list the molecular weight of any expected band(s).

How many bands would you expect after SDS-PAGE WITHOUT mercaptoethanol. ?
 (0) (1) (2) (3) (4) (5) (>5) For an explanation you need only list the molecular weight of any expected band(s).

c) Suppose GDNF normally contains 2 atoms of zinc (as the metal ion). After treatment with SDS, the protein would be expected to contain [circle all that apply and explain each possibility]:
(zinc) (peptide bonds) (beta sheet) (a net positive charge) (a net negative charge) (none of these)

5) The enzyme trypsin hydrolyzes peptides at the carboxyl side of arginine and lysine residues. However, the amino acid residue that follows the arginine or lysine can influence either the K_m or turnover number of the reaction. Suppose the curves below were generated by comparing two substrates for trypsin:
Substrate A = val-ser-arg-pro
Substrate B = ser-val-arg-phe
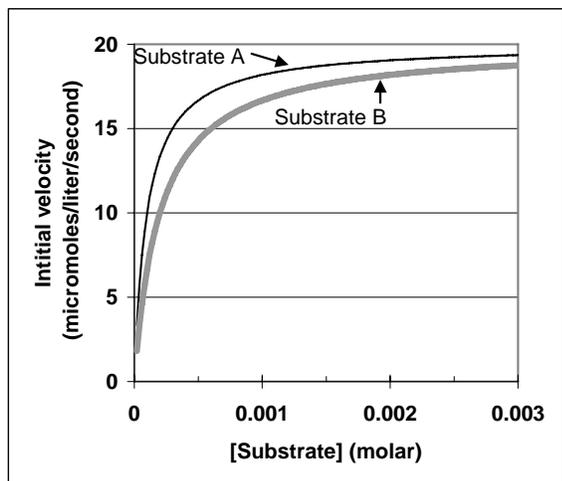
Equations that may or may not help:

$$V_o = \frac{k3E_o[S]}{K_m + [S]} \quad \text{(Michaelis-Menten equation)}$$

$$V_{max} = k3E_o \qquad Km = (k2+k3)/k1$$

No explanation needed for a, b, and c.

a) The K_m of the enzyme is higher for:
(A) (B) (same) (can't tell from this information)

b) The enzyme binds:
(more tightly to A) (more tightly to B) (same to both)
(can't tell from this information)

c) From the graph, the approximate Km for Substrate A is:
(0) (0.0001) (0.0005) (0.001) (0.002) (>0.002)

. d) The enzyme binds more tightly with the product:
(val-ser-arg) (ser-val-arg) (same) (can't tell from this information)

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e) Suppose a similar experiment using the same enzyme and Substrate A was also carried out by another laboratory, but the Vmax was only one-tenth of that found in the experiment shown above. This difference could be explained by the other laboratory's use of (circle as many as apply):
(a lower amount of substrate) (a lower amount of time) (a lower amount of enzyme)
(a lower turnover number) (none of these)

f) Suppose the enzyme concentration in the experiment graphed above was 0.1 micromoles/liter. The best guess for the turnover number of the enzyme for Substrate A is (<10)(10)(20)(100)(200) 500)(>500) per sec..

6) An oligopeptide (a nonapeptide) is subjected to fingerprint analysis using the usual separation methods. The enzyme used was trypsin, which cleaves after arginine and lysine residues. The hydrolysate was spotted onto the center of one edge of a square blotting paper (at the X), the electrophoretic step was carried out at pH7, and the second separation direction was from bottom to top. Suppose the pattern of spots seen after staining for peptides and amino acids looked like this:
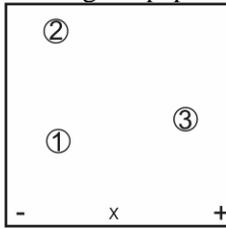
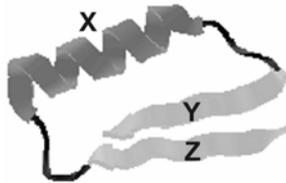a) Match the peptides below to the lettered spots in the diagram.
Spot 1 _____   Spot 2 _____   Spot 3 _____

A) ser-ser-arg
B) ser-ala-glu
C) val-val-lys

b) The N-terminal (amino terminal) tripeptide in the original nonapeptide must be:
(A) (B) (C) (A or B) (A or C) (B or C) (A or B or C)   (cannot tell from the information given)

7) Consider the protein domain pictured below.

a) The bonds responsible for the association of strands Y and Z in this 3-dimensional structure include [circle as many as apply]:
 (ionic) (hydrogen) (hydrophobic forces) (backbone atoms) (side chains)

b) The bonds responsible for the association of strands X and Y in this 3-dimensional structure include [circle as many as apply]: (ionic) (hydrogen) (hydrophobic forces) (backbone atoms) (side chains)