21. There are two significant amplification stages. The binding of one epinephrine to a receptor stimulates the formation of many molecules of $G_{\alpha s}$. In turn each molecule of $G_{\alpha s}$ (when bound to adenylate cyclase) stimulates the formation of many molecules of cAMP.

22. The mutatied α-subunit would be defective for signaling because it would be turned "on" at all times, even in the absence of an activated receptor. The inability to turn "off" the signaling pathway would be a serious flaw.

23. Epinephrine initiates a pathway that raises the level of cAMP within the muscle cell. The high level of cAMP ultimately will mobilize glucose (make more glucose available). Inhibitors of cAMP phosphodiesterase also will raise the level of cAMP within the cell. Therefore the phosphodiesterase inhibitors will act similarly to epinephrine to increase the mobilization of glucose.

24. A. Higher ph = lower [H] = higher oxygen affinity (Stabilize R)
    B. Stabilize T
    C. Stabilize T
    D. Stabilize R

25. If both patients have a Factor VIII deficiency, a mixture of the two bloods will not clot. However, if the second patient's bleeding disorder is due to the deficiency of another factor, a mixture of the two bloods should clot. This type of assay is called a complementation test.

26. The Ala-64 subtilisin lacks the critical histidine in the catalytic triad of the active site and therefore cleaves most substrates much more slowly than does normal subtilisin. However, the histidine in substrate B can act as a general base thereby the substrate itself partially compensates for the missing histidine on the mutant enzyme.

27. A reasonable prediction is that the substrate specificity of the mutant protease would resemble that of trypsin. The mutant enzyme would be predicted to hydrolyze peptide bonds that follow either lysine or arginine in the sequence (i.e., peptide bonds whose carbonyl groups are from either lysine or arginine).

28. For (a) and (b) proper graphing of the data given will provide the correct answers:
    A. In the absence of inhibitor, Vmax is 47.6 umol/min and Km is 1.1×10^{-5} M. In the presence of inhibitor, Vmax is the same and the apparent Km is 3.1×10^{-5}.
    B. Since Vmax is not altered by the inhibitor, this is competitive inhibition.
    C. Since this is competitive inhibition, Vmax doesnt change. If you mix equations, you can say that new Km = Km (1+[I]/Ki). (From Lecture).

Therefore using the data in (a) and (b), $K_i=1.1 \times 10^{-3}$ M.

D. The [S]/(Km+[S]) term in the Michaelis-Menten equation tells us the fraction of enzyme molecules bound to substrate. Thus f_{ES} = 0.243. Since $K_i=[E][I]/[EI]=1.82$. However the sum of [EI]=[E] is only 0.757 since the remaining is bound to substrate. Therefore, $1.82=f_{ES}/(0.757-f_{EI})$. $f_{EI}=0.488$.

E. Using the same eq as in (d), then f_{ES} = 0.73. With an inhibitor, $f_{ES}=0.49$. This ratio 0.73/0.49 and 33.8/22.6 are equal.

29. By subsitituting [S] = 0.1 Km into the MM eq,
v = Vmax * ([S] / [S] + Km), we can show that:
v = 1/11 Vmax
So when v = 1.0 umol/min, Vmax = 11 umol/min

33. The amino acid sequence of insulin does not determine its 3D structure. By catalyzing disulfide-sulfhydryl exchange, this enzyme speeds up the activation of scrambled ribonuclease because the native form is the most thermodynamically stable. In contrast, the structure of active insulin is not the most thermodynamically stable form. The 3D structure of insulin is determined by the folding of the preproinsulin which is later processed to mature insulin.

34. Appropriate hydrogen-binding sites on the protease might induce formation of an intermolecular β pleated sheet with a portion of the target protein. This process would effectively fully extend α helices and other folded portions of the target molecule.

35. Assume that HCl in the solution is completely ionized. The concentration of H+ = Cl-

$pH = -\log [H] = 2.1$

$[H] = 10^{-2.1}$

$= 10^{0.9} \times 10^{-3}$

$= 7.94 \times 10^{-3}$ M

Thus, $[H] = [Cl] = [HCl] = 7.94 \times 10^{-3}$ M

36. Even though individual atoms can be delineated at a resolution of 1.5 Å, the structure of individual side chains that are similar in shape and size cannot be clearly established. The primary structure of the polypeptide chain must be available. The path of the polypeptide backbone can be traced and the positions of the side chains established. Those that are similar in size and shape can be distinguished by using the primary structure as a guide as they are fitted by eye to the electron density map.