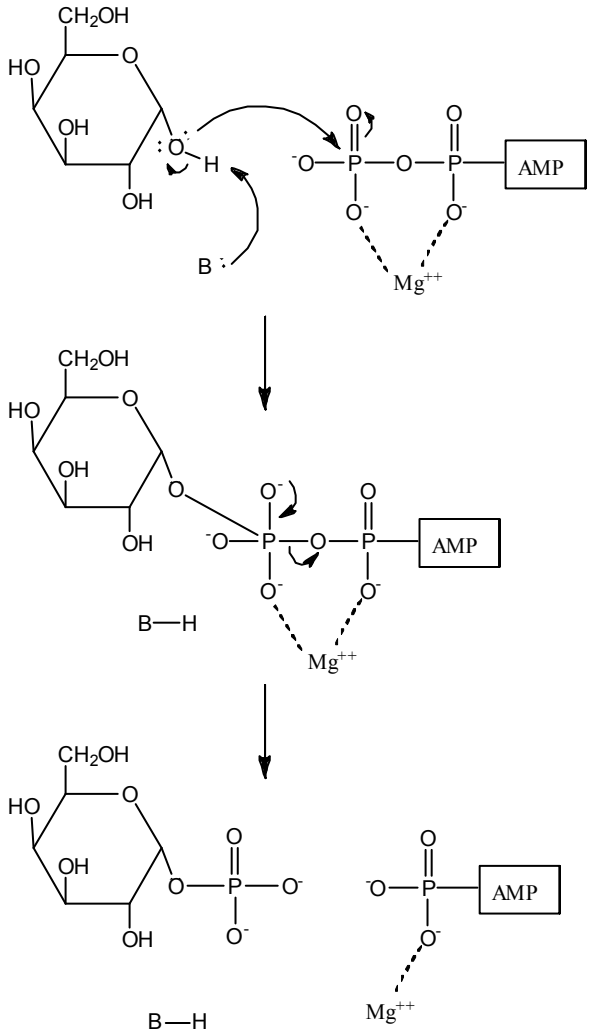
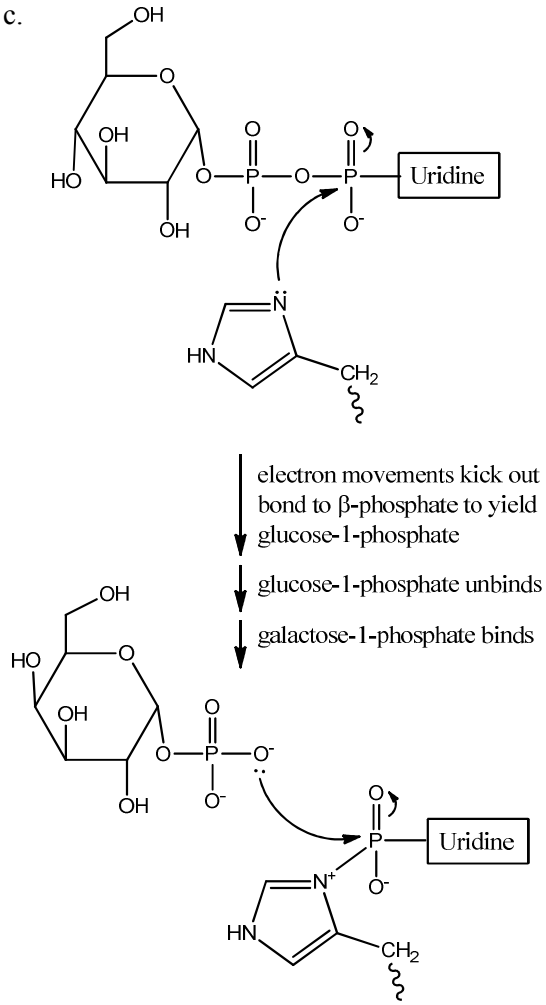
1. No. (All are formed within each subunit.)
2. 22 (10 in α subunit, 12 in β)
3. d (Asn is necessary since there is an N-linked glycosylation)
4. b
5. a. Heating would separate and denature the subunits because it breaks the weak interactions that stabilize 2°, 3°, and 4° structure.
   b. D
6. a. C
   b. B
7. a. B
   b. The protein hormone, in its normal conformation, with its carbohydrates attached
8. a
9. The lack of sequence similarity suggests convergent evolution (in which 2 sequences start out different). However, the structures are so similar that it's possible the subunits started as the same sequence and diverged to the point where they no longer show any sequence similarity.
10. d
11. True
12. a
13. hydrophobic (van der Waals)
14. a. glucose + ATP $\rightarrow$ glucose-6-phosphate + ADP + H^+
    b. PIPES. The reaction produces H^+, so a buffer that has more molecules in the deprotonated state (pK_a < pH) will be better able to resist the change in pH.
    c. $pH = pK_a + \log [A^-]/[HA]$
    $[A^-]/[HA] = 10^{pH-pKa} = 10^{7.2-6.8} = 10^{0.4} = 2.51$
    $[A^-]+[HA] = 100$ mM; $[HA] = 100mM - [A^-]$
    $[A^-]/[HA] = [A^-]/(100mM - [A^-]) = 2.51$
    $[A^-] = 251mM - 2.51[A^-]$
    $3.51[A^-] = 251mM$
    $\underline{[A^-] = 71.5\ mM}$
    $\underline{[HA]} = 100\ mM - 71.5\ mM = \underline{28.5\ mM}$
    d. Mg^{2+}
    e. A, D, G, H
    f. $\Delta G'^{\circ} = -RT\ln K'_{eq} = -RT\ln\left(\frac{[G6P][ADP]}{[Glc][ATP]}\right)$
    [ADP]=[G6P] and [ATP]=[Glc], so $K'_{eq} = ([ADP]/[ATP])^2 = e^{-\Delta G'^{\circ}/RT} = e^{16.7/(0.00831)(298)} = 848.7$
    $[ADP]/[ATP] = (848.7)^{0.5} = \underline{29.1}$
    g. [ADP]+[ATP] = 10 mM, so
    $[ATP] = 10mM - [ADP]$
    $[ADP]/[ATP] = [ADP]/(10mM - [ADP]) = 29.1$
    $[ADP] = 291mM - 29.1[ADP]$
    $30.1[ADP] = 291mM$; $\underline{[ADP] = 9.67\ mM}$
    h. $[ADP] = [H^+]$ produced = 9.67 mM
    so, 9.67 mM deprot. buffer $\rightarrow$ prot.
    $pH = pK_a + \log([A^-]/[HA])$
    $= 6.8 + \log\{(71.5 - 9.67)/(28.5 + 9.67)\}$
    $= 6.8 + 0.2 = \underline{7.0}$
15. a. Production of glycogen in sheep relies on the activity of (non-glucokinase) hexokinase.
    b. double-reciprocal or Lineweaver-Burk
    c. Sheep hexokinase has a lower K_m than rat hexokinase.
    d. Yes. Since the [glucose] in sheep is lower, you would expect the K_m of sheep hexokinase to be lower. (Sheep hexokinase has higher binding affinity for glucose.)
    e. The higher purity sample has less of a non-competitive inhibitor.
    f. The authors cannot be sure that all inhibitors have been removed.
    g. True

16. a. transferase, kinase

b.



c.



d. A
e. isomerase, mutase
f. Phosphoglycerate mutase (PGM)
g. Enzyme 1. This step couples ATP hydrolysis to galactose phosphorylation, so it's likely to be highly spontaneous (like the hexokinase reaction).
h. ATP, NADH
i. galactose, ADP, AMP, P_i, NAD^+
j. D

17. a. Triacylglycerols or triglycerides

    b. 1-myristoyl-2-myristoyl-3-palmitoyl-glycerol

    c. Reactant: ATP, products: ADP + H^+; enzyme 1 is a transferase (class) and kinase (subclass)

    d. Either glyceraldehyde-3-phosphate or dihydroxyacetonephosphate is produced by enzyme 2. Enzyme 2 is an oxidoreductase (class) and dehydrogenase (subclass)

    e. enz 1: -1 ATP
    enz 2: +1 NADH
    GAPDH: +1 NADH
    PGK: +1 ATP
    PK: +1 ATP
    PDH complex: +1 NADH
    isocitrate DH: +1 NADH
    α-KGDH complex: +1 NADH
    sucCoA synthetase: +1 GTP
    succinate DH: +1 $FADH_2$
    malate DH: +1 NADH
    Total: ATP+GTP: 2; NADH: 6; $FADH_2$: 1

    f. 3: oxidoreductase, dehydrogenase; 4: lyase, (hydratase); 5: oxidoreductase, dehydrogenase; 6 transferase, acyltransferase

    g. Because the β-carbon of the fatty acid is oxidized.

    h. 2x myristic acid (14 carbons) → 2 × 7 acetyl-CoA
    1x palmitic acid (16 carbons) → 8 acetyl-CoA
    14 + 8 = <u>22 acetyl-CoA</u>

    i. transport across mb: -3 ATP
    β-oxidation: produces 1 $FADH_2$ and 1 NADH per round
    6 rounds for myristic acid; 7 for palmitic
    2×6 + 7 = 19 rounds, so 19 $FADH_2$ & 19 NADH
    TCA: 3 NADH, 1 $FADH_2$ & 1 GTP per round
    for 22 acetyl-CoA: 66 NADH, 22 $FADH_2$, 22 GTP
    Total: ATP+GTP: 19; NADH: 85; $FADH_2$: 41

    j. 2+19 directly from ATP+GTP = 21
    (6+85 NADH)×2.5 ATP/NADH = 227.5
    (1+41 $FADH_2$))×1.5 ATP/$FADH_2$ = 63
    total ATP equivalents = <u>311.5</u>

    k. 1 glucose yields 32 ATP

$$\frac{311.5\ \text{ATP/lipid}}{750\ \text{Da}} \div \frac{32\ \text{ATP/glucose}}{180\ \text{Da}} = \mathbf{2.3}\boldsymbol{x}$$