Module 2: Study Guide Question Answers
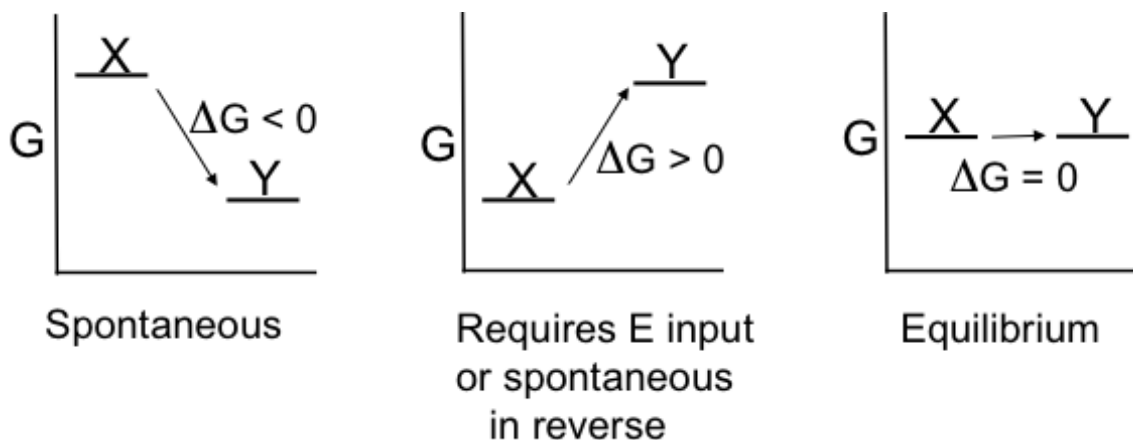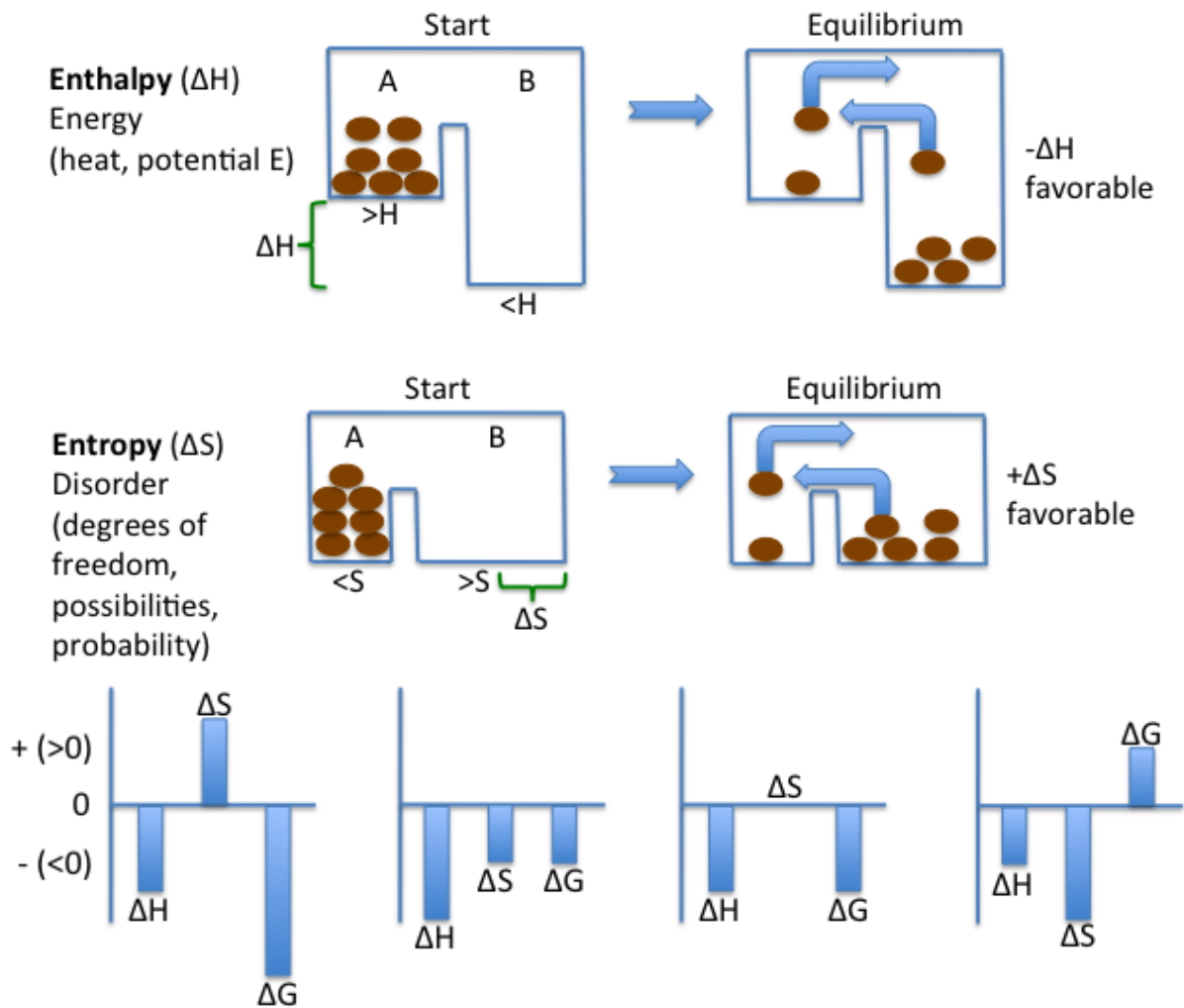
1. (A) [P]/[R] = 2 (>1), so $\Delta G° = -RT\ln>1$ = neg. number and favorable
(B) [P]/[R] = 0.5 (<1), so $\Delta G° = -RT\ln<1$ = pos. number and unfavorable
(C) the intrinsic difference between their relative free energies (Gs), if they are increasing or decreasing as the reactants become the products. If they are increasing the reaction as written is unfavorable and requires coupling to another reaction that has a greater decrease in free energy to proceed as written. If decreasing the reaction is favorable as written. Unfavorable reactions can potentially be driven by a high [P]/[R] concentration ratio.
(D) You must also know the actual concentration of the reactants and products in the cell to determine the ΔG of the reaction in the cell.

2.

Spontaneous   Requires E input   Equilibrium
                     or spontaneous
                     in reverse

3. (A) The second law of thermodynamics states that the universe tends toward randomness or disorder.
(B) A small amount of cells is added to nutrient containing medium in a flask and grown in a calorimeter (box to measure change in heat, temperature) until there is a large amount of cells.
(C) Nutrients (small molecules, less order) are taken up and used to synthesize the cells (larger molecules, whole cells, more order) while releasing heat into their surroundings (creating a large amount of disorder). Thus, the cells create order to produce cell parts and more cells, but offset this increased order with greater disorder in their system (their universe).

4. The hydrolysis of ATP to ADP, Pi and H$^+$ (H_2O is ignored since the concentration stays near 56 M) is favorable
(A) due to the $\Delta G°'$ and $RT\ln K$ being negative values.
(B) $\Delta G°'$, an intrinsic property of this reaction, is quite negative due to the neutral pH inside the cell (so stays 10^{-7} M, pulling the reaction to the right).

Start   Equilibrium

Enthalpy (ΔH)
Energy
(heat, potential E)

A   B

>H

ΔH

<H

-ΔH
favorable

Start   Equilibrium

Entropy (ΔS)
Disorder
(degrees of
freedom,
possibilities,
probability)

A   B

<S   >S
ΔS

+ΔS
favorable

+ (>0)

0

- (<0)

ΔS

ΔH

ΔG

ΔS   ΔG

ΔH

ΔH

ΔS

ΔG

ΔG

ΔH

ΔS

(C) the concentration of ATP, a system property, is kept much higher than the concentration of ADP and Pi in the cell, so RTlnK (K = [ADP][Pi]/[ATP] = < 1, ln < 1 is a negative number. We will get back to this later.

5. (A) The first law of thermodynamics, energy is conserved in the universe, relates to enthalpy or H. The second law of thermodynamics, the universe tends toward randomness or disorder relates to entropy or S.
(B)
(C)
6. (A) $\Delta G° = - RTlnKeq$; Keq is the ratio of product (chamber B) to reactant (chamber A) at equilibrium (when the ratio stops changing). As described above in the jumping bean analogy, this is a function of both enthalpy H, and entropy S. A decrease in H and increase in S lead to more product than reactant at equilibrium, a decrease in G and a favorable reaction. K is the actual ratio of product to reactant in the cell. When the concentration of reactant (chamber A) is greater than the concentration of product (chamber B) then this system property contributes to a decrease in the free energy of the overall reaction.
(B) the [products]/[reactants] or [ADP][Pi]/[ATP] in cells is << 1; at equilibrium it is >>1.

(C)

K or Keq	$\Delta G°$ (ΔG_{rxn} = 0)	ΔG_{rxn} ($\Delta G°$ = 0)
10^3	-4.3 kcal/mole	4.3 kcal/mole
10^1	-1.4 kcal/mole	1.4 kcal/mole
1	0	0
10^{-1}	1.4 kcal/mole	-1.4 kcal/mole
10^{-3}	4.3 kcal/mole	-4.3 kcal/mole

7. (A) Thermodynamically unfavorable reactions have a positive ΔG_{rxn}, and so require energy input.

(B) Cells usually "drive" an unfavorable reaction through coupling with a reaction, like ATP hydrolysis, that is energetically favorable (ΔG_{rxn} negative) enough to off-set or the positive ΔG_{rxn} of that reaction.

(C) Synthesis of glutamine from glutamate and NH_4^+ ($\Delta G°$ = +4 kcal/mole) is driven by coupling the reaction with ATP hydrolysis ($\Delta G°$ = -7.3 kcal/mole) with a net $\Delta G°$ = -3.3 kcal/mole, which is quite favorable. Mechanistically, this is done on an enzyme the transfers the high energy gamma phosphate from ATP to glutamate forming phosphoglutamate. The P-glutamate + NH_4^+ → glutamine + Pi reaction is favorable ($\Delta G°$ is negative).

8. Since the dissolution reaction is spontaneous, the ΔG must be negative. Since the reaction absorbs heat, the ΔH must be positive. Given $\Delta G = \Delta H - T\Delta S$, this is possible if the ΔS is very large and positive, as one would expect for a solid dissolving.

9. Covalent bonds (50-250 kcal/mole, unaffected by water); Ionic bond (80 kcal/mole in a vacuum- 3-20 kcal/mole in water); Hydrogen bond (3-7 kcal/mole in vacuum- ≤1-3 kcal/mole in water); van der Waals bond (0.1-0.2 kcal/mole, unaffected by water).

10. False. Some single ionic bonds could be strong enough (up to 20 kcal/mole). However, the answer is generally true. A single non-covalent van der Waals attraction, many hydrogen bonds, and some ionic bonds (especially in water) are too weak to withstand the thermal motions that tend to knock/pull molecules apart. Functioning singly, non-covalent bonds would not be sufficient to hold macromolecules together for a significant amount of time. Multiple H-bonds and ionic bonds will withstand the energy of collisions, etc. at room temperature. Therefore, this sort of interaction involves several non-covalent bonds.

11. Hydrophobic forces/interactions. Non-polar molecules cluster together to reduce the surface area exposed to the water. For example, oil forms droplets in water and eventually separates into a separate phase. Since non-polar (hydrophobic) groups and molecules cannot participate in H-bonding with water molecules, the surrounding water molecules are driven to interact more between themselves. This increased interaction stabilizes the crystal lattice structure of the water immediately surrounding the hydrophobic functional groups or molecules, forming an ice like water crystal lattice or "clathrate cage". This increased ordering of many water molecules decreases the entropy ("randomness") of the system. Bringing together the hydrophobic molecules increases the entropy (+ΔS) by decreasing the hydrophobic surface area, thus decreasing the amount of structured water.

12. Van der Waals interactions
- Weakest, require very close approach of atoms in molecules, no room for competition by H_2O molecules, so their strength is unaffected by H_2O or ions.
- Involve forming induced dipoles in interacting atoms, are strongest at the balance point between repulsion between the electron clouds and attraction between the induced dipoles.
Hydrogen bonds
- Partly covalent, partly electrostatic due to H^+ sharing/transfer between the proton donor and acceptor group (N or O atoms)
- Have directionality, are affected by the alignment of the bond, the donor and acceptor groups have the strongest H-bond when at an 180˚ alignment.
- Functional groups that form H-bonds are polar, so they H-bond with water, so water competes with and weakens H-bonds.
Ionic bonds
- Purely charge-charge or electrostatic interactions
- Are not directional
- Their strength is described quantitatively by Coulombs's law, which has terms for the strength of the positive or negative charges of the interacting functional groups, their distance from each other and the dielectric constant of the solvent/solution (a measure of its ability to compete with the two groups for interacting).
- Are strongly competed for or weakened by water (Dielectric constant of 80).
Hydrophobic forces/interactions
- Hydrophobic functional groups, for example hydrocarbons, do not interact with water to form hydrogen bonds
- The water molecules must interact with each other in the vicinity to satisfy their tendency to form H-bonds forming an ordered crystal lattice, decrease the enthalpy and the free energy of the system. The association of hydrophobic functional groups minimizes the surface area interacting with the water solvent, decreasing the order (increasing the enthalpy and free energy) of the system.
- Hydrophobic forces do not exist in the absence of water, so they are not weakened by water, rather they are dependent on it.

13. Ethanol can form hydrogen bonds with water molecules, but ethane cannot. When ethanol dissolves, the decrease in the system's entropy that results from formation of ordered arrays of water around the $CH_3CH_2^-$ group is partly compensated by the favorable interactions (hydrogen bonds) of the hydroxyl group of ethanol with water molecules. Ethane cannot form such hydrogen bonds.

14. For each of the pairs below, the conjugate base (proton acceptor group):

   1b. $RCOO^-$

   2a. RNH_2

   3a. $H_2PO_4^-$
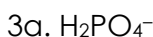
4b. HCO_3^-

15. Phosphoric acid (H_3PO_4) has three dissociable protons, with the pK_a's shown below. The form of phosphoric acid that predominates in a solution at pH 4 is $H_2PO_4^-$. A solution of phosphoric acid will reach pH 4 after addition of approximately one equivalent of OH- and will be close to half way between the first and second pKa. At pH 4 essentially all of the first proton on phosphoric acid will have dissociated but nearly none of the second proton will have begun to dissociate. I suggest you practice plotting this out on a pH versus –OH equivalents graph.

Acid	pK_a
H_3PO_4	2.14
$H_2PO_4^-$	6.86
HPO_4^{2-}	12.4

16. (1) $pK_a = -\log K_a$;
(2) See Fig. 2-17, p. 59; pK_a is the value of pH at the inflection point in a plot of pH vs. extent of titration of the weak acid. At the pK_a, the concentration of ionized acid equals the concentration of un-ionized acid.

17. 1. All amino acids found in naturally occurring proteins have an α carbon to which are attached a carboxylic acid, an amine, a hydrogen, and a variable side chain.

Functional (R) Groups differentiate a.a.

http://jmol.sourceforge.net/demo/aminoacids/
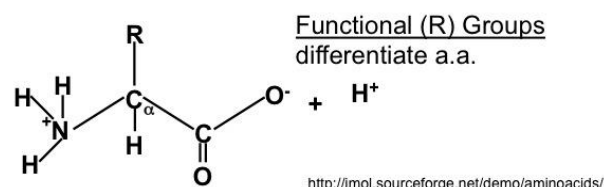
18. The three main classes are polar, nonpolar, and special amino acids. Since all amino acids have the same structure except for their R-groups, it is the R-group that determines how each amino acid is classified. Glutamate and lysine are negatively and positively charged polar amino acids, respectively. Serine is an uncharged polar amino acid. Leucine is a nonpolar amino acid. Proline is a special amino acid. See Lecture 8 PowerPoint slides for details. In your textbook the amino acids are subdivide further and slightly differently into nonpolar aliphatic and aromatic, polar uncharged, negatively charged and positively charged (page 75 Figure 3-5).

19. Most amino acids are soluble in water due to having at least two polar, charged functional groups; the amino group and the carboxyl group. Amino acids have at least one weak base and one weak acid functional group, the amino group and the carboxyl group. Some amino acids have a third functional group, the R group that is a weak acid or a weak base (see page 75 Figure 3-5, positively and negatively charged R groups). Glycine has a net charge of – 1 at pH 11 and above (see page 79 Figure 3-10). The net charge of any amino acid at its pI is 0. The pKa of the amino and carboxyl groups are similar (~9-10 and ~ 2,

respectively, see page 73 Table 3-1), but do vary due to the effects of electronegative atoms on their R groups (see page 80 Figure 3-11), so no they are not all the same.

20. Aspartate has a polar (hydrophilic) side chain, which forms hydrogen bonds with water. In contrast, phenylalanine has a nonpolar (hydrophobic) side chain. (See Fig. 3-5, p. 79 for structures.)

21. The pKa of the histidine side chain is 6.0.

a. The R group pKa = 6.0

b. The COOH pKa = 1.8 and the $^+NH_3$ pKa = 9.2

c. More than half

d. The overall net charge will equal 0.

e. The correct diagram is mod2_Q21e_B.png

f. The correct diagram is mod2_Q21f_A.png