# Analytical Chemistry Cumulative Exam Solutions
9/24/05

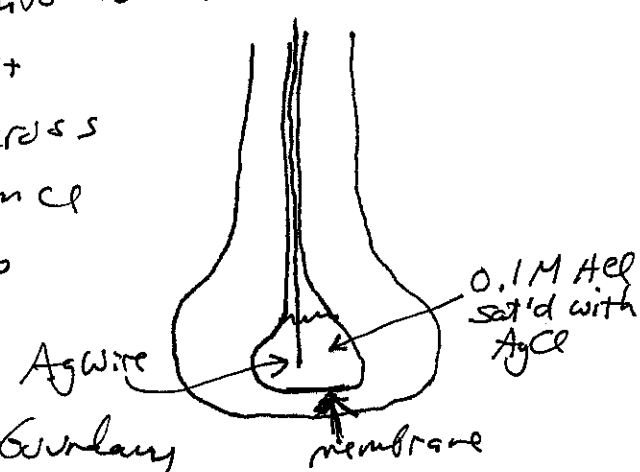
1.) A glass pH electrode senses a potential that develops across a glass membrane that separates the test and reference solutions. The hydrated glass contains silicate oxygens that are negatively charged. These sites exchange cations with the solution, as shown in the following simplified ion-exchange equilibria:

$$H^+(aq) + Na^+(glass^-) \rightleftharpoons Na^+(aq) + H^+(glass^-)$$

(10/20)

$$H^+(glass^-) \rightleftharpoons H^+(aq) + glass^-$$

A typical glass electrode contains an internal Ag/AgCl reference electrode inserted into an internal standard reference solution of fixed $a_{H^+}$




A "boundary potential" is established across the membrane because of the difference in charge states of the two surfaces caused by the difference in pH

(5) between the internal reference and external test solution. The boundary potential is measured by the internal Ag/AgCl electrode, with a cell diagram shown as follows:

$$Ag(s)|AgCl(s)|Cl^-(aq)\,||\,H^+(test)\,|\,H^+(ref), Cl^-(aq)\,|\,AgCl(s)|Ag(s)$$

membrane — internal ref electrode

The response of the glass electrode is typically described by this equation:

$$E = K + 0.059 \log \frac{a_{H^+(test)}}{a_{H^+(ref)}}$$

(2) A buffer solution can be prepared from a weak acid and its conjugate base (or a weak base and its
(5) conjugate acid). By rearranging the equilibrium constant expression, we obtain:

$$pH = pKa + \log \frac{[A^-]}{[HA]}$$

If the concentrations of $[A^-]$ and $[HA]$ are equal $pH = pKa$, so, one selects a weak acid with a pKa equal to the pH that is desired for a calibration point. For a large buffering capacity, one uses relatively large concentrations of the weak acid and conjugate base.

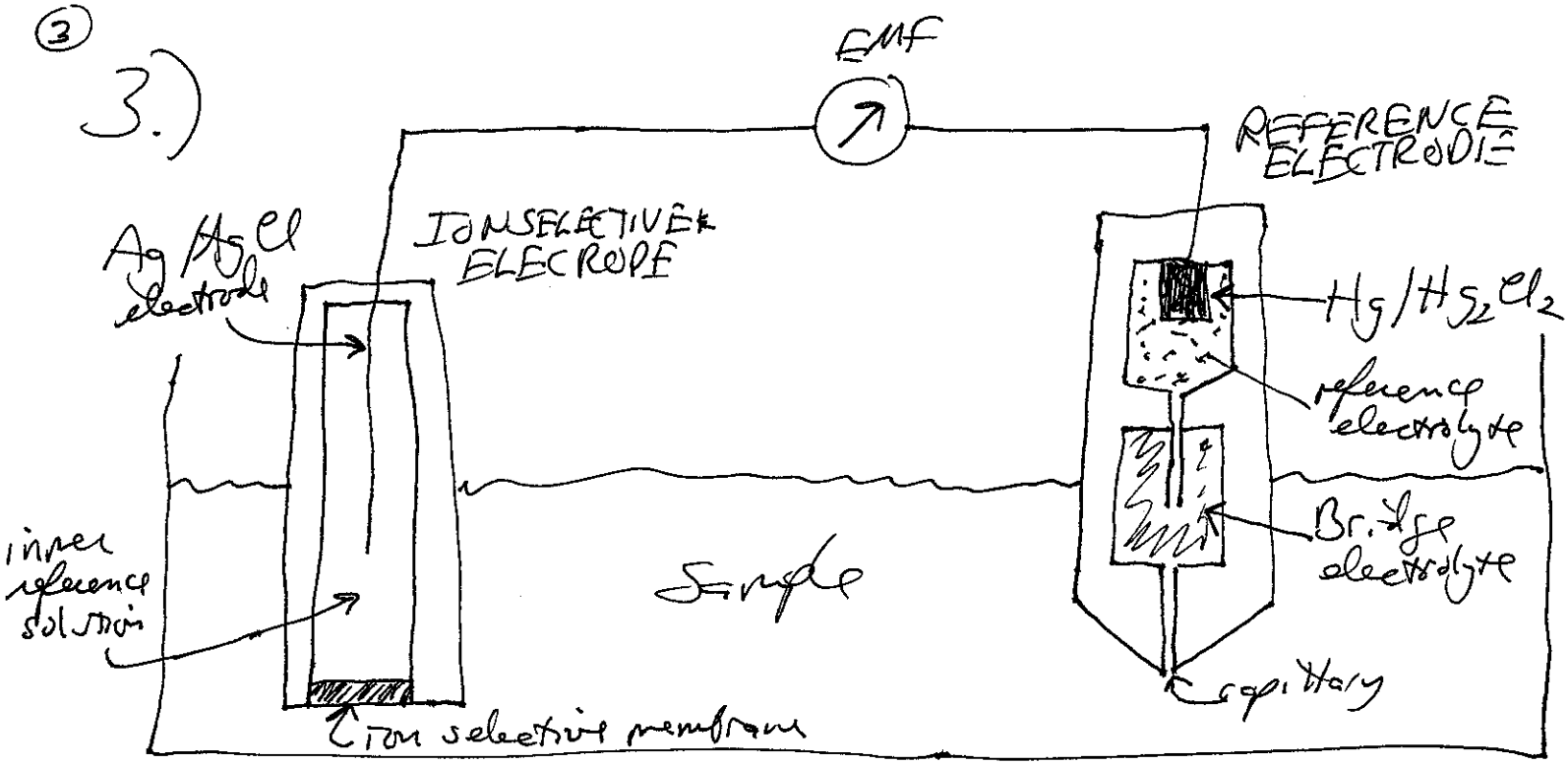
2.) $a_X \equiv [X] \cdot f_X$, where $f_X$ is the activity coefficient for X. The activity coefficient depends on the ionic strength of the solution, where the ionic strength, $I = \frac{1}{2}\sum z_i^2 [i]$
(10) A simple means of estimating the activity coefficient is through the Debye-Huckel Limiting Law:

$$-\log f_X = 0.512 Z_X^2 \sqrt{I}$$

In ISEs, the membrane potential is measured relative to the reference electrode potential, which
(10) is assumed to be fixed, i.e. sample-independent, and known.

(3)

3.)




2 electrodes, complete circuit (5)
membrane electrode + labels (5)

4.) At the membrane-sample solution interface,

(10) $$E = \frac{-\mu^\circ(\text{membrane}) - \mu^\circ(aq)}{zF} + \frac{RT}{zF}\ln\frac{a_I(aq)}{a_I(\text{membrane})}$$

where I is the analyte cation

If $a_I$(membrane) is not altered by the sample solution, a simple Nernstian response can be achieved. To keep $a_I$(membrane) constant and small, a lipophilic complexing agent must selectively bind with the analyte cations in the membrane. The binding of the analyte

(10) prevents ion exchange reactions with other interfering cations. To achieve Nernstian response, the membrane must have ion-exchanger properties, and must be lipophilic. Typically, a material such as PVC is used as membrane material.

(4)

5.) A good definition of selectivity is a favorable differential response of a detector for one (or a class of) analyte, relative to

(10) interfering sample constituents. The selectivity in the case of ISEs that use an ionophore in the membrane depends on the ratio of complex formation constants for the analyte ion and the interfering ion(s). Actually, it is important to know, and maximize the ratio of the complex formation constants ~~for the analyte~~ within the lipophilic membrane phase. Quantitatively, the selectivity can be described as follows: $E = E_I^\circ + \frac{RT}{zF}\ln\left(a_I + K_{IJ}^{pot} a_J\right)$

(10) where $a_I$ is the activity of analyte I, $a_J$ is the activity of analyte interference J, and $K_{IJ}^{pot}$ is a selectivity coefficient, which, for a very selective electrode, is very small. In the case of $Mg^{2+}$ and $Ca^{2+}$,

$$K_{IJ}^{pot} = K_{IJ} \cdot \frac{\beta_{JL}}{\beta_{IL}}$$

where $K_{IJ}$ is the equilibrium constant for exchange of the ions I ($Ca^{2+}$) and J ($Mg^{2+}$) between the aqueous and organic phases, and the $\beta$'s are the complex formation constants. So, we want a large ratio of $\frac{\beta_{JL}}{\beta_{IL}}$

(5) (c) the lower limit of detection can be determined (caused) by two primary factors:

1.) leaching of the analyte ion from the membrane into the region of the membrane-solution interface, so that there is a sample-independent local minimum concentration, and

(5) 2.) interference by similar ions, as discussed above, e.g. by $Mg^{2+}$ in this example.

(5)

Proteins can change in concentration and the degree to which they are post-translationally modified in response to regulatory stimuli, i.e.

$$[\mathrm{mRNA}] \rightarrow [\mathrm{P_i}] \rightarrow [\mathrm{P_i^*}]$$

where $P_i$ is a specific protein and $P^*_i$ is the post-translationally modified form of that protein. The concentration of either may increase or decrease as a consequence of the regulatory stimulus. This means that expression, degradation, and the rate of interconversion between $P_i$ and $P^*_i$ all play a role in the concentration of a protein at any moment in time.

1. How would you determine the degree to which $P_i$ and $P^*_i$ changed in concentration as a result of a stimulus. If your answer is based on the use of a separation system to separate the two forms of the protein, explain whether the method you propose will work with all forms of post-translational modification.

2. Assuming that $P_i$ increased in concentration and $P^*_i$ decreased in concentration as a result of a stimulus, explain all the ways this could have occurred.

The question could be answered in multiple ways. Several are given below.

**Answer**. Question 1.

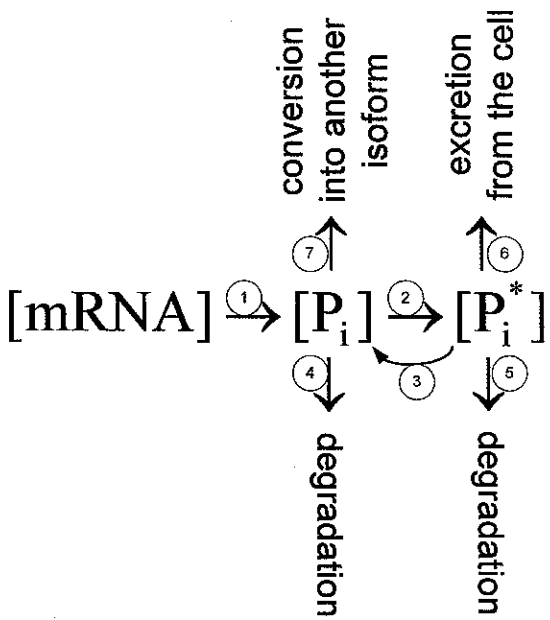
- It is necessary to discuss post-translational modifications (PTM) first.
  - There are over a hundred types of PTM.
  - Some occur at a single sit in a protein while others occur a multiple sites.
  - Thus it is possible to have PTM isoforms of a protein.
  - In the case of glycosylation it is possible to have 50 or more glycan variants at single site in a protein and one to greater than five glycosylation sites in the protein.

- There are at least three ways you could answer this question. If still another method is proposed that would work it will be accepted
  - One way is through mass spectrometry (MS) of the intact protein. This probably the weakest of the possible methods because all isoforms of the protein would have to be ionized at the same time in equal proportions. First, this is very unlikely to occur and second you would have to pre-purify the protein before MS analysis.
  - A second way is to isolate the isoforms of the proteins and quantify each separately. This requires that the isoforms be separated either by 2-D gel electrophoresis or multidimensional liquid chromatography. This requires that the separation mechanism in either the 2-D gel electrophoresis (2-DGE) or liquid chromatography method be described that was chosen as the separation method.

- The third way is to tryptic digest the protein into peptide fragments. In this approach PTM's are located on peptides. Non-PTM carrying peptides can be used to determine the total concentration of forms of the protein in the system. When compared to PTM carrying peptides the difference in concentration give the relative amount of the protein that has been modified. This approach works for virtually all types of glycosylation and does not require separation of the parents prior to beginning the analysis.
- Next it is necessary to describe unique features about several types of PTM that make them amenable to a particular type of separation.
  - Phosphorylation variants differ in charge and thus it would be possible to separate most by 2-DGE. Anion exchange chromatography would do the same.
  - Glycovariants differ in charge also, but not in all cases. 2-DGE will resolve many glycovariants but not all. In fact, there is no method that will resolve all glycovariants. For that reason there is no definitive answer for this question in the case of glycosylation.
  - Methylation is much the same a glycosylation.
  - Prenylated proteins vary be hydrophobicity. Reversed phase chromatography is more likely to separated the parent protein from the isoform carrying the PTM.
  - You only have to address several post-translational modifications. There are oxidized forms, sulfonylated forms, cleavage fragments, and many, many more.

**Answer**. Question 2.

- Again it is necessary to begin the answer to this question with a discussion of the phenomenon. There are a number of phenomena that impact the concentration of a protein and its isoforms.



- One is the rate of synthesis, both of the protein and the various isoforms from the parent protein.
- Second PTM isoforms can often be converted back to a less modified for as in the case of phosphorylation and often glycosylation.
- Third, the rate of degradation of either the parent or isoforms can have a major impact on the concentration of a particular form of a protein..
- Fourth, it is often the case that isoforms are excreted from a cell. This is widely seen in glycosylation. Excretion has much the same effect as degradation. It removes isoforms form the intracellular pool.
- Finally, it is possible for a protein to undergo further modification, either through another PTM or by coupling to another protein.

- You were to assume that $P_i$ increased in concentration and $P^*_i$ decreased in concentration as a result of a stimulus and to explain how this could happen.
  - $P_i$ could increase in a number of ways. In all cases it would require 1) an increase or decrease in the expression of the regulatory enzymes involved or 2) direct inhibition or enhancement of the activity of these enzymes.
    - One would be by an increase in the rate of either reaction 1 or 3 above, or both.
    - Another would be by decreasing the rate of reaction 2, 4, or 7 either individually or in combination.
  - A decrease in $P^*_i$ concentration could occur in a number of ways also as a result of changes in the concentration or activity of enzymes responsible for these processes.
    - One would be decreasing the rate of $P^*_i$ synthesis for the rate or conversion back into the parent protein.
    - Another way would be to increase either its rate of degradation through reaction 5 or the rate of excretion from the cell in reaction 6.
  - Next it is necessary to describe unique features about several types of PTM that make them amenable to a particular type of separation.
    - Phosphorylation variants differ in charge and thus it would be possible to separate most by 2-DGE. Anion exchange chromatography would do the same.
    - Glycovariants differ in charge also, but not in all cases. 2-DGE will resolve many glycovariants but not all. In fact, there is no method that will resolve all glycovariants. For that reason there is no definitive answer for this question in the case of glycosylation.
    - Methylation is much the same a glycosylation.
    - Prenylated proteins vary be hydrophobicity. Reversed phase chromatography is more likely to separated the parent protein from the isoform carrying the PTM.
    - You only have to address several post-translational modifications. There are oxidized forms, sulfonylated forms, cleavage fragments, and many, many more.

**Inorganic Chemistry Cumulative Exam**

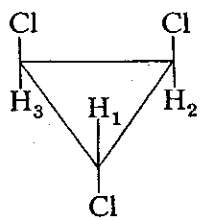
Purdue University

September 24, 2005

There are 100 possible points in this exam.

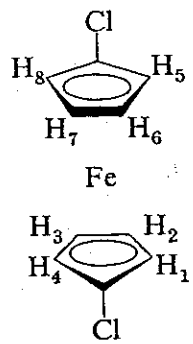
1. (20 points) Determine the point groups of the following molecules, and find the requested equivalent atoms within these molecules.

(a) Which protons, if any, are equivalent to $H_1$



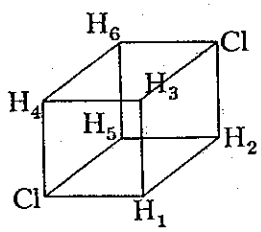

**$C_s$; None**

(b) Which protons, if any, are equivalent to $H_6$?




**$C_{2h}$; H2, H3, H7**

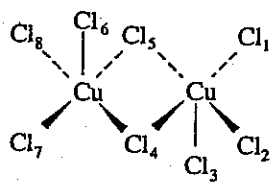
(c) Which protons, if any, are equivalent to $H_1$?




**If you assumed H1-H2 = H1-H3**
**$D_{3d}$; H2, H3, H4, H5, H6**

**If you assumed H1-H2 > H1-H3**
**$C_{2h}$; H2, H4, H6**

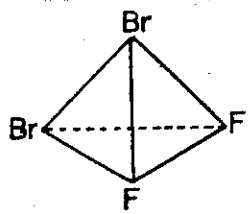
(d) Which chlorides, if any, are equivalent to $Cl_1$?



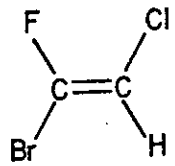

**$C_{2h}$; Cl2, Cl7, Cl8**

2. (10 points) Molecules with a mirror plane, center of inversion, or improper axis of rotation cannot be optically active. Molecules without such symmetry elements can be active. Using these criteria, determine whether or not each of the following molecules is optically active.

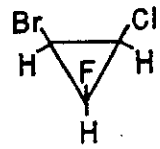
(a) **Inactive**



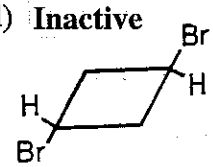

(b) **Inactive**




(c) **Active**

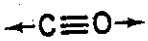



(d) **Inactive**

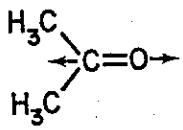



3. (10 points) In order that a molecular vibration may give rise to IR absorption, the dipole moment of the molecule must change during the vibration. Determine whether or not each of the following molecular vibrations is IR active.

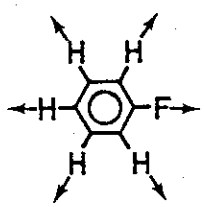
(a) **Active**



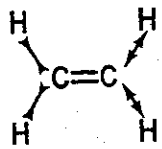

(b) **Active**




(c) **Active**



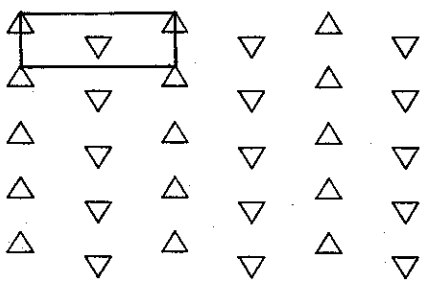

(d) **Active**



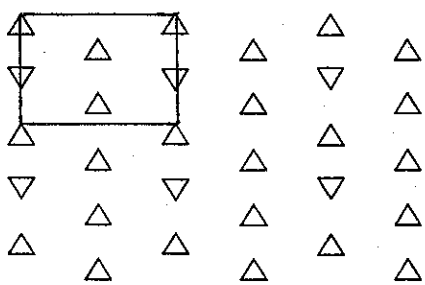

→ bond stretching
⟶⟵ bond compression

4. (10 points) A plane lattice is an infinite array of points in two dimensions such that <u>every point is identical, having the same surroundings in the same orientation.</u> A unit cell of a plane lattice is a parallelogram of two unit translations with lattice points at the corner and is perfectly representative of the lattice. Draw a unit cell for the following 2D patterns (Remember to draw your answers in your blue book!).

(a)



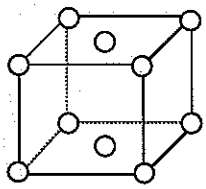
(b)



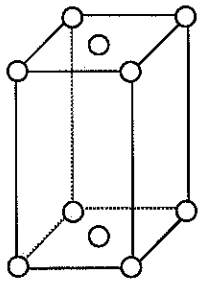
5. (20 points) The monoclinic system is characterized by one diad (2-fold rotation or mirror plane). The orthorhombic system is characterized by three mutually perpendicular diads.

tetragonal system is characterized by one tetrad (4-fold axis). The cubic system is characterized by four triads (3-fold rotational axis). To which crystal system must each of the following belong?

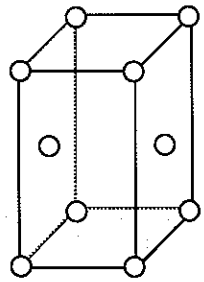
(a) **Tetragonal**



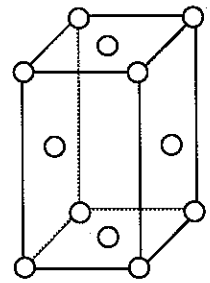
(b) **Tetragonal**



(c) **Orthorhombic**

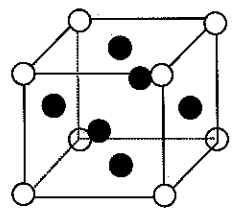


(d) **Orthorhombic**



6. (10 points) What is the lattice type of the following structure (white circles at 8 corners of a cube and black circles at the centers of 6 faces)? Explain your answer.

(1) Primitive cubic
(2) Body-centered cubic
(3) Face-centered cubic
(4) Primitive orthorhombic
(5) Face-centered orthorhombic



**(1) Primitive Cubic: Every lattice point must be identical.**

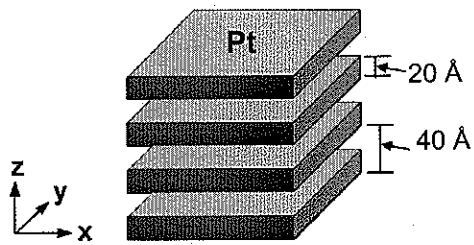
7. (10 points) Material A crystallizes in the primitive cubic structure with a = 4.0 Å. Calculate the 2θ position for (200) reflection when Cu Kα radiation (λ = 1.54Å) is used.

[Bragg's equation: $\lambda = 2d_{hkl} \sin\theta$]

**$d_{200}$ = 2.0 Å**
**1.54 Å = 2 x 2.0 Å x sinθ**
**2θ = 45.3°**

8. (10 points) Platinum metal shows typical X-ray diffraction patterns for a face-centered cubic structure (a = 3.92 Å). Suppose that this material is prepared as a 2 nm thick layer that repeats every 4 nm along the direction that is perpendicular to the layers. Sketch (or describe) the expected XRD patterns resulting from this nanostructure.

**This nanostructure has an ordering only along the z-axis. Therefore, it will generate x-ray diffraction patterns composed of only (00*l*) reflections (e.g. 001, 002, 003…). Since the repeating unit is 40 Å, the peaks generated by this nanostructure will appear at much smaller 2 theta positions than those expected for the atomic level ordering (a = 3.92 Å).**



(Bonus, 10 points) Calculate the $2\theta$ position for the first x-ray reflection (with the largest d-spacing) created by this nanostructure ($\lambda = 1.54$Å).

$$\mathbf{d_{001} = 40\ \text{Å}}$$
$$\mathbf{1.54\ \text{Å} = 2 \times 40\ \text{Å} \times \sin\theta}$$
$$\mathbf{2\theta = 2.21^\circ}$$

# Organic Cumulative Exam: Stereochemistry and Conformational Analysis
# 09/24/05

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**I.1 (18 pts)** Provide general definitions (with aid of illustrations, if necessary) for the following terms:

*i.* 'allylic 1,3-strain'
*ii.* '*meso* compound'
*iii.* 'optically active'
*iv.* 'prochiral'
*v.* 'staggered conformation'
*vi.* '*syn*-pentane interaction'

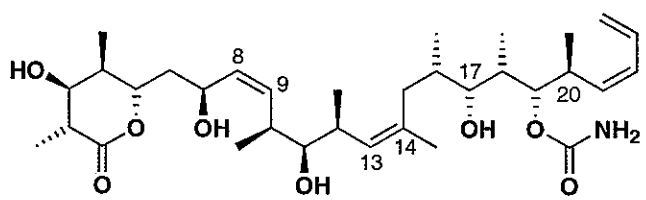
**I.2 (6 pts)** An object or a molecule is *achiral* if it possesses a plane of symmetry. Rank the following molecules by the number of symmetry planes that they possess:

*i.* $H_2$ **(∞)**
*ii.* methane **(6)**
*iii.* chloroform **(3)**
*iv.* dichloromethane **(2)**
*v.* *trans*-1,2-dimethylcyclopentane **(0)**
*vi.* *cis*-1,2-dimethylcyclopentane **(1)**

**I.3 (16 pts)** Draw schematic $^1$H-NMR spectra for both *cis*- and *trans*-1,2-dichloro-cyclopropanes, assuming sufficient resolution to provide well-resolved multiplets. Indicate integration values and label *diastereotopic* protons.

***Cis:*** **dd (2), dt(1), dt(1); methylene protons are diastereotopic.**
***Trans:*** **dd (2), t(2)**

**I.4 (40 pts)** (+)-Discodermolide is a marine metabolite possessing potent anticancer activity due to its tubulin-stabilizing property.



a) **(13 pts)** Please indicate configurations of all of the asymmetric centers in (+)-discodermolide according to the Cahn-Ingold-Prelog rules.

**C2:R, C3:S, C4:R, C5:S, C7:S, C10:S, C11:S, C12:S, C16:S, C17:R, C18:S, C19:S, C20:S**

b) **(7 pts)** Rationalize the preference for a boat-like conformation of the tetrasubstituted δ-lactone fragment (*JACS* **2001**, *123*, 9535).

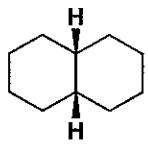
**Boat conformation allows all of the substituents to remain equatorial**

c) **(20 pts)** The solution structure of (+)-discodermolide suggests that nonbonded (*e,g.*, allylic 1,3-strain, *syn*-pentane, etc.) interactions play a major role in defining the overall helical-like configuration of the natural product (*Org. Lett.* **2001**, *3*, 696). Propose and briefly explain conformational preferences for the $C^7$–$C^{10}$, $C^{10}$–$C^{12}$, $C^{12}$–$C^{15}$, $C^{16}$–$C^{20}$, and $C^{21}$–$C^{24}$ fragments.

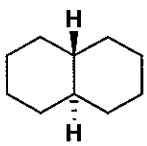
**$C^7$–$C^{10}$: allylic1,3-strain forces C7 & C10 protons to be in the same plane as C8=C9 double bond;**
**$C^{10}$–$C^{12}$: minimization of *syn*-pentane interaction between C10 and C12 substituents;**
**$C^{12}$–$C^{15}$: similar argument to $C^7$–$C^{10}$;**
**$C^{16}$–$C^{20}$: similar argument to $C^{10}$–$C^{12}$ (two *syn*-pentane interactions );**
**$C^{21}$–$C^{24}$: *s*-trans diene conformation will be preferred to *s*-cis (1,6-interaction should be invoked)**

**I.4 (20 pts)** Fused ring systems are ubiquitous in nature, most notably in steroids. With a few exceptions, all steroidal ring junctions are *trans*. Synthetic approaches to fused systems, however, can lead to different stereochemical outcomes, and therefore it is important to consider the energetic parameters involved.

a) **(5 pts)** Draw all available all-chair conformations for both *cis*- and *trans*-decalins and comment about their relative energetic stability.



*cis*-decalin



*trans*-decalin

**One all-chair conformation for *trans*-decalin and two iso-energetic all-chair conformations for the *cis* isomer.**

b) **(5 pts)** *trans*-Decalin, but not the *cis* isomer, can serve as a good model system to determine differences in reactivity of functional groups in axial vs equatorial environments. Explain.

**'Ring flip' in the *cis*-decalin system interconverts axial and equatorial substituents**

c) **(10 pts)** Perform an energy analysis on both *cis*- and *trans*-decalins in their lowest energy forms, using the following enthalpy costs: anti butane: 0 kcal/mol, gauche butane: 0.9 kcal/mol, *syn*-pentane interaction: 3.7 kcal/mol, eclipsed butane (120°): 3.7 kcal/mol, eclipsed butane (0°): 4.5 kcal/mol.

*Hint:* A systematic carbon-by-carbon "walk" may be helpful in identification of nonbonded interactions, which are only present in one system and not in the other.

**The difference between the bicyclic structures is that three gauche butane interactions in the cis-decalin are replaced by three anti interactions in the trans isomer. Cis-decalin is less stable by 2.7 kcal/mol.**

1.

Physical Cumulative Exam

September 24, 2005

1a. (40 pts) From Eqs. (1.2) and (1.3)

(i) (20 pts)

$$\bar{x} \longrightarrow \langle y \rangle = 0$$

and

$$\sigma \longrightarrow \Delta y = \left(\frac{\hbar}{2m\omega}\right)^{1/2}$$

Also in Eq. (1.1)

$$x \rightarrow y.$$

Thus combining gives

$$P(x) = \left(\frac{1}{2\pi\sigma^2}\right)^{1/2} \exp\left[-\frac{1}{2}\left(\frac{(x-\bar{x})}{\sigma}\right)^2\right] \longrightarrow$$

$$P(y) = \left[\frac{1}{2\pi(\Delta y)^2}\right]^{1/2} \exp\left[-\frac{1}{2}\frac{y^2}{(\Delta y)^2}\right]$$

or using $\Delta y = (\hbar/2m\omega)^{1/2}$ yields

$$\boxed{P(y) = \left[\frac{m\omega}{\pi\hbar}\right]^{1/2} \exp\left[-\frac{m\omega}{\hbar}y^2\right]}$$

(ii) (20 pts) Assuming $\psi(y)$ is real, $P(y) = \psi^*(y)\psi(y) = \psi^2(y)$ or $\psi(y) = P^{1/2}(y)$. Combining with the above expression for $P(y)$ gives

$$\boxed{\psi(y) = \left[\frac{m\omega}{\pi\hbar}\right]^{1/4} \exp\left[-\frac{m\omega}{2\hbar}y^2\right]}$$

2.

b. (40 pts)

(i) (30 pts)

$$\langle p_y \rangle = \int_{-\infty}^{\infty} \psi^*(y) \frac{\hbar}{i} \frac{d}{dy} \psi(y) dy =$$

$$\underbrace{\left(\frac{\hbar}{i}\right)}_{\text{pure imaginary}} \underbrace{\left(\frac{m\omega}{\pi\hbar}\right)^{1/2}}_{\text{pure real}} \underbrace{\int_{-\infty}^{\infty} \exp\left[-\frac{m\omega}{2\hbar} y^2\right] \frac{d}{dy} \exp\left[-\frac{m\omega}{2\hbar} y^2\right] dy}_{\text{pure real}}$$

As indicated the above expression for $\langle p_y \rangle$ is pure imaginary. However since $\frac{\hbar}{i}\frac{d}{dy}$ is Hermitian, $\langle p_y \rangle$ must be real. This contradiction is resolved only if the integral vanishes. Then, however,

$$\boxed{\langle p_y \rangle = 0}$$

(ii) (20 pts). First given the above result, Eq (1.46) may rewritten as

$$\Delta p_y = [\langle p_y^2 \rangle]^{1/2}$$

Thus we calculate $\langle p_y^2 \rangle$ as

$$\langle p_y^2 \rangle = \int_{-\infty}^{\infty} \psi^*(y) \left(\frac{\hbar}{i}\frac{d}{dy}\right)^2 \psi(y) =$$

$$-\hbar^2 \left(\frac{m\omega}{\pi\hbar}\right)^{1/2} \int_{-\infty}^{\infty} \exp\left[-\frac{m\omega}{2\hbar} y^2\right] \frac{d^2}{dy^2} \exp\left[-\frac{m\omega}{2\hbar} y^2\right] dy.$$

But

$$\frac{d}{dy} \exp\left[-\frac{m\omega}{2\hbar} y^2\right] = -\frac{m\omega}{\hbar} y \exp\left[-\frac{m\omega}{2\hbar} y^2\right]$$

and thus

$$\frac{d^2}{dy^2} \exp\left[-\frac{m\omega}{2\hbar} y^2\right] = \left[-\frac{m\omega}{\hbar} + \left(\frac{m\omega}{\hbar}\right)^2 y^2\right] \exp\left[-\frac{m\omega}{2\hbar} y^2\right].$$

Pulling this together gives

$$\langle p_y^2 \rangle = \hbar^2 \left(\frac{m\omega}{\pi\hbar}\right)^{1/2} \int_{-\infty}^{\infty} \left[\frac{m\omega}{\hbar} - \left(\frac{m\omega}{\hbar}\right)^2 y^2\right] \exp\left[-\frac{m\omega}{\hbar} y^2\right] dy .$$

We next use the following integrals (standard) for $a = m\omega/\hbar$,

$$I(a) = \int_{-\infty}^{\infty} \exp\left[-ax^2\right] dx = \left(\frac{\pi}{a}\right)^{1/2}$$

and

$$\frac{d\, I(a)}{da} = -\int_{-\infty}^{\infty} x^2 \exp\left[-ax^2\right] dx = -\frac{1}{2}\frac{\pi^{1/2}}{a^{3/2}} ,$$

to evaluate $\langle p_y^2 \rangle$ as $\langle p_y^2 \rangle = m\hbar\omega/2$, which gives Eq. (1.46) for $\Delta p_y = \langle p_y^2 \rangle^{1/2}$.

2. (20 pts). The orthogonality arises since the spherical harmonics $Y_{\ell=0,m=0}(\theta,\phi)$ and $Y_{\ell=2,m=0}(\theta,\phi)$ are orthogonal. This may be seen by evaluating the angular integral

$$\int_0^{\pi} \sin\theta\, d\theta \int_0^{2\pi} d\phi\, Y_{\ell=0,m=0}(\theta,\phi)\, Y_{\ell=2,m=0}(\theta,\phi) \overset{\text{put in explicit forms}}{=}$$

$$\left(\frac{1}{4\pi}\right)^{1/2} \left(\frac{5}{16\pi}\right)^{1/2} \int_0^{\pi} \sin\theta\, d\theta \left[3\cos^2\theta - 1\right] \int_0^{2\pi} d\phi =$$

$$2\pi \left(\frac{1}{4\pi}\right)^{1/2} \left(\frac{5}{16\pi}\right)^{1/2} \int_0^{\pi} \sin\theta \left[3\cos^2\theta - 1\right] d\theta .$$

Next consider the integral in the above equation which we will denote by

4.

$$I = \int_0^{\pi} \sin\theta \left[3\cos^2\theta - 1\right] d\theta .$$

Let $x = \cos\theta$ and $dx = -\sin\theta \, d\theta$. Then $I$ becomes

$$I = \int_{-1}^{1} \left[3x^2 - 1\right] dx = \left[x^3 - x\right]_{-1}^{1} = \left[(1-1) - (-1+1)\right] = 0 .$$

Thus $I = 0$ and, hence 3s and 3d orbitals are orthogonal.