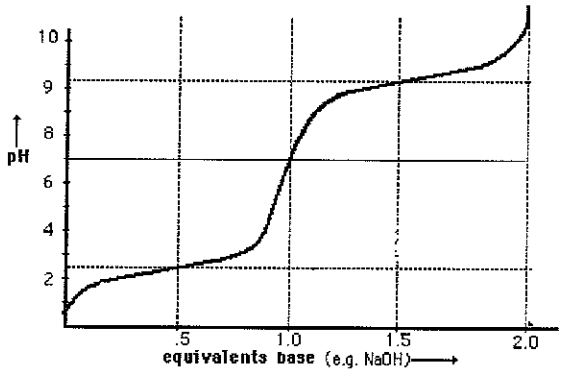
BITS PILANI, INTERNATIONAL ACADEMIC CITY ,DUBAI
II YEAR BIOTECH SECOND SEMESTER,2012-2013
COMPREHENSIVE EXAMINATION

Course Title :Biophysics **Course No:BIOT F215**
Date:5.06.2013 **Total Marks:40**
Time: 3 Hours **Weightage:40%**

1. Answer all questions sequentially
2. Useful data : $c = 3 \times 10^8$ m/s, $h = 6.626 \times 10^{-34}$ J s, 1 amu = 1.660×10^{-27} Kg, R= 0.0821 liter·atm/K/mol, Atomic mass H=1, C=12, O=16

1.(i)Write the structure for the tripeptide gly-ala-leu.
(ii)From the titration curve of alanine , assign the pK_a values of the ionizable groups present in it. Find the characteristic pH at which the net charge is zero.



(iii) Differentiate between configuration and conformation with appropriate examples.
(iv) Calculate the force constant for a single bond between ^{12}C and ^{1}H .The vibrational frequency for the single C-H bond is 3032 cm^{-1} .
(v) Describe the experiment used to determine the hydrogen bond energy of biomoleules in water.

(1+1+2+2+2M)

2.(i)Write the significance of cyclic symmetry in protein structures .
(ii)Write the Schrodinger equation for a one molecule system and the terms involved in it.
(iii)Explain the α –helix structure of proteins.
(iv)Write a note on the factors that stabilize the quaternary structure of proteins.
(v) Schematically represent all the major interactions involved in the tertiary structure of proteins. Write one example for each type of interaction.

(1+1+2+2+2M)

3.(i) Write the interactions disrupted in proteins while denaturation is carried out by heat.
(ii) Explain the various phases seen in a pressure area isotherm of a monolayer.
(iii) A solution is prepared by dissolving 1.08 g of human serum albumin, a protein from blood plasma, in 50 cm^3 of aqueous solution. The solution has an osmotic pressure of 5.85 mm Hg at 298 K. Calculate the molar mass of albumin.
(iv) Write the common features and varying parameters of secondary structure of DNA.
(v) Calculate the R_C and R_G for a freely jointed randomly coiled polymer chain if the number of monomeric units is 4500 and the bond distance is 143 pm .
(vi) Explain the random flight and rotational isomeris state theory of protein folding.

(1+1.5+1.5+2+1+2M)

4.(i)Write the expression for the potential energy of a chemical bond V_{bond} .
(ii)Give any two applications of molecular dynamics with reference to macromolecules.
(iii)Outline any two criteria needed for the growth of crystals from an aqueous solution of macromolecules.
(iv)With a neat diagram explain Laue's transmission method used in the study of X-ray diffraction of crystals.
(v)X rays of wavelength 154 pm are diffracted from a crystal at an angle of 14.17^0. Assuming that $n = 1$, Calculate the distance (in pm) between layers in the crystal.

(1+1+1+2+1M)

5.(i)Describe the principle involved in NMR spectroscopy. Based on NMR predict the splitting patterns for the molecule 1,1-Dibromoethane.(classify each proton as splitting into a singlet, doublet, triplet, etc.)
(ii)Write any two applications of CD spectroscopy with reference to protein molecules.
(iii)Briefly explain the instrumentation involved in fluorescence spectra with a block diagram.
(iv)Explain the terms Optical tweezers and Overtones.
(v) Draw the apparatus used in the Atomic force microscopy technique.
(vi)List out the possible electronic transitions taking place in ethanol .

(2+1+2+2+1+1M)

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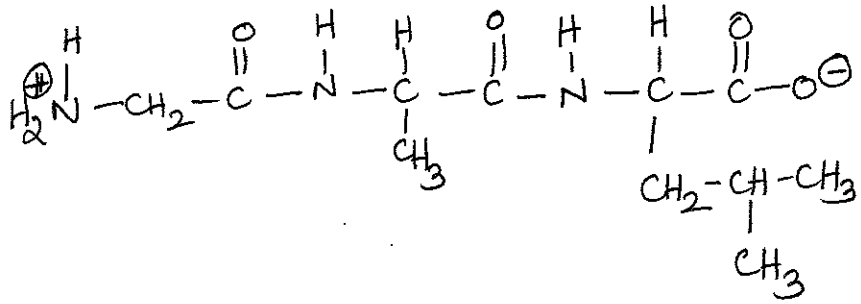
II YEAR BIOTECH SECOND SEMESTER,2012-2013
COMPREHENSIVE EXAMINATION

Course Title :Biophysics **Course No:BIOT F215**
Date:5.06.2013 **Total Marks:40**
Time: 3 Hours **Weightage:40%**

ANSWERING AND MARKING SCHEME

(1) (i) Structure of gly-ala-leu.



(1M)

(ii) $pKa_1 = 2.3$

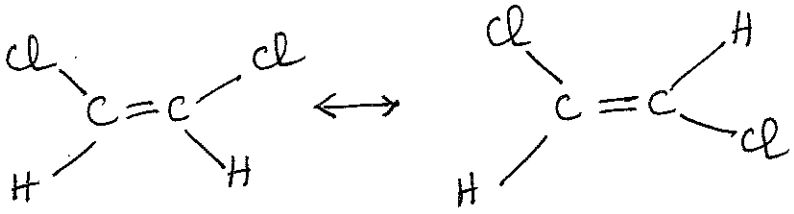
$pKa_2 = 9.7$ (aminium group)

$pI = \frac{1}{2}(2.3 + 9.7) = 6.0$

At pH = 6.0 net charge is zero. (1M)

(iii) Configuration – defines the position of groups around one or more nonrotating bonds or around chiral centres.

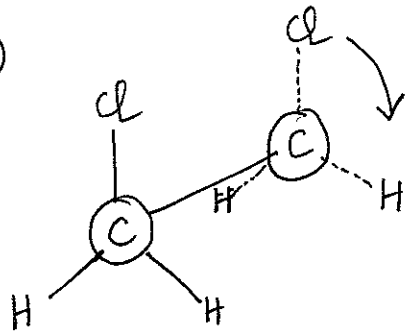
(eg) cis and trans 1,2-Dichloroethylene



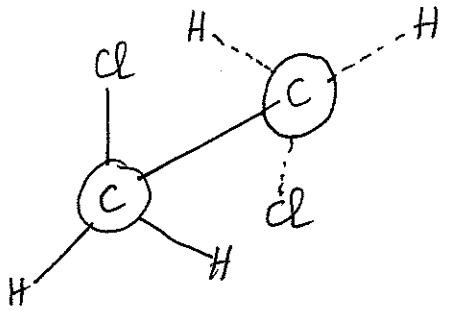
(1M)

<u>Conformation</u> - describes the spatial arrangement of groups about one or more freely rotating bonds.

(eg)



Eclipsed gauche



Staggered anti (1M)

(iv)

$$\bar{\nu} = \frac{1}{2\pi c}\sqrt{\frac{k}{\mu}}$$

$$k = (2\pi c \bar{\nu})^2 \mu \quad (1/2\,M)$$

$$\mu\ ^{12}C \text{ and } ^{1}H = \frac{12\times 1}{12+1} = \frac{12}{13} = 0.9230\,u \quad (1/2\,M)$$

$$k = (2\times 3.14 \times 3\times 10^{10}\ cm/s \times 3032\ cm^{-1})^2 \times 0.9230u \times 1.660\times 10^{-27}\ kg \quad (1/2M)$$

$$k = 499.9\ Nm^{-1} \quad (1/2\,M)$$

(v) * Biomolecules are immersed in water. Intra as well as intermolecular H bonds are formed and it stabilizes the structure.

* There is net H bond energy - it is estimated from partitioning experiments as follows.

Water G_1 $\xrightarrow{\Delta G_{trs}(1) \text{ of amino acid}}$ wet hexane (C_6H_{14}) containing G_2 ≈ 2.5 mM H_2O. (½M)

This process is favoured by −5.3 Kcal/mole.

* In this case the H-bonding makes large contribution to ΔG_{trs}. This is because the H-bonds made with water cannot be replenished in hexane and only amino acid - amino acid intermolecular hydrogen bond forming is possible in hexane.

Water G_1 $\xrightarrow{\Delta G_{trs}(2) \text{ of amino acid}}$ Wet Octanol ($C_8H_{17}OH$) containing ≈ 2.5 mM H_2O. (½M)

* This process is favoured by −1.1 Kcal/mole.

H-bonding makes small contribution to ΔG_{trs}. This is because the hydrogen bonds made with water can be replaced in octanol and both amino-acid solvent and amino acid - amino acid H-bond forming are possible. (½M)

(4)

Energy of H-bonding is $\Delta G_{trs(1)} - \Delta G_{trs(2)}$

$= -5.3 - (-1.1)$

$= -4.2$ Kcal/mole.

* Knowing that the peptide group can form 3 bonds, one can predict that energy per hydrogen in competition with solvent water is -1.4 Kcal/mole. (½ M)

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(2) (i) Proteins in cyclic group are specialized in functions that require directionality or sidedness such as a formation of hollow tube or chamber or interaction with membranes. (1M)

(ii) Schrodinger equation for a one molecule system

$$-\frac{\hbar^2}{2m}\frac{d^2\psi_a}{dx_a^2} + V_a\psi_a = E_a\psi_a$$

$\hbar = \frac{h}{2\pi}$

m = mass of oscillating particle

V_a = potential energy

E_a = Total energy. (1M)

(iii) α- Helix structure:

* In the helix the residues are held by H-bond (between NH and $-\overset{\overset{O}{\|}}{C}-$ units), vanderwaals interaction, coulombic interactions, polar interactions play a role in helical structure. (½M)

* Distance between 2-amino acid residues are 1.5 Å along the helix axis. (½M)

* α- helix has 3.6 amino acid residues per turn. (½M)

* Gradient angle $\phi = P/2\pi r = \tan\phi$

Pitch $= (3.6 \times 1.5) = 5.4$ Å (½M)

* Most of the α- helices in proteins are right handed.

(iv) * Vander waals contact : A single contact between two subunits worth ∩ 100 cal. There are 100 such contacts ∩. So net energy will be $100 \times 100 = 10$ K.cal/mole. (½M)

* Loss of solvent contacts between the interfaces.

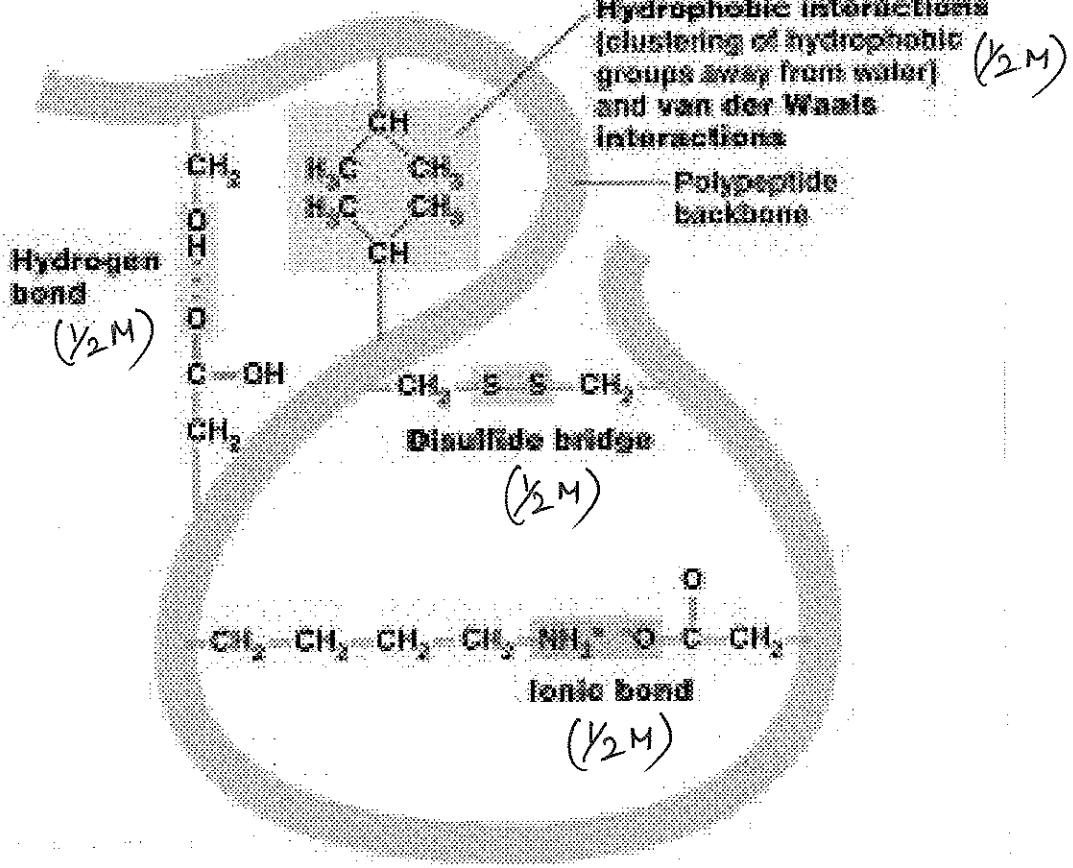
A substantial loss of such contacts and loss of Vander waals interaction occurs. consequently net vander waals energy of subunit association is negligible. (½M)

* Loss of translational and rotational degrees of freedom.

$\Delta G_{dimerization}$ = −11 to −22 K·cal/mole at 25°C. ΔS = 70 − 100 cal/°K/mole. (½M) (½M)

* Hydrophobic interaction. (½M)

(V) Major interactions involved in the tertiary structure of Proteins



(3) (i) Heat can be used to disrupt hydrogen bonds and non-polar hydrophobic interactions. (1M)

(ii) A monolayer pressure-area isotherm shows varieties phases.

* At large area they are two dimensional gas.
* On condensation a new phase appears and chains are having mutual interaction but they are disordered ... Liquid expanded (LE) (½M)
* Further compression leads to liquid condensed phase where they are more ordered. (LC) (½M)
* Finally at high pressure, they are two dimensional solid (S). With further increase in pressure the monolayer collapse to form a 3D structure. (½M)

(iii) $\pi V = n_B RT$ (½M) $\quad n_B = \frac{w_B}{m_B}$

$$m_B = \frac{1.08\,g \times 0.0821\,\ell\cdot atm/mol\cdot K \times 298\,K}{(5.85/760)\,atm \times 0.05\,\ell} \quad (½M)$$

$$= 68655\,g/mol. \quad (½M)$$

(iv) Secondary Structure of DNA:

Common features:

* All are right handed helices (except Z DNA)
* All have symmetry axis.
* Antiparallel structure is important for base pairing within a single strand (t RNA). Parallel pairing does not allow hairpin loops. (1M)

Varying parameters:

* Number of bps per turn
* Tilt of bp (angle b/w bps and helix axis)
* Diameter and groove of the helix. (1M)

— any 2 points in each.

(v) $R_c = Nl = 4500 \times 143 \times 10^{-12} m = 6.435 \times 10^{-7} m$

$R_G = \sqrt{\frac{N}{6}}\, l = \sqrt{\frac{4500}{6}} \times 143 \times 10^{-12} m = 3.916 \times 10^{-9} m$ (1M)

(vi) Random flight and rotational isomeri state Theory:

* A Local interaction stabilizes the helices and they contribute to the elastic entropy of

folding of globular protein.

* Under special solvent conditions the non-local interactions can be neglected.

* To measure whether local or non-local interactions are important, find the characteristic ratio which takes the form, where $\langle R^2 \rangle$ is mean square end to end distance and l^2 is mean square bond length.

* Three major states like trans and two Gauche can be assumed like alkanes. (2M)

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(4) (i) $$V_{bond} = V^{o}_{bond} + k_{bond}(r - r_o)^2$$ (1M)

(ii) * A low-temperature simulation facilitates the process of finding the lowest energy conformation of a system.

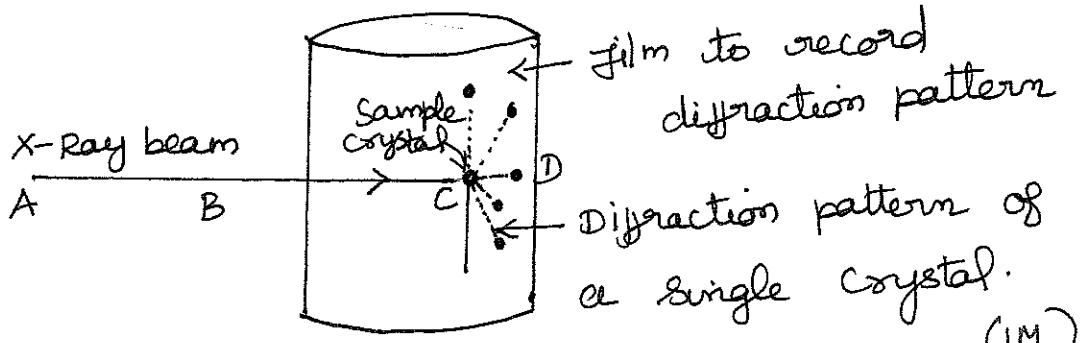
* The molecule is allowed to melt during the molecular dynamics simulation and reanneal during energy minimization (simulated annealing) — any 2 points (1M)

(iii) * Growing a crystal requires bringing the concentration of the material in solution to supersaturation.

* A molecule comes out of the solution when its concentration exceeds the intrinsic solubility S°.

—any 2 points (1M)

(iv) Laue's Transmission Method :



(1M)

A - Source of x-rays - This emits continuous beam of λ known as white radiation, obtained from a tungsten target at about 60,000 Volts.

B - Pinhole collimator : By passing through this, a fine pencil of x-rays is obtained.

C - C is a crystal. It is set on a holder to adjust its orientation.

D - is a film arranged on a rigid base. This film is provided with a beam stop to prevent

direct beam from causing excessive fogging of the film.

* The position of the crystal is held stationary in a beam of X-rays. The X-rays after passing through the crystal are diffracted and are recorded on a photographic plate. (1M)

(v) $n\lambda = 2d \sin\theta$

$$d = \frac{n\lambda}{2 \times \sin\theta} \quad (\frac{1}{2}M)$$

$$= \frac{1 \times 154}{2 \times \sin 14.17^\circ} = \underline{314.67 \text{ pm}} \quad (\frac{1}{2}M)$$

(5) (i) The origin of the signal in NMR:

* The nuclei of certain elements and isotopes have spin states that are quantized.

* ^1H has a spin quantum number $I = \frac{1}{2}$ and has allowed spin states of $+\frac{1}{2}$ or $-\frac{1}{2}$.

* Nuclei with $I = 0$ do not have spin and do not respond to an external magnetic field.

* In the presence of an external magnetic field

the nuclei orient either with (α- state) or against the magnetic field (β- state).

* Protons in an external magnetic field absorb at different frequencies depending on the e^- density around that proton.
* High e^- density around the nucleus shields the nucleus from external magnetic field — signals are upfield.
* Low e^- density — deshields the nucleus → signals are downfield. (1M)

* CH_3-CHBr_2

(a) (b) → Quartet

(a) → Doublet

Splitting is based on (n+1) coupling with neighbouring protons. (1M)

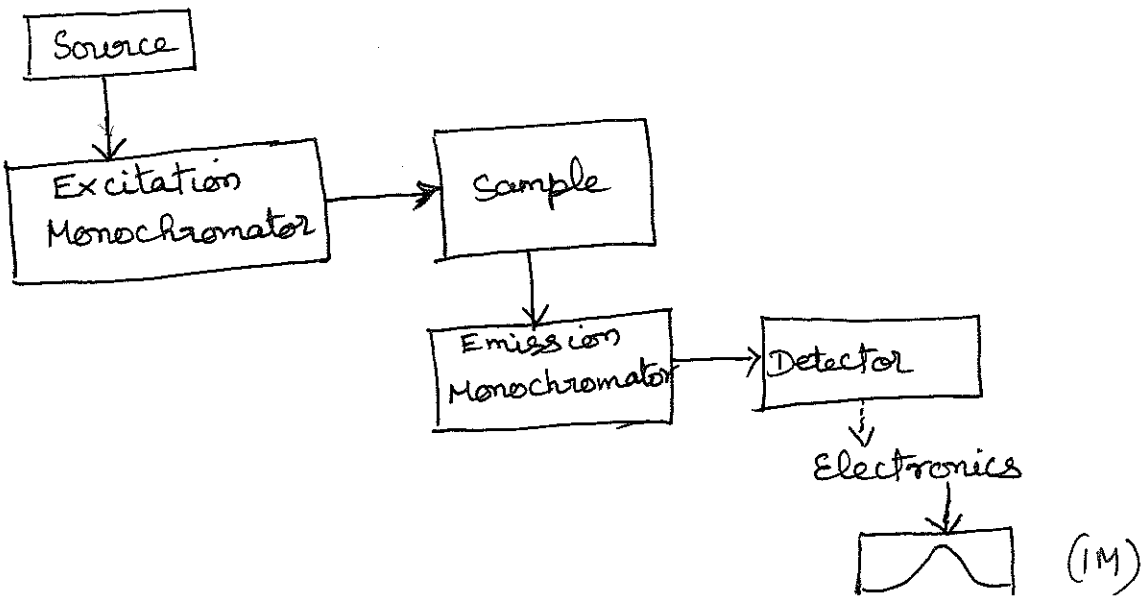
(ii) * CD spectrum of a protein can provide information about the relative amount of the major types of secondary structure (α, β and random coil)

* CD spectra is used to study the conformational changes (denaturation) of proteins.

(1M)

(iii) Fluorescence Instrumentation:

* The source is generally a high pressure Xenon arc fed by a stable direct current power supply.
* Fluorescence instruments use light to excite the sample and observe the fluorescence at right angles.
* Monochromator before the sample chooses the λ of the exciting light and a monochromator after the sample scans the λ of the emitted light.
* The fluorescence radiation from the excitation monochromator is passed on to the photomultiplier detector through a slit.
* The output is further amplified and then displayed on a recorder or meter. (1M)



(1M)

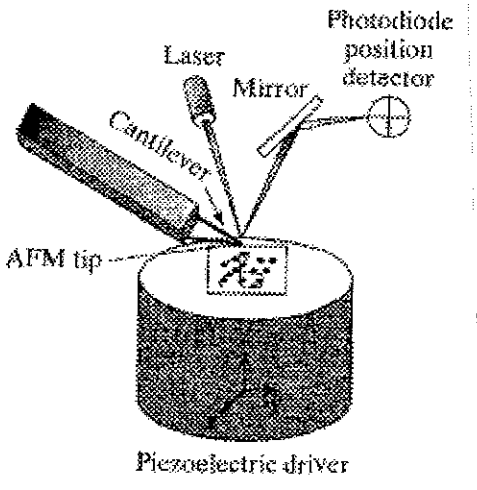
(iv) Optical Tweezers:

* Optical tweezers use light to manipulate microscopic objects as small as a single atom.
* The radiation pressure from focussed laser beam is able to trap small particles. (Momentum transfer associated with bending light). (1M)

Overtones:

* At higher quantum levels there is deviation from simple harmonic oscillators and the vibration becomes anharmonic.
* Anharmonicity accounts for the appearance of additional weak absorption lines called overtones. (1M)

(v)



(1M)

(vi) Electronic Transitions in ethanol $CH_3CH_2\ddot{O}H$

$\sigma \rightarrow \sigma^*$
$n \rightarrow \sigma^*$ } (1M)

C. Vijaya
3/6/2013

BITS PILANI-DUBAI,INTERNATIONAL ACADEMIC CITY ,DUBAI
II YEAR BIOTECH SECOND SEMESTER,2012-2013
TEST- 2 (Open book)

Course Title :Biophysics **Course No:BIOT F215**
Date:29.04.2013 **Total Marks:20**
Time: 50 min **Weightage : 20%**
Answer all questions sequentially

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1. A 95% alcohol solution cannot be used as a disinfectant on the skin, Justify. **(2M)**

2. Determine the rate of diffusion (flux) for aspirin dissolving through the stomach lining. C_1= 50 mg/L and C_2 = 290 mg/L. The diffusivity constant of aspirin is 0.29 x 10^{-9} cm^2/s and the thickness of the stomach lining is approximately 0.5 cm. **(3M)**

3. What are molecular chaperones? Give example. **(2M)**

4. If a solution containing 30.0 g of protein per liter has a measured osmotic pressure of 9.4 mm Hg at 25°C, Calculate the molar mass of the protein. **(3M)**

5. Explain the terms Levinthal's paradox and Simulated annealing. **(4M)**

6. Give the limitations of heteropolymer collapse theory. **(2M)**

7. Write a note on the forces and factors that favour the aggregation state in bilayer and monolayer. **(2M)**

8. Schematically represent the potential energy for the deformations associated with any bond length as in the case of harmonic springs. **(2M)**

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Date:29.04.2013 | **Total Marks:20**
Time: 50 min | **Weightage : 20%**

ANSWERING AND MARKING SCHEME

(1) 95% alcohol solution merely coagulates the protein on the outside of the cell wall and prevents any alcohol from entering the cell. So it cannot denature the proteins inside of the cell. (2M)

(2)

$$J = -D(dC/dx) \quad (1M)$$

$$D = 0.29 \times 10^{-9}\ cm^2/s$$

$$dC = (C_1 - C_2) = 50 - 290\ mg/L = -240\ mg/1000cm^3$$

$$dx = 0.5\ cm$$

$$J = -(0.29 \times 10^{-9}\ cm^2/s) \times (-240\ mg/cm^3)/(0.5\ cm) \quad (1M)$$

$$= 1.392 \times 10^{-10}\ mg/s.cm^2. \quad (1M).$$

(3) Chaperones are proteins that assist the non-covalent folding/unfolding of other macromolecular structures

but do not occur in these structures, when the latter are performing their normal biological functions (eg) $H_{sp}90$. (2M)

(4)

$$\pi V = n_B RT$$

$$n_B = \frac{w_B}{m_B} \quad (1M)$$

$$m_B = \frac{30\,g \times 0.0821\ l.atm/mol.K \times 298\,K}{(9.4/760)\,atm \times 1\ litre} \quad (1M)$$

$$= 5.9383 \times 10^4\ g/mol. \quad (1M)$$

(5) Levinthal's Paradox:

* It is a thought experiment in the theory of protein folding dynamics.
* Cyrus Levinthal noted that because of very large number of degrees of freedom in an unfolded polypeptide chain, the molecule has an astronomical number of possible conformations. The enormous difference between actual folding time and the time taken (calculated) by the process of random search is called Levinthal's paradox. (2M)

Simulated annealing:

* In molecular dynamics, a low-temperature simulation facilitates the process of finding the lowest energy conformation of a system.
* At any time interval the state of the system along the dynamics trajectory can slowly reduced to T = 0 K to a sample of new energy well.
* The molecule is allowed to melt during the molecular dynamics simulation and reanneal during energy minimization. The entire process is known as simulated annealing. (2M)

(6)
* The thermodynamic parameters are calculated using a pathway between the denatured and native state by two-sequential processes. (collapse and then ordering at the surface). Other pathways are not considered.
* The theory does not address regarding kinetics, barriers or whether the transition is first order. (2M)

(7) * Hydrophobic effect - it is due to water structural effect. 2 nonpolar entities have a tendency to come close in aqueous media

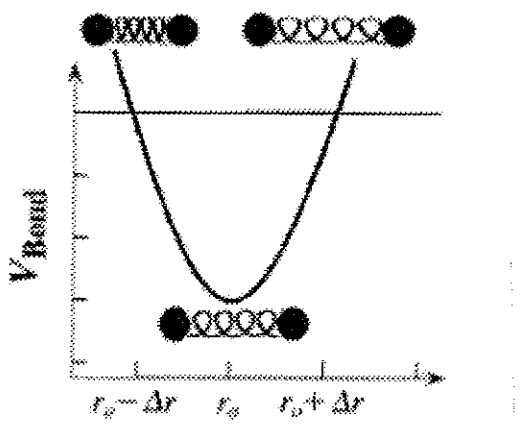
$\Delta G_{monomer} \longrightarrow$ bilayer/monomer (aggregate) is large negative

* Vanderwaal's interaction : in monomer state the amphipheles are far separated. In aggregated state they have vander waal's interaction due to close contact

$\Delta G_{monomer} \longrightarrow$ aggregated state is large -ve.

$\Sigma \Delta G$ must be -ve for a stable monolayer or bilayer. (2M)

(8) Potential energy for the deformations associated with bond length.



(2M)

C. Vijaya
28/4/2013

BITS PILANI, INTERNATIONAL ACADEMIC CITY ,DUBAI
II YEAR BIOTECH SECOND SEMESTER,2012-2013
TEST- 1 (Closed book)

Course Title :Biophysics **Course No:BIOT F215**
Date:11.03.2013 **Total Marks:25**
Time: 50 min **Weightage:25%**

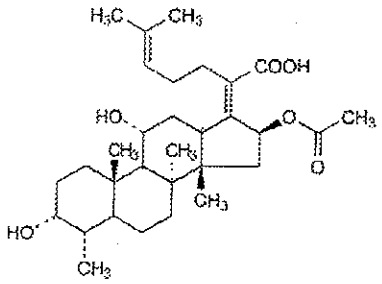
Useful Data: c = 3 x 10^8 m/s , e = 1.602 x10^{-19}C, ε_0 = 8.854 x$10^{-12}$$J^{-1}C^2m^{-1}$, h= 6.626 x 10^{-34} J.s
1 amu = 1.660 x 10^{-27}Kg.
Answer all questions sequentially

1. Calculate the vibrational frequency (cm^{-1}) of ^{12}C ^{16}O , the force constant k = 1.86 x 10^3 Kgs^{-2}. Calculate the vibrational energy of a normal mode in its ground state of n=0. **(5M)**

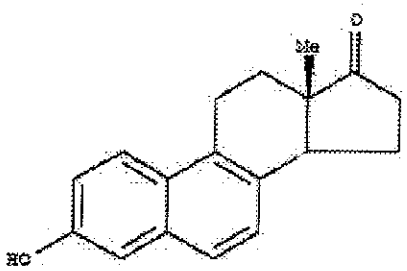
2. The ionic radius of barium ion and sulphide ion are 0.143 nm and 0.174 nm, respectively. Calculate the attractive force between a pair of barium and sulphide ions that just touch each other. **(4M)**

3. Identify the chiral centres and indicate the number of stereoisomers possible for the structures given below. **(3M)**

Fusidic acid



Equilenin



4. Write a note on origin of hydrophobic effect. **(2M)**

5. How will you quantify the polarity of amino acids using the thermodynamic parameter free energy ? **(3M)**

6. Amino acids with an amide on the side chain do not produce basic solution. Justify. **(2M)**

7. Covalent bond lengths can be decomposed into covalent radii of the individual atomic radii. However a hydrogen bond cannot be decomposed in the similar way. Why? **(2M)**

8. Schematically represent the torsion angles and dihedral angle of the four atoms around the bond A-B-C-D. **(3M)**

9. Write the significance of cubic symmetry in protein structures with an example. **(1M)**

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Time: 50 min | **Weightage:25%**

ANSWERING AND MARKING SCHEME

(1)

$$\bar{\nu} = \frac{1}{2\pi c}\sqrt{\frac{k}{\mu}} \quad (\tfrac{1}{2}\,M)$$

$$\mu = \frac{m_A m_B}{m_A + m_B} = \frac{12\times 16}{12+16} \times 1.660\times 10^{-27}\,kg = 1.138\times 10^{-26}\,kg \quad (1M)$$

$$\bar{\nu} = \frac{1}{2\times 3.14\times 3\times 10^{10}\,cm/s}\sqrt{\frac{1.86\times 10^{3}\,kg\,s^{-2}}{1.138\times 10^{-26}\,kg}} \quad (\tfrac{1}{2}\,M)$$

$$= \underline{2145.6\ cm^{-1}} \quad (1M)$$

$$E_0 = \tfrac{1}{2} h\nu \quad (\tfrac{1}{2}\,M)$$

$$= \tfrac{1}{2} \times 6.626\times 10^{-34}\ J.s \times \frac{1}{2\pi}\sqrt{\frac{1.86\times 10^{3}\,kg\,s^{-2}}{1.138\times 10^{-26}\,kg}} \quad (\tfrac{1}{2}\,M)$$

$$= \underline{2.132\times 10^{-20}\ J.} \quad (1M)$$

(2)

$$F_{attractive} = -\frac{Z_1 Z_2 e^2}{4\pi\varepsilon_0 a^2} \quad (1M)$$

$$a = \text{sum of } r_{Ba^{2+}} + r_{S^{2-}} = 0.143 + 0.174 = 0.317\,nm \quad (1M)$$

$$= \frac{-(+2)(-2)(1.602 \times 10^{-19}\ C)^2}{4 \times 3.14 \left[8.854 \times 10^{-12}\ C^2/(N.m)^2\right](0.317 \times 10^{-9}\ m)^2}$$

(1M)

$$= 9.18 \times 10^{-9}\ N \quad (1M)$$

(3) In Fusidic acid there are 10 chiral carbons

$\therefore$ the no of stereoisomers is $2^n = 2^{10} = 1024$. (1½ M)

In Equilenin there are 2 chiral centres

$\therefore$ the no of stereoisomers is $2^2 = 4$. (1½M)

(4) * Hydrophobic effect arises from the strong attractive forces between water molecules which being isotropically arranged, must be disrupted.

* Non-polar groups cannot compensate the disruption.

* When a solution of non-polar solute is made in water, they prefer to occupy the same cavity. (like oil droplets in water). This attraction is Hydrophobic attraction.

* Driving force in folding of macromolecules, binding of substrates to enzymes etc. (4)

(5) * solubility of amino acid is considered in a polar solvent (Water) and a non-polar solvent (ethanol). (½M)

* Free energies are measured for the amino acid in water (ΔG_1) and ethanol (ΔG_2). The free energy will give an idea how the transfer is favoured. (½M)

* for glycine as side chain $G_{Transfer} = \frac{-4.63}{Kcal/mole}$ (being -ve) glycine would transfer spontaneously from C_2H_5OH to H_2O. (1M)

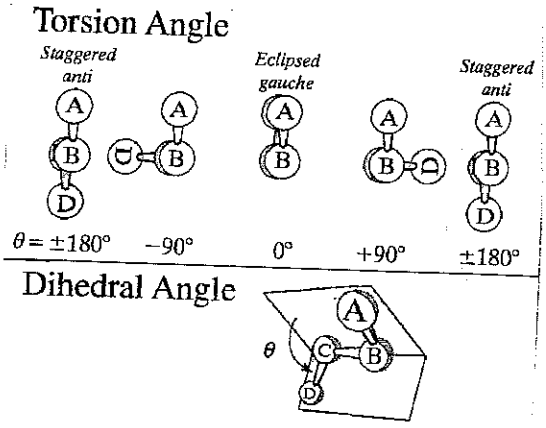
* for phenylalanine side chain $G_{Transfer} = \frac{+2.65}{Kcal/mole}$. The calculation shows that a phenylalanine side chain would prefer to go spontaneously from water to ethanol. They stay interior of protein which is relatively non-polar (compared to the exterior of protein). (1M)

(6) The lone pair of e⁻s on N atom is involved in the resonance with carbonyl group. The e⁻ pair

of N is not easily available for protonation. So the basic character is decreased. (2M)

(7) H-bonds are group-pair properties. The properties of H-bonds are dependent not only on the first neighbour but also on the sequential nature of the total pattern of bonding. (2M)

(8)



(2M)

(1M)

(9) This group of protein structure plays an important role in storage and transport particularly the icosahedral symmetry (eg) Ferritin (1M)

C. Vijaya
10/3/2013

BITS, PILANI – DUBAI CAMPUS

SECOND SEMESTER 2012 – 2013

Course Code: BIOT F21 | **SECOND YEAR** | Date:13.05.2013
Course Title:Biophysics | QUIZ-2 | Max Marks:7
Duration : 20 minutes | Weightage: 7%

Name: ..... **ID No:** ..... **Sec / Prog:** .....

Instructions: (if any) Over writing will be taken as wrong answer

1. The X-ray wavelength from a copper X-ray is 154.2 pm. If the inter-planar distance from NaCl is 286 pm, Calculate the angle θ for n=1. **(1M)**

2. Write any two advantages of Atomic Force Microscopy over Scanning Electron Microscopy. **(1M)**

3. What happens during the tapping mode of operation in the Atomic Force Microscopy technique ? **(1M)**

4. Give the three distinct steps required in the X-ray diffraction technique from single crystals. **(1M)**

5. Write the expression for minimum wavelength λ_{min} and λk_{β} of x-rays. **(1M)**

6. What is meant by the term Bremsstrahlung ? **(1M)**

7. Calculate the R_{rms} and R_G for a linear polymeric chain containing 350 monomeric units each being 55 Å long. **(1M)**

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BITS, PILANI – DUBAI CAMPUS

SECOND SEMESTER 2012 – 2013

Course Code: BIOT F21 | **SECOND YEAR** | Date:13.05.2013
Course Title:Biophysics | QUIZ-2 | Max Marks:7
Duration : 20 minutes | Weightage: 7%

Name: ..... **ID No:** ..... **Sec / Prog:** .....

ANSWERING and Marking Scheme

Instructions: (if any) Over writing will be taken as wrong answer

1. The X-ray wavelength from a copper X-ray is 154.2 pm. If the inter-planar distance from NaCl is 286 pm, Calculate the angle θ for n=1. **(1M)**

$$n\lambda = 2d \sin\theta$$

$$\sin\theta = \frac{n\lambda}{2d} = \frac{1 \times 154.2\,pm}{2 \times 286\,pm} = \underline{15.63^\circ}$$

2. Write any two advantages of Atomic Force Microscopy over Scanning Electron Microscopy. **(1M)**

AFM provides

* a three-dimensional surface profile
* high resolution
* AFM do not require any special treatment.

—any 2 points.

3. What happens during the tapping mode of operation in the Atomic Force Microscopy technique ? **(1M)**

* In the tapping mode, the cantilever is made to oscillate, so the tip taps its way across the sample, which has been deposited on a very smooth surface.

4. Give the three distinct steps required in the X-ray diffraction technique from single crystals. **(1M)**

* Growing a crystal
* Collecting the XRD pattern from the crystal
* constructing and refining a structural model to fit the XRD pattern.

5. Write the expression for minimum wavelength λ_{min} and λk_β of x-rays. **(1M)**

$$\lambda_{min} = hc/ve = 1240/V$$

$$\lambda k_\beta = hc/(E_M - E_K)$$

6. What is meant by the term Bremsstrahlung ? **(1M)**

This is radiation given off by the electrons as they are scattered by the strong electric field near the high-Z (proton number) nuclei. These x-rays have a continuous spectrum.

7. Calculate the R_{rms} and R_G for a linear polymeric chain containing 350 monomeric units each being 55 Å long. **(1M)**

$$R_{rms} = \sqrt{N}\, l = \sqrt{350} \times 55\,\text{Å} = 1028.9\,\text{Å}$$

↓

root mean square separation

$$R_G = \sqrt{\frac{N}{6}} \times l = \sqrt{\frac{350}{6}} \times 55\,\text{Å} = 420\,\text{Å}$$

radius of gyration

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C. Vijaya
12/5/2013

BITS, PILANI – DUBAI CAMPUS

SECOND SEMESTER 2012 – 2013

Course Code: BIOT F215 **SECOND YEAR** Date:1.04.2013
Course Title:Biophysics Max Marks: 8
Duration : 20 minutes Weightage: 8%

Name: ..... **ID No:** ..... **Sec / Prog:** .....

Instructions: (if any) Over writing will be taken as wrong answer

1. Which gives rise to the net dipole moment in proteins? **(1M)**

2. . Calculate the number of modes of vibration for ethane molecule. **(1M)**

3. What is meant by Pitch in the alpha helix geometry of proteins ? Give its relation with the gradient angle . **(1M)**

4. Schematically represent all the major interactions involved in the tertiary structure of proteins. **(2M)**

5. Schematically illustrate the phosphodiester bond. **(1M)**

6. In a double stranded DNA the amount of guanine residues was found to be 30 % . Determine the amount of thymine residues in the same. **(1M)**

7. Write any 2 features of Quaternary structure of RNA. **(1M)**

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BITS, PILANI – DUBAI CAMPUS

SECOND SEMESTER 2012 – 2013

Course Code: BIOT F215
Course Title:Biophysics
Duration : 20 minutes

SECOND YEAR

Date:1.04.2013
Max Marks: 8
Weightage: 8%

Name: ..... **ID No:** ..... **Sec / Prog:** .....

ANSWERING and MARKING SCHEME

Instructions: (if any) Over writing will be taken as wrong answer

1. Which gives rise to the net dipole moment in proteins? **(1M)**

Anisotropic charge distribution.

2. . Calculate the number of modes of vibration for ethane molecule. **(1M)**

Ethane Non-linear molecule $3N-6$

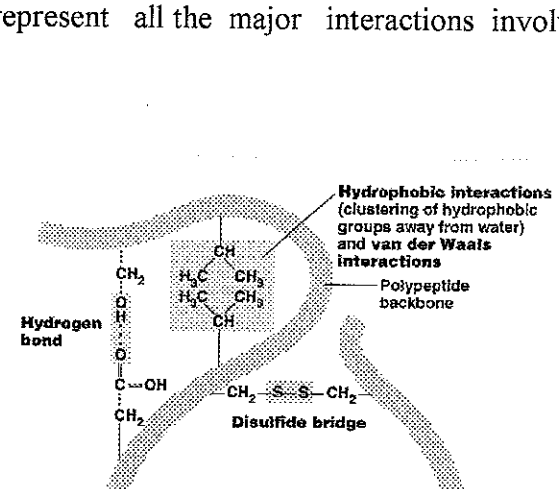
C_2H_6 $\therefore 3(8)-6 = 18$

3. What is meant by Pitch in the alpha helix geometry of proteins ? Give its relation with the gradient angle . **(1M)**

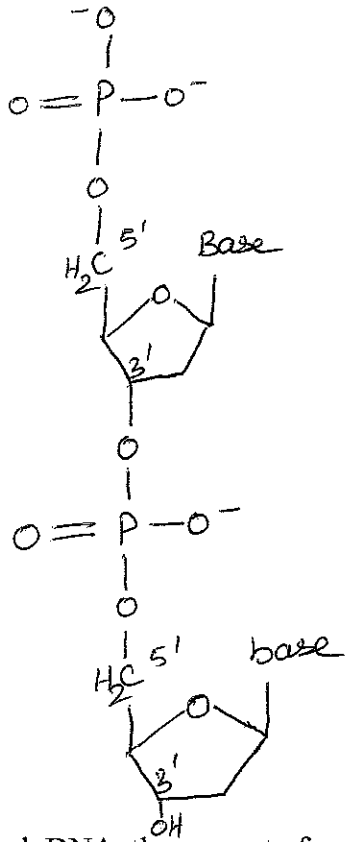
The distance a point moves in the direction of its axis per revolution is called Pitch.

$P/2\pi r = \tan\phi$, where r is the radius of helix.

4. Schematically represent all the major interactions involved in the tertiary structure of proteins. **(2M)**



5. Schematically illustrate the phosphodiester bond. **(1M)**



6. In a double stranded DNA the amount of guanine residues was found to be 30 % . Determine the amount of thymine residues in the same. **(1M)**

G = 30%. Hence C = 30%.

Therefore A + T = 40 % Hence T = 20 %

7. Write any 2 features of Quaternary structure of RNA. **(1M)**

* They are formed by identical subunits and are stabilized by interstrand base pairing, but not intrastand.
* Complementary base pairing possibility may have a role in quaternary structure formation.

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C. Vijaya
31/3/2013