INDIAN INSTITUTE OF TECHNOLOGY GUWAHATI

MID SEMESTER EXAMINATION - BT 305

Maximum Marks: 40. Time: 2 hours. Total 8 questions, all questions carry 5 marks

Q1. A) The internal coordinates of ethane molecule in staggered conformation is shown below. Re-write the internal coordinate file for the eclipsed conformation. **(3 marks)**

1	C						
2	C	1.54	1				
3	H	1.0	1	109.5	2		
4	H	1.0	2	109.5	1	180.0	3
5	H	1.0	1	109.5	2	60.0	4
6	H	1.0	2	109.5	1	−60.0	5
7	H	1.0	1	109.5	2	180.0	6
8	H	1.0	2	109.5	1	60.0	7

B) The VADAR output file of first 26 amino acids of a protein molecule is shown below. Study the details in this file, and answer the following questions.

RES. NUM.	RES. NAME	SCND STRUC	HBOND HBOND	BTURN BTURN	RES. ASA	FRAC. ASA	RES. VOL.	FRAC. VOL.	PHI PHI	PSI PSI	OMEGA OMEGA
Chain A											
1	MET	CCC C			221.9	1.02	151.2	0.92	0.0	151.9	169.7
2	THR	CBC C			126.3	0.81	109.3	0.91	-83.8	150.2	-179.8
3	PRO	CBC C			90.0	0.59	105.7	0.91	-64.5	147.5	173.7
4	ALA	CBC C			88.6	0.72	87.5	0.99	-74.2	128.0	178.1
5	VAL	BBB B			81.4	0.47	119.9	0.88	-113.0	146.3	179.9
6	THR	BBB B	25A,25A		49.5	0.32	114.6	0.95	-117.4	144.1	169.7
7	THR	BBB B			71.9	0.46	111.7	0.93	-88.8	123.5	176.3
8	TYR	BBB B	23A,23A		7.1	0.03	188.9	0.97	-107.0	147.7	179.8
9	LYS	BBB B	57A,55A		92.8	0.40	188.1	1.11	-114.0	145.8	170.1
10	LEU	BBB B	21A,21A		0.0	0.00	150.7	0.92	-118.9	124.0	172.2
11	VAL	BBB B	59A,57A		37.7	0.22	131.3	0.96	-98.8	120.1	-175.5
12	ILE	BBB B	19A,19A		2.6	0.01	160.5	0.99	-113.6	117.1	175.0
13	ASN	BBB B	61A,59A		78.1	0.45	120.3	0.97	-113.8	70.0	-178.1
14	GLY	BBC B	17A		4.8	0.05	64.9	1.01	-92.8	170.3	176.6
15	LYS	CCC C			169.7	0.74	161.2	0.95	-66.1	-39.9	179.0
16	THR	CBC C			140.7	0.90	110.2	0.91	-121.8	-19.7	-179.4
17	LEU	CBC C	14A		54.1	0.26	163.1	0.99	-108.9	123.9	-179.1
18	LYS	CBC C			167.1	0.72	156.9	0.93	-141.0	145.5	172.3
19	GLY	CCC C	12A,12A		38.7	0.44	63.3	0.98	137.6	-143.1	-176.7
20	GLU	BBB B			105.8	0.55	126.1	0.91	-140.4	149.8	170.8
21	THR	BBB B	10A,10A		42.2	0.27	115.6	0.96	-142.8	174.6	-176.1
22	THR	BBB B			77.3	0.50	109.2	0.91	-139.7	159.4	170.1
23	THR	BBB B	8A,8A		34.5	0.22	114.0	0.94	-147.6	158.1	177.1
24	LYS	BBB B			154.9	0.67	161.4	0.95	-111.2	136.2	178.5
25	ALA	BBB B	6A,6A		6.8	0.06	89.2	1.01	-155.6	161.4	176.8
26	VAL	BCC C			80.6	0.47	118.9	0.87	-74.0	-24.1	-177.8

1. The fractional Solvent accessible surface area of Residue number 10 LEU is 0.00. What inference do you make from this information? **1 mark**
2. By examining the Phi, Psi coordinates, how many beta sheet and beta strand can you see from this structure file. **1 mark**

Q2. A shortened list of most influential scientists converted to peptide sequences are shown in the below table. Write your name and surname as a peptide sequence as the first entry. Ignore letters that do not represent amino acids. Which scientists' name converted to peptide sequence aligns with your name most favourably and which one is least favourable.

ALERTEINSTEIN
A_D_ITY_AINDAL

ALERTEINSTEIN
ADI TYAIN DAL

LISPASTER

Notes:

1. Insertions and deletions are permitted
2. Residue exchange matrix is provided (following) for scoring

Your NameSurname (as one sequence)	IsaacNewton
AlbertEinstein	CharlesDarwin
LouisPasteur	JohannesKepler
FrancisCrick	GustavKirchhoff

_L_ISPA-STE--R
ADITYAINDAL

FRANCIS_CRICK__
--AD-ITYA-IN-D-AL

B, J, O, U, Z, X

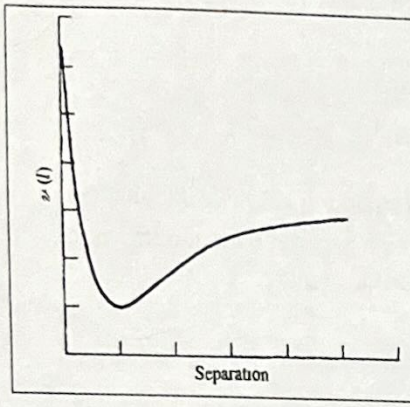
ISAAC NEWTN
--A

Residue Exchange Matrix

	A	R	N	D	C	Q	E	G	H	I	L	K	M	F	P	S	T	W	Y	V
A	4	-1	-2	-2	0	-1	-1	0	-2	-1	-1	-1	-1	-2	-1	1	0	-3	-2	0
R	-1	5	0	-2	-3	1	0	-2	0	-3	-2	2	-1	-3	-2	-1	-1	-3	-2	-3
N	-2	0	6	1	-3	0	0	0	1	-3	-3	0	-2	-3	-2	1	0	-4	-2	-3
D	-2	-2	1	6	-3	0	2	-1	-1	-3	-4	-1	-3	-3	-1	0	-1	-4	-3	-3
C	0	-3	-3	-3	9	-3	-4	-3	-3	-1	-1	-3	-1	-2	-3	-1	-1	-2	-2	-1
Q	-1	1	0	0	-3	5	2	-2	0	-3	-2	1	0	-3	-1	0	-1	-2	-1	-2
E	-1	0	0	2	-4	2	5	-2	0	-3	-3	1	-2	-3	-1	0	-1	-3	-2	-2
G	0	-2	0	-1	-3	-2	-2	6	-2	-4	-4	-2	-3	-3	-2	0	-2	-2	-3	-3
H	-2	0	1	-1	-3	0	0	-2	8	-3	-3	-1	-2	-1	-2	-1	-2	-2	2	-3
I	-1	-3	-3	-3	-1	-3	-3	-4	-3	4	2	-3	1	0	-3	-2	-1	-3	-1	3
L	-1	-2	-3	-4	-1	-2	-3	-4	-3	2	4	-2	2	0	-3	-2	-1	-2	-1	1
K	-1	2	0	-1	-3	1	1	-2	-1	-3	-2	5	-1	-3	-1	0	-1	-3	-2	-2
M	-1	-1	-2	-3	-1	0	-2	-3	-2	1	2	-1	5	0	-2	-1	-1	-1	-1	1
F	-2	-3	-3	-3	-2	-3	-3	-3	-1	0	0	-3	0	6	-4	-2	-2	1	3	-1
P	-1	-2	-2	-1	-3	-1	-1	-2	-2	-3	-3	-1	-2	-4	7	-1	-1	-4	-3	-2
S	1	-1	1	0	-1	0	0	0	-1	-2	-2	0	-1	-2	-1	4	1	-3	-2	-2
T	0	-1	0	-1	-1	-1	-1	-2	-2	-1	-1	-1	-1	-2	-1	1	5	-2	-2	0
W	-3	-3	-4	-4	-2	-2	-3	-2	-2	-3	-2	-3	-1	1	-4	-3	-2	11	2	-3
Y	-2	-2	-2	-3	-2	-1	-2	-3	2	-1	-1	-2	-1	3	-3	-2	-2	2	7	-1
V	0	-3	-3	-3	-1	-2	-2	-3	-3	3	1	-2	1	-1	-2	-2	0	-3	-1	4

Q3.

The equilibrium bond length of few bonds is given below.



Bond	l_0 (Å)	k (kcal mol^{-1} Å^{-2})
Csp^3-Csp^3	1.523	317
Csp^3-Csp^2	1.497	317
$Csp^2=Csp^2$	1.337	690
$Csp^2=O$	1.208	777
Csp^3-Nsp^3	1.438	367
C–N (amide)	1 345	719

How much would be the change in energy (in kcal mol^{-1} A^{-2}) if the C----N and C----C(=O) single bonds of amino acid alanine is stretched to 0.16 nm and compressed to 0.14 nm respectively. Rationalise your answer. You may assume that the strain in the bonds follow Hooke's Law.

Q4. A) In MD simulations, we allow the system to evolve in time indefinitely, that system will eventually pass through all possible states with a hope of generating enough representative conformations. What is the statistical relevance of this exercise? What do we achieve from this?

2 marks

B) 'The Verlet algorithm uses positions and accelerations at time t and the positions from time t-dt to calculate new positions at time t+dt'. Prove this statement from first principles. **3 Marks**

Q5. Define force field. What are the constituent energy terms in classical force fields used for MD simulations? What is the consequence if we switch off improper dihedral angle term?

1 + 3 + 1 = 5 Marks

Q6. Explain briefly the following concepts.

A) Solvent Accessible Surface B) Solvent Excluded Surface and C) van der Waals surface. In an ideal calculation of rolling probe method, how is probe size important? **1+1+1+2 = 5 marks**

Q7. Examine the structure of methane molecule given in the following diagram (Figure 1A). Assume that you define force field with a potential energy (u) Vs angle (ɵ). Draw and spot the position of Potential Energy in the graph (Figure 1B) in your answer book after giving appropriate scales for x and y axis as per your calculations. Attempt it for all possible angle combinations, while there is a bend of 3° and 2° in angle between **H_1, C, H_3** and **H_2, C, H_3** of methane molecule respectively.

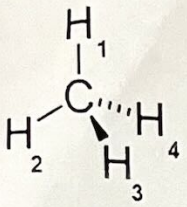


Figure 1A

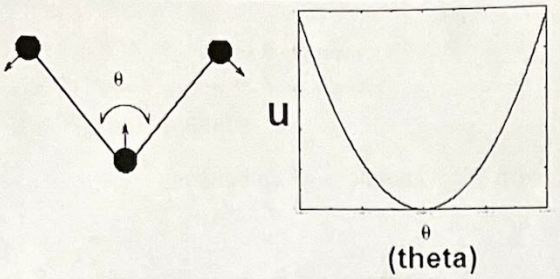
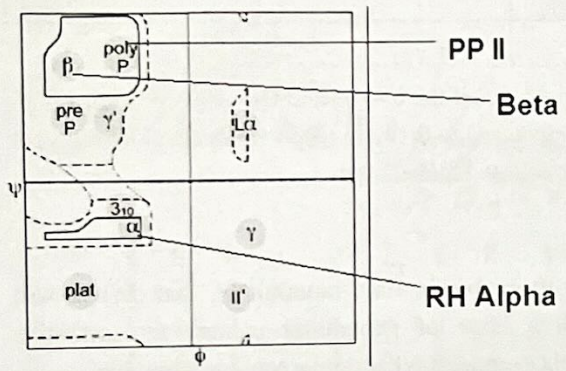


Figure 1B

Q8. In the following Ramachandran map, β (beta), Polyproline (PP II) and α (alpha) helical region are shown. Write approximate dihedral angles for a nine residue poly-glycine peptide to get the structure of A) Right handed alpha helix; B) Beta sheet; C) Beta strand and D) Random coil.



1+2+1+1 = 5 marks

----------End of Questions----------