



Semester I Examinations 2010 / 2011

Exam Code(s)	3BS9, 3BPM
Exam(s)	Third year Chemistry and Third year Biopharmaceutical Chemistry
Module Code(s)	CH328
Module(s)	Molecular Modeling and Drug Design
Paper No.	
External Examiner(s)	Professor Paul Seakins
Internal Examiner(s)	Professor Paul V. Murphy Professor Leif A. Eriksson Professor Rob Woods
<u>Instructions:</u>	Answer <u>four</u> questions: <u>One</u> from each Section
	All questions carry 100 marks
Duration	2 hours
No. of Pages	2
Discipline(s)	Chemistry
Requirements	None

Section A

Molecular Mechanics / Structure (answer one of the two questions – 100 marks)

1. What type of structural and experimental information do you expect to find in the Protein Databank (PDB)? Name two experimental methods commonly used to determine molecular 3D structures.
2.
 - a. What is the difference between a local energy minimum and a global energy minimum?
 - b. Why it is difficult to initiate the formation of an α -helix?
 - c. Why is a parallel β -sheet less stable than an anti-parallel β -sheet?

Section B

Quantum Chemistry (answer one of the two questions– 100 marks)

3. Explain, in a few sentences, each of the following terms:
 - a. Transition state
 - b. LCAO-MO
 - c. Electron correlation
 - d. Coulomb integral
 - e. Slater determinant
4. What is the difference between the van der Waals surface and the Solvent accessible surface of a (macro)molecule? Why do we compute surfaces in computational chemistry, and what information can these provide?

Section C

Bioinformatics (answer one of the two questions– 100 marks)

5. Explain the main features of Structure based virtual screening *versus* Ligand based virtual screening.
6. Assume that you have been given a gene sequence by an experimental colleague (at the Biochemistry department), and they ask you if it is possible to determine the corresponding protein structure. Describe how you would go about this.

Section D

Molecular Dynamics Simulations (answer one of the two questions– 100 marks)

7. Why do we perform free energy calculations to describe molecular interactions? (Hint: definition of free energy in the context of thermodynamic equilibrium). Name two computational methods you can use to evaluate free energy, together with advantages and shortcomings of one method relative to the other.
8. When studying biomolecules, why is molecular dynamics simulation preferable to energy minimization? Why is data from an MD simulation more similar to data from NMR spectroscopy than to data from X-ray crystallography?