

Indian Institute of Technology (IIT) Delhi
Department of Biochemical Engineering and Biotechnology

I SEMESTER 2008 – 2009
BEL722 – GENOMICS AND PROTEOMICS

MAJOR TEST

Date	Nov 22, 2008
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Time = 2 hours

Max. Marks = 40

Answer all the questions

Question #	Question	Marks
1	<p>a) Discuss the salient features of the human genome as put forth by the IHGSC with respect to the evolution, repeats and GC content. (4)</p> <p>b) Define the process of genome annotation. Why is it necessary to annotate genome sequences? (3)</p> <p>c) In an EST project, how does the kind of information that comes from 5'-sequencing differ from 3'-sequencing? Results coming out of EST projects are said to be "low quality, but very informative". What does this mean? (3)</p>	
2	<p>a) How will you detect SNPs and describe the implications of SNPs. (3)</p> <p>b) What is the difference between an ortholog and a paralog? If you did a BLAST search with a sequence from species "A" and found several "hits" from species "B", how might you decide which are orthologous and which are paralogous? (3)</p> <p>c) What is chain-terminator sequencing reaction? Describe the outcome of a chain-terminator sequencing procedure in which (i) too little ddNTP is added (ii) too much ddNTP is added (iii) too few primers are present (iv) too many primers are present. (4)</p>	
3	<p>a) What are the differences between open and close column chromatography? Explain with examples. (4)</p> <p>b) What kind of chromatographic techniques should be used for the high through put protein purification and checking of purity of protein molecules? Explain with justifications. (4)</p>	
4	<p>a) What should be the level of purity of the protein molecules for carrying out X-Ray crystallography, NMR spectroscopy, Mass spectrometric analysis, CD and fluorescence spectroscopy on them? Explain with proper justifications. (6)</p> <p>b) Explain the basic principle of N-terminal amino acid sequence analysis of the protein molecules. Explain the protein sequence analysis using Mass spectrometry based method. (6)</p>	