

CENTRE FOR COMPUTATIONAL BIOLOGY AND BIOINFORMATICS

Course: M.Sc. Bioinformatics Subject: Computational Genomics and Proteomics Semester: 2nd
 Course Code: BIN-466 Maximum Marks: 20 Credit: 2 Time: 1:00 Hr

I. Section -A (All Questions are COMPULSORY)

(5 X 1 = 5)

Q1). ANSWER ALL THE FOLLOWING QUESTIONS

A). Which of the following is not a type of post-translational modification?

- a) Proteolysis b) Protein folding ~~a)~~ Glycosylation d) Lipid addition

B). Pick the correct Gene Expression pathway

a) Gene → Translation → m-RNA → Transcription → Protein

~~b)~~ Gene → Transcription → m-RNA → Translation → Protein

c) Gene → m-RNA → Transcription → Translation → Protein

d) Gene → Transcription → Translation → m-RNA → Protein

C). Which of the following has unusual bases

a). m-RNA

b) t-RNA

~~c)~~ r-RNA

d) hn_RNA

D). Glycosylation is the addition of _____ to the protein.

a) Carbohydrate

b) Lipid

c) Fat d) Minerals

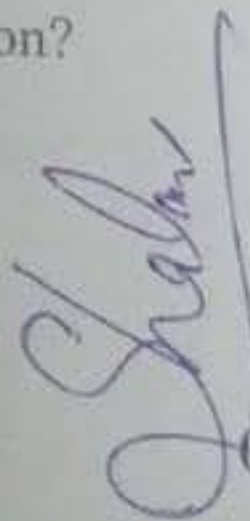
E). Nearly CPA is composed of _____ proteins.

II. Section -B (Attempt any TWO Question)

(2 X 2.5 = 5)

~~Q2)~~ Write a detailed short note on Protein degradation?~~Q3)~~ Differences between the Prokaryotic and Eukaryotic transcription?

Q4). Write about prokaryotic m-RNA processing

~~Q5)~~ Write about mRNA Splicing


(2 X 5 = 10)

III. Section - C (Attempt any TWO Question)

~~Q6)~~ Write about Post-Translation modification?

Q7). Explain Eukaryotic Transcription?

Q8). Write about Cleavage and 3'-Polyadenylation in Eukaryotic m-RNA Processing.

~~Q9)~~ Explain about Prokaryotic Transcription?