

**BIO 316 – BIOINFOMATICS**

**Time: 1½ Hours**

**Credit Unit: 1**

**Instruction: Answer question ONE (1) and any other THREE (3) questions.**

1a. Outline the steps involved in searching for relevant entries on the enzyme human neutrophil elastase to get detailed information, including the sequence of the enzyme. (5 marks)

1b Using bioinformatics facilities determine the position of gene in the human genome. (5mark)

1c. Write briefly on the following:

i. BLAST (5 marks)    ii. BOOTSTRAP (5 marks)    iii. NEME (5 marks)

2a. Give a detail account of local alignment in sequence alignment analysis. (7 marks)

2b. In hemoglobin comparison, outline the steps involved on comparing Amino Acid Sequence for Protein in different organisms (8 marks)

3 a. Briefly elucidate on the following:

i). A ACOMP (Ident, Sim) (3marks)    ii). A ACompident (3 marks)    iii). Accession Number (3 marks)  
 iv). Conserved Domain Database (3 marks)    v). Dot Matrix (3 marks)

4. Write concisely on the following:

i). Parsimony (4 marks)    ii). Phi-blast (4 marks)    iii). Grail (2 marks)  
 iv). Phylogenetic Analysis (5 marks)

**5. Complete the table using coding for Amino Acid in Sequence Information**

S/N	Amino Acid	3-letter code	1- letter code
1.	Alanine		
2.	Arginine		
3.	Asparagine's		
4.	Aspartic Acid		
5.	Cysterine		
6.	Glutamine		
7.	Glutamine Acid		
8.	Glycine		
9.	Histidine		
10.	Leucine		
11.	Lysine		
12.	Methionine		
13.	Phenylalanine		
14.	Proline		
15.	Serine		

(15 marks)