



W1-2-60-1-6

JOMO KENYATTA UNIVERSITY OF AGRICULTURE AND TECHNOLOGY  
UNIVERSITY EXAMINATIONS 2019/2020

EXAMINATION FOR THE DEGREE OF MASTER OF SCIENCE IN  
MOLECULAR MEDICINE

**TIM 3112 : GENOMICS AND BIOINFORMATICS**

DATE: FEBRUARY 2020

TIME: 3 HOURS

**INSTRUCTIONS:**

**ANSWER ANY FOUR QUESTIONS**

**QUESTION ONE [25 MARKS]**

- (a) Describe genome assembly and mapping using paired-end reads obtained from next generation sequencing technologies to identify single nucleotide polymorphisms and structural variants. [15 marks]
- (b) Describe the process of drug development using computer aided drug design (CADD) starting from the gene. [10 marks]

**QUESTION TWO [25 MARKS]**

- (a) Discuss phylogenetic analysis considering acquiring of sequences, multiple sequence alignment and building of phylogenetic tree. [15 marks]
- (b) Give a protein ID. Explain how you can identify potential glycosylation sites of the protein (Describe the steps you will take and the tools you will use). [10 marks]

**QUESTION THREE [25 MARKS]**

- (a) Discuss Basic Local Alignment Search Tool (BLAST) homology search algorithm. [15 marks]
- (b) Describe comparative modeling and its application in drug discovery. [10 marks]

**QUESTION FOUR [25 MARKS]**

- (a) Explain five parameters that can be computed for a given protein sequence using protparam tool. [10 marks]
- (b) Describe on the following databases:
- (i) Uniprot KB [5 marks]
  - (ii) Eupath DB [5 marks]
  - (iii) OMIM [5 marks]

**QUESTION FIVE [25 MARKS]**

(a) Describe the following models of nucleotide substitution.

(i) Kimura – 2- parameter

[5 marks]

(ii) Jukes and cantor 1969

[5 marks]

(iii) Hasegawa, Kishino and Yano (HKY88)

[5 marks]

(b) Discuss two distance based methods for estimating phylogenetic trees.

[10 marks]

**QUESTION SIX [25 MARKS]**

(a) Describe any four DNA sequence formats [10 marks]

(b) Discuss protein-ligand docking and its applications [10 marks]

(c) Distinguish between assembly and mapping of genomes. [5 marks]