



**NATIONAL UNIVERSITY OF SCIENCE AND TECHNOLOGY**

**FACULTY OF APPLIED SCIENCE**

**DEPARTMENT OF APPLIED BIOLOGY AND BIOCHEMISTRY**

**BACHELOR OF SCIENCE HONOURS IN BIOTECHNOLOGY**

**BIOINFORMATICS (SBT4101)**

**Special Examination Paper**

**AUGUST 2024**

This Examination Paper consists of 2 pages

Time Allowed: 3 hours  
Total Marks: 100  
Special Requirements: NONE  
Examiner: PROF J. MBANGA

**INSTRUCTIONS**

1. Answer (4) Questions.
2. Where a question contains subdivisions, the mark value for each subdivision is given in brackets.
3. Illustrate your answer where appropriate with large, clearly labelled diagrams.

**MARK ALLOCATION**

QUESTION	MARKS
1.	25
2.	25
3.	25
4.	25
5	25
6	25
<b>TOTAL</b>	<b>100</b>

1. (a) Outline key considerations when designing primers. (7 marks)
- (b) Distinguish between the following:
- (i) Similarity and Homology. (4 marks)
  - (ii) Paralogs and Orthologs. (4 marks)
- (c) Briefly discuss whether it is better to align DNA or protein sequences. (10 marks)
2. Describe the main criteria for building a multiple sequence alignment (MSA) and discuss the applications of MSA in bioinformatics.
3. Using named examples, compare primary and secondary databases highlighting their applications.
4. (a) Distinguish between local and global alignment. (4 marks)
- (b) Write short notes on the following algorithms:
- (i) Smith – Waltherman. (5 marks)
  - (ii) Needleman – Wunsch. (5 marks)
- (c) Explain how substitution matrices work, detailing how the scoring may be done. (11 marks)
5. Discuss the variants and practical applications of BLAST.
6. Write an essay on protein structural and functional databases, highlighting their applications.

**END OF EXAMINATION PAPER**