UNIVERSITY OF ESWATINI
FACULTY OF SCIENCENCE & ENGINEERING
DEPARTMENT OF BIOLOGICAL SCIENCES
MAIN EXAMINATION PAPER 2018/2019

COURSE CODE: BIO451

TITLE OF PAPER: BIOINFORMATICS

TIME ALLOWED: THREE HOURS

INSTRUCTIONS: 1. ANSWER **ALL** QUESTIONS

2. CANDIDATES MAY USE SCIENTIFIC CALCULATORS

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QUESTION 1:
BIOINFORMATICS APPLICATION & DATABASES

(a) Briefly explain the role of public biological databases. [2 marks]

(b) Distinguish between primary and secondary databases. [3 marks]

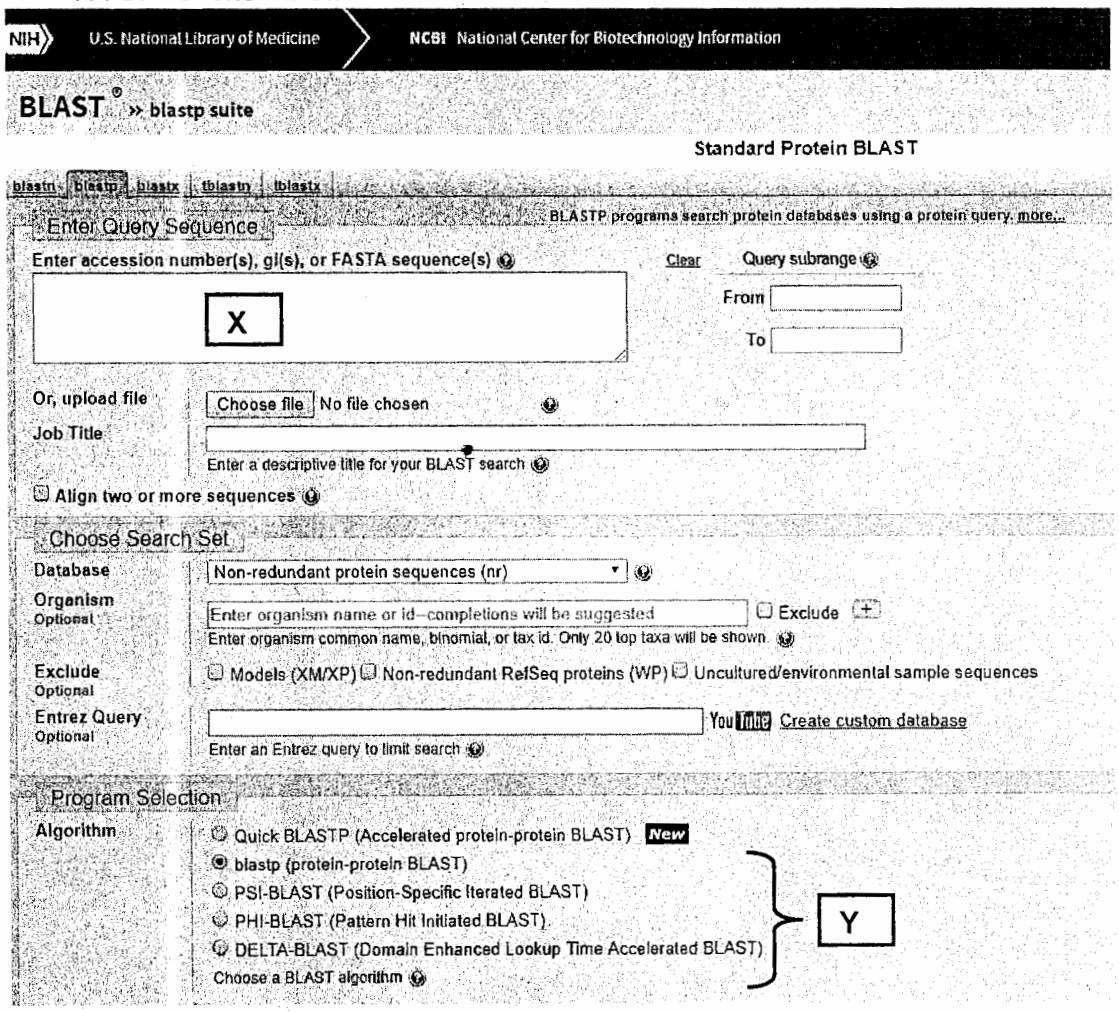
(c) Describe the following databases:
(i) GenBank, ENA and DDBJ [2 marks]
(ii) UniprotKB, [2 marks]
(iii) Refseq, [2 marks]
(iv) OMIM [2 marks]
(v) MEDLINE [2 marks]

(c) A recent enteric disease epidemic in the Manzini region of Eswatini has been reported to be caused by an unknown species of bacteria whose treatment is not yet known. A pure culture of this pathogen is brought to your consultancy lab for identification with a view to suggesting probable treatment for this disease. Describe the molecular biology and bioinformatics tools you can use to identify the species and/or genus this bacteria species may belong to. [10 marks]

[Total marks = 25]

QUESTION 2:
NUCLEIC ACID/PROTEIN SEQUENCE ANALYSIS, MULTIPLE-SEQUENCE ALIGNMENT & HOMOLOGY/PATTERN-BASED SEARCH ALGORITHMS

(a) Answer the following questions based on the screenshot of a BLAST page from NCBI website below.

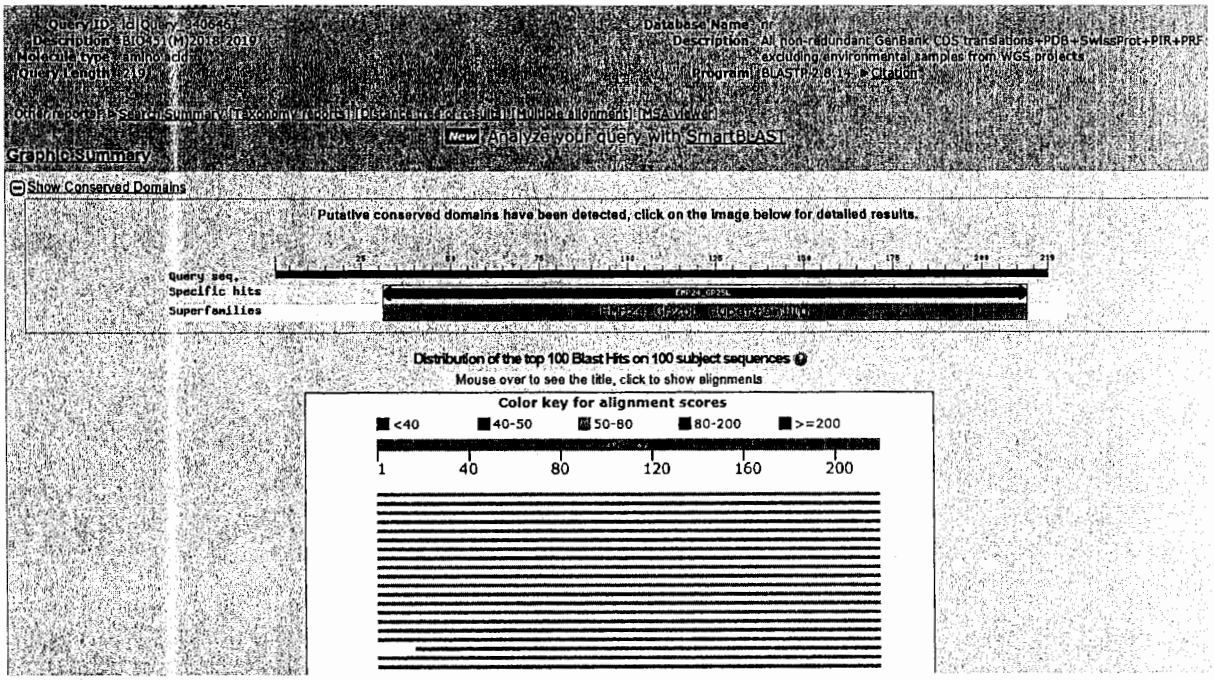


(i) Describe the nature and format of the sequence in the panel labelled **X**. [2 marks]
(ii) Discuss the principle of the different algorithms in the section marked **Y**.[8 marks]

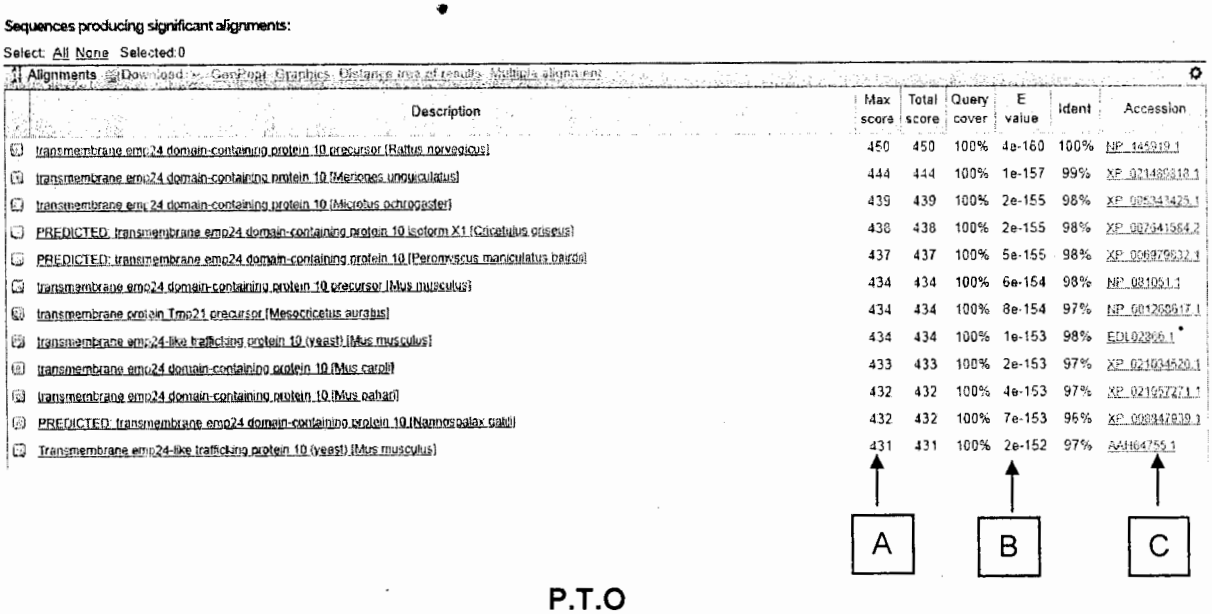
(b) (i) Explain the difference between PAM and BLOSUM scoring matrices. [6 marks]
(ii) Explain the significance of "62" on the BLOSUM62 matrix. [1 mark]

(c) Explain the difference between the following sequence alignment concepts:
(i) Smith–Waterman and Needleman–Wunsch algorithms, [4 marks]
(ii) Progressive and iterative MSA, [2 marks]
(iii) Global and local MSA. [2 marks]

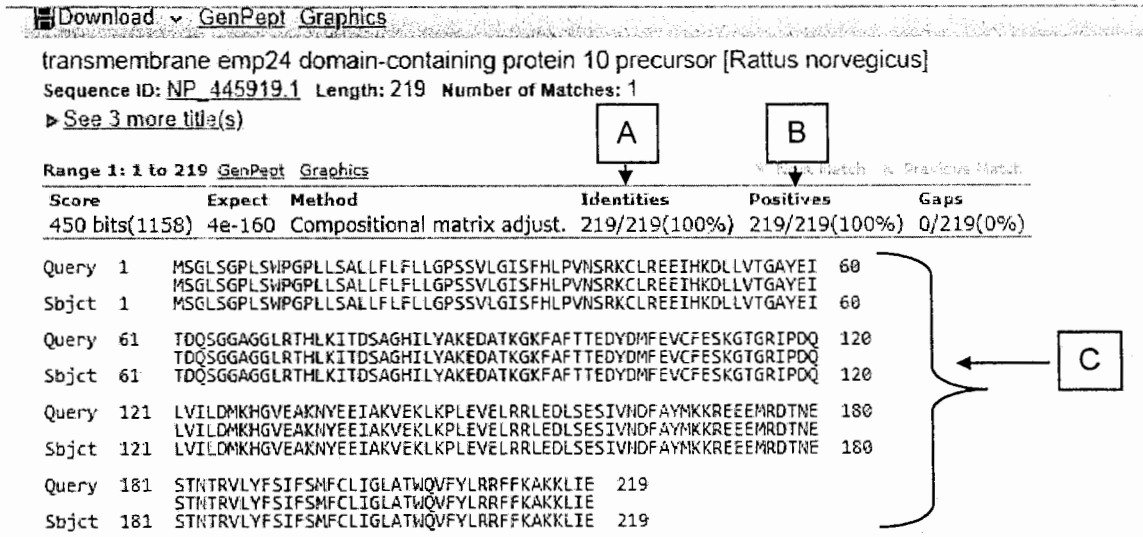
(d) Shown below is a typical graphic summary of BLAST result. Identify important information can you extract from it. [3 marks]



(e) Shown below is a screenshot of a typical BLAST HIT result. Identify and explain the labelled items. [6 marks]



(f) Shown below is a screenshot of a typical BLAST alignment result. Identify and explain the labelled items. [6 marks]



[Total marks = 40]

QUESTION 3:
GENE & PROTEIN MOTIFS/DOMAIN PREDICTION AND GENOME ANNOTATION

(a) Briefly discuss the advantages and disadvantages of having long versus short k-mers in genome assembly [6 marks]

(b) Describe using any bioinformatics tool, how CpG islands in a genome can be detected. [5 marks]

(c) Discuss the use of the Burrows-Wheeler transform in genome assembly, including its algorithmic complexity. [6 marks]

[Total marks = 17]

QUESTION 4:
MOLECULAR PHYLOGENETICS

(a) Explain why a heuristic approach is required for constructing phylogenetic trees when the number of taxa is large. [6 marks]

(b) Explain the difference between the Jukes-Cantor and Kimura 2-parameter models when inferring a phylogenetic tree from DNA sequences. [6 marks]

(c) What is an outgroup and why is it important to include one or more outgroups in phylogenetic analysis? [6 marks]

[Total marks = 18]

END OF EXAMINATION PAPER