NATIONAL UNIVERSITY OF SCIENCE AND TECHNOLOGY

FACULTY OF APPLIED SCIENCE

DEPARTMENT OF APPLIED BIOLOGY AND BIOCHEMISTRY

MASTER OF SCIENCE DEGREE IN APPLIED MICROBIOLOGY AND BIOTECHNOLOGY

ANALYTICAL BIOTECHNOLOGY AND BIOINFORMATICS (SBB5212)

Main Examination Paper

MARCH 2025

This examination paper consists of **6** pages

Time Allowed : 3 hours

Total Marks : 100

Examiner's Name : Dr W.T.CHOGA

Special Requirements : (1) Calculator, (2) Amino Acid codon Chart provided

INSTRUCTIONS

1. Answer **Four (4)** questions. Each question carries 25 marks.
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**
TOTAL	**100**

1. Discuss how bioinformatics can be applied to investigate a disease outbreak, including key computational methods and databases used, and steps to isolate the responsible pathogen.

2. (a) Define the following types of mutations:

(i) Silent.	(1 mark)
(ii) Nonsense.	(1 mark)
(iii) Missense.	(1 mark)

   (b) Perform a mutation profiling analysis based on the provided protein alignment insert (page 4 and 5) and comment on the most prevalent mutation. (6 marks)

   (c) Solve the following ambiguous nucleotide codons and analyse their potential mutations:

- Position: 124. Reference Codon: AGA (Arginine) → Observed: RGG	(4 marks)
- Position: 99. Reference Codon: TTT (Phenylalanine) → Observed: TTY	(4 marks)
- Position: 3. Reference Codon: CAA (Glutamine) → Observed: CAR	(4 marks)
- Position: 240. Reference Codon: CCG (Proline) → Observed: CCV	(4 marks)

3. Using a named example, describe how you would design and develop an epitope-based vaccine, including computational and experimental approaches.

4. (a) Describe the major post-translational modifications (PTMs) involved in protein processing. (10 marks)

   (b) Discuss the functional significance of PTMs and explain how analytical techniques such as mass spectrometry and Western blotting can be used to detect and characterise them. (15 marks)

5. (a) Compare and contrast Oxford nanopore technology and Illumina sequencing, highlighting their major applications. . (15 marks)

   (b) Discuss **two** types of protein purification techniques, and explain their applications in biomedical research. (10 marks)

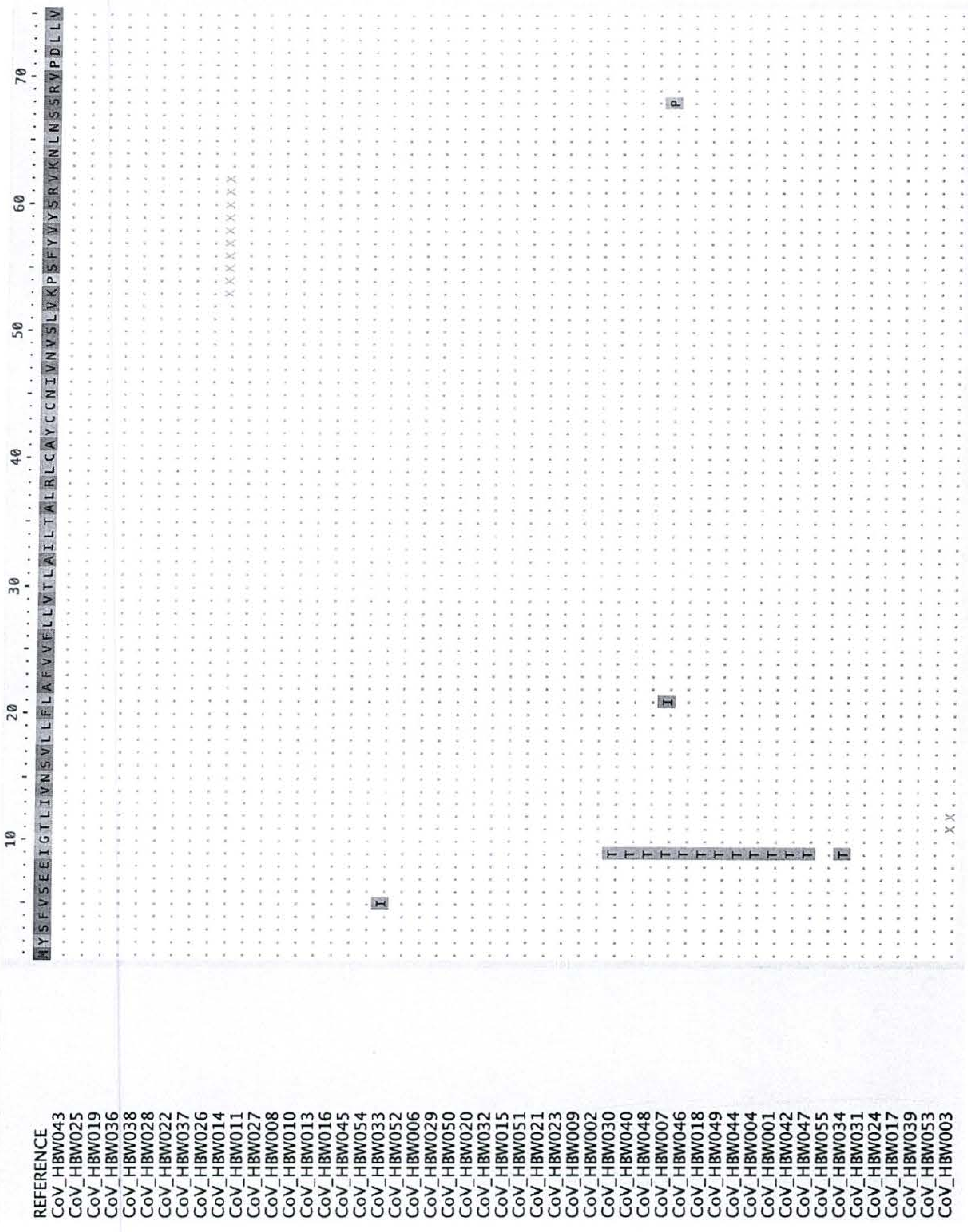
6. (a) List and briefly describe any 15 essential Linux commands used in bioinformatics workflows. (15 marks)

   (b) Using the Needleman-Wunsch algorithm, align the following sequences and compute the alignment score:

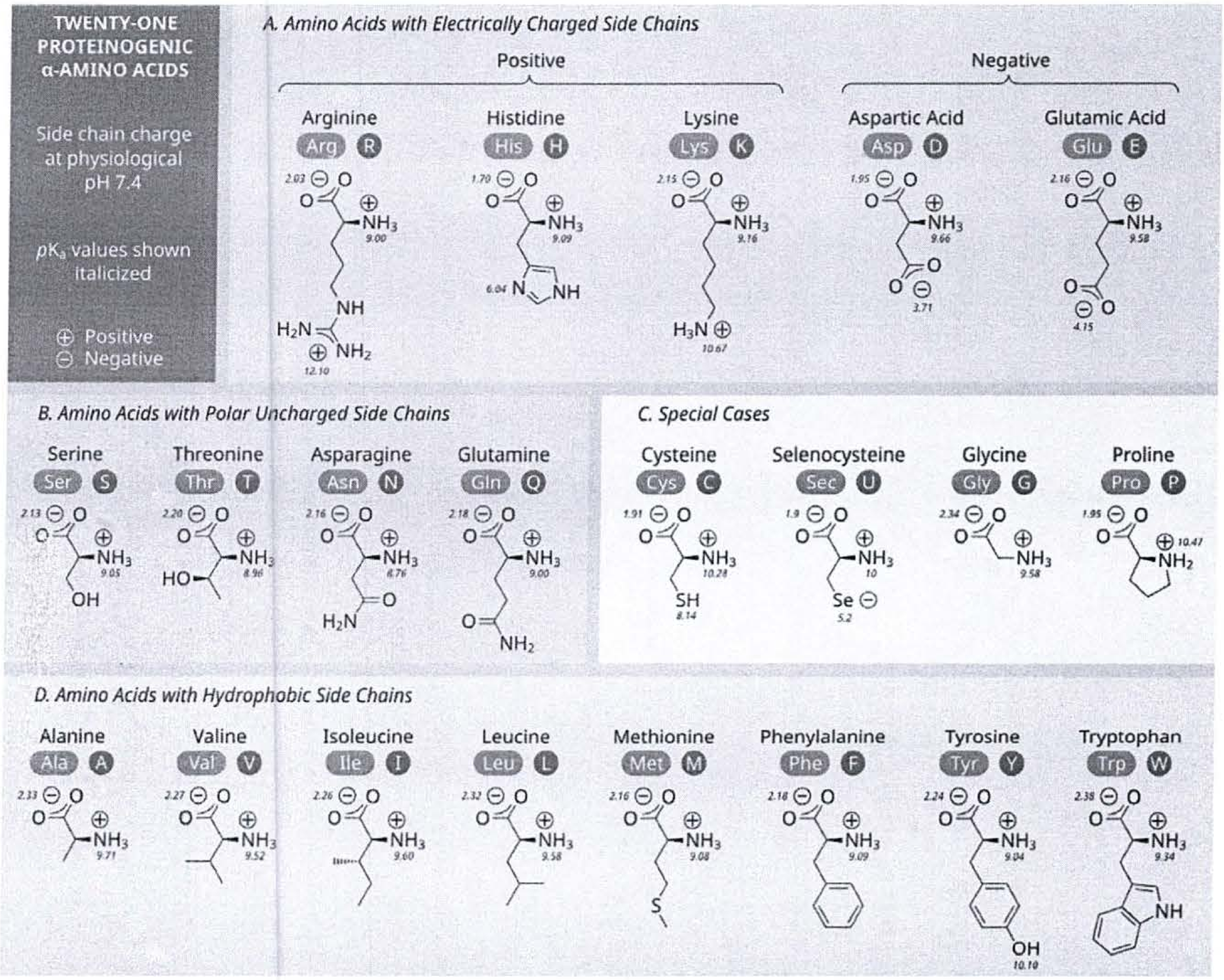
   - Seq001: **AATCG** vs. Seq002: **AACG** (10 marks)

END OF EXAMINATION

Protein alignment provided for Question 2b.



Additional Materials



First Letter	Second Letter: T		C		A		G		Third Letter
T	TTT TTC TTA TTG	Phe Leu	TCT TCC TCA TCG	Ser	TAT TAC TAA TAG	Tyr STOP STOP	TGT TGC TGA TGG	Cys STOP Trp	T C A G
C	CTT CTC CTA CTG	Leu	CCT CCC CCA CCG	Pro	CAT CAC CAA CAG	His Gln	CGT CGC CGA CGG	Arg	T C A G
A	ATT ATC ATA ATG	Ile Met	ACT ACC ACA ACG	Thr	AAT AAC AAA AAG	Asn Lys	AGT AGC AGA AGG	Ser Arg	T C A G
G	GTT GTC GTA GTG	Val	GCT GCC GCA GCG	Ala	GAT GAC GAA GAG	Asp Glu	GGT GGC GGA GGG	Gly	T C A G