



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:

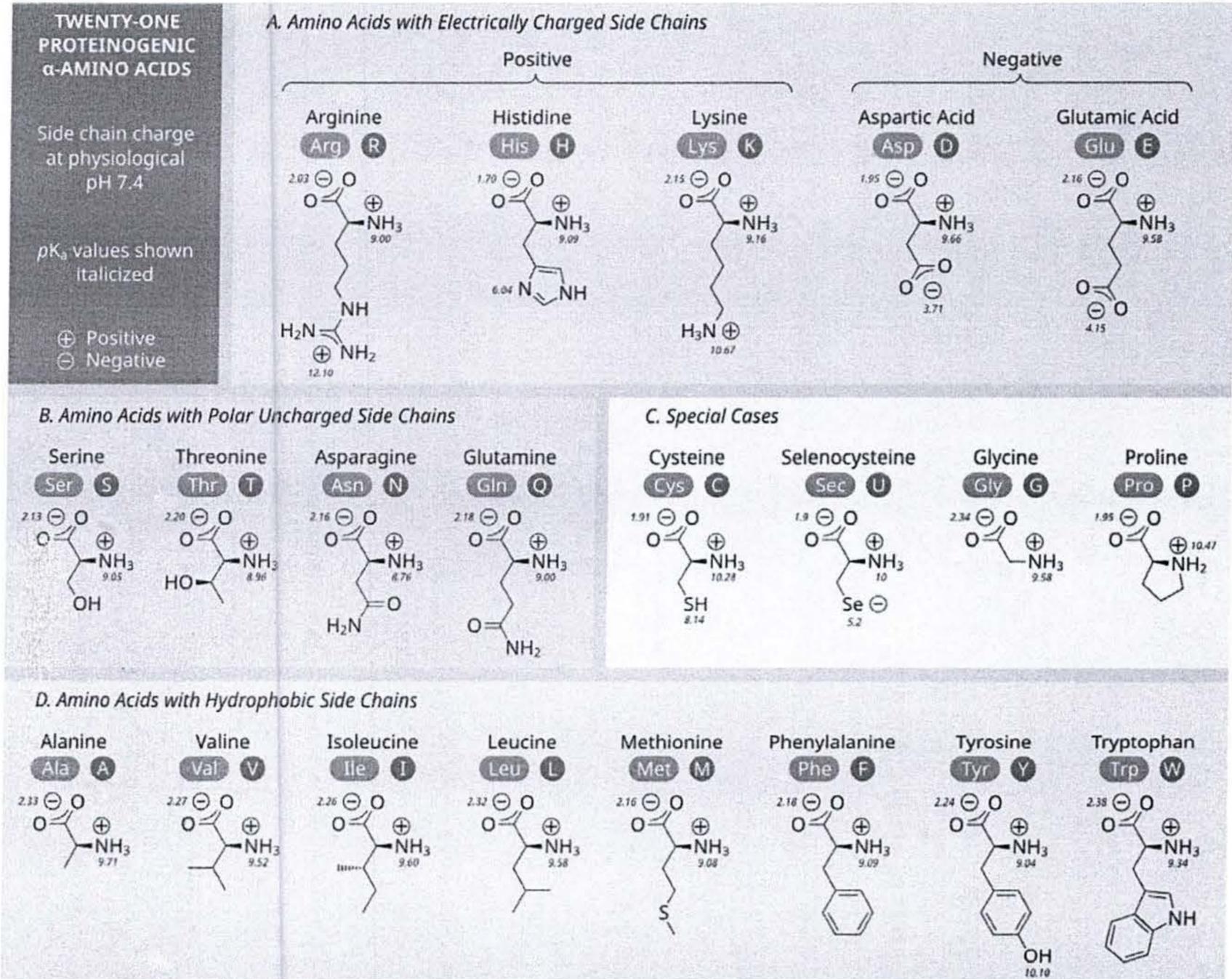
- Seq001: **AATCG** vs. Seq002: **AACG** (10 marks)

END OF EXAMINATION

Protein alignment provided for Question 2b.

REFERENCE	10	20	30	40	50	60	70
CoV_HBW043	MYSFVSE	EIGTLIIVN	SVLLFLAFVVF	LLVTLAI	LTA	LRCLCA	YCCNIVN
CoV_HBW025							
CoV_HBW019							
CoV_HBW036							
CoV_HBW038							
CoV_HBW028							
CoV_HBW022							
CoV_HBW037							
CoV_HBW026							
CoV_HBW014							
CoV_HBW011							
CoV_HBW027							
CoV_HBW008							
CoV_HBW010							
CoV_HBW013							
CoV_HBW016							
CoV_HBW045							
CoV_HBW054							
CoV_HBW033							
CoV_HBW052							
CoV_HBW006							
CoV_HBW029							
CoV_HBW050							
CoV_HBW020							
CoV_HBW032							
CoV_HBW015							
CoV_HBW051							
CoV_HBW021							
CoV_HBW023							
CoV_HBW009							
CoV_HBW002							
CoV_HBW030							
CoV_HBW040							
CoV_HBW048							
CoV_HBW007							
CoV_HBW046							
CoV_HBW018							
CoV_HBW049							
CoV_HBW044							
CoV_HBW004							
CoV_HBW001							
CoV_HBW042							
CoV_HBW047							
CoV_HBW055							
CoV_HBW034							
CoV_HBW031							
CoV_HBW024							
CoV_HBW017							
CoV_HBW039							
CoV_HBW053							
CoV_HBW003							

Additional Materials



Second Letter

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