BCH2333B **Exam 2** **16th March 2018**

Student name (Last, First): ______________________________

Student number: ____________________________

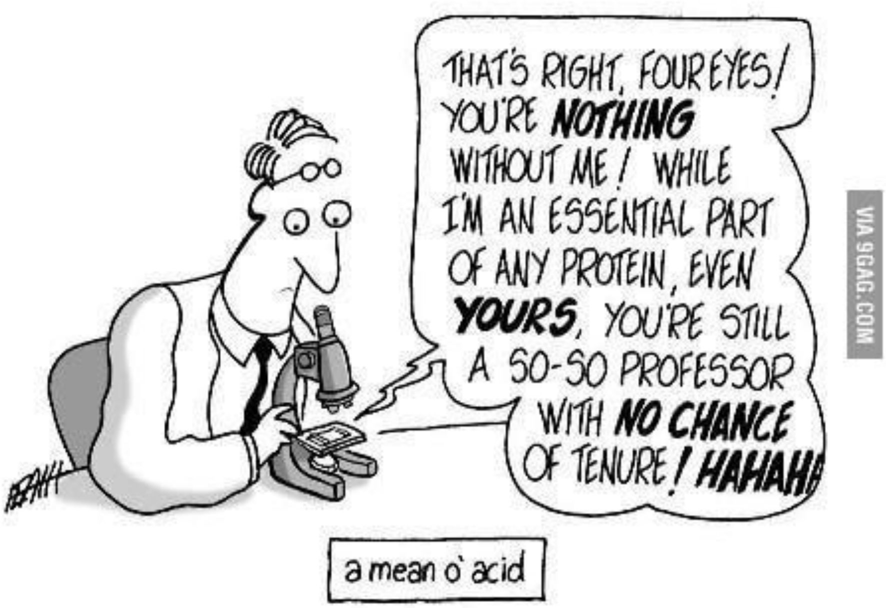
Instructions:

- Calculator permitted (Faculty approved or any other kind)
- Molecular model kits are permitted
- The exam will last 80 minutes (2:30pm-3:50pm)

Cellular phones, unauthorized electronic devices or course notes (unless an open-book exam) are not allowed during this exam. Phones and devices must be turned off and put away in your bag. Do not keep them in your possession, such as in your pockets. If caught with such a device or document, the following may occur: academic fraud allegations will be filed which may result in your obtaining a **0** (zero) for the exam.

By signing below, you acknowledge that you have ensured that you are complying with the above statement.

Sign here: ______________________________________



TRUE/FALSE SECTION

Point distribution: 3 pts per question for a total of 15 pts for the section. You receive 1 pt for correctly selecting true or false and 2pts for the explanation. If an explanation is not necessary, 3 pts is allocated to for correctly selecting true or false.

β-mercaptoethanol is used to oxidize disulfide bonds linkages in polypeptides.

True

False. If false, explain why.

BME is an reducing agent that reduces the disulfide bond to generate thiols.

Only L-amino acid enantiomers are used by cells.

True

False. If false, explain why.

Either answer is acceptable, given textbook description

In globular proteins, the majority of β-sheets prefer to be in a parallel orientation.

True

False. If false, explain why.

Majority of β-sheets in globular proteins prefer to be in an anti-parallel orientation, given stabilizing effect of linear hydrogen bonds

Trypsin will hydrolyze the peptide bond at the N-terminus of lysine and arginine residues in a protein.

True

False. If false, explain why.

Trypsin will hydrolyse the peptide bond at the C-terminus of lysine and arginine

The native folded state of any protein is usually not the lowest energy state possible for the protein.

True

False. If false, explain why.

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MULTIPLE CHOICE SECTION
Point distribution: 3 pts per question for a total of 24 points.

1. Give the following statements about protein folding:
    - I. The ΔH becomes less negative for hydrogen bonding, VDW, and electrostatic interactions
    - II. The $-T\Delta S$ contribution from the chain conformation energy becomes less positive
    - III. The $-T\Delta S$ contribution from the hydrophobic effects becomes more negative
    - IV. The Gibbs free energy becomes more negative

    Which of the statement(s) above can be used to describe the impact of increasing the temperature on protein unfolding?
    - a. I, II, & III
    - b. I & III
    - c. II & IV
    - d. I, III, & IV
    - e. II, III, & IV
2. Given the following statements:
    - I. The ΔH becomes more negative for hydrogen bonding, VDW, and electrostatic interactions
    - II. The $-T\Delta S$ contribution from the chain conformation energy become more positive
    - III. The $-T\Delta S$ contribution from the hydrophobic effects becomes less negative
    - IV. The Gibbs free energy becomes more positive

    Which of the statement(s) above can be used to describe the impact of extreme cold on protein unfolding?
    - a. I & III
    - b. I & IV
    - c. III & IV
    - d. IV only
    - e. III only
3. Given the following statements:
    - I. 3.6 amino acid residues per helical turn
    - II. 4.4 amino acid residues per helical turn
    - III. A pitch of approximately 5.4 Å
    - IV. A pitch of approximately 6 Å

    Which of the statement(s) above best describe the characteristics of an α-helical structure?
    - a. IV only
    - b. II &III
    - c. I & IV
    - d. II & IV
    - e. I & III
4. Given the following statements:
    - I. The ribosome translocates along the mRNA molecule in the 3' to 5' direction
    - II. The ribosome translocates along the mRNA molecule in the 5' to 3' direction
    - III. The aminoacyl-tRNA binds to the A-site of the ribosome
    - IV. There is a nucleophilic attach from A-site amino acid to the C-terminal amino acid in the P-site
    - V. The growing peptidyl-tRNA is located in the A-site of the ribosome

    Which of the statement(s) above best describes the process of protein translation?
    - a. II, III, and IV
    - b. I, III, and IV
    - c. III, IV, & V
    - d. II & III
    - e. III & IV

5. Given the following statements:
   - I. They generally exist as zwitterions at physiological pH
   - II. They have a characteristic isoelectric point
   - III. Each has three pKas
   - IV. They can act as buffers
   - V. Are all found in the L-form in cells

   Which of the statement(s) above best describe the characteristics of the 20 proteogenic amino acids?
   - a. I, IV, & V
   - b. I, II, & IV
   - c. I, II, IV, and V
   - d. III only
   - e. II, IV, & V

   either answer is okay

6. Given the following statements:
   - I. All are strongly hydrophilic
   - II. Histidine's ring structure results in its being categorized as aromatic or basic, depending on pH
   - III. On a molar basis, tryptophan absorbs more ultraviolet light than tyrosine
   - IV. The major contribution to the characteristic absorption of light at 280 nm by proteins is the phenylalanine R group
   - V. The presence of a ring structure in its R group determines whether an amino acid is aromatic

   Which of the statement(s) above do/does describe aromatic amino acids?
   - a. III only
   - b. I, II, IV, & V
   - c. IV & V
   - d. I, II & III
   - e. All of the statements above describe aromatic amino acids

   Removed from exam
   +3 pts to all students

7. Given the following statements:
   - I. Interactions occur when two or more bases are positioned with their rings anti-parallel to each other
   - II. Interactions are hydrophilic in nature
   - III. Involves the combination of van der Waals and dipole-dipole interactions between the bases
   - IV. Helps to minimize contact of the bases with water
   - V. Interactions are important in stabilizing the three-dimensional structure of nucleic acids

   Which of the statement(s) above are not true about base stacking when nucleic acids are in a double-stranded conformation?
   - a. II & III
   - b. I & III
   - c. I, II, & III
   - d. II & IV
   - e. II, IV, & V

   Either answer is okay

8. Osmosis is the movement of a:
   - a. Charged solute molecule (ion) across a membrane
   - b. Gas molecule across a membrane
   - c. Non-polar solute molecule across a membrane
   - d. Polar solute molecule across a membrane
   - e. Water molecule cross a membrane

SHORT ANSWER QUESTIONS
Total points: 16

9. **(2 pts)** How many protein fragments will be generated if trypsin is used to hydrolyze the polypeptide below:

GPR|GTILAGYTCUGTNQVR|AGLMFWHDKPEDGTLAVYFMLPHTNQCUGMLIFYWR|HSTTNQ

Answer: 4

10. **(2 pts)** What amino acid is principally found at the i + 2 position on a type II β-turn?

Glycine

11. **(2 pts)** Helical interactions between two alpha helices are stabilized by what two forces/interactions?

Hydrophobic (van der Waals) and electrostatic (salt bridge)

12. **(2 pts)** What chromatographic method separates proteins based on their size?

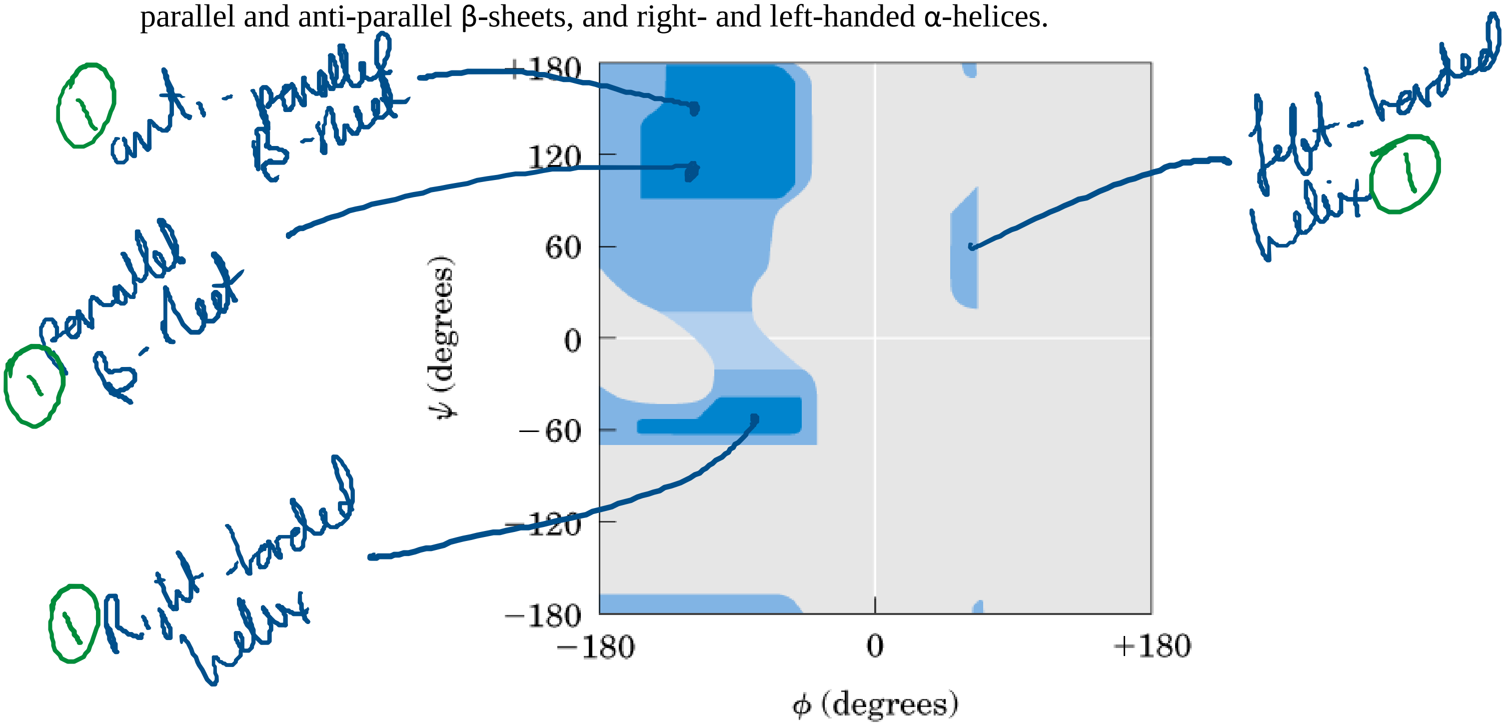
Gel filtration chromatography

13. **(2 pts)** What is the side chain pKa of C?
Acceptable range: 8.1-8.5

14. **(2 pts)** What metals are used in metal-exchange chromatography? Include their charge state.

Cobalt 2+ and nickel 2+

15. **(4 pts)** On the Ramachandran plot below, indicate the regions that represent the phi and psi angles for parallel and anti-parallel β-sheets, and right- and left-handed α-helices.



LONG ANSWER QUESTIONS

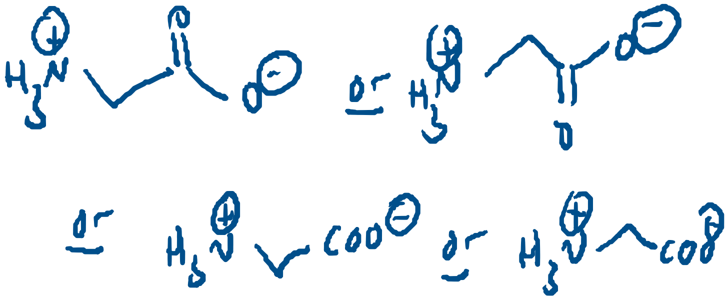
16. (**20 pts; partial marks are allocated**) Draw all the aliphatic & aromatic non-polar amino acids, assuming they are found at biological pH (Be sure to draw the structures in an orientation that displays their Cahn-Ingold-Prelog configuration). In addition, for each amino acid include the (a) three-letter code, (b) one-letter code, and (c) side-chain pKa value (if relevant).

Point allocation:

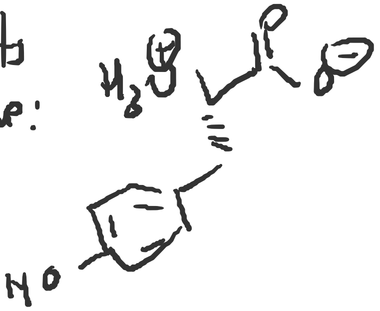
- 0.5 pt/structure = 5 pts
- R/S configuration = 3 pts (-1.5 pts if one structure is incorrect)
- Side-chain pKa for tyrosine = 2 pts
- 3 letter-code (0.5pts/structure) = 5 pts
- 1 letter-code (0.5pt/structure) = 5 pts
- Total points : 20pts

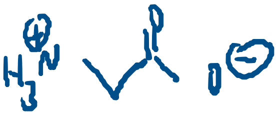
* if student draws A.A.s that are polar and/or charged, remove 0.5 pts/structure

okay if structures are:

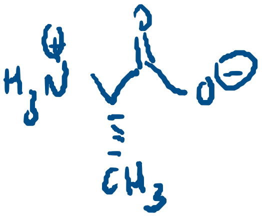


okay if students include Tyrosine:

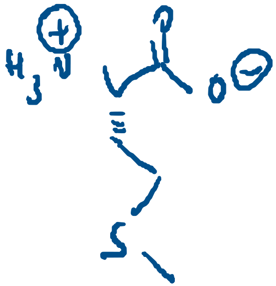




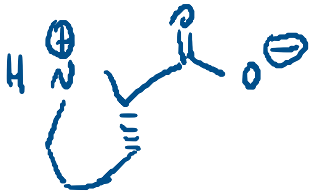
glycine
Gly
G



alanine
ala
a



Methionine
Met
M

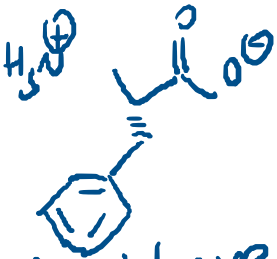


Proline
Pro
P

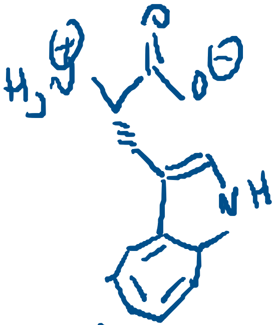
Valine
Val
V

Leucine
Leu
L

Isoleucine
Ile
I



Phenylalanine
Phe
F



Tryptophan
Trp
W

17. (**25 pts, partial marks are allocated**) Given the sense DNA sequence below:

strand must be read
Left → Right.

ACACGATTATACAGAGAT

Using the codon table, draw the polypeptide that would be formed by the DNA strand above, given that mRNA is the intermediate biomolecule that is read by ribosomes (ensure that the amino acids are in their correct Cahn-Ingold-Prelog orientation) and assume that the polypeptide is in a solution with pH 10.5. Indicate (a) the single-letter code underneath each drawn amino acid in the polypeptide, the (b) pka of the side chain (if relevant), and (c) the specific chromatographic method that could be used to purify this peptide given the pH abov

- Properly identified the amino acids from the codon table? 3pts
- Converted the sense DNA strand to mRNA? 3 pts
- Linked together the polypeptide? 2pt/amino acid = 12pts (wrong R/S no R/S: -8 pts) (not linked in a polypeptide? -12 pts) (drawn in Fischer projection? -8 pts)
- Single letter code for each amino acids? 0.5pts/amino acid = 3 pts
- Overall charge on the polypeptide given pH 10.5? 1 pt
- Chromatography method? 1pt
- Side-chain pKa values indicated? 2 pts
- Total points: 25

· Since the above strand is the sense strand, then that means:

DNA
3' ———— 5' ← sense (non-template) strand
5' ———— 3' ← anti-sense (template) strand

· Therefore: 3'-ACA-CGA-TTA-TAC-AGA-GAT-5' (DNA)

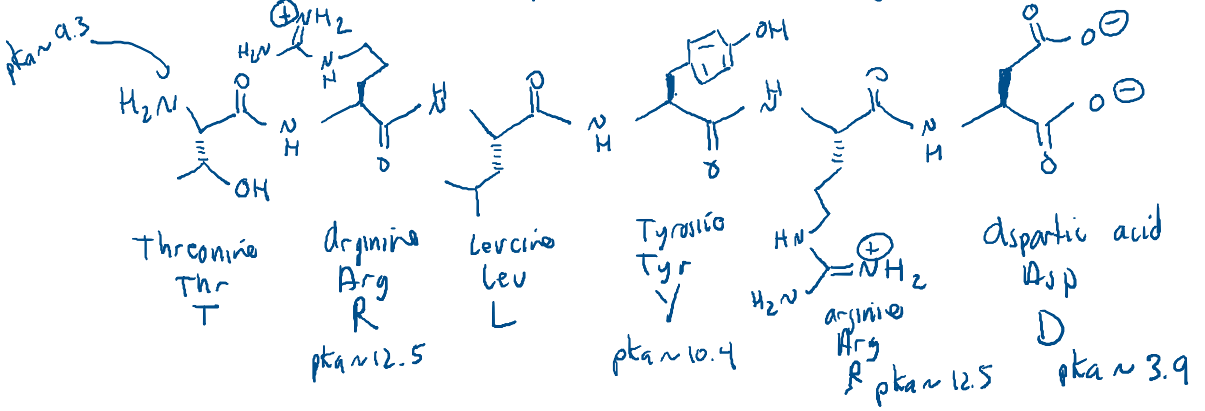
↓

5'-ACA-CGA-UUA-UAC-AGA-GAU-3' (mRNA)

· Since the table on the exam represents the codon and not the anti-codon table, then can compare the mRNA nucleotide sequence directly wiy the table:

TRLYRD (polypeptide)

· Draw the structure of the polypeptide considering the R/S configuration @ pH 10.5.



overall charge

Either: neutral

or: (−)

due to tyrosine

To purify this polypeptide, can use either anion exchange (if ⊖) or gel filtration (if neutral)

⇒ BELOW IS OTHER OPTION FOR ANSWER to THIS QUESTION (max points 12.5/25)

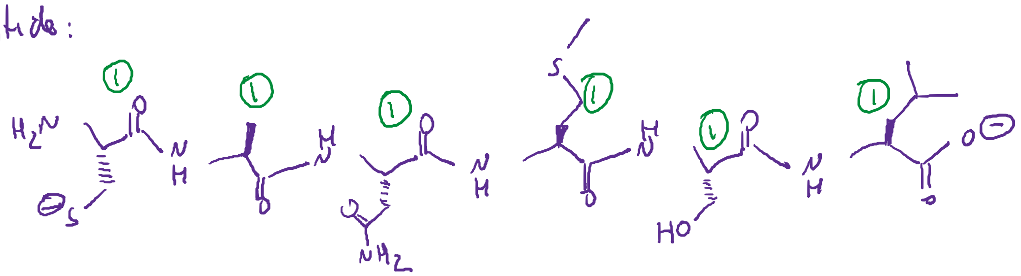
- students assumed codon table was anti-codon table:

5' - ACA - CGA - UUA - UAC - AGA - GAU - 3' (mRNA)

(0.5) ⇒ UGU GCU AAU AUG UCU CUA anti-codon

UGU	GCU	AAU	AUG	UCU	CUA
⇓	⇓	⇓	⇓	⇓	⇓
Cysteine	alanine	Asparagine	Methionine	Serine	Leucine
Cys	ala	Asn	Met	Ser	Leu
C	A	N	M	S	L
pKa≈8.5 (0.5)	(0.5)	(0.5)	(0.5)	(0.5)	(0.5)

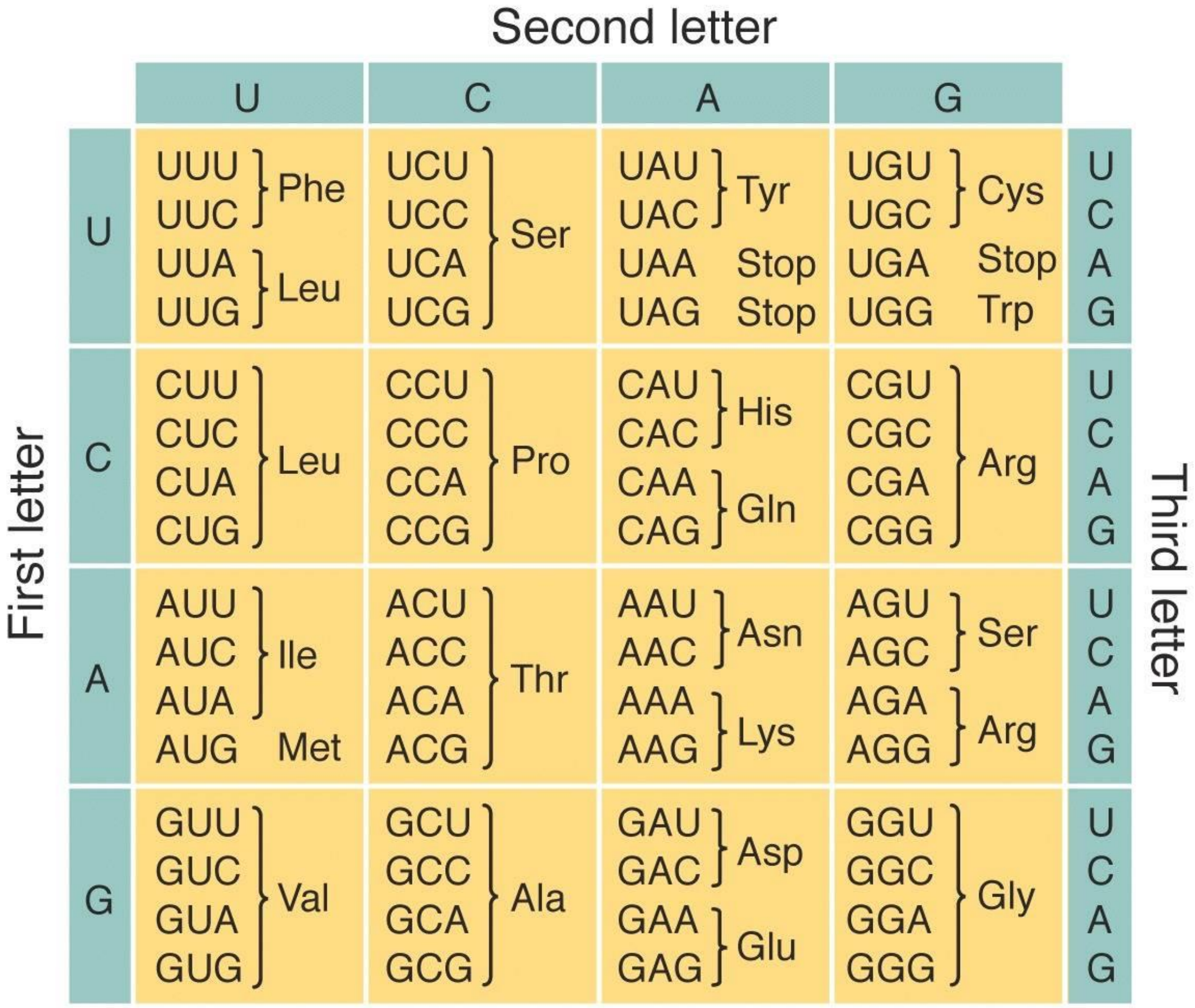
- Polypeptide:



overall charge (1)

$\boxed{-2}$

- Can purify w/ anion-exchange chromatography. (2)



Second letter

First letter	U	C	A	G	Third letter
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC	UCC	UAC	UGC	C
	UUA Leu	UCA	UAA Stop	UGA Stop	A
	UUG	UCG	UAG Stop	UGG Trp	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC	CCC	CAC	CGC	C
	CUA	CCA	CAA Gln	CGA	A
	CUG	CCG	CAG	CGG	G
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
	AUC	ACC	AAC	AGC	C
	AUA	ACA	AAA Lys	AGA Arg	A
	AUG Met	ACG	AAG	AGG	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC	GCC	GAC	GGC	C
	GUA	GCA	GAA Glu	GGA	A
	GUG	GCG	GAG	GGG	G