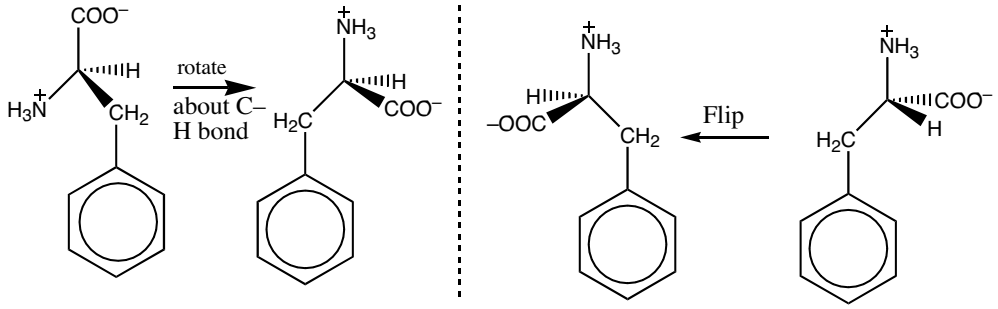
NESA Final Answer Key – Summer 2002 (Total Points: 66)

1. B(3) 2. C (2) Note that the question specified the **anti**-cordon sequence.
3. A (2)

If you rotate the second Phe so that the amine is pointing the same direction as on the first Phe you will notice that the two amino acids are not the same compound. The are in fact non-superimposiable mirror images or enantiomers.



4. A (2)
5. All answers were taken and others were possible. The first two numbers were found if the empirical numbers for the electron transport chain (ETC) were used. The second two were obtained if the theoretical values for the ETC were used. The numbers in each pair show the different treatments of the activation of fatty acids. By one interpretation 1 ATP is used and by another 2 are used. (4)
6. C (2)
7. (12)
    a. (1,4) glycosidic bonds (partial credit given, don't worry about sterochem, position important)
    a. 6 (all or nothing)
    a. Per glucose molecule

(6 separate sugars 1 pts, Glycolysis 2 pts, Oxidative decarboxylation 1 pts, CAC 2 pts, ETC 2 pts. Math error –1)

Glycolysis –
Used: 2 ATPs
Produced:
4 ATPs
2 NADH
2 pyruvate

Oxidative decarboxylation
Used: 2 pyruvate
Produced:
2 NADH
2 Ac-SCoA

Citric Acid Cycle
Used: 2 Ac-SCoA
Produced:
6 NADH
2 $FADH_2$
2 ATPs

Electron transport and oxidative phosphorylation.

TotalNADH: 2+2+6 = 10

Total $FADH_2$: 2

Ideal (3 ATP/NADH, 2 ATP/ $FADH_2$)	Empirical (2.5 ATP/NADH, 1.5 ATP/ $FADH_2$
10 • 3 + 2 • 2 = 34 ATPs	10 • 2.5 + 2 • 1.5 = 28 ATPs
From *Glycolysis:* 4	4
Used in *Glycolysis*: – 2	– 2
From *CAC*: 2	2
Total/glucose: 38	32
Overall production: 228 ATPs	192 ATPs

8. (17)

Original 5' – AGT TCG ATG ATG CCT GGC TTC CAA TCG GGC GAC GGT TAG GGA ATT – 3'

a. 3' – TCA AGC TAC TAC GGA CCG AAG GTT AGC CCG CTG CCA ATC CCT TAA – 5'

b. 5' – AGU UCG AUG AUG CCU GGC UUC CAA UCG GGC GAC GGU UAG GGA AUU – 3'

c. Ser Ser Met Met Pro Gly Phe Gln Ser Gly Asp Gly Stop Gly Ile

produced Met Met Pro Gly Phe Gln Ser Gly Asp Gly Stop

Start codon

Stop codon

(a. Sequence 3 pt, Ends 2 pts)

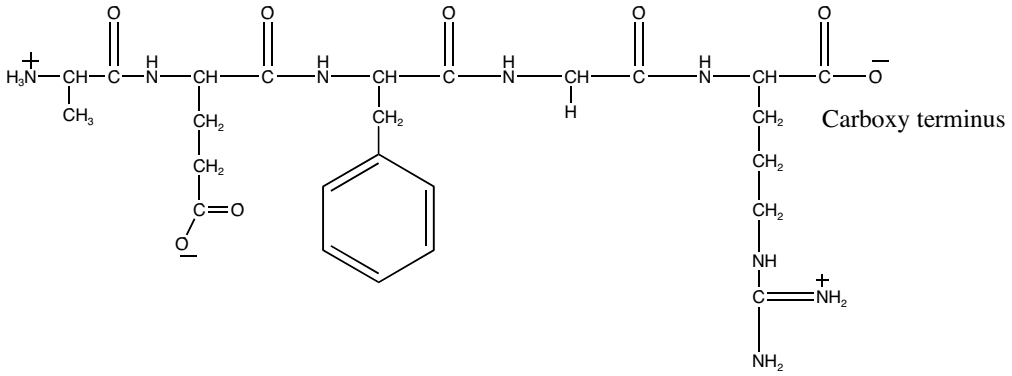
(a. Label 2 pts, sequence 2 pts)

(c. Sequence 3 pt, start 1 pts, stop 1 pts) Partial credit given

d. In replication and transcription complimentary nucleic acid strands are produced. One main reason for this characteristic is the existence of complimentary bases held specifically to each other by stable hydrogen bonds. This property is also seen during translation. The anti-codon of a tRNA must be complimentary to the section of mRNA being read. Again, the two segments match up mainly due to the hydrogen bonding observed in Watson-Crick base pairs. (3 pts)

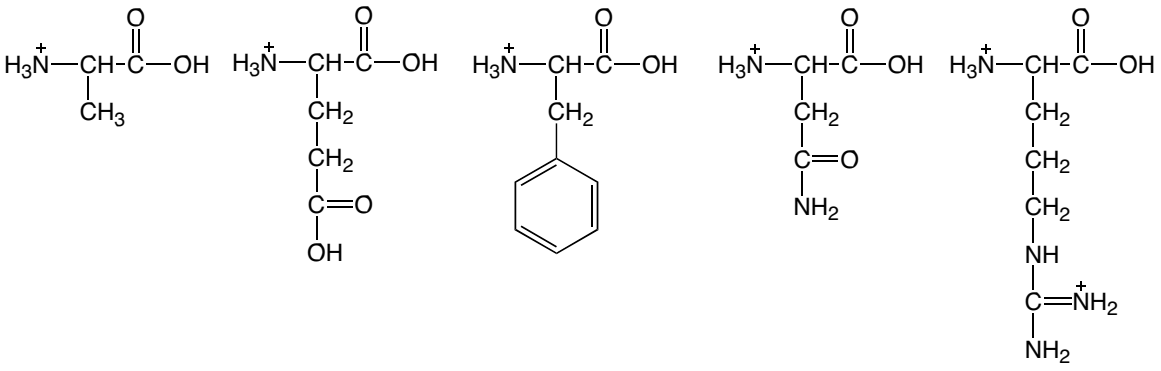
9. (9)

Amino terminus



a.

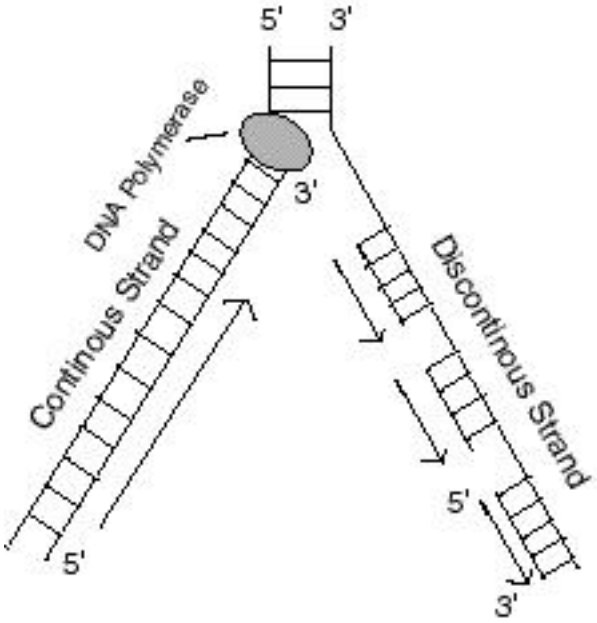
(peptide bonds 1 pt, structures 1 pt, termini 1 pts, charges 2 pts, Total 5)



b.
(Structure 2, charges 2, total 4)

10. Recall that: the percentage of A equals the percentage of T, the percentage of C equals the percentage of C, and all percents add to 100%. If a DNA molecule contains 22% A, it will also contain 22% T, 28% C and 28% G. If you check the list of available nucleoside triphosphates, you should notice that only 22% dCTP is available for replication. dCTP is the nucleoside triphosphate that is limiting to the replication and dTTP is in excess. (2 pt answer, 3 pts explanation, total: 5)

11.



(4 pts directions, 3 pts polymerase, 1 discontinuous, total: 8)

12. (10 pts Extra credit)

a. The replication mechanism of DNA is semi-conservative, meaning that each strand from a double stranded parent DNA will act as a template and will be incorporated in each daughter, double stranded DNA. For generation 0, all of the nitrogen atoms in the bacterial DNA are ^{15}N, so this band will have the highest mass. Starting with generation 1, newly synthesized DNA will contain only ^{14}N. DNA is replicated in between generations 0 and 1. Since DNA replication is semi-conservative, one strand of the DNA in generation 1 will contain ^{15}N (from the parent DNA, synthesized before generation 0) and the other will contain ^{14}N. One band (there is one pattern of labeling) will show during the sedimentation technique and its mass will be less than that of the DNA from generation 0. For generation 2 we observe two different masses, one is the same isotope enrichment pattern as in generation 1 and the lower mass one is DNA made of two ^{14}N labeled strands. The last sample, a mixture of generations 0 and 2, shows that we in fact have three different masses of double stranded DNA.

b.