1. What are the codons for Trp, Glu, Ile, Leu and Ser?

   Trp UGG  Ile AUI  Leu CUC UUA  Ser UCU AUC
   Glu GAA GAG  Leu CUA CUC UUC
   Ile AUI AUA  Val UCA UCU

2. What is the minimum number of tRNAs required to recognize all of the codons for each amino acid in problem 1? What are their corresponding anticodon sequences?

   Trp CCA  Glu UVC  Ser GUA
   Ile IAU  Leu GAG  Ser GCA
   Leu GAG  Ser GCA

   9 codons

3. How many codons can be deduced using the repeating block copolymer (CAGU)n as mRNA? What are they, and which amino acids do they code for?

   CA6  Glu
   AGU  Ser
   GUC  Val
   UCA  Ser

4. Reconstruct in a standard chemical structure drawing the structures of the bases, sugars and phosphates, and their molecular interactions depicted in the electron density contour map (i) in your tRNA handout.
5. Referring to the tRNA structure on your tRNA handout or in RASMOL, determine which pairs of nucleotides are closer to each other:

(a) 5 and 8 vs. 7 and 49
(b) 10 and 14 vs. 15 and 59
(c) 10 and 56 vs. 19 and 57
(d) 5 and 67 vs. 22 and 53
(e) 9 and 46 vs. 10 and 47

6. Which bases in tRNA are not stacked? For each of them, can you explain why?

- D16 is non-aromatic, non-planar
- D17 
- G20 Local structure requires non stacking
- U47
- A76 at 3' end of tRNA

7. Peptide bond formation is one step in protein synthesis that does not require ATP or GTP. Explain where the energy of peptide bond formation comes from.

The aminoacyl-tRNA ester linkage is high energy.
8. To study genes at the molecular level, it is often important to obtain large quantities of DNA containing a purified gene. List two fundamentally different ways of accomplishing this.

cloning
PCR

9. Give two steps of recombination that require ATP.

recA-mediated strand invasion
rnuB-dependent branch migration
recBC - dependent unwinding

10. During the original studies on isolation of RNA polymerase, why did extensive purification of RNA polymerase give preparations that were found to transcribe DNA inefficiently and non-specifically?

sigma factor was lost

11. The following represents the nucleotide sequence of one strand of a DNA duplex near the start of transcription of a highly transcribed E. coli gene. Identify (by boxing):

(a) The −10 promoter element
(b) The −35 promoter element
(c) The likely transcriptional start site (i.e., nucleotide #1 of the RNA transcript)

\[\text{(5') TCAGAAAATTTTAAATTTTCTGTTCAAGGCCGGA}\]
\[\text{ATAACTCCCTATAATGCACCGACACTGACACGG (3')}\]

12. How was it shown that the genetic code is (a) "comma-less" and (b) non-overlapping?

crossing of "+" (or "+") acridine mutations to give a "+++" (or "---") triple mutation gave revertant phenotype.