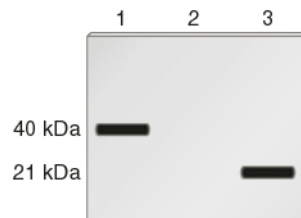
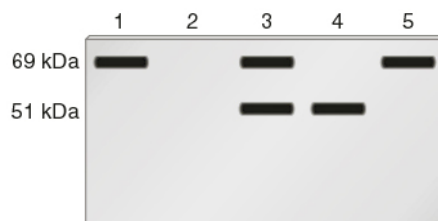


- E1. A codon contains three nucleotides. Since G and C are present at 50% each, if we multiply $0.5 \times 0.5 \times 0.5$, we get a value of 0.125, or 12.5%, of each of the eight possible codons. If we look the codons up in Table 13.2, we would expect 25% glycine (GGG and GGC), 25% alanine (GCC and GCG), 25% proline (CCC and CCG), and 25% arginine (CGG and CGC).
- E2. A. There could have been other choices, but this template would be predicted to contain a cysteine codon, UGU, but would not contain any alanine codons.
 B. You do not want to use ^{35}S because the radiolabel would be removed during the Raney nickel treatment.
 C. There would not be a significant amount of radioactivity incorporated into newly made polypeptides with or without Raney nickel treatment. The only radiolabeled amino acid in this experiment was cysteine, which became attached to tRNA^{CYS}. When exposed to Raney nickel, these cysteines were converted to alanine but only after they were already attached to tRNA^{CYS}. If there were not any cysteine codons in the mRNA template, the tRNA^{CYS} would not recognize this mRNA. Therefore, we would not expect to see much radioactivity in the newly made polypeptides.
- E3. The threonine has been changed to serine. Based on their structures, a demethylation of threonine has occurred. In other words, the methyl group has been replaced with hydrogen.
- E4. The initiation phase of translation is very different between bacteria and eukaryotes, so they would not be translated very efficiently. A bacterial mRNA would not be translated very efficiently in a eukaryotic translation system because it does not have a cap structure. A eukaryotic mRNA would probably not have a Shine-Dalgarno sequence near its 5' end, so it would not be translated very efficiently in a bacterial translation system.
- E5. The overall function of the ribosome is to facilitate translation of mRNA. That is already clear, and an understanding of the molecular structure of the ribosome would not affect that knowledge. However, molecular biologists are interested in the steps that occur so that the process of translation can be elucidated. In this regard, an understanding of the structure of ribosomes can be quite helpful. For example, the sequencing of bacterial 16S rRNA showed that a sequence within this rRNA was complementary to the Shine-Dalgarno sequence. This helped molecular biologists understand how mRNA initially binds to the small ribosomal subunit. Electron microscopy studies revealed how the mRNA, ribosomal subunits, and tRNAs “fit together” during the translation process. Overall, the studies of molecular biologists provide bits and pieces to the puzzle of how a large macromolecular complex can catalyze the synthesis of a polypeptide with a defined amino acid sequence based upon an mRNA with a defined nucleotide sequence.
- E6. Looking at the figure, the 5' end of the template DNA strand is toward the right side. The 5' ends of the mRNAs are farthest from the DNA, and the 3' ends of the mRNAs are closest to the DNA. The start codons are slightly downstream from the 5' ends of the RNAs.
- E7.



E8.



- E9. The sample in lane 2 came from an individual who is homozygous for a mutation that introduces an early stop codon into the coding sequence. As seen in lane 2, the protein is shorter than normal. The sample in lane 3 came from an individual who was homozygous for a mutation that prevented the expression of this polypeptide. It could be a down promoter mutation (i.e., a mutation in the promoter that decreases the rate of transcription), or it could be a mutation in the coding sequence that causes the protein to be degraded very rapidly. The sample in lane 4 came from an individual who is homozygous for a mutation that changed one amino acid to another amino acid. This type of mutation, termed a missense mutation, may not be detectable on a gel. However, a single amino acid substitution within a polypeptide may block protein function. This would explain the albino phenotype.
- E10. A. If codon usage were significantly different between kangaroo and yeast cells, this would inhibit the translation process. For example, if the preferred leucine codon in kangaroos was CUU, translation would probably be slow in a yeast translation system. We would expect the yeast translation system to primarily contain leucine tRNAs with an anticodon sequence that is AAC because this tRNA^{leu} would match the preferred yeast leucine codon, which is UUG. In a yeast translation system, there probably would not be a large amount of tRNA with an anticodon of GAA, which would match the preferred leucine codon, CUU, of kangaroos. For this reason, kangaroo mRNA would not be translated very well in a yeast translation system, but it probably would be translated to some degree.
- B. The advantage of codon bias is that a cell can rely on a smaller population of tRNA molecules to efficiently translate its proteins. A disadvantage is that mutations, which do not change the amino acid sequence but do change a codon (e.g., UUG to UUA), may inhibit the production of a polypeptide if a preferred codon is changed to a nonpreferred codon.