

1. The draft of the human genome project will be completed in May, 2000. That means the DNA sequence of every human gene will be known soon. The key method of this great project is DNA sequencing. Please describe one of the methods for DNA sequencing and its principle (15 %).

2. Assume the following portion of an mRNA. Find a start codon, and write the amino acid sequence that is coded for (10%). (Some of the amino acids and their corresponding codons are provided.)

5'-...GCCAUGUUUCCGUCUUAUCCCAAAGAUAAAAAAGAG...-3'

Asp: GAU or GAC Glu: GAA or GAG Lys: AAA or AAG
 Met: AUG Phe: UUU or UUC Pro: CCU, CCC, CCA or CCG
 Ser: UCU, UCC, UCA or UCG Tyr: UAU or UAC.

3. Once the sequence of the entire human genome is known, the next question is to ask what are the functions of each gene. If you have a new gene in hand, how will you study the functions of this gene (15%)?

4. Extracellular signals interact with cells through specific receptors. For each of the four receptors listed in column A, identify all characteristics listed in column B, by number, which accurately describe that receptor (20%).

Column A	Column B
a. An adrenergic receptor	1. Located at the cell surface
b. A steroid receptor	2. Located in the cell interior
c. An integrin receptor	3. Contains two subunits
d. The insulin receptor	4. A transmembrane protein
	5. A DNA binding protein
	6. Receptor-ligand becomes concentrated in the nucleus
	7. The hormone-receptor complex activates specific gene transcription
	8. Links to guanine nucleotide-binding proteins
	9. Not known to act through a second messenger
	10. Links to cytoskeletal proteins

5. The way we can see is a combination of many biochemical pathways. Please use the following key words to make a story of the sequence of these pathways (10%)

Key words: light, retinal, rhodopsin, transducin, cGMP phosphodiesterase, cGMP-gated channel, membrane potential, neurotransmitter

6. Choose five of the following terms or techniques and briefly describe them (30%).

- a. Glycolysis b. Gluconeogenesis c. The tertiary structure of protein d. Adenylyl cyclase
- e. High-density lipoprotein f. IP₃ g. cDNA
- h. Alternative splicing i. Restriction enzyme length polymorphism
- j. Gene knockout