

Solutions to 7.014 Problem Set 1

Question 1

a) Describe the conditions of the atmosphere on prebiotic earth and how these conditions differ from what is found today.

Prebiotic earth had an atmosphere that lacked oxygen, but was rich in H_2 , N_2 , CO_2 , H_2O , and sulfurous gases. In the absence of O_2 and O_3 , the UV light penetrated in far greater strength than it does now. Today, we have an atmosphere rich in oxygen and an ozone that protects us from the sun's UV light.

b) Describe the proposed first organism as it compares to modern organisms; include the type of genetic material and the source of energy it may have used.

The first cells were anaerobic and likely absorbed free organic compounds from the primordial seas. They are thought to have used RNA as their genetic material. Some modern anaerobic prokaryotic organisms may resemble these early cells. However, these modern cells do not freely absorb the organic compounds needed, they make them. They also use DNA as their genetic material.

c) Describe the process that led to an O_2 atmosphere on earth and how this change in atmospheric conditions influenced the course of evolution.

At some point, photosynthetic organisms developed the ability to use the highly abundant H_2O instead of H_2S as a source of electrons. This released oxygen into the seas that reacted with dissolved ions and precipitated as oxides (predominantly iron oxide). As the ions were exhausted, the seas became saturated with O_2 , and finally, O_2 escaped, began oxidizing the iron on land and finally began accumulating in the atmosphere. The change from a reducing environment to a more oxidizing one took hundreds of millions of years after the evolution of oxygenic photosynthesis. This change likely resulted in the extinction of many organisms adapted to the reducing conditions, and created an ozone shield that allowed the introduction of many aerobic life forms.

Question 2

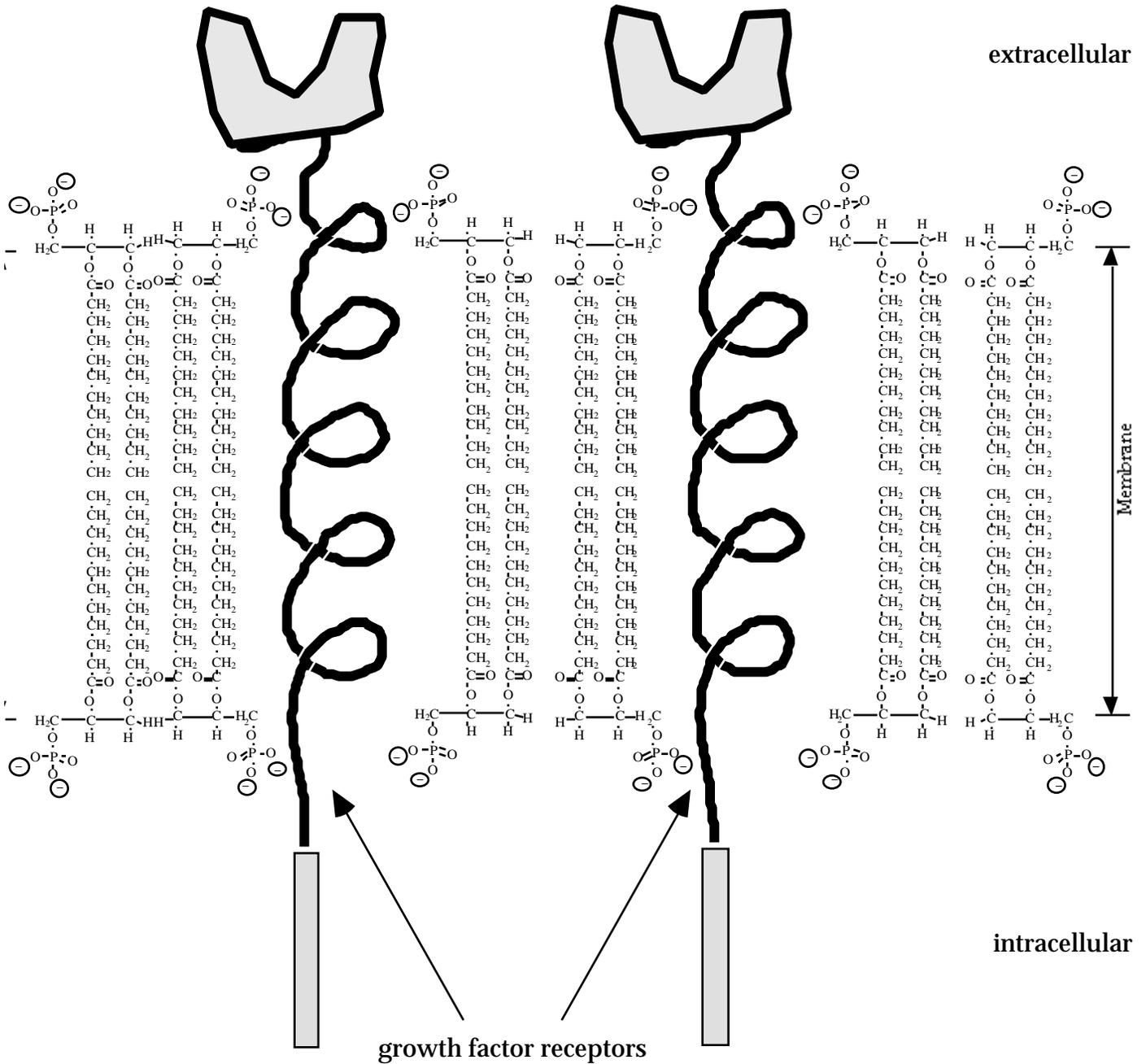
You are given four test tubes, each contains cells from a different organism. One tube contains bacterial cells, one contains yeast cells (eukaryotic), one contains human cells and the last contains dinosaur cells.

Can you identify the cells from each tube if you are given a light microscope? Explain your answer.

With a light microscope you could easily distinguish the prokaryotic bacteria from the other cell types. The prokaryotic bacteria would not have a nucleus, the other cell types would. The yeast cell wall would distinguish yeast cells from human and dinosaur cells. Distinguishing human and dinosaur cells with a simple microscope may not be possible.

Question 3

Growth factor receptors (shown below) are transmembrane proteins found on the cell surface.



a) The molecules that form the above membrane belong to what class of macromolecules?

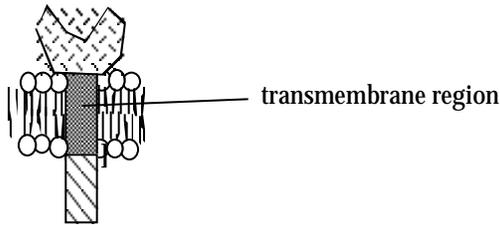
_____ *Phospholipids*

Explain the important qualities/properties of these molecules that allow them to form membranes.

The phospholipid molecules have hydrophilic heads that prefers to interact with aqueous environments and hydrophobic tails that cluster together to exclude water.

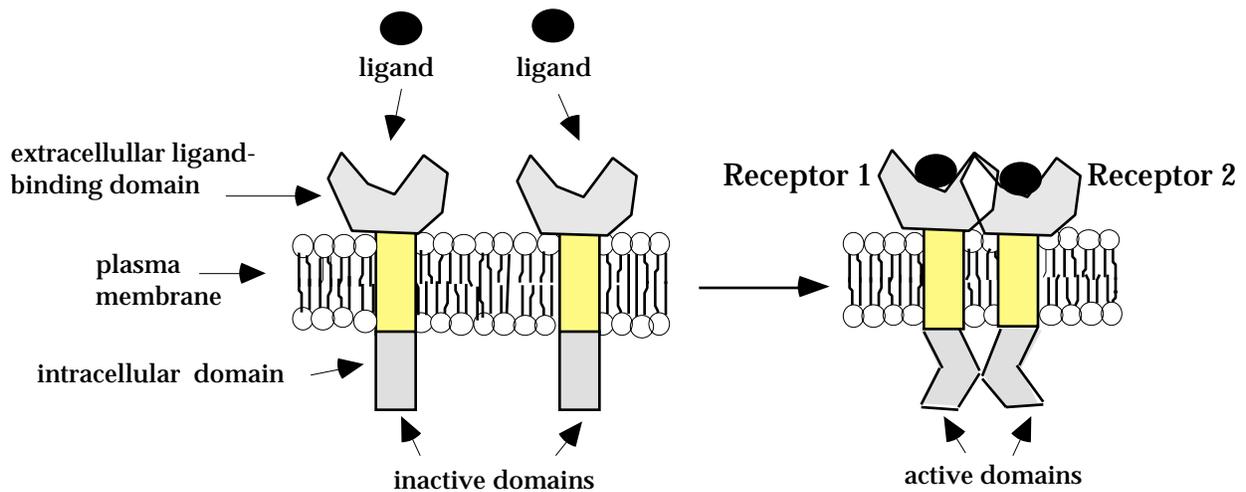
Question 3, continued

A smaller schematic of the growth factor receptor is shown here.



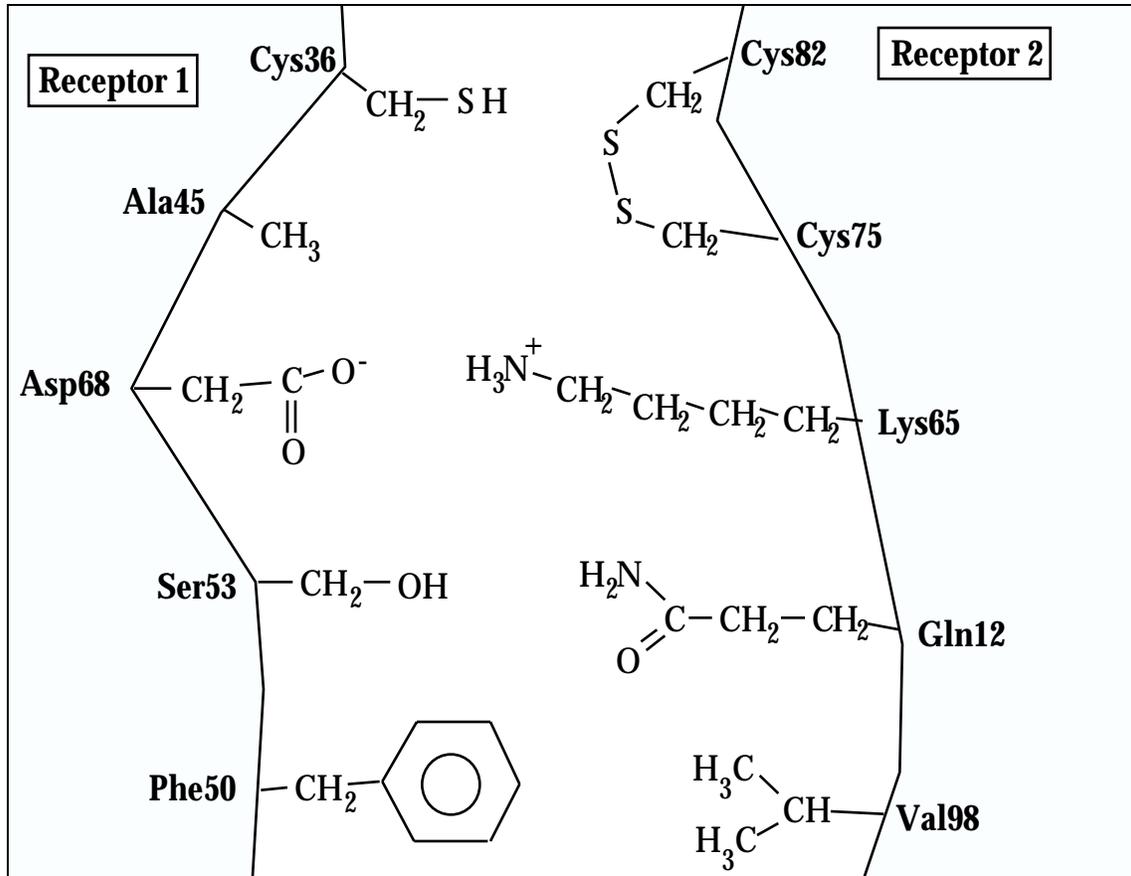
b) Which amino acids would you expect to find in the transmembrane region of the receptor?
Alanine, cysteine, glycine, isoleucine, leucine, methionine, phenylalanine, proline, tryptophan, tyrosine, valine.

When growth factor binds to the extracellular domain of the receptor, a conformational change occurs in the receptor. Growth factor binding causes dimerization of two adjacent receptors in the cell membrane. Upon dimerization, the intracellular domains of the receptors become activated. See schematic below.



Question 3, continued

c) Regions of the two receptors that interact upon dimerization shown below. In parts (i - iv) below, name the strongest type of interaction (choose from; **hydrogen bond**, **ionic**, **covalent**, **van der Waals**) that occurs between the side chains of the amino acids indicated.



<u>Interacting Side chains</u>	<u>Type of interaction</u>
i) Phe50 : Val98	van der Waals
ii) Asp68 : Lys65	ionic
iii) Cys75 : Cys82	covalent
iv) Ser53 : Gln12	hydrogen

d) Explain how Gln12 and Val98, which are far apart in the primary sequence of the protein, can be close to each other in the region of the protein diagrammed above.

When the linear chain of amino acids folds into its three dimensional shape, non-adjacent amino acids can be found in close proximity to one another.

Question 4

You have discovered a new enzyme, enzyme E, which breaks down proteins by cleaving peptide bonds after tyrosine or phenylalanine.

a) Enzyme E is the product of gene G that encodes a protein with the molecular weight of 50 kilodaltons (50 kD). When purify enzyme E, only the expected polypeptide is present. However, active enzyme E has a molecular weight of 250 kilodaltons (250 kD), not 50 kD.

i) Why might active purified enzyme E be larger than the product encoded by gene G?
The active enzyme must have multiple subunits. Likely it is a pentamer of the 50 kD polypeptide encoded by gene G.

ii) Define primary, tertiary, and quaternary structure.
*The primary structure is the linear sequence of amino acids.
The tertiary structure is the 3 dimensional shape.
The quaternary structure is the association of distinct polypeptide chains with each other.*

iii) Is the primary structure of the 50 kD protein the same or different than the primary structure of the 250 kD protein? Explain briefly.
The primary structure is the same. The linear sequence of amino acids is the same.

iv) Is the tertiary structure of the 50 kD protein the same or different than the tertiary structure of the 250 kD protein? Explain briefly.
The tertiary structure is the same. Each polypeptide folds to form the same 3 dimensional shape.

Alternative answer:

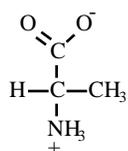
The tertiary structure is different. Although each polypeptide can fold to form the same 3 dimensional shape in isolation, when more than one polypeptide interact, the 3 dimensional shape can change.

v) Is the quaternary structure of the 50 kD protein the same or different than the quaternary structure of the 250 kD protein? Explain briefly.
The 50 kD protein, as a single polypeptide does not have quaternary structure, the quaternary structure of the 250 kD protein is the five subunit nature of this protein.

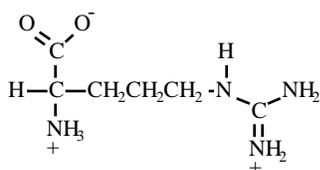
b) You test enzyme E activity on a large protein substrate. This substrate is not cleaved by enzyme E. You then treat the substrate with DTT (a compound that disrupts disulfide bonds) and test the enzyme E activity again. This time the substrate is cleaved by enzyme E. Why was enzyme E able to cleave the protein substrate only after the substrate was treated with DTT?

Enzyme E binds and cuts at specific sites. These site are not present on the exterior of the substrate when the substrate is properly folded. When the disulfide bonds within the substrate protein are disrupted, the 3 dimensional shape is altered, and the protein unfolds. This allows enzyme E access to sites that were previously protected within the substrate protein.

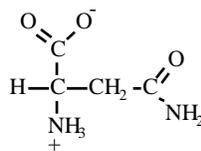
STRUCTURES OF AMINO ACIDS at pH 7.0



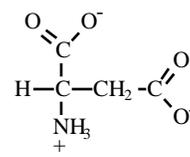
ALANINE
(ala)



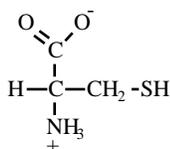
ARGININE
(arg)



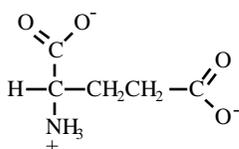
ASPARAGINE
(asn)



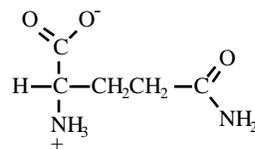
ASPARTIC ACID
(asp)



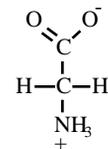
CYSTEINE
(cys)



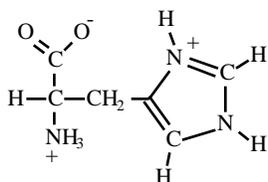
GLUTAMIC ACID
(glu)



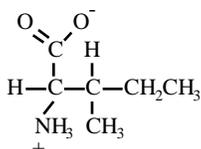
GLUTAMINE
(gln)



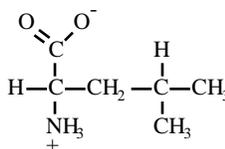
GLYCINE
(gly)



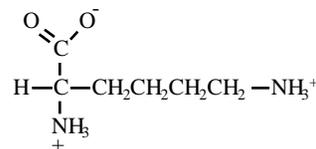
HISTIDINE
(his)



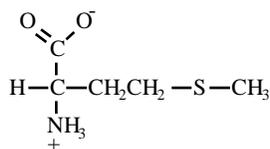
ISOLEUCINE
(ile)



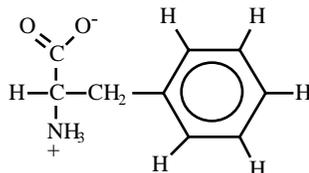
LEUCINE
(leu)



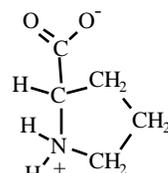
LYSINE
(lys)



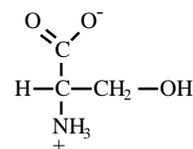
METHIONINE
(met)



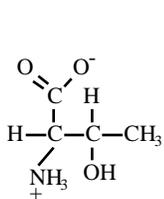
PHENYLALANINE
(phe)



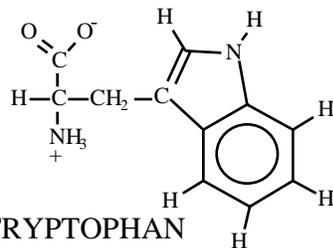
PROLINE
(pro)



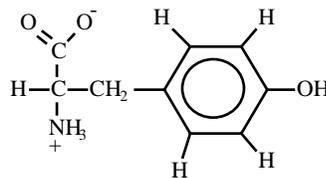
SERINE
(ser)



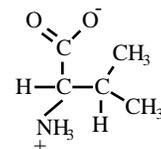
THREONINE
(thr)



TRYPTOPHAN
(trp)



TYROSINE
(tyr)



VALINE
(val)