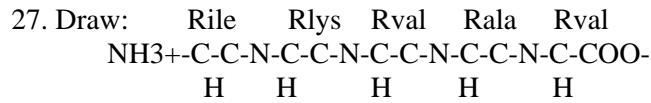


1. Organization is missing, the organized structure that carries out the functions necessary to maintain and extend the structure.
2. Life on earth: 3600 million years or 3.6 billions
 angstroms per nm: 10
 tetrahedral angle: 109°
 torsion angle of transpeptide = 180°
3.

DNA	→	DNA	→	RNA	→	protein
	Replication		transcription		translation	
4. a. $\Delta G = \Delta H - T \Delta S$.
 b. exergonic, since renaturation at 37° is spontaneous
 c. $\Delta G = 0$, since it doesn't prefer either direction
 d. $\Delta G = 0 = \Delta H - T \Delta S = \Delta H - (324K)(50J/K) = \Delta H - 16.2 \text{ KJ}$
 so $\Delta H = 16.2 \text{ KJ}$ (either + or-, since I didn't specify whether denaturation or renaturation)
5. d.
6. b. $A = ecl = 38L/\text{mole-cm} \times .01 \text{ moles/L} \times 1 \text{ cm} = 0.38$
7. c.
8. b.
9. c. Fully protonated Asp will be $+1+0+0 = +1$. Will be zero between 1.99 and 3.9 and -0.5 at 3.9
10. b. ...and precisely zero half way between 1.99 and 3.9.
11. a.
12. d.
13. c.
14. a. "d" is enticing... but the whole AA doesn't flit between + and -. Most of the time, it's just + on the amino end and - on the carboxyl end, a double ion, or zwitterion.
15. e. They are not ionized by the light.
16. Sure, as long as it is treated as an open system. Solar energy entering the glass house is equal and opposite to thermal energy leaving. However, the interior is able to maintain its organization because the sunlight is a low-entropy form of energy and the thermal energy is a high-entropy form. The system "sucks neg-entropy" out of its environment. [Notes: (a) "no" is wrong cuz there's a hundred year history of applying Td to open systems. The Biosphere II is much like Biosphere I, ie the earth. (b) Just because Biosphere II was a failure in its original form doesn't mean that the laws of Td are a failure; it didn't start failing as a Td system just because it failed as a biological experiment.]
17. $\Delta G = -RT \ln K_{eq}$, so $K_{eq} = \exp(-9.15/2.5) = \exp(-3.66) = 0.026$
18. Must circle the C-C-N-C in the middle of the picture plus the =O and -H attached to the C-N.
19.

NH ₃ ⁺	H	
H - C - CH ₂ - S - HO	...or it could be an H from water to the sulfur
COO-	H	
20. a. 12 amino acid residues x 110 daltons/residue = 1320 daltons for an estimate.
 b. There are 3 basic residues - Lys, His, and Arg - and 1 acidic residue - Asp. Thus, it will be predominantly positively charged at pH 7, and the pH must adjusted upward to gain neutrality, ie $pI > 7$.
 c. C, H, N, O, S
21. See Fig 2-15. Curve of pH vs [OH⁻] should rise upward except where it flattens out as it passes thru pH 4.76.
22. $pH = pK + \log(\text{base/acid})$
 $\log(\text{base/acid}) = pH - pK = 5.30 - 4.76 = 0.54$
 $\text{base/acid} = \text{acetate/ acetic acid} = 10^{(0.54)} = 3.5$
23. $5\text{nm} \times 10,000 = 50,000 \text{ nm} = .05 \text{ mm}$. That's $1/20^{\text{th}}$ of a mm, which sounds about right.
24. The tops of the amphiphiles are negatively charged so they repel each other. The bottoms are nonpolar and might tend to be squeezed out of the water (by hydrophobic interactions), but not into any very closeknit structure, due to the electrostatic repulsion between the heads.

25. Cations neutralize the negative charges on the Glu residues, or shield them. Therefore, they no longer suffer electrostatic repulsion, and they can now form micelle-like or lipid-bilayer-like structures. However they are sufficiently "pointed" that they tend to form cylinders instead of spheres or bilayers. [It's not enough to say that ionic bonds are formed between Glu and Ca/Na. That's not what forms the nanofiber structure. Still need to explain why the monomeric amphiphile molecules now aggregate.]
26. The carboxyl sidechains of the Glutamic acid R groups are deprotonated at pH 7.4



except with the appropriate R group substituted, and the Rlys in the protonated state. Thus the net charge at this pH 7.4 would be +1+0+1 = +1.

Common mistake to write a tetrapeptide; (Val should appear twice) and in wrong sequence.

28. The charge is +1 at 7.4, so the pI would be above 7.4, or between 9.5 and 10.54, or pI = 10.
29. Each slot could be any of 20, so the total varieties would be: 20x20x20x20x20 = 3.2 million
30. 5 amino acids require 15 base pairs to code for them, (triplet code)
31. a. Hexokinase b. Myoglobin c. Hexokinase d. Myoglobin e. cytochrome c
32. C-A-D-B [Note: SDS-PAGE uses an externally applied elec field; Anion Exchange Chr does not.]
33. Total activity/Total protein = 14, 85, 378, and 10,265.
 Thus the purification has been 10,265/14 = 733.