1. Volume V=100000 μ^3+10000$\mu^3 \approx 10^5 \mu^3$. Number of protein molecules is N= 500molecules/minute*60minutes/hour*24hours/day*7days/week/N_a, N_a - Avogadro number
Concentration C=N/V=8.4*10^{-8}M

2. Dynamic equilibrium: $dN_{\text{syntetized molecules}}/dt=dN_{\text{transported to axon}}/dt=$
=1000molecules/minute=K
$dN_{\text{transported to axon}}/dt=v*A*C$, v-rate of transport (5mm/day), A-cross-sectional area, C stable concentration
C=K/(v*A)= 2.4*10^{-7}M

3.
   a. $2Dt=<\Delta X^2>$, t=$(0.05cm^2)^2/2D=6.25*10^4$s

   b. Presumably the diffusion doesn't have directional preference, so half of synthesized molecules will be in dendrite, and half will be in axon.
   In dendrite: C=(N/2)/(N_a*V_{dendrite})=~21uM, volume $V_{\text{dendrite}}=4\mu^2*1$mm
   In axon: the first 1 mm (==2*$<\Delta X^2>$) contains ~95% of molecules diffused in axon (two standard deviations of normal distribution), so average concentration C=0.95*(N/2)/(N_a*V_{axon})=~79uM, volume $V_{\text{axon}}=1\mu^2*1$mm

4. pH_{medium}=7.4, so $[H^+]=10^{-7.4}$M=40nM=C_c
Surface is negatively charged to V=-50mV, and negative charges are distributed by Boltzmann distribution: surface concentration of positive ions (protons) $C_s=C_c*\exp[zeV/kT]$, and surface pH=-lgC_s=6.5

5. The surface area of sphere is proportional ("$\propto$") to the r^2. We have ~25% of radius change ([7.5μ-6μ]/6μ), so we have $(1.25)^2 \approx 1.56$ of initial membrane area (~56% stretching). But even 4% stretching leads to lysis, so lymphocytes can swell due to smoothing of folds in membrane.

6. At the beginning we have K^+ -defined membrane potential: V_K=RT/(zF)ln[3mM/140mM]=~-90mV, where is z=1. At the end we can calculate voltage difference again by Nernst equation, but for Ca^{2+}: V_{Ca}=RT/(zF)ln[0.5mM/2μM]=~+66mV, where is z=2. The change in potential will be $\Delta V=V_K-V_{Ca}$=~-156mV

7. Donnan equilibrium (see also Lecture#11): $C_{K\text{ inside}}/C_{K\text{ outside}} = C_{Cl\text{ outside}}/C_{Cl\text{ inside}}$, Also we know that $C_{K\text{ outside}}$=1mM $C_{Cl\text{ outside}}$=110mM. Another equation – electroneutrality inside the cell (assuming that there are only K & Cl): $C_{K\text{ inside}}=C_{Cl\text{ inside}}$. Also x – change in concentrations inside: $C_{K\text{ inside}}$=140+x, and $C_{Cl\text{ inside}}$ = 4 + x. By substituting one equation to another : x^2+144x+450=0, the meaningful solution of this square equation (which will keep concentrations positive) x= -3.2mM, so $C_{Cl\text{ inside}}$=4+x=0.8mM, and $C_{K\text{ inside}}$=~136.8mM.
Potential difference by Nernst equation (for example for potassium):
V=56mV*lg[1/136.8]=~ -118mV.

8.

a. Bending energy for the membrane with constant curvature $E=(B/2)*(1/R_t)^2*A$. Area of cylinder $A=\pi*d*l=\sim 5\mu^2$
$E=7.8*10^{-17}$ N*m, $KT=\sim 4*10^{-21}$ N*m (T=300K)
So $E= \sim KT*10^4$

b. Affinity of enhancer (E) to DNA gives us the change in free energy: $\Delta G_1 = = RT*\ln[K_{E\text{-}DNA}] = \sim -5.5$ Kcal/mole. For binding E to transcription factor (TF) we know change in entropy and enthalpy of binding, so we also can calculate change in free energy: $\Delta G_2 = \Delta H - T*\Delta S = -4-1 = -5$ Kcal/mole. For full reaction: $\Delta G = \Delta G_1 + \Delta G_2 = -10.5$ Kcal/mole, and equilibrium constant: $K_A = \exp[-\Delta G/(RT)] = \sim 4*10^7$ 1/M, and $K_D = 2.5*10^{-8}$ M ; We also know that we need enhancer concentration equal to dissociation constant for 50% activation of transcription. By knowing the volume of nucleus we can calculate the actual number of molecules: $N=K_D*Na*V = = \sim 1700$ molecules

9. $D=kT/(6\pi\eta r)=2.2*10^{-7}$ cm^2/s (You also can calculate it by using the $D \propto 1/r$ proportionality from this formula (see comments for (5) of the provided to exam equations): $D_{1\mu \text{ radius sphere}}=4.4*10^{-9}$ cm^2/s, so $D_{0.05\mu \text{ radius virus particle}}=2.2*10^{-8}$ cm^2/s)

10. The first mechanism – linear movement of scanning protein complex with the rate v=30b.p./s=~$6x10^{-4}$ cm/s (3Å/b.p.), so scanned distance will be l=t*v

For diffusion model scanned distance defined by $d=\Delta X/2$, and $<\Delta X^2> = 2D*t$.
For t=1 min= 60 s: l=~$5.4x10^{-2}$ cm=~1800b.p., and $d=(1/2)*(2DT)^{1/2}$ =~1.7um= =~5800 b.p.
For t=1 h = 3600s: l=~3cm=108 Kb.p., d==~13.4um= 45Kb.p.

11. L=5000bp, rate of synthesis is v=50bp/s, so time of synthesis is T=L/v=100s. Time between moment of transcription initiations t=300bp/v=6 s. 100^{th} copy of RNA will be synthesized in $99*6=594^{th}$ second after beginning of synthesis of the first RNA molecule, and will finish synthesis in next T=100s, so cycle for synthesis of 10 molecules is t+T=~700 s. And the gene should be activated 700s/30min=~39% of time.

12. Reynold's number: $R = \upsilon L\rho/\eta$, L- here is diameter, υ – speed, ρ – density of obnject (particles), η – viscosity of media (we can use viscosity of water here – brain slices are usually covered by thin layer of some liquid). So υ= ~1.7m/s