1. The packing ratio of DNA is defined as the ratio of its contour length to the length of its container. This ratio is maximal when the container is a sphere (if the container were a cube, for example, its longest dimension, its body diagonal, would be larger than the diameter of a sphere of equal volume).

The volume, $V$, occupied by a $10^6$ bp DNA is a 20-Å diameter cylinder that is $3.4 \times 10^6$ Å long.

$$V = \pi \left( \frac{d}{2} \right)^2 = 3.14 \times \left( \frac{20}{2} \right)^2 \times 3.4 \times 10^6 \text{ Å}^3 = 1.07 \times 10^9 \text{ Å}^3$$

The radius of sphere of this volume ($V = 4\pi r^3/3$) is

$$r = \left[ \frac{3V}{4\pi} \right]^{1/3} = \left[ \frac{3 \times 1.07 \times 10^9}{4 \times 3.14} \right]^{1/3} = 635 \text{ Å}$$

$$\text{Packing ratio} = \frac{\text{contour length}}{\text{diameter of sphere}} = \frac{3.4 \times 10^6 \text{ Å}}{2 \times 635 \text{ Å}} = 2680$$
For a $10^9$ bp DNA, repeating the calculations:

$$r = \left( \frac{3 \times 1.07 \times 10^{12}}{4 \times 3.14} \right)^{1/3} = 6350 \, \text{Å}$$

Packing ratio = $\frac{3.4 \times 10^9 \, \text{Å}}{2 \times 6350 \, \text{Å}} = 268,000$

2. (a) A nucleosome core particle contains 147 bp of DNA. Thus for yeast (\textit{S. cerevisiae}), the fraction of the DNA associated with nucleosome core particles is $\frac{147}{147 + 18} = 0.89$. For humans, this quantity is $\frac{147}{147 + 38} = 0.79$.

(b) The haploid yeast genome has 12,070 kb so that its diploid genome has $2 \times 12,070,000 = 24,140,000$ bp. A yeast nucleosome contains $147 + 18 = 165$ bp. Hence a diploid yeast nucleus contains $24,140,000 \text{ bp} / 165 \text{ bp} = 146,000$ nucleosomes. Similarly, a human diploid nucleus has $(2 \times 3,038 \times 10^6 \text{ bp}) / (147 + 38 \text{ bp}) = 33,000,000$ nucleosomes.

3. A chromosome consists of a single molecule of dsDNA in noncovalent association with histone octamers and numerous other proteins. Hence, cleaving the DNA in even a few places will cause the chromosome to fragment, whereas degrading a few of the DNA’s associated proteins will have little structural effect on the chromosome.

4. If the DNA double helical winding was unaffected by supercoiling around the nucleosome, the SV40 minichromosome would be supercoiled by nearly $-2$ superhelical turns per nucleosome (left-handed toroidal turns, by definition, have negative supercoils; Section 29-3Aa). The observed $-1$ superhelical turns per nucleosome implies that the missing superhelical turns are taken up by the duplex helix. This, in turn, implies that the duplex DNA in a nucleosome is overwound in its relaxed state by about one turn per nucleosome (which is $360^\circ / 146 \text{ bp} \approx 2.5^\circ / \text{bp}$).

5. Histones have a great tendency to form nonspecific aggregates. The presence of the polyanion polyglutamate apparently electrostatically shields the histones from each other and thereby allows them to specifically aggregate with DNA to form nucleosomes. Thus, polyglutamate, much like the acidic protein nucleoplasmin, acts as a molecular chaperone in the formation of nucleosomes.
6. The DNA molecule consists of $60\%$ repeated sequences of complexity $x = 400$ and $40\%$ unique sequences with $x = 400,000$. Hence, the $C_{0t_{1/2}}$ values of these two types of sequences should differ by a factor of 1000. There should be little, if any, difference between the $C_{0t}$ curves of DNA sheared to lengths of 1000 bp and 100 bp because the rate of collision between complimentary sequences is the same in both cases. Hence, in both cases, the $C_{0t}$ curve has the shape:

![Graph showing $C_{0t}$ vs. $f$]

7. Single-strand nucleases would remove the non-base paired loop of the foldback structures:

![Diagram showing single-strand nuclease digestion]

Since the sequences of these foldback structures vary in their complexity as much as the rest of the DNA sample from which they are taken (at least to the limit of their length), cleaved and denatured foldback structures can take varied amounts of time to renature.
8. (a) The rDNA transcripts (rRNA) are used directly to form ribosomes. However, many copies of a ribosomal protein can be translated from a single copy of ribosomal mRNA. Thus, in a sense, the ribosomal proteins are "amplified" in the normal course of their synthesis.

(b) Assuming that the rate of rRNA synthesis is proportional to the number of rDNA copies (that is, that the availability of template DNA is the limiting factor in its transcription), in the absence of gene amplification, rRNA synthesis should occupy $1500 \times 2$ months = 250 years.

9. Hb Kenya most probably arose in a manner similar to Hb Lepore (Figure 34-43): by an unequal crossing-over between the $\lambda$-gene and the corresponding position of the $\beta$-gene.

10. Red-green color blindness is conferred by a mutation in an X-linked gene so that female carriers of this condition, who do not appear to be red-green color blind, have one wild-type gene and one mutated gene for this condition. In placental mammals such as humans, females are mosaics of clones of cells in which only one of their two X chromosomes is transcriptionally active. Hence, in a female carrier of red-green color blindness, the transcriptionally active X chromosome in some of these clones will contain the wild-type gene and others will contain the mutated gene. The former type of retinal clone is able to differentiate red and green light, whereas the latter type of retinal clone is unable to do so. Apparently, these retinal clones are small enough so that a narrow beam of light is necessary to separately interrogate them.

11. The band is indicative of a region in the DNA made DNase I hypersensitive by the binding of Sp1.

12. A sequence located downstream of the gene’s promoter (i.e., within the coding region) could regulate gene expression if it were recognized by the appropriate transcription factor such that the resulting DNA–protein complex successfully recruited RNA polymerase to the promoter.

13. Calico cats are genetic mosaics in which some patches of skin grow orange fur as specified by one X chromosome and the remaining patches grow black fur as specified by the second X chromosome (Section 34-3Aa). Normal XY male cats, having only one X chromosome, cannot be calico cats. However, genetically abnormal XXY male cats can be calico cats since one of their two X chromosomes in each cell is inactivated to form a Barr body, just as in normal females.

14. The $esc$ gene is apparently a maternal-effect gene. Thus, the proper distribution of the $esc$ gene product in the fertilized egg, which is maternally specified, is sufficient to permit normal embryonic development regardless of the embryo’s genotype.
15. If the cancer cell's transformed state results, at least in part, from the absence of a functional tumor suppressor gene such as that expressing pRb, and if the chromosomes that the normal cell contribute to the fused cell express that tumor suppressor gene, then the fused cell will have a nontumorogenic phenotype. This is because tumor suppressor gene products suppress uncontrolled cell proliferation (cancer) so that cells requiring such a gene product for normal growth, but lacking it, will assume the cancerous state.