

Your name:

1. (3 points) You isolate DNA from yeast that has been arrested in G1 (prior to the initiation of DNA synthesis) or in G2 (prior to the initiation of mitosis). In separate reactions of the same volume you allow DNA from the same number of cells (e.g. 10^8) from each preparation to denature and hybridize. You measure hybridization rate as the time required for half of the DNA to become double-stranded (not the initial reaction rate).

- a) DNA from the G1-arrested cells would hybridize faster by a factor of 4
- b) DNA from the G1-arrested cells would hybridize faster by a factor of 2
- c) DNA from the two samples would hybridize at the same rate
- d) DNA from the G2-arrested cells would hybridize faster by a factor of 2
- e) DNA from the G2-arrested cells would hybridize faster by a factor of 4

2. (3 points) You repeat this experiment using the same amount of DNA (e.g. exactly 100 micrograms) from each sample. Once again, you use the same volume. This time

- a) DNA from the G1-arrested cells would hybridize faster by a factor of 4
- b) DNA from the G1-arrested cells would hybridize faster by a factor of 2
- c) DNA from the two samples would hybridize at the same rate
- d) DNA from the G2-arrested cells would hybridize faster by a factor of 2
- e) DNA from the G2-arrested cells would hybridize faster by a factor of 4

(3 points each for questions 3-28). In each of the following there are two or more statements. One is true (generally, it is taken directly from your textbook or another reliable source) and the others have been modified so as to be untrue, misleading, false, wrong, unlikely or bogus. Circle, check or otherwise designate the correct statement. Ambiguous marks (checking both, placing a mark between the two statements, etc.) will be considered wrong.

- 3.
 - a) Human alpha globin and mouse beta globin are **homologs**.
 - b) Human alpha globin and mouse beta globin are **orthologs**.
- 4.
 - a) In *E. coli*, *trpA* and *trpB* are two **alleles** of the same gene.
 - b) In *E. coli*, *trpA* and *trpB* are two **genes**.
- 5.
 - a) The bacterial origin of DNA replication "fires" only **after** the prior round of DNA replication is complete.
 - b) The bacterial origin of DNA replication can "fire" **before** the prior round of DNA replication is complete.
- 6.
 - a) In conjugation, donor DNA is **transferred directly** to the recipient through a connecting tube.

Your name:

- b) In conjugation, donor DNA is **taken up from the medium** by a recipient cell.
7. a) The recipient of (successful) transfer from an Hfr strain **becomes F⁺**.
b) The recipient of (successful) transfer from an Hfr strain **remains F⁻**.
8. a) Common plasmid vectors are capable of carrying up to **15 kb.** of foreign DNA.
b) Common plasmid vectors are capable of carrying up to **40 kb.** of foreign DNA.
c) Common plasmid vectors are capable of carrying up to **80 kb.** of foreign DNA.
9. a) A single base mismatch in an allele-specific oligonucleotide used in **hybridization** will provide maximal discrimination (the greatest possible difference in T_m) when located **at the 3' end** of the oligonucleotide.
b) A single base mismatch in an allele-specific oligonucleotide used in **hybridization** will provide maximal discrimination when located **in the center** of the oligonucleotide.
10. a) A single base mismatch in an allele-specific primer used in **PCR amplification** will provide maximal discrimination when located **at the center** of the primer.
b) A single base mismatch in an allele-specific primer used in **PCR amplification** will provide maximal discrimination when located **at the 3' end** of the primer.
11. a) **SNPs** are highly polymorphic DNA markers that are useful in linkage studies.
b) **Microsatellites** are highly polymorphic DNA markers that are useful in linkage studies.
12. a) CODIS, the combined DNA index system, makes use of **STR** (short tandem repeats) polymorphisms.
b) CODIS, the combined DNA index system, makes use of **SNPs** (single nucleotide polymorphisms).
13. a) In PCR-based mutagenesis methods desired sequence changes are designed into the **5'** end of the PCR oligonucleotides.
b) In PCR-based mutagenesis methods desired sequence changes are designed into the **3'** end of the PCR oligonucleotides.
14. a) The initiating event for meiotic recombination is a double-strand break generated by a cellular protein.
b) The initiating event for mitosis is a double-strand break generated by a cellular protein.
c) Double-strand breaks are damaging to DNA. No cellular proteins cause double-strand breaks in healthy cells.
15. a) For automated sequencing, the Sanger protocol is performed in four **separate** reactions, each with a different labeled terminating nucleotide.

Your name:

- b) For automated sequencing, the Sanger protocol is performed with all four individually labeled terminating nucleotides present in a **single** reaction.
16. a) New methods for the rapid and inexpensive sequencing of entire genomes are under active development and **dramatic improvements are expected**.
b) New methods for the rapid and inexpensive sequencing of entire genomes are **unlikely to emerge** because of natural limits on DNA sequencing technology based on physical laws.
17. a) **DNA footprinting** uses end-labeled DNA to map the position of protein binding sites.
b) **The electrophoretic mobility shift assay** uses end-labeled DNA to map the position of protein binding sites.
18. a) The human genome is about **40** times the size of bacterial genomes.
b) The human genome is about **200** times the size of bacterial genomes.
c) The human genome is about **1,000** times the size of bacterial genomes.
19. a) Mammals have **less than 15** times as many genes as typical bacteria.
b) Mammals have **between 15 and 50** times as many genes as bacteria.
c) Mammals have **between 50 and 200** times as many genes as bacteria.
20. a) In shotgun sequencing, fragments are sequenced by annealing **random oligonucleotide primers** to the cloned insert.
b) In shotgun sequencing, fragments are sequenced using a common oligonucleotide primer that is complementary to a vector sequence that is immediately adjacent to a **random and unknown insert**.
21. a) **Intron** sizes vary more between species with genomes of different sizes (e.g. humans vs. Arabidopsis)
b) **Exon** sizes vary more between species with genomes of different sizes (e.g. humans vs. Arabidopsis).
22. a) **Myc/Max heterodimers** bind to DNA and activate the transcription of genes that control growth but **Max/Max homodimers bind without activating**.
b) **Max/Max homodimers** bind to DNA and activate the transcription of genes that control growth but **Myc/Max homodimers bind without activating**.
23. a) The **primer-walking** protocol is a reasonable and commonly used approach to sequence whole genomes.
b) The **shotgun sequencing** protocol is a reasonable and commonly used approach to sequence whole genomes.
24. a) Long terminal repeats are found in mobile genetic elements that use **DNA polymerase** during their replicative cycle.

Your name:

- b) Long terminal repeats are found in mobile genetic elements that use **reverse transcription** during their replicative cycle.
25. a) Cytosine deamination in DNA is repaired by a mechanism involving **nucleotide excision repair**.
b) Cytosine deamination in DNA is repaired by a mechanism involving **base excision repair**.
26. a) A lysogenic bacterium **carries a prophage**.
b) A lysogenic bacterium **lyses to release infectious bacteriophage**.
27. a) Different **sigma** factors allow *E. coli* RNA polymerase to recognize different promoters.
b) Different **alpha** factors allow *E. coli* RNA polymerase to recognize different promoters.
28. a) A core promoter is defined as the minimal sequence element that is **sufficient** to confer transcriptional activity *in vivo* in the absence of additional regulatory sequences.
b) A core promoter **has little or no** transcriptional activity *in vivo* in the absence of additional regulatory sequences.
29. (8 pts.) Rank the following types of DNA with respect to the fraction of the human genome it makes up (place a 1, 2, 3 or 4 next to each type of DNA where 1 indicates the largest amount of DNA, 2 the next largest, 3 the third and 4 the least abundant class of DNA).
- a) ___ Sequences that code for amino acids.
b) ___ Non-LTR retroelements such as SINEs and LINEs.
c) ___ LTR-retrotransposon and retroviral proviruses.
d) ___ Conserved (and therefore presumably functional) noncoding sequences.
30. (8 pts.) Explain why CG dinucleotides are so rare in mammalian DNA and why they are more frequent in the vicinity of active genes.