科目:分子生物學【生科系碩士班甲組選考、乙組選考】

題號:4033

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一、配合題:每題2分(10 points)

For the following enzymes involved in DNA replication indicate which activities from the right-hand Activities column match. Note there may be more than one activity that matches a particular enzyme so list as many as apply, also each enzyme will have at least one activity

	Enzymes	Activities
1.	DNA polymerase III	A. DNA template dependent
2.	Ligase	B. breaks hydrogen bonds between base pairs
3.	Primase	C. 5' to 3' DNA polymerase
4.	Helicase	D. 3' to 5' exonuclease
5.	Telomerase	E. 5' to 3' RNA polymerase
		F. joins two DNA fragments
		H. requires an RNA primer

二、是非題:正確敘述請答(O),若是不正確敘述請答(X),每題2分(20 points)

- 1. Epigenetic inheritance is the transfer of information that is not based on DNA sequence from parent to progeny.
- 2. An open-reading frame is a long stretch of nucleotide sequence that contains no chain-terminating (stop) codons.
- 3. About half of the human genes identified by sequencing can be assigned a function by homology to previously characterized genes, and the other half represent new genes of unknown function.
- 4. Analysis of single nucleotide polymorphisms (SNPs) may enable physicians to tailor treatment strategies to match the genes of individual patients.
- 5. The consequences of errors in transcription are less than those of errors in DNA replication.
- 6. The differences in the patterns of proteins produced in different specialized cell types are accurately reflected in the patterns of expressed mRNAs.
- 7. Many gene regulatory proteins in eucaryotes can act even when they are bound to DNA thousands of nucleotide pairs away from the promoter that they influence.
- 8. By far the most important advantage of cDNA clones over genomic clones is that they can contain the complete coding sequence of a gene.
- 9. Loss-of-function mutations are usually recessive.
- 10. If two mutations have a synthetic phenotype, it usually means that the mutations are in genes whose products operate in the same pathway.

三、選擇題:選出一個正確的答案,每題2分(40 points)

- 1. A gene can be defined as a segment of DNA that codes for
 - (a) a protein.
- (b) a functional product.
- (c) mRNA.

- (d) mRNA or rRNA.
- (e) mRNA, rRNA, or tRNA.
- 2. Introns can encode
 - (a) small nuclear RNAs. (b) microRNAs. (c) sequences that control RNA processing
 - (d) All of the above.
- (e) None of the above.

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3. Synthesis of different proteins from the same gene is due to

(a) intron shuffling.

(b) exon shuffling.

(c) alternative splicing.

(d) exon splicing.

(e) alternative transcription.

- 4. Telomeres are
 - (a) microtubule binding sites in the center of chromosomes.
 - (b) chromosome structures that form during telophase.
 - (c) sites at the ends of chromosomes where DNA replication begins.
 - (d) chromosome end structures required for complete replication of linear chromosomes.
 - (e) sites at the ends of chromosomes where microtubules bind.
- 5. To sequence the human genome, the International Human Genome Sequencing Consortium
 - (a) used the shotgun approach to sequence fragments and assemble them in order using overlaps between the sequences.
 - (b) used BAC clones as substrates for sequencing.
 - (c) sequenced cloned DNA and then mapped it by FISH.
 - (d) All of the above
- 6. The main difference between the genomes of the bacteria *Haemophilus influenzae* and *E. coli* is that
 - (a) the genome of *H. influenzae* is a circular molecule and that of *E. coli* is linear.
 - (b) the *H. influenzae* genome encodes a larger number of genes.
 - (c) a higher percentage of the genome of *H. influenzae* contains genes encoding proteins.
 - (d) the genome of E. coli is approximately three times the size of H. influenzae.
- 7. Bioinformatics is defined as
 - (a) an electronic copy of genomic sequences that is exchanged between scientists across the world.
 - (b) a quantitative understanding of integrated dynamic behavior of complex biological systems and processes.
 - (c) a field of biology that lies at the interface between biology and computer science, and is focused on developing the computational methods needed to analyze and extract useful biological information from the sequences of DNA.
 - (d) the systematic inactivation of each gene in the genome by homologous recombination.
- 8. Polytene chromosomes
 - (a) are *Drosophila* chromosomes present in hundreds of copies and aligned in parallel.
 - (b) are a pair of homologous *Drosophila* chromosomes aligned side by side.
 - (c) are visible by light microscopy due to their highly condensed nature.
 - (d) can be stained to yield bands that correspond to 200 kilobases of sequence.
- 9. Partial digestion of chromatin with micrococcal nuclease was found to yield DNA fragments approximately 200 base pairs long. What accounts for this phenomenon?
 - (a) The low pH environment of the nucleus renders the nuclease able to cut only in 200-base-pair increments.
 - (b) The nuclease cleaves at specific DNA sequences that occur every 200 base pairs in the genome.
 - (c) This is a random phenomenon, and its significance is unknown.
 - (d) This result suggests that the binding of proteins to DNA in chromatin protects regions of DNA from nuclease digestion.

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10	Th	e wobble hypothesis predicts that codons coding for the same amino acid
		may differ at the first position (b) may differ at the second position
		may differ at the third position (d) may differ at the first two positions
		may differ at all three positions
11.		nonsense suppressor mutation is a mutation
	a)	that alters the reading frame
	b)	that changes the amino acid sequence of the gene product
	c)	that creates a termination codon
	d)	in a tRNA gene that allows it to recognize a termination codon
		that allows a ribosome to bypass termination codons
12	Tr	ansposons, or jumping genes, are DNA elements that move within the genome. In
	wł	nich organismic groups are transposons found?
		bacteria b) eukaryotes c) mammals
	d)	ancient bacteria e) all organismic groups
13	. A	n aminoacyl tRNA synthase Valine is mutated so that it now attaches the amino acid
!	gl	yoine to the tRNA Valine instead of valine. What will happen at translation?
	a)	There will be glycines at all valine positions and valines at all glycine positions.
ľ	b)	There will be valines at all glycine positions and glycines at all valine positions.
	c)	There will be valines at all glycine positions and at all valine positions.
		There will be glycines at all glycine positions and at all valine positions.
	_	There will be no translation.
14		aring bacterial translation initiation, the mRNA
		binds to the large subunit
		is oriented so that the AUG start codon is in the A site
		only binds f-Met tRNA after the entire ribosome has been assembled
	d)	is oriented by its Shine-Delgarno sequence through base-pairing with an rRNA
1		requires ATP hydrolysis for binding to the ribosomal subunit
15		major difference between the <i>E. coli lac</i> and <i>ara</i> operons is that
		the substrate of the enzyme coded by ara is not the inducer
		the ara regulator protein interacts with two regions of the operon
	•	ara does not have a CAP-binding site ara is expressed constitutively
	,	ara does not have an operator site
16	•	protein causes the acetylation of histones. What affect do you think this will have on a
10		ne in that region?
	a)	It will cause a decrease in expression.
İ		It will cause an increase in expression.
	c)	It will cause the methylation of that DNA.
	d)	It will permit DNA replication only, but will silence the gene.
	e)	It will only change the chromatin structure, with no effect on gene expression.
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17	. The advantage of RNAi over other functional genomic techniques is that				
	a) RNAi does not affect any gene but the targeted one				
	b) other techniques cannot target single genes				
	c) other techniques cannot make specific mutagenic changes				
	d) RNAi introduces no mutations to the organism				
	e) All of the above				
18	. A mutation in one gene that counteracts the effects of a mutation in another gene is known				
	as a				
	a) temperature-sensitive mutation b) recessive mutation c) conditional mutation				
	d) suppressor mutation e) nonsense mutation.				
19.	. Which of the following clusters of terms applies when addressing enhancers or silencers as				
	elements associated with eukaryotic genetic regulation?				
	a) cis-acting, fixed position, fixed orientation				
	b) trans-acting, fixed position, fixed orientation				
	c) cis-acting, variable orientation, variable position				
	d) cis-acting, variable position, fixed orientation				
20	e) trans- and cis-acting, variable position				
ZU.	Under strictly controlled conditions, a probe can be used that will hybridize only with its complementary sequence and not with other sequences that may vary by as little as one				
	nucleotide. What are such probes called?				
	a) generation-specific probes b) short, variable repeats c) VNTRs				
	d) microsatellites e) allele-specific oligonucleotides (ASOs)				
	d) merosatemes e) anero specime ongonacionaes (rises)				
79	、問答題 (30 points)				
	What is the difference between telomerase in cancer cells and telomerase in normal somatic				
	cells of an adult, and what is the significance of that difference? (5 points)				
	What does the term "replication licensing" refer to in the process of eukaryotic DNA				
	replication? (5 points)				
	Describe briefly the maturation of eukaryotic mRNA transcript, i.e. what is the				
	posttranscriptional processing of eukaryotic mRNA transcript. (5 points)				
	(a) List three major structural classifications of DNA-binding domains that are found in				
	eukaryotic transcription factors. (3 points)				
	(b) Name three consensus sequences or modular DNA sequences that exist upstream from				
	the coding regions of some eukaryotic genes. (3 points)				
	Assume that a plasmid (circular) is 3200 base pairs in length and has restriction sites at the				
	following locations: 400, 700, 1400, 2600. Give the expected sizes of the restriction				
	fragments following complete digestion. (4 points)				
6.	Nucleotide excision repair (NER) occurs through two distinct mechanisms; what are these,				
;	and how do they differ? (5 points)				