QUESTION	YOUR SCORE	FULL SCORE
I		40
II		40
III		40
IV		40
V		40
TOTAL		200

YOUR NAME: \_\_\_\_\_ (Please PRINT your name in ink on this line as legibly as possible.) YOUR SIGNATURE: \_\_\_\_\_\_\_\_\_(Please SIGN your name in ink on this line.) YOUR STUDENT ID NUMBER: YOUR LAB ROOM / TA (circle one): Dale Aromdee Jane Klimenko Jesse Patterson

**QUESTION I.** Multiple Choice. Please CIRCLE <u>clearly</u> the letter that corresponds to the <u>most</u> correct conclusion to each of the following statements or queries. [40 points total]

(1) An organism whose cells contain two copies of each and every chromosome is called: [4 points]

- (a) Homozygous
- (b) Heterozygous
- (c) Homogeneous



(2) All of the following terms are appropriate descriptions for the growth and duplication of a yeast cell in liquid medium, EXCEPT: [4 points]

- (a) Vegetative multiplication
- (b) Mitotic proliferation
- (c) Meiotic progression
- (d) Cell cycling

(3) The most appropriate definition for the genetic term "allele" is: [4 points]

(a) one of a series of possible alternative forms of a given gene

- (b) alternative genes at two different genetic loci
- (c) one of two different forms of a specific chromosome
- (d) sequences that encode each of the domains of a bifunctional gene product

(4) In a eukaryotic cell, like budding yeast (*Saccharomyces cerevisiae*), transcription and translation take place: [4 points]

- (a) In the cell nucleus and the cytoplasm, respectively
- (b) In the nucleolar compartment of the nucleus and the cytoplasm, respectively



(d) In the nucleolus and on the surface of the rough endoplasmic reticulum, respectively

(5) For propagation of *Saccharomyces cerevisiae*, it is essential that all of the following nutrients be present in the growth medium, EXCEPT: [4 points]



- (b) Ammonia
- (c) Sulfate
- (d) Phosphate

(6) The degree of relatedness (in percent sequence identity) between an *Saccharomyces cerevisiae* gene product and its clearly homologous counterpart in a mammalian cell is usually in the range of: [4 points]

- (a) 20-40%
- (b) 40-60%
- (c) 60-80%
- (d) 80-100%

(7) If a mutation in one gene in *MAT***a** cell masks the phenotypic effect of a mutation in a different gene, this genetic behavior is called: [4 points]

- (a) Haploinsufficiency
- (b) Synthetic lethality
- (c) Dominance
- (d) Epistasis

(8) Each of the following conditions listed can be used to counter-select (i.e. provides a positive selection) for loss-of-function mutations in the indicate marker genes, EXCEPT [4 points]

- (a) addition of the toxic arginine analog, canavanine, to isolate *can1* (Arg permease-minus) mutants.
- (b) addition of the toxic pyrimidine analog, 5-fluoro-orotic acid (plus Ura), to isolate *ura3* mutants.

(c) addition of the toxic histidine analog, 3-amino-triazole (plus His), to isolate his3 mutants.

(d) addition of the toxic lysine precursor, *alpha*-aminoadipic acid (plus Lys), to isolate *lys2* mutants.

(9) To occur efficiently, all of the following events require DNA sequence homology, EXCEPT: [4 points]

- (a) Site-specific mutagenesis
- (b) Meiotic recombination
- (c) Gene transplacement
- (d) Plasmid integration

(10) A standard genetic procedure to determine whether two recessive mutations that display a similar phenotype are likely located in the same gene is called: [4 points]

- (a) A dominance test
- (b) A suppression test
- (c) A loss-of-function test



A complementation test

**QUESTION II**. TRUE or FALSE. Put a <u>clear</u> "X" mark in the box that is the most appropriate response to each of the statements on the left. [40 points total]

	TRUE	FALSE
(1) All yeasts are fungi. [4 points]	x	
(2) All plasmids are episomes. [4 points]	x	
(3) Extragenic suppressors of nonsense mutations are often mutant tRNA genes. [4 points]	x	
(4) Most prokaryotic ( <i>E. coli</i> ) genes cannot function in yeast, and vice-versa. [4 points]	x	
(5) A dominant-negative mutation interferes with the function of the wild-type version of the same gene. [4 points]	x	
<ul><li>(6) A dosage suppressor must be overexpressed in order to manifest its phenotypic effect.</li><li>[4 points]</li></ul>	x	
(7) Genetics can be used to infer what residues are critically involved in the biological function of protein-coding genes, i.e. polypeptides. [4 points]	x	
(8) These terms— data, bacteria, spectra, media, maxima, criteria, and optima —are all plural words. [4 points]	x	
(9) The cell wall of <i>Saccharomyces cerevisiae</i> is very thick and made up of the same complex protein- and polysaccharide-containing polymers (peptidoglycan) as the prokaryotes (Gram-positive bacteria) that also have very thick cell walls. [4 points]		x
(10) Lactose is Gal( $\beta$ 1—>4)Glc, whereas melibiose is Gal( $\alpha$ 1—>6)Glc. [4 points]	X	

**III**. Fill in the blank with the LETTER corresponding to the <u>most</u> appropriate term, phrase, word or abbreviation from the column on the right. [40 points total]



**IV**. Fill in the blank with the LETTER corresponding to the <u>most</u> appropriate genetic convention, nomenclature term, or abbreviation from the column on the right. [40 points total]

(1) Designates an insertion mutation that prevents			
catabolism of the carbon source, galactose. [4 points]	B	Α.	leu2
(2) Designates a dominant allele that permits constitutive		B.	gal7::HIS3
(2) Designates a dominant affele that permits constitutive			11151-24 20021/ADE2
necessary for catabolism of galactose [4 points]	Y		
	^	<u>C</u> .   F	Cvh <sup>R</sup>
(3) Designates the product of a wild-type gene.		G	aal80∧…l FU2
[4 points]	Q	H.	his3-∆200
[]	~	1.	Ade
(4) Designates a chimeric polypeptide in which a yeast		J.	[cox3]
protein has been fused to another protein sequence.		K.	Psi⁺
[4 points]	U	L.	LEU2
		M.	[KIL-k1]
(5) Designates a double mutation at the indicated locus.		N.	P <sub>GAL1</sub> -lacZ
[4 points]	V	0.	ARG4
		P.	p[ <i>LYS2</i> ]
(6) Designates a mutation in a mitochondrial gene.		Q.	His3
[4 points]	J	R.	GAL80°
(7) Designates a fusion of a native vesat promotor to a		S.   T	hisg::URA3::hisg
(7) Designates a rusion of a native yeast promoter to a	N		$trp1-64^{mn}$
reporter gene. [4 points]	N		
(8) Designates an antibiotic-resistance phenotype		V.	Russe GEP
[4 noints]	F	X X	$G\Delta I 4-5$
	*	Y.	TRP1
(9) Designates a null (deletion) allele and not a		Z.	URA3
deletion-insertion allele. [4 points]	Н		
		·	
(10) Designates the heterozygous condition at a			

particular locus in a diploid [4 points]

\_\_\_\_D\_\_\_\_

#### YOUR NAME:

**QUESTION V**. Complete the sentence, phrase, paragraph or thought, with the <u>most</u> appropriate word, term, concept, reaction, or subject that you are able to provide. [40 points total]

(1) Access to the codon for translation initiation downstream of the 5'-end of eukaryotic mRNAs, which is called the 5'-untranslated region (or 5'-UTR), is almost always blocked by rather extensive \_\_\_\_secondary and tertiary structures\_\_\_[4 points] in the RNA itself. The eukaryotic translation initiation factor most responsible for dealing with this specific problem is termed \_\_\_\_elF4A\_\_\_\_[4 points]. This protein is able to alleviate this problem because it possesses a catalytic function known as \_\_\_\_RNA helicase\_\_\_\_\_activity [4 points].

(2) The eukaryotic translation initiation factor, termed \_\_\_\_\_elF4G\_\_\_\_\_ [4 points], is considered a platform that organizes the entire process of translation initiation because it is able to associate physically and directly with the the mRNA itself, as well as with the factor discussed in part (1) immediately above, and also with the following additional components that are all essential for efficient initiation of translation: the factor known as \_\_\_\_\_elF4E\_\_\_\_\_ [4 points] that binds to the extreme 5'-end of the mRNA; a factor that binds to mature 3'-end of the mRNA, termed \_\_\_\_PABP\_\_\_\_ [4 points]; and, a factor that is necessary to recruit the 40S subunit of ribosomes, known as \_\_\_\_\_elF3\_\_\_\_\_ [4 points].

(3) Using DNA-mediated transformation of a  $MATa/MAT\alpha$  his3/his3 diploid cell, you replace the chromosomal copy of *GENEX* on chromosome V with a geneX $\Delta$ ::HIS3 construct by selecting for His<sup>+</sup> transformants. As a control, you transform the same strain with just HIS3 DNA and select the resulting His<sup>+</sup> transformants. You subject both the *MATa/MATa* his3/his3 geneX $\Delta$ ::HIS3/GENEX and the *MATa/MATa* his3/HIS3 diploids to sporulation. You then dissect the meiotic products on a rich medium (YPD). You find that from each ascus of the *MATa/MATa* his3/his3 geneX $\Delta$ ::HIS3/GENEX diploid strain only two of the spores of each tetrad are able to grow (and all are His<sup>-</sup>), whereas all four spores are viable in every acus examined from the control *MATa/MATa* his3/HIS3 diploid. What does this result tell you about the function of *GENEX* in the physiology of the yeast cell? Explain your reasoning. [12 points]

This segregation pattern of 2 live spores-to-2 dead spores (abbreviated 2 live:2 dead) is the hallmark of a loss-of-function mutation in an <u>essential</u> gene (i.e. one that is required for the yeast cell to grow under any condition). Moreover, since the function of this gene is essential, even on rich medium (where all of the small molecules required for yeast growth are being supplied), the product of GENE X most likely has a role in macromolecular synthesis, cell structure, energy generation, or some other essential aspect of cell physiology that cannot be satisfied by low molecular weight nutrients, vitamins, trace minerals or other metabolites.