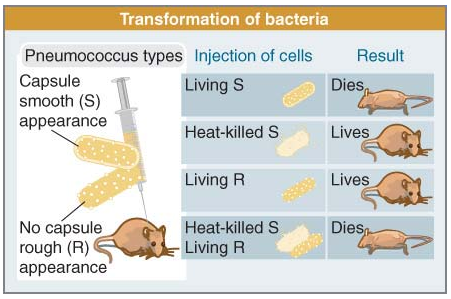
BIOL 4620 Molecular Biology
Exam 1 Name KEY

PLEASE WRITE LEGIBLY. **IF THE GRADER CANNOT READ YOUR ANSWER IT WILL BE MARKED WRONG**.

There are 15 multiple choice questions below. Each question is worth 1 point. Please write the letter for the correct answer in the appropriate space in the table. **Only answers written in the table will be graded**.

1. B	2. B	3. D	4. A	5. C
6. C	7. B	8. D	9. D	10. A
11. C	12. B	13. D	14. C	15. A



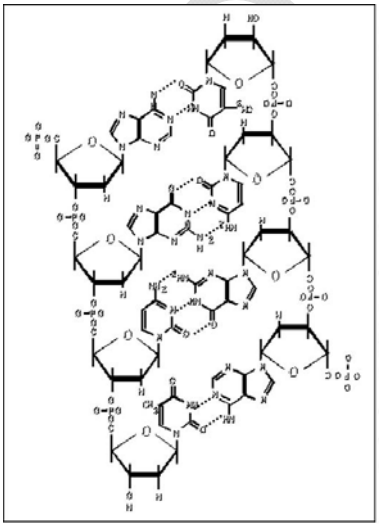
16. (3pts) Frederick Griffith's experiments indicated that transformation of R cells was the result of a transforming principle in heat killed S cells. How did Avery, McLeod and McCarty use enzymes to show that the transforming principle is DNA?

Treat with RNAse -- no effect on transforming principle

Treat with protease no effect

Treat with DNAse destroy the transforming principle

17 (4pts) If the GC content of DNA duplex is 0.44 (44%) , what are the proportions of each of the four bases? A 0.28 C 0.22 G 0.22 T 0.28



Label 5' and 3' ends of the leftmost strand

What is the sequence of the leftmost strand?

Is this DNA or RNA?

Identify one structural difference that distinquishes DNA nucleotide from RNA nucleotide

18 8pts.

2 points correct 5'/ 3' 2 points correct seq (1pt if miss 1 or 2)
Top to bottom 5' AGCT 3' (sequence is the same both strands)
DNA: Because (any of these acceptible)—2'H on sugar (vs 2'OH for RNA), contains thymine (not uracil), double stranded,

19. (4pts) Genetic maps and physical maps show distances between DNA markers. How are genetic maps different from physical maps?

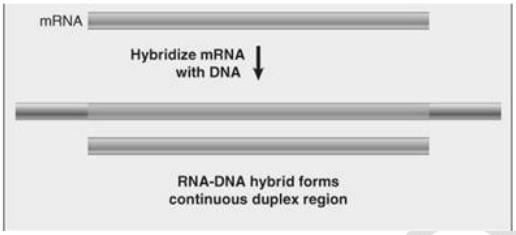
Genetic maps based on recombination frequency (measured in centimorgan)

Physical maps distances are physical distance (base pairs)

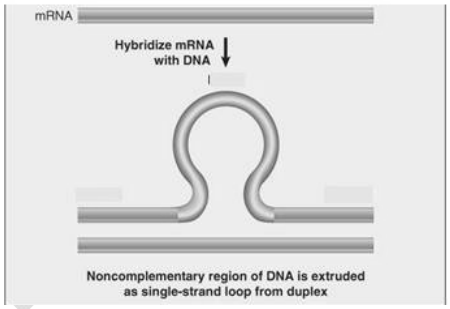
20 (4pts) Distinguish between a silent mutation and a null mutation in a protein coding gene.
Silent mutation is change in the nucleotide sequence that does not affect the amino acid sequence (will also accept amino acid change that does not affect protein function)
Null mutation prevents expression of functional protein. This can be result of gene deletion or premature termination or amino acid replacement which results in nonfunctional protein

21 (6pts) You've done a hybridization experiment with DNA and mRNA which of the following results (A or B) do you expect? Why? 1pt correct A/B 1 pt correct why

A



B



a) hybridization of bacterial genomic DNA with beta galactosidase mRNA _____A__
Why?_____in bacteria genomic DNA and mRNA are collinear -- no introns

b) hybridization of human genomic DNA with human beta globin mRNA _____B_____
Why?_____human genomic DNA contains introns which are removed from the mRNA

c) hybridization of human beta globin cDNA with human beta globin mRNA_____A_____
Why?__ cDNA DNA is generated from reverse transcription of the mRNA – it is a DNA copy of the mRNA and should completely hybridize

22 (4pts) Why might it be difficult to express an **intact** human protein coding gene inserted into bacterial cell?
Most human protein coding genes contain introns. (Bacterial genes do not).

Presence of introns likely to introduce premature stop codon

23. 2pts. You have two computer files, one containing the complete *Escherichia coli* genomic sequence and the other containing the complete *Zea mays* (maize) genomic sequence. A new student in the lab made a mistake and renamed the files "A" and "B." However, you do know

that **file A is 1,125,000 bytes** while file **B is 305,000,000 bytes in size**. Without opening the file and examining the sequence, predict which file is more likely to contain the genomic sequence for *E. coli* and which file contains the genomic sequence for *maize*? Why?

File A is likely to contain the *E. coli* genomic sequence, and file B is likely to contain the *maize* genomic sequence. In general, procaryotic genomes are smaller than eucaryotic genomes

24 (2 pts) Give **one** reason why the size of the proteome is not an accurate estimate of the numbers of genes?

In eukaryotes, one gene can give rise to more than one protein due to to alternative splicing.

other reasons include:In some organisms, more than one protein can be generated from one gene due to use of alternative start or stop sites

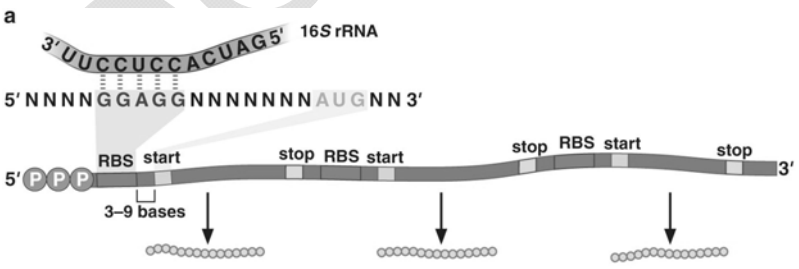
25 (4pts) Why is bacterial gene expression generally faster than eukaryotic gene expression?

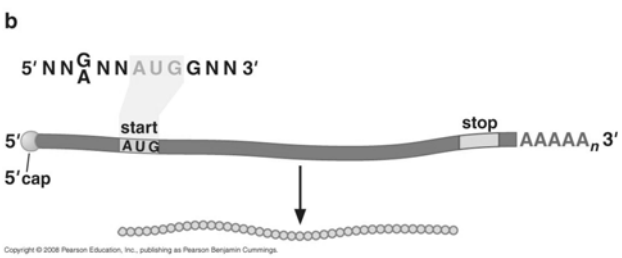
Bacteria) transcription and translation coexist, that is they occur simultaneously

Eukaryores) RNA transcribed, then processed before being transported to cytoplasm for translation

26 (6) Compare the human nuclear genome with the human mitochrondrial genome 1pt each

	Nuclear genome	Mitochondrial genome
Mendellian or maternal inheritance?	Mendellian inheritance	Maternal inheritance
Linear or circular chromosomes?	Linear chromosomes	circular
Encodes rRNA genes?	Yes (tandem repeats)	Yes





27. (6pts) 1pt each Is the mRNA shown in panel A more likely to be prokaryotic or eukaryotic?

prokaryotic

What are 2 features that support your answer?

Polycistronic RNA

no 5' cap/ no 3' polyA

Is the mRNA shown in panel B prokaryotic or eukaryotic? eukaryotic

What are **2** features of the mRNA that support your answer?

5' cap monocistronic (only one protein produced from mRNA)

3' poly A ANY 2 of these

28 (3pts) Transfer RNA evolved from gene duplication and specialization. Is this type of gene family more similar to the ribosomal RNA gene family or the globin gene family? Explain.

tRNA family is more like globlin family. tRNA related but distinct

Ribosomal gene family – nearly exact copies repeats

globin family gene duplication / specialization although related they have distinct features

29. (2pts) What is satellite DNA? Highly repetitive DNA in which base composition is different from bulk DNA. Form satellite band on density gradient

30 (6) a. Microsatellites are also called short tandem repeats or variable nucleotide repeats. What process is responsible for the expansion of repeats in **microsatellite DNA**?

Replication slippage (2)

b. How are variable nucleotide repeats used to determine heredity relationships via DNA fingerprinting?

Examine a few well studied VNTR to determine repeat copy number (size of repeat).

Repeat lengths are unique (derive from unique events) and inherited from parents (Mendellian). 2 Although two unrelated individuals may share the same repeat length when examining only one VNTR, it is unlikely that unrelated individuals share the same repeat lengths when examining multiple VNTRs. 2

31 (4) Why do silent substitutions in coding regions (silent sites) occur at a much higher rate than replacement substitutions?

Since silent substititutions do not alter the protein (polypeptide) sequence, there is less constraint on substitution compared to replacement substitutions.

Replacement results in change in amino acid sequence. Most replacements are deleterious and eliminated.

32 (2) If a unicellular yeast is expressing about 75% of its genes under normal conditions, why aren't the other 25% of genes expressed?

Some genes only need to be expressed under special circumstances (stresses) and are not required under normal conditions

33. (2) Antibiotics such as tetracycline and erythromycin interfere with ribosomes. Why do these antibiotics inhibit protein synthesis in bacterial cells, but not affect protein synthesis in humans?

Although bacterial and eukaryotic ribosomes have similar functions they are distinct - differentrRNA and different proteins make up the ribosomal subunits

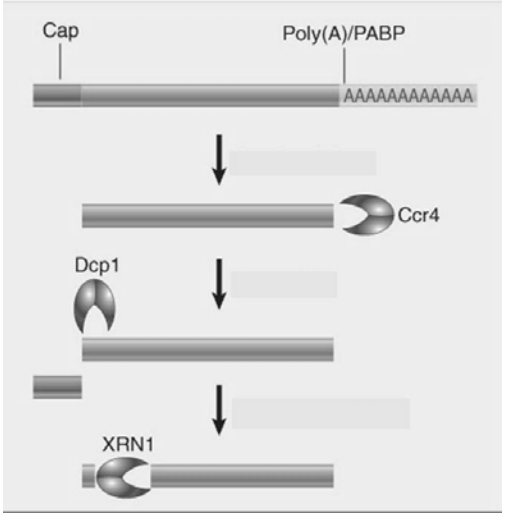
34. (2). The human genome contains 4 $tRNA^{Ser}$. How many serine tRNA synthetases are required to charge these 4 isoaccepting $tRNA^{Ser}$ with serine? One- (there is one tRNA synthetase for each amino acid)

35 (2 pts) Would the amino acid sequence of the encoded peptide change if amino acid on $tRNA_{cys}$ is desulfurated (amino acid is now Ala)? Why?

Yes Ala would be inserted at Cys codon. tRNA selected solely by codon-anticodon interaction

36. (5 pts). Write the letter of the choice that best fits the statement. A choice may be used once, more than once or not at all. 1 pt each

D	DNA synthesized from RNA template	a. 5' to 3'
A	DNA synthesis occurs in this direction	b. 3' to 5'
A or E	Movement of ribosome on mRNA template	c. transcription
C	RNA synthesized from DNA template	d. reverse transcription
A	RNA synthesis occurs in this direction	e. translation
		f. reverse translation



37. (4pts) One mechanism for RNA degradation is shown in the figure

Does this mechanism occur in bacteria, eukaryotes or both bacteria and eukaryotes? 2
Eukaryotes – note cap and polyA

Which enzyme is cutting the mRNA in the 3' to 5' direction? Ccr4 (3' to 5' exonuclease) 2