BIOL 4620 Exam 3 3513 Apr 8, 2013 Name [redacted] 78 78

PLEASE WRITE LEGIBLY in ball point pen.
IF THE GRADER CANNOT READ YOUR ANSWER IT WILL BE MARKED WRONG.

1 (4pts) a. Cro and lambda repressor have important roles in controlling the developmental pathway of bacteriophage lambda. Describe the molecular interactions that occur if cI accumulation predominates over Cro accumulation.

XX

if CI predominates over ~~Cro~~ Cro then the complex to the left is formed. CI will bind specific sites on the nucleic acid and prevent the shaded region from being expressed.

b. Would this lead to the lytic or lysogenic pathway?

lysogenic ✓

2. (2pts) What is function of lambda N protein?

the lambda N ~~protein~~ is a distinguishing protein which inhibits activity of other ~~[redacted]~~ promoters ~~and~~ in a regulatory fashion. antiterminator

-2

3 (4pts) Describe the mechanism by which **steroid receptors** (glucocorticoid receptor, estrogen receptor) only are able to activate transcription when in the hormone bound state.

Steroid receptors normally reside in the cytoplasm and contain two-binding domains. when the receptor is bound, it enters the nucleus and recruits other proteins which activate transcription. ✓

4. (2pts) Why is attenuation absent in eukaryotic organisms?

attenuation is absent in eukaryotic organisms because RBPs stabilize newely synthesized RNA and prevent them from forming loops

-2

separate compartments

5 (4pts) Sir proteins are involved in maintenance of the HMLalpha and HMRa mating type cassettes in yeast. Sir2 is a histone deacetylase. How does this affect expression of the mating type cassette genes?

sir 2 deacetylase removes the expression of the targeted genes by removing ~~Ba~~ acetygroups from the histones, makes them harder to transcribe. sir 2 removes expression of HMRa. ✓

-4

6. (4pts) List 2 similarities between transfer RNA and ribosomal RNA processing to yield mature molecules

both require nucleolytic process in order to splice introns.

both are modified post transcriptionally w/ various types of modifications (i.e. deamination, methylation, acetylation)

7 (2 pts) Identify two functions of the 5' cap of eukaryotic mRNAs

The cap protects the mRNA from 5'-3' exonucleases

The cap serves as a binding site for formation of the complex that creates the necessary loop for translation

8 (2pts) What is the role of RNA polymerase II in eukaryotic mRNA processing?

produces other types RNA (other than mRNA) including ~~mRNA~~ ? + tRNA

-2

CTD

9. (4pts) Compare the processes of self- splicing (group I and group II introns) and pre-mRNA splicing. Answer should include at least one similarity and one difference

in self splicing, ~~no proteins are required and~~ the interactions that occur all happen between the nucleic acid involved (opposed to proteins binding to the pre-mRNA @ specific points. +

-2

In both cases, specific sequences in the intron are recognized and expelled from the RNA.

10. (4pts) Explain how the correct 5' and 3' splice sites are recognized by the cell splicing apparatus using exon or intron definition.

GU AG

the splice sites (located on the intron) contain GU at the 5' and AG at the the 3' end. ~~Seg~~ the intron sequences at these points are recognized by proteins.

-2

U1, U2

11. (2pts) What is the role of SR proteins in RNA processing?

SR proteins recognize sequences and bind to exons exclusively which aids in the splicing process.

-1

recruits spliceosome

12. (2pts) Explain why tRNA is called the physical link between mRNA and polypeptide. - specific

tRNA is the physical link because it is charged with the polypeptide and it is the tRNA that also binds the appropriate mRNA codon which allows for protein production.

13. (4pts) What are the functional roles of bacterial 16S and 23S rRNAs in translation?

16S rRNA

binds the the shine delgaro sequence to help initiate translation

23S rRNA

-2 plays an important role in initiation by identifying a specific sequence on mRNA

peptidyl transferase

Multiple choice questions 1pt each

14. ~~A~~ C In the presence of thyroid hormone, TR-RXR heterodimer activates transcription. What happens in the absence of hormone?
   a. TR-RXR associates with corepressors that deacetylate histones and repress transcription.
   b. TR-RXR is targeted for degradation in the proteasome
   c. Heterodimer formation is prevented because TR is sequestered in the cytoplasm
   d. Heterodimer formation is prevented because RXR is sequestered in the cytoplasm

15. C Which of the following statements about riboswitches is *FALSE*?
   a. Riboswitches can block the production of mRNAs.
   b. Riboswitches can control the translation of mRNAs.
   c. Riboswitches are made from rRNAs.
   ~~d. Riboswitches can bind metabolites.~~

16. ~~B~~ a Dicer and RISC complexes are NOT involved in:
   a. Transcriptional gene silencing in response to dsRNA
   b. modulation of viral translation in response to dsRNA ✓
   c. Modulation of translation of specific mRNA via cellular miRNA ✓
   d. Generating 20-30nt siRNA from ds RNA ✓

17. ~~✓~~ d Which sequence is found at the 3' end of all tRNAs?
   a. TATA3' b. AGGAGG3' c. AUG3' d. CCA3'

-24

18. b rRNA base modifications are determined by
   a. interactions with U snRNA
   b. interactions with snoRNA
   c. specific rRNA maturases
   d. specific rRNA methylases

19. b Maturation of mammalian pre rRNA includes
   a. specific cleavages to yield mature sized rRNA and base modifications
   b. nucleolar intron splicing and base modifications
   c. autocatalytic intron splicing and base modifications
   d. base modifications only

20. d Eukaryotic cells are able to carefully regulate level of transcription in specific genes via
   a. Histone phosphorylation
   b. Transcription attenuation
   c. Controlled activation of transcription factors
   d. Histone methylation

21. a The consensus splice site for intron splicing contains only a few highly conserved sequences. Nearly invariant sequences found in the mRNA are:
   a. GU-AG. These sequences are found at the 5' and 3' ends of the intron (respectively)
   b. GU-AG. These sequences are found at the 5' and 3' ends of the exon (respectively)
   c. GU-AG. These sequences are found both ends to the intron and mark the exon - intron border
   d. GU-AG. These sequences are found in the 5' and 3' UTR

22. b U1 snRNA initiates intron splicing by binding to:
   a. the central part of the first exon
   b. the 5' splice site of the intron
   c. the branch sequence of the intron
   d. the 3' splice site of the intron

23. b As a general rule, alternative splicing involving different 5' sites may be influenced by:
   a. formation of secondary structures that contains several domains formed by base-paired stems and single-stranded loops.
   b. proteins in the spliceosome assembly that either stimulate or repress the usage of one of the possible sites for splicing.
   c. a single type of spliced mRNA formed when an interrupted gene is transcribed into an RNA.
   d. the type of RNA ligase that functions in the reaction

24. d mRNA splicing joins
   a. two intron sequences
   b. two DNA molecules
   c. two polypeptides
   d. two exon sequences

-2

25. C RNA editing in trypanosome mitochondria involves:
   a. modification of U to pseudoU via snoRNA
   b. deamination of a C to a U
   c. insertion or deletion of several U bases via base pairing with guide RNA
   d. insertion or deletion of several C bases via base pairing with guide RNA

26. b The "near universality" of the genetic code suggests that
   a. all organisms are basically the same
   b. the genetic code arose early on in evolution of life
   c. any changes in codon meaning would be disruptive
   d. the third position of a codon has no use

27. a What is the role of the nuclear localization sequence in a nuclear protein?
   a. It is bound by cytoplasmic proteins that direct the nuclear protein to the nuclear pore.
   b. It is a hydrophobic sequence that enables the protein to enter the nuclear membranes.
   c. It aids in protein unfolding so that the protein can thread through nuclear pores.
   d. It prevents the protein from diffusing out of the nucleus through nuclear pores

28. b Which of the following is NOT a function of molecular chaperones in protein folding?
   a. Molecular chaperones can stabilize partially folded proteins and prevent them from aggregating with other proteins
   b. Molecular chaperones specify the tertiary structure of a protein
   c. Molecular chaperones assist protein in finding their correct structure
   d. Molecular chaperones can shield and protect exposed hydrophobic regions of proteins

29. d The proteasome is characterized by all of the following EXCEPT
   a. the proteasome is a structure comprised of two caps at both ends of a hollow cylinder through which proteins enter
   b. Proteolytic degradation by proteasomes generates short peptides approximately 4-10 amino acids in length.
   c. In bacteria, molecular recognition sequences on N- and C- termini target proteins for degradation by the proteasome
   d. Proteins do not need to be unfolded to enter the proteasome, but they must be bound to chaperone

30. d What allows the insertion of Seleno-Cys-tRNA at certain UGA codons?
   a. SelB
   b. a downstream stem-loop (SECIS) in the mRNA
   c. a downstream stem-loop (SECIS) in the mRNA AND EF-Tu
   d. a downstream stem-loop (SECIS) in the mRNA AND SelB

31. C Which of the following statements about disulfide bond formation is FALSE?
   a. Disulfide bonds do not form under reducing environments.
   b. Disulfide bonding stabilizes the structure of proteins
   c. Disulfide bonding occurs spontaneously by the oxidation of pairs of cysteine side chains on the protein when the protein enters the ER
   d. Disulfide bonds form in the oxidizing environment of the ER lumen via protein disulfide isomerases

32. a Two common features of programmed frameshifting are _____.
   a. slippery sequence and ribosome delay
   b. slippery sequence and less frequency than errors at nonprogrammed sites
   c. very high efficiency and ribosome delay
   d. occurs more often than nonprogrammed mutation and slippery sequence

33. a What 3 main features are commonly used by aminoacyl-tRNA-synthetases to recognize their tRNAs?
   a. discriminator base, bases in the acceptor stem, and a base in the anticodon.
   b. discriminator base, position of modified bases in D loop, and a base in the codon
   c. G and C nucleotide content, bases in the acceptor stem, and a base in the codon
   d. discriminator base, A and U nucleotide content, and a base in the anticodon

34 (4pts) Compare and contrast translation initiation in bacteria and eukaryotes. Identify 2 significant similarities and 2 significant differences

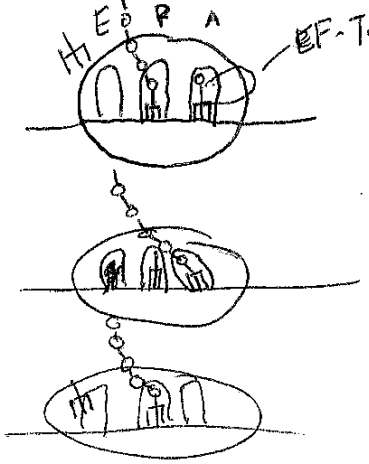
similarities: both utilize 2 subunits (large and small) that must converge on the mRNA.

both utilize a special $t\text{-}RNA^{met}$ for initiation that is not the same as normal $t\text{-}RNA^{met}$s.

Differences: Bacterica initiation includes SD sequence recognition by ~~the~~ 16S, eukaryotes do not have the SD sequence.

In bacteria, the ~~initiator t-RNA met~~ small subunit binds the mRNA directly, eukaryotes require proteins to mediate the process and a special loop to be formed.

35 (4 pts) Describe the major events that take place during bacterial translation elongation



EF-Tu uses energy from GTP to place a new charged tRNA into the A sight. EF-G ~~stabs~~ rachets the ribosome so that the new amino acid ~~chain~~ becomes the carboxy terminus of the chain after accepting the preexisting polypeptide from the tRNA in the P-site. In the final step the tRNA, now ~~chain~~ bound to the polypeptide moves to the P site and the original tRNA in the P site is moved to the E site and expelled.

36. (4pts) How is the initiator methionine tRNA distinct from the elongator methionine tRNA?

the initiator tRNA contains an extra, unpaired, base at the peptide-binding site and also contains an A-U rich region.

to prevent A entry

-1

37. (2pts) Why is it important that aminoacyl tRNA-EF-Tu-GTP, EF-G and class-1 release factors all have similar 3 dimensional conformations?

They must all be able to interact with the same protein (ribosome) and fit into the same regions to be effective

what region?

-1

38 (6pts) Which step in translation is affected by the following interactions?. Be sure to state whether the molecule affects bacterial or eukaryotic protein synthesis

a) Kasaugamycin interacts with 16S rRNA and 30S ribosomal protein S7

bacterial, initiation

b) Cycloheximide binds peptidyl transferase center of the 60S ribosome

bacterial, ends elongation

-1

c) Kirromycin - prevents release of EF-TuGDP

bacterial, elongation

39(2pts) eIF4A has helicase activity. What role does this have in eukaryotic translation initiation?

as eIF4A is a protein factor neccesary in initiation, it's helicase activity allows it to perform the neccesary measures for the scan before initiation

40 (2pts) Viruses such as picornavirus inhibit cap-dependent translation yet translate viral mRNAs using host translation machinery. How are viral mRNAs able to be translated?

the viruses promote a proccess which is cap-independant translation (seen in humans as an emergency responce to some stimuli) which allows them to translate their ~~cap-independent~~ RNAs IRES

-1

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-4

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All of the following statements are false. Explain why (2pts each)

41. In prokaryotes degradation begins via exonuclease digestion of the 3' end of mRNA

degredation begins via endonuclease digestion of the insider mRNA regions

42. In trans-splicing, the order of exons within an RNA transcript is rearranged to yield a different mRNA sequence

ie. 5' [E1] [E2] [E3] 3'

exon order cannot be rearranged ✓ can become 5' E1-E3 3' or 5' E2-E3 3' but never 5' E3-E1 3'

OK

43. The ~~ubiquitination~~ of the initiation factor eIF-2 results in a repression of global translation initiation in eukaryotic cells

phosphorylation, ~~[illegible]~~ results in repression ✓

44. Codon-anticodon interactions involve the formation of covalent bonds.

codon-anticodon interactions are based upon hydrogen bonds

45. N-linked glycosylation involves modification of the side chains of ~~aspartic acid~~.

-2 ~~[illegible]~~ arginine is glycosylated

asparagine

46 Nuclear localization signals are cleaved after protein enters the nucleus

-2 Nuclear localization ~~signals~~ sequences

47 Protein synthesis is terminated when an uncharged tRNA enters the A site enabling release of polypeptide.

-2 Protein synthesis is terminated by specific protein(s) which bind the stop codon

48 The most common single stranded RNA binding motif is the ~~PAZ~~ domain found in mRNA splice factors.

-2 the most common motif is the HEF (sp?) domain which contains beta sheet & 2 helicies

49. In heterochromatin, methylated DNA is bound by methylated DNA binding proteins that recruit transcription ~~activators.~~

transcription repressors are recruited by most DNA binding proteins

50. Noncoding RNA has no effect on the translatability of an mRNA.

Noncoding RNA can form siRNAs and also affect splicing, both of which influence mRNA expression. ✓

8

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