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Fall Quarter, 2016 – LS 3-1
Dr. Lin
Midterm II
November 3, 2016
6pm-7:50pm

VERSION 1

1. Write and bubble in your name and student UID on the **Scantron.**
2. Write and bubble in your test version in column K, under 'Special Codes' on the **Scantron.**
3. Check the exam to make sure that you have every page before you start. Read the questions and the multiple choices carefully. You should select the **BEST** answer and register your answer on both the Scantron and the exam pages.
4. Hand in the Scantron and Question Packet to the TAs after you complete the exam.
5. Midterm II has 40 multiple-choice questions, worth 2.5 points each
6. Use your common sense. Do not spend too much time on any single question. ***Good luck!***

Total Exam Points: ___ / 100

1. Which of the following about transcription is incorrect?
A). Transcription requires the functions of many proteins
B). Transcription requires DNA replication
C). Transcription requires DNA as the template
D). Transcription is the only cellular process that synthesizes RNAs
E). Transcription may be coupled with translation.

2. Which of the following is correct about transcription initiation?
A). Transcription initiation may not occur *in vitro*
B). Transcription is usually initiated by a protein kinase
C). Sigma factor is not required for prokaryotic transcription initiation
D). The β'-subunit of E. coli RNA polymerase initiate transcription
E). None of above

3. Which of the following is incorrect about transcription regulation?
A). Transcription regulation involves specific DNA sequences.
B). Transcription factors regulate transcriptional activity of genes.
C). Transcription regulatory proteins may increase or decrease the activity of RNA polymerase.
D). Transcription of different genes are regulated by different mechanisms.
E). Transcription regulation requires DNA modification but not protein modification.

4. Which of the following statements about sigma factor is incorrect?
A). Sigma factor is considered part of bacterial DNA polymerase core enzyme
B). It can bind to both -10 box and the core RNA polymerase
C). One cell may have more than one type of sigma factor.
D). One type of sigma factor may bind to more than one type of regulatory DNA sequences.
E). Sigma factor has no detectable RNA polymerase activity

5. Which of the following is not true about a transcription termination?
A). Special DNA sequences and specific proteins determine transcription termination
B). The Rho protein facilitates transcription termination of some bacterial genes
C). Transcription termination is always determined by a Riboswitch
D). A terminator may contain inverse repeats
E). A terminator may contain the A/U rich sequence

6. What is an operon?
A). A bacterial gene encoding multiple proteins or a group of genes coordinately regulated by an operator
B). An human lactose gene
C). An Arabidopsis photoreceptor gene
D). A heat-shock gene.
E). A RNA polymerase

7. Which of the following about gene expression is correct?

A). Transcription of most prokaryotic genes produces a single polypeptide.
B). Transcription of most eukaryotic genes produces multiple polypeptides
C). Transcription of most prokaryotic genes produces only one mRNA.
D). Transcription of most prokaryotic genes produces more than one mRNA.
E). None of above

8. Adam used a NC (nitrocellulose) filter-binding assay to test how a bacterial RNA polymerase interacted with DNA. He added holoenzyme or core enzyme to ^{3}H-labeled DNA. He then added excessive amount of unlabeled DNA (of the same sequence) to compete with the labeled DNA, applied the reactions to NC filters at various times, and measured ^{3}H on the NC filters. Her result is shown in Fig. 1. Which would be the most appropriate interpretation of his result?

A). The holoenzyme but not the core enzyme binds to DNA
B). The core enzyme binds DNA with higher specificity
C). The holoenzyme binds DNA tighter than the core enzyme
D). The holoenzyme releases DNA faster than the core enzyme
E). The core enzyme but not holoenzyme binds to DNA

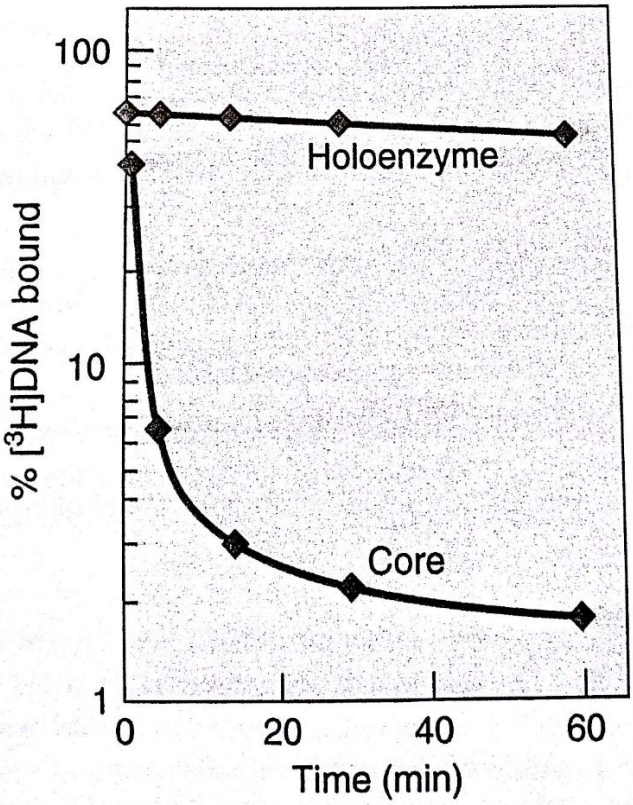

Fig. 1. The results of the NC filter-binding experiment. "%(^{3}H)DNA bound" indicate the amount of DNA-RNA polymerase formed in the reaction. "Time" indicate duration of the reaction after the excessive non-labeled competitive DNA was added.

9. A *trp* mutant contains the normal *trp* promoter and operator, but deletion of the leader sequence encoding the 5'UTR (5' untranslated region) upstream of the *trpE/D/C/B/A* mRNA. Which of the following will most likely be observed in this mutant?
A). Increased abundance of tryptophan in this bacterial mutant continues to suppress transcription of the *Trp* operon
B). Increased abundance of tryptophan in this bacterial mutant continues to activate transcription of the *Trp* operon
C). The *Trp* operon will no be negatively regulated.
D). This mutation will not affect transcription of the *Trp* operon.
E). None of above.

10. Which of the following is most likely to occur if the level of lactose is high in a bacterial cell?
A). The lac repressor is activated to bind the lac operator
B). The CAP activitor is activated to bind the lac operator.
C). The CAP activitor is activated to bind the lac promoter.
D). The lac repressor is activated to bind the lac promoter.
E). None of above.

11. Bacterium *Basillus subtilis* can undergo either vegetative growth when there are lots of nutrients or sporulation when there is not enough nutrition. Which of the following would mostly likely happen to *Basillus subtilis* when there is not enough nutrition around?
A). Shutdown transcription to save energy
B). Activate transcription of vegetative genes to grow out of the poor condition
C). Delete vegetative genes to accelerate sporulation
D). Undergo sigma-switching to change gene expression
E). Undergo DNA methylation to turn off all genes

12. Which of the following conditions does not lead to a change of gene expression in bacterial cells?
A). Sporulation
B). Heat shock
C). Nutrient availability
D). Nitrogen deprivation
E). None of above.

13. Which of the following about T7 RNA polymerase is true?
A). The bacterial RNA polymerase is associated with T7 polymerase.
B). The bacterial RNA polymerase is inactivated by the T7 polymerase.
C). T7 RNA polymerase does not transcribe bacterial genes.
D). T7 RNA polymerase needs T7 sigma factor.
E). T7 RNA polymerase encodes a new β subunit of the bacterial RNA polymerase.

14. How many types of eukaryotic RNA polymerase have been found?
A). 1
B). 2
C). 3
D). 4
E). 5

15. Which of the following techniques should be used to examine whether a known transcription activator may bind to chromatin of a known enhancer *in vivo*?
A). DNA finger printing
B). Chromatin immunoprecipitation
C). DNA sequencing
D). RT-PCR
E). DNA footprinting

16. Why are eukaryotic transcriptional regulation generally more complicated than that of the prokaryote transcription?
A). Eukaryotes are often multicellular organisms that need to coordinate between different cells and organs.
B). Eukaryotes usually have larger genomes.
C). Eukaryotes have more complex protein-protein interactions.
D). Eukaryotes need to respond to not only external signals but also internal signals.
E). All above are correct.

17. Which of the following about DNA footprinting experiment is correct?
A). A limited RNA hydrolysis reaction is needed for this experiment
B). DNA footprinting experiment can be used to distinguish genetic diversity of individuals.
C). DNA footprinting experiment can be used to analyze protein-DNA interaction
D). A complete DNA hydrolysis reaction is needed for this experiment.
E). A specific restriction enzyme is needed for this experiment.

17. C

18. Which of the following about ChIP (chromatin immunoprecipitation) is incorrect?
A). ChIP can be used to analyze transcription regulation *in vivo*
B). ChIP can be used to identify enhancer sequences *in vitro*
C). ChIP can be used to analyze effect of chromatin structure on transcription
D). ChIP is used to investigate how histone modification affect transcription
E). All of above.

18. B

19. Which of the following about histone is correct?
A). Histones are chromatin proteins.
B). Histones are found in eukaryotes but not prokaryotes.
C). Histones may be covalently modified by acetylation or methylation
D). Histones are non-covalently associated with DNA.
E). All of above.

20. Which of the following statements about prokaryotic promoter is incorrect?
A). Some prokaryotic promoters have GC-rich sequence.
B). Different prokaryotic promoters may have different operators
C). All prokaryotic promoters have a TATA box that bind to TBP
D). Prokaryotic promoters are usually free of nucleosome
E). Some prokaryotic genes are transcribed by σ^{70}.

21. Joanne wants to study the effect of decreased transcription of the β-globin gene without significantly inhibiting transcription of most rRNA genes needed to synthesize the β-globin protein. Which of the following inhibitors would be most useful to her experiment?
A). α-amanitin
B). DMS
C). IPTG
D). SDS
E). DTT.

22. Which of the following best explains the function of histone modification?
A). Histone acetylation increases positive charges of the core histones, resulting in increased density of nucleosomes and decreased transcription
B). Histone acetylation reduces positive charges of the core histones, resulting in decreased density of nucleosomes and increased transcription.
C). Histone methylation increases hydrophobicity of the core histones, resulting in increased condensation of nucleosomes and increased transcription.
D). Histone phosphorylation increases negative charges of DNA, resulting in increased density of nucleosomes and decreased transcription.
E). Histone acetylation and methylation both reduce positive charges of the core histones, resulting in increased density of nucleosomes and increased transcription.

23. Which of the following about transcription is incorrect?
A). The CTD domain of RNA polymerase II undergoes progressive phosphorylation to change the activity of RNA polymerase
B). A transcription factor may be ubiquitinated to decrease its abundance in the cell.
C). Protein acetylation or methylation may change structure of the protein
D). Epitope-tagging is a method often used to study protein complexes associated with transcription
E). Epitope-tagging is a method often used to study DNA/RNA complexes associated with transcription

24. John did an experiment to characterize four bHLH transcription factors, CIB1, CIB2, CIB4, and CIB5. He used a gel shift assay to analyze how CIB proteins interact with DNA). shown in Fig. 2. In this experiment, John first mixed one or two proteins indicated with one of the two different DNA probes indicated in Fig. 2, and analyzed the DNA-protein complex by a native gel electrophoresis. What would be the most appropriate explanation of the result shown in Fig. 2?

A). CIB1 has no DNA-binding specificity
B). All CIB proteins bind to the E-box as the homodimers
C). All CIB proteins specifically bind to E box as heterodimers
D). CIBs are transcription activators
E). None of above

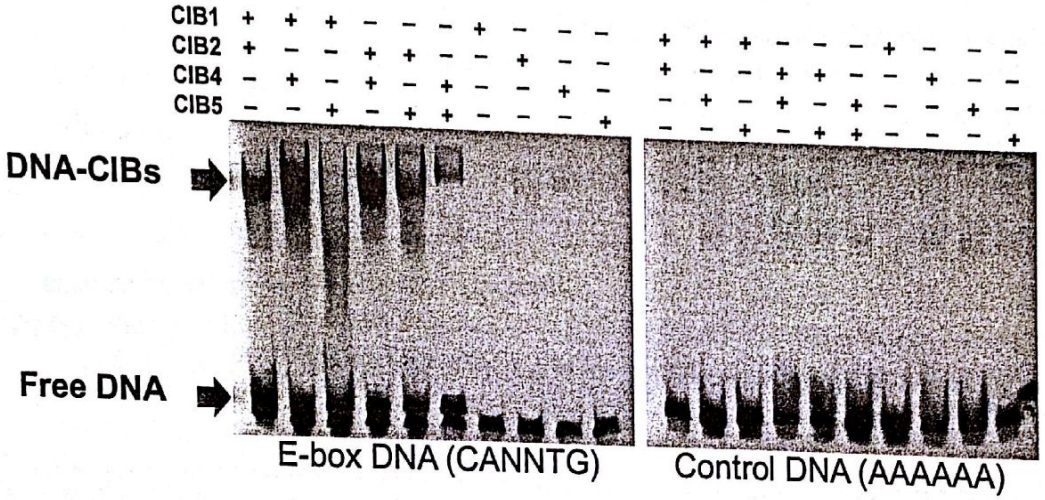

Fig. 2 Result of John's gel shift experiment. Proteins used in each reaction are indicated on the upper left, sequences of the DNA probe used in this experiment are shown below the gel images. Arrows indicate DNA-protein complexes or free DNA.

25. Which of the following about eukaryotic promoters are incorrect?

A). The rRNA genes usually have the class I promoter
B). Genes that have the class III promoters do not need TFIIH for transcription.
C). Genes that have the class II promoters are usually transcribed by RNA polymerase II
D). Genes that have the class II promoters may or may not have the TATAAA sequence
E). The tRNA genes are driven by the class III promoter and transcribed by RNA polymerase III.

26. Transcription factors contain at least two domains, which of the following proteins is most likely classified as a transcription factor?

A). A protein contains a basic domain and an polymerase domain
B). A protein contains a RNA-binding domain and a phosphorylation domain
C). A protein contains a PAS protein-interaaction domain and a kinase domain
D). A protein contains a nulear importation domain and E3 ligase domain

E). A protein contains a DNA-binding domain and transcription repression domain

27. Which of the following about the eukaryotic general transcription factors is incorrect?
A). Many general transcription factors are required to form preinitiation complex, and they are released after transcription initiation.
B). Some general transcription factors may be commonly used by different RNA polymerases.
C). Different general transcription factors are usually needed to transcribe different genes.
D). At least one general transcription factor has at least two enzymatic activities.
E). All of above

28. Which of the following is correct about TFIID?
A). TFIID acts as a helicase to unwind DNA for transcription
B). TFIID acts as an ATPase to provide energy for transcription initiation
C). TFIID activates RNase activity of RNA polymerase to prevent transcription arrest
D). TFIID binds DNA to promote formation of the preinitiation complex
E). All of above are correct

29. In the study of transcription in yeast, temperature-sensitive mutants are often used because those mutants can be grown at relatively low temperatures, and they can also be exposed to higher temperature to detect the effect of the mutations in critical genes. Which of the following is most likely observed for a yeast mutant strain that encodes a temperature-sensitive TFIIH mutant protein?
A). Higher temperature would affect RNA polymerase I.
B). Higher temperature would affect RNA polymerase II.
C). Higher temperature would affect RNA polymerase III
D). Higher temperature would affect RNA polymerase I and III
E). All of above.

30. All of the following are true regarding homeodomain proteins except
A). Homeodomain proteins usually bind DNA as dimers.
B). Homeodomain proteins have the DNA-binding domains that are structurally related to the bacteiral helix-turn-helix proteins.
C). Homeodomain proteins bind to the DNA of homeoboxes.
D). Homeodomain proteins are often involved in the regulation of organ development.
E). Homeodomain proteins usually bind to zinc ions.

31. Which of the following protein domains may be found in a transcription activator?
A). zinc fingers
B). glutamine-rich regions
C). bZIP motifs
D). proline-rich regions
E). All of above

32. The glucocorticoid receptor is a transcription factor that is activated by binding to
A). its hormone ligand in the mitochondria.
B). its hormone ligand in the cytosol and moving to the nucleus.
C). its hormone ligand in the nucleus and moving to the cytosol.
D). to DNA first and then to its hormone ligand.
E). to hsp90 and moving together with hsp90 to the nucleus.

33. Which of the following is a reasonable hypothesis to explain how an enhancers may act at a distance from the promoter to activate transcription?
A). The activator binds to an enhancer, changing the supercoiling state of the DNA to make the promoter located far away more accessible to general transcription factors.
B). The activator binds to an enhancer, slides along the DNA until it encounters the promoter, and activates transcription.
C). An activator binds to an enhancer, creating loops in the DNA, which leads to the interaction of proteins at the promoter and activation of transcription.
D). An activator binds to an enhancer and a downstream segment to form a loop, which causes the protein to track toward the promoter and activate transcription.
E). All of the above are plausible hypotheses.

34. Transcriptional insulators are the DNA sequences that
A). block gene activity by binding to the operator regions.
B). regulate movement of other proteins on chromatins.
C). modify phosphorylation of other transcription factors.
D). shield genes from activation by binding the terminator regions.
E). activate transcription activity by binding to the promoter DNA.

35. What are heterochromatins?
A). heterozygous chromosomes
B). heterozygous chromatides
C). highly expressed regions of the genome
D). condensed chromatins that usually does not transcribe
E). transcription activator-binding sequences

36. Predict the effect to transcription by addition of excess acetyltransferase.
A). It will abolish chromosome remodeling.
B). It will lead to a tighter association of histone with DNA, resulting in reduced transcription.
C). It will have no effect on the interaction of DNA with histones.
D). It will likely loosen the interaction of histone with DNA.
E). None of above.

37. Which of the following about the histone code is correct?
A). Histone Code refers to the combined patterns of histidine phosphorylation and arginine methylation.
B). Histone Code defines the genetic code transmitted into amino acid sequence of four different histones.
C). Histone Code refers to the combined patterns of lysine acetylation and tryptophan ubiquitination.
D). Histone Code is the combination of all chemical modifications of nucleosomal histone proteins.
E). Histone Code is the combination of all genetic modifications of nucleosomal histone proteins.

38. Which of the following general features about genes are not known to us?
A). A gene may have two different promoters encoding one protein
B). A gene may encode two different proteins from one promoter
C). Genes may be transcribed by different sigma factors but the same RNA polymerase III
D). One repressor binds to one operator to regulate expression of multiple proteins associated with the same metabolic pathway
E). None of above

39. Which of the following methods can be used to study how a DNA regulatory element is associated with transcriptional regulation?
A). Promoter bashing and linker scanning
B). DNA footprinting
C). Reporter gene assays
D). Electrophoretic mobility shift assay
E). All of above

40. Which of the following about signal transduction is incorrect?
A). Proteins involved in signal transduction are often modified in response to external signals
B). Transcription factors are major downstream targets of signal transductions in plants and animals
C). Signal transduction networks regulate combinatorial control of transcription
D). Many signal transduction proteins are encoded by proto-oncogenes or tumor suppressor genes
E). None of above