Molecular Biology
Midterm Exam 4

1. Based on your understanding of the article entitled "An appointment with chance" which of the following is a true statement?
A. Many adult tissues including the heart and brain, which were once thought not to require cell renewal, actually contain stem cell populations.
B. Stem cells, when transplanted into damaged brain tissue, can migrate to the injury site while stem cells that were transplanted into healthy brains did not move.
C. Brain injury patients with transplanted stem cells fared better on behavioral tests than patients who did not receive the stem cell transplant.
D. All of the above.

2. Based on your understanding of the article entitled "Name, rank and serial number" which of the following is a false statement?
A. The idea behind DNA barcoding is to generate a unique identification tag for each species based on a short stretch of DNA – in case of animals the tag is from the cytochrome oxidase I (CO1) gene.
B. DNA barcoding has been used to catalog different mosquito species, different plants that produce herbal medicines, and agricultural pests such as fruit flies.
C. DNA barcoding, however, is unable to distinguish between different types of *Hirudo medicinalis*, the medicinal leech that has been approved by the FDA as a prescription device for stopping blood clots.
D. The CO1 gene is useful as all animals have it, the gene varies just enough to identify different species and it is easily extracted (because it is located within mitochondria).

3. Based on your understanding of the article entitled "The evolution of primate color vision" which of the following is a false statement?
A. For most human beings any color can be reproduced by mixing together just three fixed wavelengths of light at certain intensities (this is called trichromacy).
B. Trichromacy is common in primates but is not a universal trait within the animal kingdom
C. The M and L pigment genes reside on the X-chromosome and are inherited in a sex-linked manner while the S pigment gene resides on an autosome and is inherited in classical Mendelian ratios.
D. Red-green color blindness (which results from mutations in the M and L genes) is more common in females due to X chromosome inactivation.

4. Based on your understanding of the number and location of pigment genes (described in the article "The evolution of primate color vision") why are all Old World monkeys trichromatic while all male and most female New World monkeys dichromatic?
A. The number of long-wavelength pigment genes (located on the X-chromosome) differs between Old and New World monkeys.
B. New World monkeys undergo X-chromosome inactivation while Old World monkeys do not.
C. The number of short-wavelength pigment genes (located on the autosomes) differs between Old and New World monkeys.
D. mRNAs that are transcribed from pigment genes in Old World monkeys are alternately spliced to generate different protein isoforms that have different spectral properties.

5. Based on your understanding of the article entitled "Regulating evolution" which of the following statements about enhancer elements is a true statement?
A. Enhancers are sequences of non-coding DNA that are bound by transcription factors.
B. Enhancers can be located on either side of a gene, within intronic sequences, close to the promoter or can be found at considerable distances (several thousands of nucleotides away).
C. Enhancers regulate the spatial and temporal aspects of gene expression.
D. All of the above.

6. Based on your understanding of how the *yellow* gene is regulated in Drosophila (described in the article entitled "Regulating evolution") which of the following is a true statement?
A. Expression of the yellow gene is controlled by two separate enhancers: one for the abdomen and one for the wing.
B. In spotted species the wing enhancer has acquired new binding sites for additional transcription factors. This increases expression of yellow in small areas of the wing without altering the pattern of level of expression in other tissues such as the abdomen.
C. In species lacking a black abdomen the abdominal enhancer contains mutations, which have disrupted the binding sites of transcription factors that are required for expressing yellow at high levels.
D. All of the above.

7. Levels of the amino acid tryptophan (trp) are regulated in bacterial cells by the trp operon. As discussed in class the 5` end of the mRNA transcript contains sequences that code for a 14 amino acid leader peptide as well as four sequences that can form a variety of stem loop structures. Which of the following is a true statement regarding the operon?
A. The two consecutive trp codons within the 5` end of the mRNA transcript serve as the "sensor" for tryptophan levels within the cell.
B. Under adequate/moderate levels of trp, a termination stem loop forms thereby preventing RNA polymerase from transcribing the trpA-E genes.
C. Under low levels of trp, the ribosome stalls at the two trp codons thereby allowing for the formation of a non-termination stem loop. RNA polymerase is then able to transcribe the trpA-E genes.
D. All of the above.

8. Based on your knowledge of how the trp operon functions, what would happen if two codons for the amino acid proline (pro) replaced the two trp codons that are normal present within the leader sequence (5` end of the mRNA transcript)?
A. The pro operon would be placed under the control of tryptophan levels.
B. The trp operon would now be under the control of proline levels.
C. The sensitivity of the trp operon will increase.
D. There will be no effect on the transcription of the trpA-E genes.

9. What would happen if a mistake by DNA polymerase during replication resulted in a deletion of stem sequence #4 and the poly-U stretch that follows it?
A. A termination stem loop will never form and the trpA-E genes will always be transcribed by RNA polymerase.
B. The ribosome would never initiate translation of the mRNA transcript because the ribosomal binding site (RBS) is present within stem sequence #4.
C. A termination stem loop will always form between stem sequences #2 and #3 and RNA polymerase will never be able to transcribe the trpA-E genes.
D. The deletion will prevent the first AUG codon of the trpE mRNA from being placed correctly within the P pocket of the ribosome. Thus production of the trpE protein will be blocked.

10. Imagine that the lacZ gene has been fused to an enhancer element containing five LexA binding sites. Which of the following proteins can bind to the enhancer and activate transcription of the lacZ reporter gene?
A. GAL4 DNA binding domain + LexA activation domain
B. LexA DNA binding domain
C. LexA DNA binding domain + GAL4 activation domain
D. GAL4 DNA binding domain + GAL4 activation domain

11. Which of the following repression mechanisms best describes the type of repression that is used to block transcription of the lac operon?
A. Competition
B. Inhibition
C. Direct Repression
D. Indirect Repression

12. Which of the following best describes the mechanism underlying "indirect repression"?
A. Interactions between a transcriptional repressor and a transcriptional activator block the activity of RNA polymerase.
B. A transcriptional repressor interacts with the mediator complex thereby preventing the C-terminal tail of RNA polymerase from being phosphorylated.
C. A transcriptional repressor recruits histone deacetylase (HDAC), which in turn removes acetyl groups from histones thus blocking transcription.
D. A transcriptional repressor sits down on a binding site and prevents a transcriptional activator from binding to the same recognition site.

13. Which of the following is a true statement regarding transcription factors and the enhancer elements that they bind?
A. Each gene within the genome can only be bound and regulated by a single transcription factor.
B. All genes that are repressed during development are bound by the same transcription factors.
C. Enhancers can be simultaneously bound by multiple transcription factors.
D. Each transcription factor binds to and regulates the transcription of only a single gene.

14. What type of molecule is rhodopsin and what is its role in both fly and human photoreceptors?
A. It is a transcription factor that activates expression of genes required for eye development.
B. It is a transmembrane protein that captures photons of light and initiates a cascade that converts this information into electrical signals.
C. It is a channel protein that sits in the membrane and regulates the passage of calcium, potassium and sodium ions across the membrane.
D. It is a transcription factor that represses the activity of genes that block the formation of ectopic eyes.

15. Which of the following photoreceptors will be expected to undergo retinal degeneration if the Rh3 and Rh4 rhodopsins are both deleted from the fly genome?
A. All photoreceptors (R1-8)
B. R8 photoreceptors
C. R1-6 photoreceptors
D. R7 photoreceptors

16. Based on your understanding of how transcription of the Rh5 and Rh6 genes is restricted to the R8 photoreceptor layer which of the following is a false statement?
A. The Rh5 and Rh6 genes contain enhancers that are bound by the transcriptional repressor Prospero It is expressed solely within the R7 cell and thus can bind to the Rh5 and Rh6 enhancers and inhibit expression within the R7 cell.
B. The transcriptional activator Eyeless is expressed solely within the R8 cell. It binds to the Rh5 and Rh6 enhancer elements and directs expression of these two rhodopsin genes within the R8 cell.
C. The Rh3 and Rh4 genes are transcribed early within the life of the R7 cell. These proteins recruit histone deacetylase proteins to the Rh5 and Rh6 enhancers thereby inhibiting transcription of these genes within the R7 cell.
D. The Rh5 and Rh6 genes are transcribed in both the R7 and R8 cells but the mRNA transcripts are edited in the R7 cells. The edits actually change the first methionine amino acid into a nonsense stop codon so mRNAs are not translated into protein within the R7 cell.

17. seq56 was identified as being a critical control element within the Rh5 and Rh6 enhancer elements. Experiments within the fly retina indicated that both the A and B halves of this site were required to inhibit Rh5 and Rh6 expression in the R7 cell. However, an electro mobility shift assay (EMSA) demonstrated that Prospero is only bound to the B half. Based on this data which of the following is best prediction?
A. The Prospero protein binds to both A and B halves within the fly retina but since the B site is the high affinity site it is the only site that appears bound by Prospero in the electro mobility shift assay.
B. The mutated A and B sites are now bound by transcriptional activators that can direct expression of the Rh5 and Rh6 genes in the R7 cell.
C. A second transcriptional repressor binds to the A half and together with Prospero inhibits transcription of the Rh5 and Rh6 genes in the R7 cell.
D. Since the two experiments are contradictory it suggests that seq56 is not actually important for the regulation of the Rh5 and Rh6 genes.

18. What would be the phenotypic consequence of deleting either seq56 or the prospero gene from the fly genome?
A. Rh5 and Rh6 will be ectopically expressed in the R7 photoreceptor layer.
B. Each photoreceptor cell will express all six rhodopsins (Rh1-Rh6).
C. Expression of the Rh5 and Rh6 genes will be inhibited within the R8 photoreceptor cell layer.
D. There will be no change in Rh5 and Rh6 expression patterns since seq56 functions only in the regulation of the Rh3 and Rh4 genes.

19. In order to determine which domains of the transcription factors Eyeless (Ey) and Twin of Eyeless (Toy) are required for eye development, full-length and deletion constructs were expressed in flies and the presence or absence of ectopic eyes were analyzed. Based on your memory of this lecture which of the following best describes the conclusion that was drawn from these sets of experiments?
A. The Paired DNA binding domain and the C-terminal activation domain are the only two portions of both Ey and Toy that are required for eye development.
B. All five structural domains of Ey and Toy are required for eye development.
C. Eye development requires that Ey and Toy bind to enhancer elements via both the Paired (PD) and Homeodomains (HD)
D. Only the Ey protein is required for eye formation. The Toy protein is completely dispensable.

20. Several laboratories have demonstrated that Ey can induce ectopic eyes at a higher frequency and in a broader range of tissues than Toy. Based on the analysis of the Ey and Toy proteins using yeast transcription assays, which of the following best describes why Ey is a more potent inducer of ectopic eyes (when compared to Toy)?
A. Ey binds to enhancer elements with higher affinity than Toy
B. Toy binds to and activates fewer genes that are required for eye formation than Ey.
C. Ey is a stronger transcriptional activator than Toy.
D. Ey is a dedicated transcriptional activator while Toy is a dedicated transcriptional repressor.

21. In yeast the C-terminal tail of Ey functions as a stronger transcriptional activator than even full-length Ey. Based on the molecular dissection of Ey, which of the following provides the best explanation for this observation?
A. Full-length Ey is bound to a subset of enhancers in the genome so can therefore only activate a small number of genes. The Ey C-terminal tail is not bound to DNA and is free to interact with the general transcription factor machinery at all promoters.
B. The Ey C-terminal tail (by itself) binds to and activates RNA polymerase at higher affinity than full-length Ey.
C. The Ey C-terminal tail is more stable than full-length Ey.
D. The Ey full-length protein contains a repressor domain that is located in another portion of the protein.

22. Yeast cells expressing a mutant Ey protein in which the B domain has been removed grew in media containing 250mM concentrations of the transcriptional inhibitor 3AT while cells expressing the full-length Ey protein stopped growing if the concentration of 3AT was higher than 150mM. In flies, a chimeric protein in which the B domain of Ey was replaced with the homologous domain of Toy is capable of inducing ectopic eyes on the head and genitals, two places whose fates cannot be altered by full-length Ey. Which of the following best describes the underlying mechanisms for these observations?
A. The B domain of Ey is a target for cellular protein degradation machinery therefore the deletion and chimeric proteins are more stable than the full-length Ey protein.
B. The B domain of Toy contains an additional transcriptional activation domain.
C. Ey contains a transcriptional repression domain within its B domain.
D. The chimeric protein can bind with higher affinity to enhancer elements within the genome. This higher affinity is mediated by interactions between the B domain of Toy and the general transcription factor machinery.

23. Which of the following best describes the piece of evidence indicating that Ey is a stronger transcriptional activator than Toy?
A. Ey can bind to enhancer elements with higher affinity than Toy.
B. Yeast cells expressing full-length Ey can grow on media containing higher levels of 3AT than cells expressing full-length Toy.
C. Ey binds DNA as a homodimer while Toy binds DNA as a monomer
D. Ey functions as both a transcriptional activator and a repressor while Toy is just an activator.

24. Which of following is a true statement regarding the Toll pathway?
A. The spatzle ligand is expressed and secreted by the ventrally located follicle cells.
B. The Toll receptor (which can bind the spatzle ligand) is expressed uniformly within the embryonic eggshell.
C. Upon activation of the Toll receptor by the spatzle ligand, the Dorsal protein is released from the cytoplasm and translocated into the nucleus.
D. All of the above.

25. Which of the following best describes why the twist (twi), rhomboid (rho) and short gastrulation (sog) genes are all bound by the Dorsal protein but are expressed in different patterns within the developing Drosophila embryo?
A. Each gene contains a unique number and combination of high and low affinity Dorsal binding sites.
B. Each gene is bound by different numbers of transcriptional repressors that in turn counteract the activity of Dorsal.
C. The sog, rho and twi enhancers are located at progressively further distances from the transcriptional start sites.
D. All of the above.

26. A bioinformatic search for the presence of new Dorsal binding sites identified a number of potentially new targets of Dorsal all of which were experimentally verified. Which of the following best describes the conclusions that were drawn from the bioinformatic approach?
A. Most true transcriptional targets of Dorsal contain a single high-affinity binding site.
B. Transcriptional targets of Dorsal have both high and low affinity binding sites scattered throughout the entire length of the gene.
C. True transcriptional targets of Dorsal are likely to contain several (3-4) closely clustered binding sites within a short (100-400bp) enhancer.
D. Most true transcriptional targets actually do not have any Dorsal binding sites.

27. DNA microarrays and tiling arrays were used to experimentally identify new transcriptional targets of Dorsal. Which of the two methods identified novel genes that were not already predicted by bioinformatic algorithms or known to experimentally exist.
A. DNA microarrays
B. DNA tiling arrays
C. Neither approach
D. Both approaches

28. Which of the two methods allows you to identify new exons?
A. DNA microarrays
B. DNA tiling arrays
C. Neither approach
D. Both approaches

29. DNA microarrays detect differences amongst cells and tissues in which of the following categories?
A. Replication
B. Transcription
C. RNA editing
D. Translation

30. Imagine that you are using DNA microarrays to determine the differences between the RNA profiles of wild type skin cells and that of cancerous skin cells. The RNA from wild type is labeled in red while the RNA from the cancerous cells is labeled in green. What does it mean if a gene spot on the microarray slide is red.
A. The gene is transcribed at higher levels in the wild type skin cell sample.
B. The gene is transcribed at higher levels in the cancerous skin cell sample.
C. The gene is transcribed at equal levels in both tissue samples.
D. The gene in question is not expressed

31. What does it mean if a different gene spot on the micorarray slide is yellow?
A. The gene is transcribed at higher levels in the wild type skin cell sample.
B. The gene is transcribed at higher levels in the cancerous skin cell sample.
C. The gene is transcribed at equal levels in both tissue samples.
D. The gene in question is not expressed

32. And what does it mean if a third gene spot on the microarray slide is black?
A. The gene is transcribed at higher levels in the wild type skin cell sample.
B. The gene is transcribed at higher levels in the cancerous skin cell sample.
C. The gene is transcribed at equal levels in both tissue samples.
D. The gene in question is not expressed

33. What is the purpose of the laser capture microscope (LCM)?
A. The LCM is used to isolate very small quantities of tissue whose RNA profiles can then be determined using DNA microarrays.
B. The LCM is used to isolate RNA from small quantities of tissue, which then can be hybridized to a microarray slide.
C. Genomic DNA from small quantities of cells can be isolated using a LCM. The genomic DNA can be sequenced and differences in genomic structure and organization can be determined.
D. The LCM is used to sort cells into different pools based on their protein profiles.

34. As we discussed in class DNA microarrays were used to determine the transcriptional profile of different Drosophila stages. Which of the following are true statements.
A. A subset of genes is expressed only during one specific stage of development (i.e. embryonic).
B. Some genes are expressed at all stages during development.
C. Several genes that are expressed during early stages of development (embryonic) are re-expressed again during later stages (pupal).
D. All of the above.

35. Which of the following is a true statement regarding morphogen gradients?
A. The morphogen (ligand) is secreted molecule that can diffuse long distances.
B. While cells that surround the morphogen source express the same number of receptors on their surface irrespective of their distance from the source, cells that lie closest to the source will have more occupied receptors than cells that lie farther away.
C. Differences in the numbers of occupied receptors is translated into differences in gene expression.
D. All of the above.

36. Based on our knowledge of the Bicoid and Oskar gradients which of the following best describes how these two mRNAs are localized to the poles of the embryo?
A. The bicoid and oskar mRNAs are secreted into the two poles by the anterior and posterior follicle cell populations that surround the embryo.
B. Both mRNA transcripts are localized to the poles through diffusion.
C. The two mRNAs are bound to motor proteins that move the transcripts along microtubules to the poles.
D. The bicoid and oskar genes are transcribed only within cells at the anterior and posterior poles.

37. Development of the Drosophila embryo is controlled by a series of gene regulatory networks. Which of the following subdivides the embryo into the three major subdivisions: head, thorax and abdomen.
A. Maternal Effect Genes
B. Gap Genes
C. Segment Polarity Genes
D. Hox Genes

38. Which of the following is a true statement regarding Hox genes and the homeobox (also called the homedomain) DNA binding motif?
A. The loss of a Hox gene results in loss of primary segmentation fate and replacement with a secondary segmentation fate.
B. Forced expression of Hox genes can alter tissue fate (i.e. transform antenna to leg)
C. All Hox proteins contain a homeobox but all transcription factors that contain a homeodomain are not Hox proteins
D. All of the above.

39. Which of the following combinations of tissues are not transformed into other tissues when Hox gene expression is lost (in Drosophila)?
A. Antenna-Eye-Wing
B. Proboscis-Leg-Abdomen
C. Head-Leg-Abdomen
D. T1 leg – T2 leg – T3 leg

40. Removal of the Ultrabithorax (Ubx) gene from the haltere leads to its transformation into a wing. What does this phenotype suggest about its molecular function?
A. Ubx is a transcriptional repressor that normally inhibits wing fate in the haltere.
B. Ubx is a transcriptional activator that normally promotes haltere fate.
C. Ubx has activation and repression domains – Ubx activates wing fate and represses haltere fate.
D. None of the above

EXAM 4 ANSWER KEY

1. D
2. C
3. D
4. A
5. D
6. D
7. D
8. B
9. A
10. C
11. A
12. C
13. C
14. B
15. D
16. A
17. C
18. A
19. A
20. C
21. D
22. C
23. B
24. D
25. A
26. C
27. B
28. B
29. B
30. A
31. C
32. D
33. A
34. D
35. D
36. C
37. B
38. D
39. A
40. A