Question No. 1 of 10

Instructions: (1) Read the problem and answer choices carefully (2) Work the problems on paper as needed (3) Pick the answer (4) Go back to review the core concept tutorial as needed.

<table>
<thead>
<tr>
<th>Question</th>
<th>1. Which of the following is NOT a feature of eukaryotic gene expression?</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(A) Poly polycistronic mRNAs are very rare.</td>
</tr>
<tr>
<td></td>
<td>(B) Many genes are interrupted by non-coding DNA sequences.</td>
</tr>
<tr>
<td></td>
<td>(C) RNA synthesis and protein synthesis are coupled as in prokaryotes.</td>
</tr>
<tr>
<td></td>
<td>(D) mRNA is often extensively modified before translation.</td>
</tr>
<tr>
<td></td>
<td>(E) Multiple copies of nuclear genes and pseudo-genes can occur.</td>
</tr>
</tbody>
</table>

A. Incorrect! Polycistrorn is very common in prokaryotes but very rare in eukaryotes.

B. Incorrect! The majority of the protein coding genes are interrupted by introns, which are non-coding DNA sequences.

C. Correct! RNA synthesis and protein synthesis in prokaryotes are coupled, as there is no nuclear membrane to separate these two process. In eukaryotes, RNA synthesis occurs in the nucleus and protein synthesis occurs in cytoplasm; the two processes are well-separated.

D. Incorrect! Eukaryotic mRNAs are usually extensively modified, including capping, polyadenylation, and splicing.

E. Incorrect! Eukaryotes have a large genome and multiple copies of one gene; pseudo-genes are very common.

It is important to understand how the genome is organized and how gene expression is regulated.

(C)RNA synthesis and protein synthesis are coupled as in prokaryotes.
Question No. 2 of 10

**Instructions:** (1) Read the problem and answer choices carefully (2) Work the problems on paper as needed (3) Pick the answer (4) Go back to review the core concept tutorial as needed.

### Question

2. The regions labeled A and C of the diagram are ______.

![Diagram of mRNA splicing](image)

(A) Introns  
(B) Spliceosomes  
(C) snRNPs  
(D) Exons  
(E) 5’ UTR and 3’ UTR

### Feedback

A. Incorrect!  
Intron is the labeled B region.

B. Incorrect!  
Spliceosome is the protein/RNA complex that removes the intron, not part of the DNA.

C. Incorrect!  
SnRNA is protein/RNA complex, also not part of the DNA.

D. Correct!  
Exons are interrupted by introns in hnRNA.

E. Incorrect!  
5’UTR and 3’UTR are untranslated regions for an mRNA; they are part of exons but, in this case, the labeled regions are not because the UTR regions cannot be separated by only one intron; a coding sequence is needed for a gene to be a protein-coding gene.

### Solution

Understanding the eukaryotic gene structure is an important step of the regulation of gene expression.

(D) Exons
### Question No. 3 of 10

**Instructions:** (1) Read the problem and answer choices carefully (2) Work the problems on paper as needed (3) Pick the answer (4) Go back to review the core concept tutorial as needed.

<table>
<thead>
<tr>
<th>Question</th>
<th>3. Which of the following features would you NOT expect to find in heterogeneous nuclear RNA (hnRNA)?</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(A) Introns</td>
</tr>
<tr>
<td></td>
<td>(B) 3’ poly A</td>
</tr>
<tr>
<td></td>
<td>(C) 5’ caps</td>
</tr>
<tr>
<td></td>
<td>(D) Polycistronic coding sequence</td>
</tr>
<tr>
<td></td>
<td>(E) U nucleotides</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Feedback</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>A. Incorrect!</td>
<td>hnRNA contains introns.</td>
</tr>
<tr>
<td>B. Incorrect!</td>
<td>hnRNA may also contain 3’ poly A because the polyadenylation process occurs in nucleus.</td>
</tr>
<tr>
<td>C. Incorrect!</td>
<td>5’ capping process also occurs in the nucleus and, therefore, may be found in hnRNA.</td>
</tr>
<tr>
<td>D. Correct!</td>
<td>Polycistronic coding sequence is found in prokaryotes, not in eukaryotes where hnRNA can be found.</td>
</tr>
<tr>
<td>E. Incorrect!</td>
<td>All RNA molecules contain U nucleotides.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Solution</th>
<th>Key point: post-transcriptional control, including capping, polyadenylation and splicing, all occur in the nucleus.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(D) Polycistronic coding sequence</td>
</tr>
</tbody>
</table>
### Question 4 of 10

**Instructions:**
1. Read the problem and answer choices carefully.
2. Work the problems on paper as needed.
3. Pick the answer.
4. Go back to review the core concept tutorial as needed.

#### Question

Which of the following statement is NOT true regarding translation initiation in eukaryotes?

- **(A)** The translation initiation of tRNA uses $\text{tRNA}^{\text{met}}$.
- **(B)** The 5' UTR region plays a critical role in translation initiation.
- **(C)** 5' cap is the site where the 80S ribosome binds.
- **(D)** The poly A tail plays a critical role in translation initiation.
- **(E)** Sometimes, the initiation can start without a 5’ cap.

#### Feedback

- **A. Incorrect!**
  This statement is true; the eukaryotic translation machinery use $\text{tRNA}^{\text{met}}$ for initiation.

- **B. Incorrect!**
  This statement is also true. The 5’ UTR region may contain secondary structure to inhibit translation or internal ribosome binding site for cap-independent initiation.

- **C. Correct!**
  5’ cap is where the translation initiation complex binds but, at this stage, the 80S ribosome is not formed; only the 40S small subunit of the ribosome is bound to 5’ cap and a scanning process starts. Until the AUG is found, the 60S then join the complex and form 80S ribosome.

- **D. Incorrect!**
  The poly A tail, although located at 3’ end, can interact with translational initiation complex and enhance translation.

- **E. Incorrect!**
  This statement is true; there is a cap-independent initiation mechanism.

#### Solution

Translation initiation is a key step in regulating eukaryotic gene expression and many mechanisms are involved.

**(C)5’ cap is the site where the 80S ribosome binds.**
### Question 5 of 10

**Instructions:** (1) Read the problem and answer choices carefully (2) Work the problems on paper as needed (3) Pick the answer (4) Go back to review the core concept tutorial as needed.

<table>
<thead>
<tr>
<th>Question</th>
<th>The translational control in eukaryotes includes all of the following components, except for _____.</th>
</tr>
</thead>
</table>
|          | (A) uORF  
|          | (B) 5’ cap  
|          | (C) IRES sequence  
|          | (D) Poly A  
|          | (E) TATA box  |

| Feedback | A. Incorrect!  
|          | uORF is part of the translation control mechanism for some gene expression.  
|          | B. Incorrect!  
|          | 5’ cap is where the translation initiation complex is attached; it is required for initiation.  
|          | C. Incorrect!  
|          | IRES sequences may be located within mRNA or at 5’ UTR for cap-independent translation initiation.  
|          | D. Incorrect!  
|          | Poly A can interact with translation initiation complex and enhance the translation.  
|          | E. Correct!  
|          | TATA box is part of the promoter and involved in transcriptional control, not translational. |

| Solution | The key to solve this problem is to have an overall understanding of how genes are transcribed and regulated at the translational level. |
|          | (E) TATA box |

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<table>
<thead>
<tr>
<th>Question No. 6 of 10</th>
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</thead>
<tbody>
<tr>
<td><strong>Instructions:</strong> (1) Read the problem and answer choices carefully  (2) Work the problems on paper as needed  (3) Pick the answer  (4) Go back to review the core concept tutorial as needed.</td>
</tr>
<tr>
<td><strong>Question</strong></td>
</tr>
<tr>
<td>6. Which of the statements about gene structure is correct?</td>
</tr>
<tr>
<td>(A) The regulatory regions of genes include the promoter and intervening introns.</td>
</tr>
<tr>
<td>(B) The promoter is where RNA ligase binds to initiate replication.</td>
</tr>
<tr>
<td>(C) Enhancers bind to DNA polymerase to inhibit DNA replication.</td>
</tr>
<tr>
<td>(D) A eukaryotic gene consists of an enhancer, promoter and a TATA box which is usually 300kbp away.</td>
</tr>
<tr>
<td>(E) The TATA box binds to transcription factors to regulate gene expression and is located usually within 30bp from the transcription start site.</td>
</tr>
<tr>
<td><strong>Feedback</strong></td>
</tr>
<tr>
<td>A. Incorrect! The promoter is a regulatory region, but the introns are not.</td>
</tr>
<tr>
<td>B. Incorrect! The promoter is where transcription factors bind.</td>
</tr>
<tr>
<td>C. Incorrect! Enhancers promote expression of a distal or proximal gene.</td>
</tr>
<tr>
<td>D. Incorrect! The TATA box binds to transcription factors to regulate gene expression and is located usually within 30bp from the transcription start site.</td>
</tr>
<tr>
<td>E. Correct! The TATA box binds to transcription factors to regulate gene expression and is located usually within 30bp from the transcription start site.</td>
</tr>
<tr>
<td><strong>Solution</strong></td>
</tr>
</tbody>
</table>
| Eukaryotic genes consist of: enhancer, promoter and TATA Box.  
Promoter: Proximal DNA sequence that binds to RNA polymerase for regulating gene expression.  
Enhancers: a short region of DNA that can be bound with proteins to promote expression of a distal or proximal gene.  
TATA Box: Binds to transcription factor for regulating gene expression, usually within 30bp of the transcription start site. |
| (E) The TATA box binds to transcription factors to regulate gene expression and is located usually within 30bp from the transcription start site. |
**Question:** 7. What is a Leucine-zipper?

(A) A DNA binding motif that contains a leucine residue at every other turn of the helix.
(B) An RNA binding motif that contains a leucine residue at every other turn of the helix.
(C) A leucine zipper is a basal transcription factor, which contains two cysteines and two histidines to bind Zn.
(D) It is a transcription factor that is induced only during mitosis.
(E) It is a transcription factor that contains many basic amino acids.

<table>
<thead>
<tr>
<th>Feedback</th>
</tr>
</thead>
</table>
| A. Correct!  
A leucine-zipper is a DNA-binding motif that contains a leucine residue at every other turn of the helix. |
| B. Incorrect!  
A leucine zipper is a DNA-binding motif. |
| C. Incorrect!  
A zinc finger contains two cysteines and two histidines to bind Zn. |
| D. Incorrect!  
A leucine zipper is a basal transcription factor. |
| E. Incorrect!  
A helix-loop-helix transcription factor contains many basic amino acids. |

<table>
<thead>
<tr>
<th>Solution</th>
</tr>
</thead>
</table>
| A common feature of basal transcription factors is that they all contain a motif to bind DNA (DNA-binding domain). There are three types of DNA-binding motifs:  
1. Zinc-finger is repetitive, has two cysteines and two histidines to bind a Zn, forming a “finger” structure.  
2. Leucine-zipper: leucine residue at every other turn of the helix, 7 amino acids apart.  
3. Helix-loop-helix (HLH): homeodomain contains many basic amino acids, also called basic HLH (bHLH).  

(A) A DNA binding motif that contains a leucine residue at every other turn of the helix. |
### Question No. 8 of 10

**Instructions:**
1. Read the problem and answer choices carefully
2. Work the problems on paper as needed
3. Pick the answer
4. Go back to review the core concept tutorial as needed.

<table>
<thead>
<tr>
<th>Question</th>
<th>Feedback</th>
<th>Solution</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>8. Which of the following statements about splicing is true?</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(A) Splicing removes the exons from the mRNA.</td>
<td>A. Incorrect! Splicing is a modification to remove the introns from the mRNA.</td>
<td></td>
</tr>
<tr>
<td>(B) Splicing removes the introns from the mRNA.</td>
<td><strong>B. Correct! Splicing is a modification to remove the introns from the mRNA.</strong></td>
<td></td>
</tr>
<tr>
<td>(C) The process of splicing always creates the same form of the protein.</td>
<td>C. Incorrect! Alternate splicing results in many isoforms of the same protein.</td>
<td></td>
</tr>
<tr>
<td>(D) A spliceosome is made up of tRNA and protein.</td>
<td>D. Incorrect! A spliceosome is made up of snRNA and protein.</td>
<td></td>
</tr>
<tr>
<td>(E) Improper splicing leads to a defective protein, with no effect on the cell or organism.</td>
<td>E. Incorrect! Improper splicing may cause severe disease, as well as produce a defective protein.</td>
<td></td>
</tr>
</tbody>
</table>

### Solution

Intron types include: Group I and Group II. They are found in rRNA genes and mitochondrial mRNA genes. They are self-splicing with no protein required. The third class is pre-mRNA introns. The third class is pre-mRNA introns found in nuclear mRNA genes and require a spliceosome to be removed. Alternative splicing is an important mechanism in gene regulation. Introns are spliced out at different positions. Splicing can result in many isoforms of the same protein. Improper splicing may cause severe disease.

**(B) Splicing removes the introns from the mRNA.**
## Question No. 9 of 10

**Instructions:**
1. Read the problem and answer choices carefully.
2. Work the problems on paper as needed.
3. Pick the answer.
4. Go back to review the core concept tutorial as needed.

### Question

9. mRNA stability or translation ______.

   - (A) Is maintained by the mRNA alone; there is no other factor needed.
   - (B) Is inhibited by the binding of an miRNA to the mRNA.
   - (C) Remains stable with siRNA bound.
   - (D) Increases in stability and remains stable as it moves from the nucleus to the cytosol.
   - (E) Is not under strict control and can change quickly.

### Feedback

A. Incorrect!
The stability of an mRNA is affected by the presence of a micro RNA (miRNA) and a small interfering RNA (siRNA).

B. Correct!
miRNA inhibits mRNA translation.

C. Incorrect!
mRNA can be degraded when siRNA is bound to it.

D. Incorrect!
While in the cytosol, the mRNA can be translated, remain stable or be degraded, depending on what factor is bound.

E. Incorrect!
mRNA stability and expression is under strict control.

### Solution

Once the mRNA leaves the nucleus, it may be translated immediately or translation may be inhibited by miRNA or degraded by signaling due to siRNA binding.

- **miRNA:** binds to mRNA in cytoplasm, inhibits translation.
- **siRNA:** binds to mRNA and leads to mRNA degradation.

(B) **Is inhibited by the binding of an miRNA to the mRNA.**
10. Which statement about the role of the Cap in translation is correct?

(A) CAP is a modified nucleotide that is added to the 3’ end of the mRNA.
(B) The 5’ cap binds to the 30S subunit of the ribosome.
(C) In cap-independent translation, the IRES allows the initiation of translation in the middle of the mRNA.
(D) The IRES allows the initiation of translation at the end of the mRNA, in place of the CAP.
(E) IRES is usually found as a normal factor in eukaryotic cells.

A. Incorrect!
The special nucleotide is added to the 5’ end of the mRNA.

B. Incorrect!
The 5’ cap binds to the 40S subunit of the ribosome.

C. Correct!
In cap-independent translation, the IRES allows the initiation of translation in the middle of the mRNA.

D. Incorrect!
In cap-independent translation, the IRES allows the initiation of translation in the middle of the mRNA.

E. Incorrect!
IRES is found mostly in viruses.

5’ cap (m7G) of the mRNA binds the 40S subunit of the ribosome. The pre-initiation complex is also attached to the polyA tail via other translation factors. The preinitiation complex (43S subunit or the 40S and mRNA) with the protein factors scan the mRNA for the AUG start codon. The start codon is methionine in eukaryotes and archaea. Once the AUG is found, the 60S ribosome binds. The complete ribosome 80S starts translation elongation. CAP independent translation initiation is mediated by IRES sequence, which is close to the AUG start codon. The IRES (internal ribosome entry site) allows translation initiation in the middle of an mRNA molecule. This sequence was first discovered in poliovirus RNA, which were able to bind eukaryotic ribosome to the mRNA molecule, allowing translation to occur.

(C) In cap-independent translation, the IRES allows the initiation of translation in the middle of the mRNA.