## Question 1: Interpreting and Evaluating Experimental Results — 9 points

Most proteins that are secreted from a cell must be transported to the endoplasmic reticulum (ER) either during translation or after translation.

For proteins transported during translation, this process begins in the cytosol and pauses when a specific sequence of amino acids is translated. The translation complex is then transported to the surface of the ER where translation continues. Proteins that are transported after translation are translated entirely in the cytosol and then transported to the ER. In both instances, the translated proteins enter the ER through a protein channel in the membrane of the ER.

Researchers studying the two types of protein transport identified that the ER membrane protein SR is necessary for transport during translation, while the ER membrane protein Sec62 is necessary for transport after translation. To investigate which transport mechanism is used for different proteins, researchers first created small interfering RNAs (siRNAs) that reduce expression of either SR or Sec 62. They then treated groups of cells with either the SR siRNA or the Sec62 siRNA and determined the relative amount of SR and Sec 62 protein in each group of cells compared with cells treated with a control siRNA. (Figure 1).

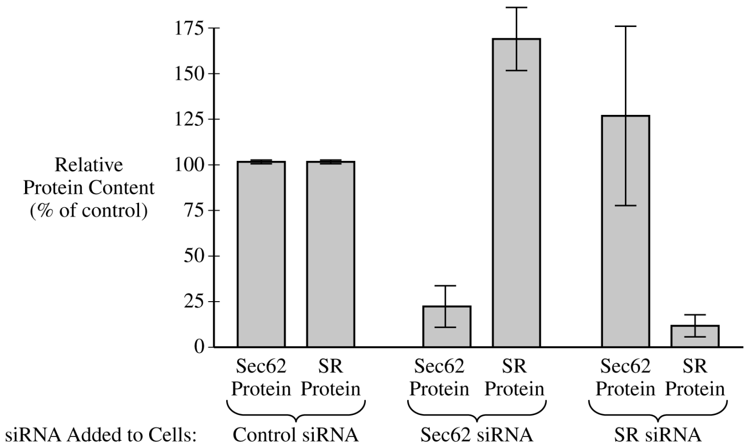


**Figure 1. Average relative amounts of Sec62 and SR proteins in cells treated with control siRNA, Sec62 siRNA or SR siRNA. Error bars represent $\pm SE_{\bar{X}}$.**

The researchers then measured the amount of each of three different proteins that was transported to the ER in cells treated with Sec62 siRNA or SR siRNA. The researchers calculated the percent transported relative to the cells treated with control siRNA (Figure 2).





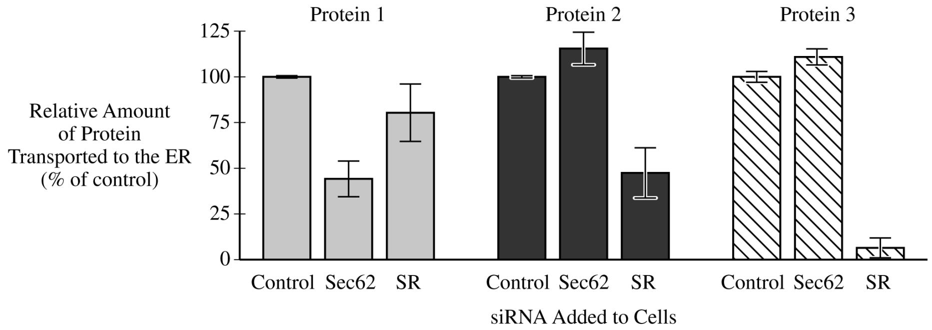


**Figure 2. Average relative amounts of three proteins that were transported to the ER when treated with control siRNA, Sec62 siRNA, or SR siRNA. Error bars represent $\pm SE_{\bar{X}}$.**

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| **A** | **Describe** the function of ribosomes.<br>Examples of acceptable responses may include the following:<br>• Ribosomes synthesize <u>polypeptides</u>/<u>proteins</u>.<br>• Ribosomes perform translation.<br>• Ribosomes are sites of <u>polypeptide</u>/<u>protein</u> synthesis. | **Point A1** |
| **B** | (i) **Identify** the dependent variable in the experiments shown in Figure 1.<br>• The (relative) <u>amount of protein</u>/<u>protein content</u> | **Point B1** |
| | (ii) **Justify** why the researchers included the control of measuring the relative amounts of both Sec62 and SR proteins in cells that were treated with Sec62 siRNA only (data shown in Figure 1).<br>Examples of acceptable responses may include the following:<br>• (The control allowed the researchers) to determine whether the (Sec62) siRNA <u>reduced</u>/<u>affected</u> the content of both proteins (relative to protein content in the presence of the control siRNA).<br>• (The control allowed the researchers) to determine whether the (Sec62) siRNA <u>reduced</u>/<u>affected</u> Sec62 (protein content) only. | **Point B2** |
| | (iii) Based on Figure 1, **describe** the effect on the production of SR protein when cells are treated with Sec62 siRNA.<br>Examples of acceptable responses may include the following:<br>• (SR protein production) increased.<br>• (SR protein production) increased by 65% (accept 50–80%). | **Point B3** |

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| **C** | (i) **Identify** the independent variable in the researchers' second experiment (data shown in Figure 2).<br>Examples of acceptable responses may include the following:<br>• (The type of) siRNA (added to the cells)<br>• The type of protein whose amount was measured | **Point C1** |
| | (ii) Based on Figure 2, **identify** the protein(s) that when treated with Sec62 siRNA showed an increase in percent transport to the ER compared with the control.<br>Examples of acceptable responses may include the following:<br>• Proteins 2 and 3<br>• Protein 2<br>• Protein 3 | **Point C2** |
| | (iii) Protein 1 is encoded by 234 nucleotides, while protein 2 is encoded by 495 nucleotides. Assuming all nucleotides for both proteins encode amino acids, **calculate** the difference in the number of amino acids between the two proteins.<br>• 87 (amino acids) [(495/3)−(234/3)] | **Point C3** |
| **D** | (i) Researchers claim that protein 1 is the only tested protein that is transported to the ER following its complete translation in the cytosol. Using data from Figure 2, **support** the researchers' claim.<br>• Only protein 1 showed a reduced <u>amount</u>/<u>percentage</u> of transport when cells were treated with Sec62 siRNA. | **Point D1** |
| | (ii) For any protein that enters the ER, researchers claim that amino acids close to the protein's amino terminus determine how likely the protein is to pass through the protein channel within the ER membrane. **Justify** the researchers' claim based on your understanding of factors that affect the transport of proteins across membranes.<br>• Amino acids (at the amino terminus) that have <u>similar polarity to</u>/<u>opposite charge to</u> (the R groups of amino acids lining) the protein channel are more likely to pass through the channel (than are proteins where the amino terminus contains amino acids with dissimilar polarity or similar charge). | **Point D2** |





## Question 2: Interpreting and Evaluating Experimental Results with Graphing

**9 points**

During meiosis, double-strand breaks occur in chromatids. The breaks are either repaired by the exchange of genetic material between homologous nonsister chromatids, which is the process known as crossing over (Figure 1A), or they are simply repaired without any crossing over (Figure 1B). Plant breeders developing new varieties of corn are interested in determining whether, in corn, a correlation exists between the number of meiotic double-strand chromatid breaks and the number of crossovers.

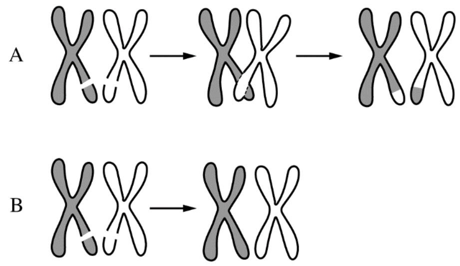


Figure 1. Double-strand breaks in chromatids are repaired with crossing over (A) or without crossing over (B).

Using specialized staining and microscopy techniques, scientists counted the number of double-strand chromatid breaks and the number of crossovers in the same number of meiotic gamete-forming cells of six inbred strains of corn (Table 1).

TABLE 1. NUMBER OF CHROMATID DOUBLE-STRAND BREAKS AND AVERAGE NUMBER OF CROSSOVERS IN INBRED STRAINS OF CORN

| Strain of Corn | Number of Double-Strand Breaks | Average Number of Crossovers ($\pm 2SE_{\bar{X}}$) |
|---|---|---|
| I | 710 | $19.5 \pm 0.5$ |
| II | 650 | $18.0 \pm 0.7$ |
| III | 600 | $17.5 \pm 1.0$ |
| IV | 510 | $16.0 \pm 1.0$ |
| V | 425 | $14.0 \pm 0.5$ |
| VI | 325 | $11.0 \pm 1.5$ |

| | | |
|---|---|---|
| **(a)** | The double-strand breaks occur along the DNA backbone. **Describe** the process by which the breaks occur.<br>Accept one of the following:<br>• (Enzymatic) hydrolysis occurs between the <u>sugars and phosphates</u>/<u>nucleotides</u>.<br>• The covalent bonds between the <u>sugars and phosphates</u>/<u>nucleotides</u> are broken. | **1 point** |

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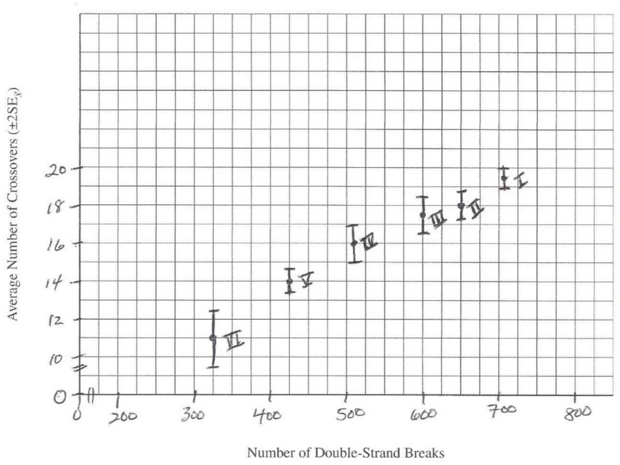
| **(b)** | Using the template in the space provided for your response, **construct** an appropriately labeled graph that represents the data in Table 1 and allows examination of a possible correlation between double-strand breaks and crossovers. | **1 point** |




- Appropriate axis scaling

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|---|---|---|
| | Using the template in the space provided for your response, **construct** an appropriately labeled graph that represents the data in Table 1 and allows examination of a possible correlation between double-strand breaks and crossovers.<br>• Accurately plotted X,Y graph with separate points for the average number of crossovers for each strain | **1 point** |
| | Using the template in the space provided for your response, **construct** an appropriately labeled graph that represents the data in Table 1 and allows examination of a possible correlation between double-strand breaks and crossovers.<br>• Accurate error bars | **1 point** |
| | Based on the data, **determine** whether corn strains I, II, and III differ in their average number of crossovers.<br>• There is no (statistical) difference (in the average number of crossovers) between strains II and III. Strain I is <u>higher</u>/<u>different</u> (in the average number of crossovers) compared with strains II and III. | **1 point** |
| | **Total for part (b)** | **4 points** |
| **(c)** | Based on the data, **describe** the relationship between the average number of double-strand breaks and the average number of crossovers in the strains of corn analyzed in the experiment.<br>• (In general) there is a <u>direct correlation</u>/<u>positive relationship</u> (between the number of double-strand breaks and the number of chromatid crossovers). | **1 point** |





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| **(d)** | Crossing over (Figure 1A) creates physical connections that are required for proper separation of homologous chromosomes during meiosis. A diploid cell with four pairs of homologous chromosomes undergoes meiosis to produce four haploid cells. Crossing over occurs between only three of the pairs. **Predict** the number of chromosomes most likely present in each of the four haploid cells.<br>• Two cells will have <u>three</u>/<u>n−1</u> chromosomes; two cells will have <u>five</u>/<u>n+1</u> chromosomes. | **1 point** |
| | Provide reasoning to **justify** your prediction.<br>• During meiosis I, (three homologous pairs separate normally, and) one pair <u>does not separate</u>/<u>experiences nondisjunction</u>. In meiosis II, the sister chromatids separate normally. | **1 point** |
| | **Explain** how plant breeders can use the information in Table 1 to help develop new varieties of corn.<br>Accept one of the following:<br>• Because crossing over increases genetic diversity, the plant breeders can breed strains with high <u>crossover numbers</u>/<u>double-strand breaks</u>.<br>• They can increase the number of double-stranded breaks, which may lead to more crossovers that increase genetic variation. | **1 point** |
| | **Total for part (d)** | **3 points** |
| | **Total for question 2** | **9 points** |

## Question 6: Analyze Data — 4 points

Researchers are studying the use of RNA vaccines to protect individuals against certain diseases. To develop the vaccines, particular cells are first removed from an individual. Then mRNAs coding for specific proteins from a pathogen are introduced into the cells. The altered cells are injected back into the individual, where the cells make the proteins encoded by the introduced mRNAs. The individual then produces an immune response to the proteins that will help to protect the individual from developing a disease if exposed to the pathogen in the future.

When introduced into cells, the mRNAs used for vaccines must be stable so that they are not degraded before the encoded proteins are produced. Researchers developed several modified caps that they hypothesized might make the introduced mRNAs more stable than mRNAs with the normal GTP cap. To test the effect of the modified caps, the researchers produced mRNAs that differed only in their cap structure (no cap, the normal cap, or modified caps I, II, or III). They introduced the same amount of each mRNA to different groups of cells and measured the amount of time required for half of the mRNAs to degrade (mRNA half-life) and the total amount of protein translated from the mRNAs (Table 1).

TABLE 1. EFFECT OF mRNA CAP STRUCTURE ON mRNA HALF-LIFE AND PROTEIN TRANSLATED FROM THE INTRODUCED mRNA

| $5'$ Cap Structure | mRNA Half-Life $\pm 2SE_{\bar{X}}$ (hours after introduction into cells) | Total Amount of Protein Translated from mRNA $\pm 2SE_{\bar{X}}$ (relative to amount in normal cap) |
|---|---|---|
| No cap | $1.41 \pm 0.02$ | $0.011 \pm 0.000$ |
| Normal GTP cap | $16.10 \pm 1.83$ | $1.000 \pm 0.007$ |
| Modified cap I | $15.50 \pm 1.57$ | $4.777 \pm 0.042$ |
| Modified cap II | $27.00 \pm 2.85$ | $13.094 \pm 0.307$ |
| Modified cap III | $18.09 \pm 0.81$ | $6.570 \pm 0.075$ |

**(a)** Based on the data, **identify** which cap structure is most likely to protect the end of the mRNAs from degradation. **1 point**

- Modified cap II

**(b)** Based on the data for the mRNAs with modified caps, **describe** the relationship between the mRNA half-life and the total amount of protein produced. **1 point**

Accept one of the following:

- A longer mRNA half-life is associated with more protein.
- There is a positive <u>correlation</u>/<u>relationship</u>.

**(c)** After examining the data on mRNA half-lives and the amount of protein produced, the researchers hypothesized that each mRNA molecule with modified cap I was translated more frequently than was each mRNA molecule with the normal GTP cap. **Evaluate** their hypothesis by comparing the data in Table 1. **1 point**

- The data support their hypothesis because the half-lives of the two mRNAs are the same, but the amount of protein produced from the mRNA with modified cap I is more than (four times as much as) that produced from the mRNA with the normal





**(d)** Introduction of mRNAs into cells allows the cells to produce foreign proteins that they might not normally produce. **Explain** why the production of a foreign protein may be more likely from the introduction of mRNA than DNA into cells. **1 point**

Accept one of the following:

- Protein production from the DNA requires (transcription) factors to initiate transcription.
- Protein production from the mRNA does not depend on (correct posttranscriptional) processing of the pre-mRNA.
- The cells may be unable to transcribe the DNA (while mRNA can be directly translated).

**Total for question 6 — 4 points**