AP BIO Unit 6 Released FRQs

2017 #3

3. Gibberellin is the primary plant hormone that promotes stem elongation. GA 3-beta-hydroxylase (GA3H) is the enzyme that catalyzes the reaction that converts a precursor of gibberellin to the active form of gibberellin. A mutation in the *GA3H* gene results in a short plant phenotype. When a pure-breeding tall plant is crossed with a pure-breeding short plant, all offspring in the F_1 generation are tall. When the F_1 plants are crossed with each other, 75 percent of the plants in the F_2 generation are tall and 25 percent of the plants are short.

Second Base in Codon

First Base in Codon	U	C	A	G	Third Base in Codon
U	UUU, UUC: Phe UUA, UUG: Leu	UCU, UCC, UCA, UCG: Ser	UAU, UAC: Tyr UAA Stop, UAG Stop	UGU, UGC: Cys UGA Stop, UGG Trp	U, C, A, G
C	CUU, CUC, CUA, CUG: Leu	CCU, CCC, CCA, CCG: Pro	CAU, CAC: His CAA, CAG: Gln	CGU, CGC, CGA, CGG: Arg	U, C, A, G
A	AUU, AUC, AUA: Ile AUG: Met or Start	ACU, ACC, ACA, ACG: Thr	AAU, AAC: Asn AAA, AAG: Lys	AGU, AGC: Ser AGA, AGG: Arg	U, C, A, G
G	GUU, GUC, GUA, GUG: Val	GCU, GCC, GCA, GCG: Ala	GAU, GAC: Asp GAA, GAG: Glu	GGU, GGC, GGA, GGG: Gly	U, C, A, G

Figure 1. The universal genetic code

(a) The wild-type allele encodes a GA3H enzyme with alanine (Ala), a nonpolar amino acid, at position 229. The mutant allele encodes a GA3H enzyme with threonine (Thr), a polar amino acid, at position 229. **Describe** the effect of the mutation on the enzyme and **provide reasoning** to support how this mutation results in a short plant phenotype in homozygous recessive plants.

(b) Using the codon chart provided, **predict** the change in the codon sequence that resulted in the substitution of alanine for threonine at amino acid position 229.

(c) **Describe** how individuals with one (heterozygous) or two (homozygous) copies of the wild-type *GA3H* allele can have the same phenotype.

2017 #3 Answer Key

(a) The wild-type allele encodes a GA3H enzyme with alanine (Ala), a nonpolar amino acid, at position 229. The mutant allele encodes a GA3H enzyme with a threonine (Thr), a polar amino acid, at position 229. **Describe** the effect of the mutation on the enzyme and **provide reasoning** to support how this mutation results in a short plant phenotype in homozygous recessive plants. **(2 points)**

Description (1 point)	**Reasoning (1 point)**
The amino acid substitution changes the shape/structure/function of the protein.	The mutation decreases/eliminates gibberellin production.

(b) Using the codon chart provided, **predict** the change in the codon sequence that resulted in the substitution of alanine for threonine at amino acid position 229. **(1 point)**

Prediction (1 point maximum)

- G ↔ A in the first position (of the codon)
- 5′-GCN-3′ ↔ 5′-ACN-3′
- 5′-NGC-3′ ↔ 5′-NGT-3′ in the template strand of DNA

(c) **Describe** how individuals with one (heterozygous) or two (homozygous) copies of the wild-type *GA3H* allele can have the same phenotype. **(1 point)**

Description (1 point)

- Enough active enzyme is produced from one wild-type/dominant allele.
- Enough gibberellin is produced in the presence of one wild-type/dominant allele.

2016 #6

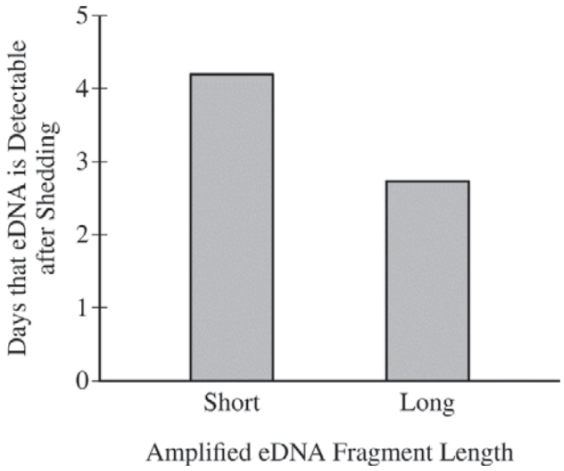


Figure 1. Detectability of eDNA fragments of varying lengths

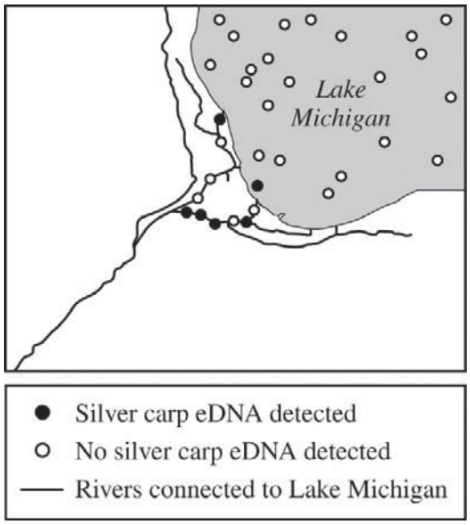


Figure 2. Map of the waterways that connect a nearby river system to Lake Michigan

6. Living and dead organisms continuously shed DNA fragments, known as eDNA, into the environment. To detect eDNA fragments in the environment, the polymerase chain reaction (PCR) can be used to amplify specific eDNA fragments. eDNA fragments of different lengths persist in the environment for varying amounts of time before becoming undetectable (Figure 1).

   To investigate whether silver carp, an invasive fish, have moved from a nearby river system into Lake Michigan, researchers tested water samples for the presence of eDNA specific to silver carp (Figure 2).

   (a) **Justify** the use of eDNA sampling as an appropriate technique for detecting the presence of silver carp in an environment where many different species of fish are found. **Propose** ONE advantage of identifying long eDNA fragments as opposed to short fragments for detecting silver carp.

   (b) The researchers tested a large number of water samples from Lake Michigan and found eDNA specific to silver carp in a single sample in the lake, as indicated in Figure 2. The researchers concluded that the single positive sample was a false positive and that no silver carp had entered Lake Michigan. **Provide reasoning** other than human error to support the researchers' claim.

2016 #6 Answer Key

(a) **Justify** the use of eDNA sampling as an appropriate technique for detecting the presence of silver carp in an environment where many different species of fish are found. **Propose** ONE advantage of identifying long eDNA fragments as opposed to short fragments for detecting silver carp. **(2 points)**

Justify (1 point)

- eDNA allows detection of the fish without visual identification/catching the fish.

Proposed advantage (1 point)

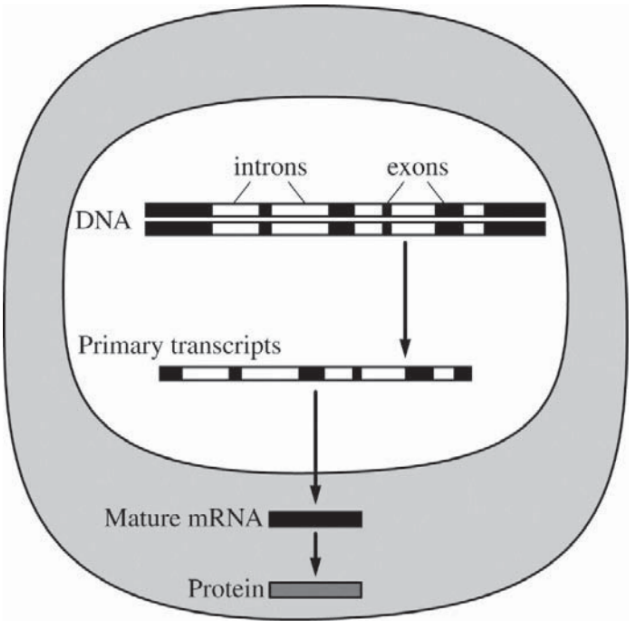
- Longer fragments indicate more recent presence of fish.
- Longer fragments are more likely to contain a sequence that is specific to silver carp.
- Longer sequences/more base pairs may increase accuracy/specificity/confidence that the eDNA is from a silver carp and not a related species.

(b) The researchers tested a large number of water samples from Lake Michigan and found eDNA specific to silver carp in a single sample in the lake, as indicated in Figure 2. The researchers concluded that the single positive sample was a false positive and that no silver carp had entered Lake Michigan. **Provide reasoning** other than human error to support the researchers' claim. **(1 point)**

Reasoning (1 point)

- eDNA entered the lake by means other than the fish (e.g., river flow, boats, waste from predators).

2016 #4



4. The figure represents the process of expression of gene *X* in a eukaryotic cell.

   (a) The primary transcript in the figure is 15 kilobases (kb) long, but the mature mRNA is 7 kb in length. **Describe** the modification that most likely resulted in the 8 kb difference in length of the mature mRNA molecule. **Identify** in your response the location in the cell where the change occurs.

   (b) **Predict** the length of the mature gene *X* mRNA if the full-length gene is introduced and expressed in prokaryotic cells. **Justify** your prediction.

2016 #4 Answer Key

(a) The primary transcript in the figure is 15 kilobases (kb) long, but the mature mRNA is 7 kb in length. **Describe** the modification that most likely resulted in the 8 kb difference in length of the mature mRNA molecule. **Identify** in your response the location in the cell where the change occurs. **(2 points)**

Describe process (1 point)

- Removal of introns
- RNA processing

Identification (1 point)

- Nucleus

(b) **Predict** the length of the mature gene *X* mRNA if the full-length gene is introduced and expressed in prokaryotic cells. **Justify** your prediction. **(2 points)**

Prediction (1 point)

- 15 kb
- Longer than the mature mRNA in the eukaryote

Justification (1 point)

- mRNA processing typically does not occur in prokaryotes

2014 #5

5. Genetically modified crops have been developed that produce a protein that makes the plants resistant to insect pests. Other genetic modifications make the crops more resistant to chemicals that kill plants (herbicides).

   (a) **Describe** TWO potential biological risks of large-scale cultivation and use of such genetically modified plants.

   (b) For each of the risks you described in part (a), **propose** a practical approach for reducing the risk.

2014 #5 Answer Key

(a) **Describe** TWO potential biological risks of large-scale cultivation and use of such genetically modified plants. (**2 points maximum**)

(b) For each of the risks you described in part (a), **propose** a practical approach for reducing the risk. (**2 points maximum**; LO 4.21, 2.23)

Description of risk (**1 point each; 2 points maximum**)	Proposed mitigation* + (**1 point each box; 2 points maximum**)
Unknown human/other animal health risk due to consuming GM proteins	• Testing/labeling product packaging • Isolate animals from crops
Disruption within food chain	• Intersperse GM plants with non-GM plants in culture • Provide alternative food source
Developed resistance in pest species	• Increased use of effective pesticides • Introduce pest predators • Further engineer the GMO to produce more resistance protein • Rotate GM and non-GM crops
Spread of genetic modifications to non-GM plants	• Contain pollen of GM plants • Disable the ability of GM plants to produce viable seeds
GM plants out-compete native species	• Contain/isolate GM plants • Disable GM plants' ability to produce viable seeds
Reduced numbers of pollinators	Contain/isolate GM plants
Loss of biodiversity	Intersperse GM plants with non-GM plants in culture
Use of herbicides harms non-target species	• Rotate GM and non-GM crops • Use organic/alternative herbicides
Invasive disease wiping out the monoculture	Intersperse GM plants with non-GM plants in culture

* Proposed mitigation of non-use of GM plants is acceptable for any described risk above.

+Mitigation must be practical for the risk given.

2012 #3

3. Information flow in cells can be regulated by various mechanisms.

   (a) **Describe** the role of THREE of the following in the regulation of protein synthesis:

   - RNA splicing
   - repressor proteins
   - methylation
   - siRNA

   (b) Information flow can be altered by mutation. **Describe** THREE different types of mutations and their effect on protein synthesis.

   (c) **Identify** TWO environmental factors that increase the mutation rate in an organism, and **discuss** their effect on the genome of the organism.

   (d) Epigenetics is the study of heritable changes in the phenotype caused by mechanisms other than changes in the DNA sequence. **Describe** ONE example of epigenetic inheritance.

2012 #3 Answer Key

Note: At least 1 point must be earned from each of parts (a), (b), (c), and (d) in order to earn a maximum score of 10.

Information flow in cells can be regulated by various mechanisms.

(a) **Describe** the role of THREE of the following in the regulation of protein synthesis:
- RNA splicing
- repressor proteins
- methylation
- siRNA

(*3 points maximum*)

	Description (1 point per box)
RNA splicing	• Exons spliced together. • Introns removed. • snRNPs/spliceosomes help remove introns.
Repressor proteins	• Inhibit **transcription**. • Inhibit **translation**. • Silence genes. • Inactivate gene expression.
Methylation	• DNA or histone methylation prevents transcription. • Protects against restriction enzymes.
siRNA	• Facilitates degradation of mRNA. • Inhibits translation.

(b) Information flow can be altered by mutation. **Describe** THREE different types of mutations and their effect on protein synthesis.
(4 points maximum)

Type of mutation (not limited to the following)	**Description (1 point per box)**	**Effect (1 point per box)**
Silent	Nucleotide change.	No change in amino acid/protein sequence.
Missense/substitution	Nucleotide change causes new codon.	Different amino acid/protein sequence.
Nonsense/substitution	Nucleotide change causes stop codon.	Protein not formed OR truncated protein.
Frameshift (insertion/deletion)	Nucleotide insertion/deletion alters reading frame after mutation.	Changes amino acid/protein sequence OR nonfunctional protein OR no protein.
Regulatory region	Nucleotide insertion/deletion/substitution.	Alters gene expression OR alters splice site.
Translocation	Chromosome segment moves to different site.	Alters gene expression.
Nondisjunction	Chromosomes fail to separate.	
Duplication	Chromosome segment doubles.	
Deletion	Chromosome segment is removed.	
Inversion	Chromosome segment is reversed.	
Transposition	Chromosome segment moves to a different site.	

(c) **Identify** TWO environmental factors that increase the mutation rate in an organism, and **discuss** their effect on the genome of the organism.
(4 points maximum)

Environmental factor (not limited to the following) (1 point each; 2 points maximum)	**Discussion (1 point each; 2 points maximum)**
• UV light	• T-T/thymine dimers.
• Carcinogens o Cigarette smoke o Asbestos o Radon gas • Radiation o X-rays o Gamma rays/cosmic rays • Chemical mutagens o Nitrites o EtBr o Aflatoxin o Pollution	• DNA is altered/damaged (e.g., deamination, depurination, double strand breaks).
• Viruses	• Disrupt gene sequence.

(d) Epigenetics is the study of heritable changes in the phenotype caused by mechanisms other than changes in the DNA sequence. **Describe** ONE example of epigenetic inheritance.
(1 point maximum)

Description of an epigenetic example (1 point maximum)

Acceptable responses include, but are not limited to, the following:

- DNA or histone modifications
- Inactivated X chromosomes (Barr bodies, calico cats)
- Heterochromatin
- Tumor suppressor genes (inactivation of *p53*)
- Cellular aging
- Environmental/in utero influences
- Maternal diet
- Agouti mice
- Heavy metals
- Famine study
- Pollution
- Twin studies (e.g., identical twin variations)
- Stress-induced alterations (e.g., post-traumatic stress disorder)
- Genomic imprinting (e.g., Prader-Willi syndrome, Angelman syndrome)

2009 #4

4. The flow of genetic information from DNA to protein in eukaryotic cells is called the central dogma of biology.

   (a) **Explain** the role of each of the following in protein synthesis in eukaryotic cells.

   - RNA polymerase
   - Spliceosomes (snRNPs)
   - Codons
   - Ribosomes
   - tRNA

   (b) Cells regulate both protein synthesis and protein activity. **Discuss** TWO specific mechanisms of protein regulation in eukaryotic cells.

   (c) The central dogma does not apply to some viruses. **Select** a specific virus or type of virus and **explain** how it deviates from the central dogma.

2009 #4 Answer Key

The flow of genetic information from DNA to protein in eukaryotic cells is called the central dogma of biology.

(a) **Explain** the role of each of the following in protein synthesis in eukaryotic cells. **(5 points maximum)**

	Description (1 point each)
RNA polymerase	DNA → RNA
Spliceosomes (snRNPs)	Removes the introns and connects (splices) the exons in RNA
Codons	Codes for amino acids/signals
Ribosomes	RNA → protein or site of protein synthesis
tRNA	Transports amino acids

(b) Cells regulate both protein synthesis and protein activity. **Discuss** TWO specific mechanisms of protein regulation in eukaryotic cells. **(4 points maximum)**

Protein Synthesis

Idea of the mechanism (1 point)	**Discussion (1 point)**
Promotor	increases RNA polymerase binding
Enhancer	increases transcription
Methylation	adding methyl group inhibits transcription
Acetylation	adding acetyl group promotes transcription
DNA packaging	loosening/tightening chromatin promotes/inhibits transcription
RNA processing	GTP cap or Poly-A tail
RNA editing	removing of introns
Alternative splicing	editing in different ways to get new/different RNA/polypeptides
mRNA degradation	targets RNA for destruction (miRNA or siRNA)
Protein processing	polypeptide → protein modifications (folding, chaperonins, cleavage, etc.)
Protein degradation	proteases break down proteins

Intracellular Protein Activity

Feedback: negative/positive	correct explanation of the identified feedback loop
Allosteric/noncompetitive	conformational change/binding to alternative site
Competitive	binding to (or blocking) active site
Environmental conditions	**intracellular** control by pH/temperature/substrate/enzyme concentration
Phosphorylation	protein kinase/phosphorylase activating enzyme/altering 3-D shape
Hormones	correct action for steroid or protein hormone
Coenzymes/Cofactors	presence/absence controls reactions

(c) The central dogma does not apply to some viruses. **Select** a specific virus or type and **explain** how it deviates from the central dogma. **(3 points maximum)**

Names a specific RNA virus or type of RNA virus (HIV, flu virus, etc.)	**(1 point)**
Deviation from the central dogma (RNA → DNA or RNA → protein or RNA → RNA)	**(1 point)**
More **detailed explanation** of the deviation from the central dogma	**(1 point)**

2009B #1

1. **Describe** how a plasmid can be genetically modified to include a piece of foreign DNA that alters the phenotype of bacterial cells transformed with the modified plasmid. **Describe** a procedure to determine which bacterial cells have been successfully transformed.

2009 B #1 Answer Key

Describe plasmid modification (8 points maximum):

Topic	Description (1 point each)
Plasmid vector	Describes plasmid as small circular DNA
Cut (cleave) DNAs	Use of restriction endonucleases (RE) Plasmid and inserted DNA must have same RE cut ends or be cut by same RE
Sticky ends	Ends of DNA should be sticky, wanting to bond with matching ends Generate ends for attachment using endonucleases
Ligase	For joining of sticky ends
Orientation	Correct orientation of insertion to ensure expression
Gene of interest	DNA cut should be a complete sequence of gene Attach piece with a promoter or insert next to promoter
Reporter gene	Gene used to identify insertion of desired DNA Insert DNA with a gene that produces a new phenotype
Selective marker	Inserted to help identify the DNA insertion (e.g., antibiotic resistance)
AUG in place	Ensure proper start codon
Uptake of plasmid	Calcium chloride and heat shock, electroporation to make competent
Alternative procedures	Blunt cuts; T4 ligase; add terminal transferase to add poly (A) to 3' end

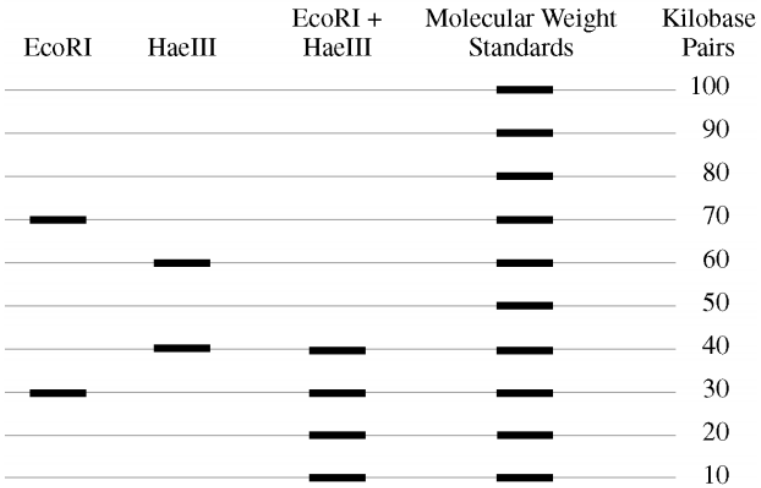
Describe plasmid uptake and how transformation is **determined (6 points maximum)**:

Topic	Description (1 point each)
Transformation	Defined process of transformation of a plasmid
Isolation	Isolate plasmids/agar plate that grows only colonies of resistance gene
Antibiotic	Use of antibiotic resistance/sensitivity genes Detailed description of antibiotic resistance lab procedure
Gel electrophoresis	Isolate plasmid using electrophoresis Detailed description of gel electrophoresis for isolation
Retrieval	Retrieve altered plasmid
Protein	Identification of new protein, possible glowing marker protein Detailed description of retrieval or protein method
Tag	Fluorescent marker, etc. Detailed description of alternate method

2007 #4

4. A bacterial plasmid is 100 kb in length. The plasmid DNA was digested to completion with two restriction enzymes in three separate treatments: EcoRI, HaeIII, and EcoRI + HaeIII (double digest). The fragments were then separated with electrophoresis, as shown.

RESULTS OF GEL ELECTROPHORESIS

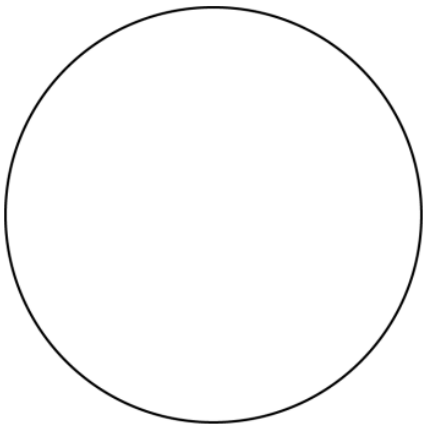


(a) Using the circle provided, **construct** a labeled diagram of the restriction map of the plasmid. **Explain** how you developed your map.

(b) **Describe** how:

- recombinant DNA technology could be used to insert a gene of interest into a bacterium
- recombinant bacteria could be identified
- expression of the gene of interest could be ensured

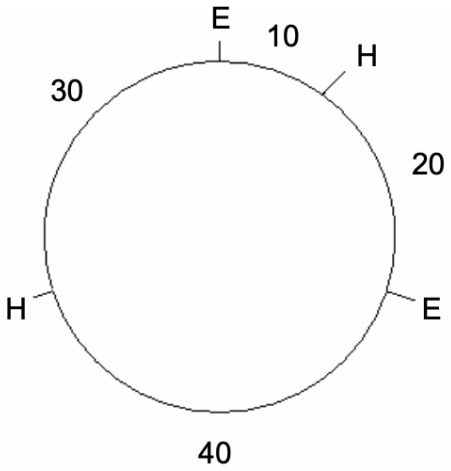
(c) **Discuss** how a specific genetically modified organism might provide a benefit for humans and at the same time pose a threat to a population or ecosystem.

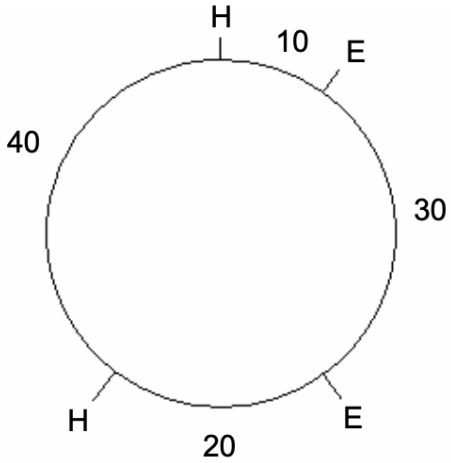


2007 #4 Answer Key

(a) Using the circle provided, **construct** a labeled diagram of the restriction map of the plasmid. **Explain** how you developed your map.

Construct a labeled map and **explain (3 points maximum)**





E = EcoRI Restriction Point
H = HaeIII Restriction Point

- Restriction sites correctly placed and kilobase sizes shown **(2 points)**
- Explanation **(1 point)**
  (NO POINTS for explanation with incorrect or missing map OR for interpreting gel only)
  - trial and error discussion
  - restriction site within larger fragment

(b) **Describe** how:

- Recombinant DNA technology could be used to insert a gene of interest into a bacterium
- Recombinant bacteria could be identified
- Expression of the gene of interest could be ensured

Describe how to: (6 points maximum)

(1) Insert gene of interest (4 points maximum)

- Cut gene of interest from source and/or cut plasmid with restriction enzyme
- Use SAME restriction enzyme on both
- Anneal/ligate/mix/combine gene of interest with vector (plasmid/virus/phage)
- "Sticky ends"/bp matches/complementarity
- Treatment for competent cells ($CaCl_2$/heat shock); incubate together
- Chemical modification can prevent restriction enzyme activity (e.g., methylation)
- Gene = cDNA (without introns) to fit into plasmid

(2) Identify recombinant bacteria (1 point)

- Phenotypic selection (antibiotic resistance/blue-white colony selection/"glo" gene, product produced [e.g., insulin])
- Radioactively/fluorescently labeled probe (tag/dye) / mRNA
- Electrophoresis of cut recombinant vs. original (gene/plasmid) **OR** with sequence comparison of recombinant vs. original (gene/plasmid) **(Not bacterial genome)**

(3) Ensure expression of gene of interest (1 point)

- Promoter [for prokaryote]
- cDNA/removal of introns for prokaryotic expression
- Operon (e.g., nutrient/arabinose induced)

(c) **Discuss** how a specific genetically modified organism might provide a benefit for humans and at the same time pose a threat to a population or ecosystem. **(3 points maximum)**

Discuss GM, benefit to humans, and threat to population/ecosystem

- Nonhuman organism with specific, heritable GM trait
- Plausible benefit to humans related to the GM trait
- Plausible or unknown threat to population/ecosystem related to GM trait/modified organism

2007B #3

3. A molecule of messenger RNA (mRNA) has just been synthesized in the nucleus of a human cell.
   (a) What types of modifications may occur to this RNA before it leaves the nucleus?
   (b) Once in the cytoplasm, how is the mRNA translated to a protein?
   (c) If the cell is a secretory cell, how is the protein from part (b) eventually targeted, packaged, and secreted to the exterior of the cell?

2007 B #3 Answer Key

A molecule of messenger RNA (mRNA) has just been synthesized in the nucleus of a human cell.

(a) What type of modifications may occur to this RNA before it leaves the nucleus?

One point for each of the following explanations/identifications (3 points maximum):

- Difference between introns and exons
- Description of splicing
- 5′ cap added or description of function
- 3′ poly A tail added or description of function

(b) Once in the cytoplasm, how is the mRNA translated to a protein?

One point for each of the following explanations/identifications (6 points maximum):

- Description of the role of tRNA in the transport of amino acids
- Description of the ribosome/rRNA
- Peptide bond formation (or the connecting of amino acids into a polypeptide chain)
- Concept of codon-anticodon binding
- Concept of the role of the genetic code (e.g., mRNA bases determine the sequence of amino acids)
- Description of stages (initiation, elongation, and termination)
- Elaboration point for a detailed explanation—examples of acceptable answers include, but are not limited to, the following:
  - Description of 40S and 60S ribosomal subunits
  - Role of aminoacyl-tRNA synthetase
  - Structure of tRNA
  - Use of GTP as energy source

(c) If the cell is a secretory cell, how is the protein from part (b) eventually targeted, packaged, and secreted to the exterior of the cell?

One point for each of the following explanations/identifications (3 points maximum):

- Role of chaperones in folding a polypeptide into the protein
- Modification of the protein or addition of sugars and/or phosphate
- Concept of the endomembrane system (description of protein moving from ER to Golgi to vesicles)
- Exocytosis through the fusion of the vesicle with the cell membrane

2005B #3

3. Protein synthesis is vital for cell growth and metabolism.
   (a) Describe transcription and translation.
   (b) Identify similarities between transcription and translation.
   (c) Identify differences between transcription and translation.
   (d) Describe structural changes that can occur to a protein after translation to make it function properly.

2005 B #3 Answer Key

NOTE: To receive 10 points, a student must earn at least 1 transcription point and 1 translation point from parts (a), (b), or (c).

Parts (a), (b), and (c) (9 points maximum)

Part (a)

Transcription	**Translation**
• DNA template • complimentary RNA (base-pairing) • RNA produced by RNA polymerase • promoter region/TATA box • transcription factors • DNA unwound (partially, temporarily) • posttranscriptional processing	• mRNA template • codon/anticodon • tRNA carries amino acid • role of ribosome • initiation (fMet, Shine-Delgarno) • elongation (peptide bond formation) • termination description

Part (b)
NOTE: Students must provide specific similarity AND explanation to earn a point.

Similarity	**Explanation**	
	Transcription	**Translation**
• base pairing	DNA–RNA, specific base examples	mRNA–tRNA (codon–anticodon), specific base examples
• polymer formed	RNA	polypeptide
• specialized protein	RNA polymerase	initiation factors, etc.
• specific start sites	promoter/TATA	initiation (start) codon

Part (c)
NOTE: Students must provide specific difference AND explanation to earn a point.

Difference	**Explanation**	
	Transcription	**Translation**
• location in cell (eukaryote)	nucleus	cytoplasm, rough ER
• product	RNA	polypeptide
• template	DNA	mRNA
• purpose	transfer information	make proteins
• enzymes	RNA polymerase	peptide bond-forming enzyme (peptidyl transferase)

Part (d) (3 points maximum)

- Folding
- Cleavage
- Chemical modification
- Elaboration—specifics of folding, chaperones, types of bonds, role of Golgi, incorporation into existing molecular arrays, etc.