**********379***

# 17 | BIOTECHNOLOGY AND GENOMICS

## REVIEW QUESTIONS

**1** How are GMOs created?

**A** Introducing recombinant DNA into an organism by any means

**B** *In vitro* fertilization methods

**C** Mutagenesis

**D** Plant breeding techniques

**Solution** The solution is (A). Recombinant DNA is DNA that has been genetically modified in the laboratory. A genetically modified organism (GMO) is created by introducing recombinant DNA into an organism.

**2** Which technique used to manipulate genetic material results in a significant increase in DNA or RNA fragments?

**A** Gel electrophoresis

**B** Nucleic acid extraction

**C** Nuclear hybridization

**D** Polymerase chain reaction (PCR)

**Solution** The solution is (D). PCR is a method used to make many copies of DNA or RNA fragments from a small number of copies.

**3** What is the role of plasmids in molecular cloning?

**A** They are used to create clones.

**B** They are used as vectors to insert genes into bacteria.

**C** They are a functional part of binary fission.

**D** They contain the circular chromosome of prokaryotic organisms.

**Solution** The solution is (B). Plasmids are vectors that can be used to insert genes into bacteria.

**4** What is meant by a recombinant DNA molecule?

**A** Chimeric molecules

**B** Bacteria transformed into another species

**C** Molecules that have been through the PCR process

**D** The result of crossing over during cell reproduction

**Solution** The solution is (A). Recombinant DNA is a chimeric molecule, as it has been genetically modified in the laboratory.

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**********380**********

**5** What is Bt toxin is considered to be?

**A** A gene for modifying insect DNA

**B** An organic insecticide produced by bacteria

**C** A nerve toxin in humans

**D** A strain of genetically modified tomatoes

**Solution** The solution is (B). Bt, or *Botulinum toxin*, is lethal to insects and is, therefore, an organic insecticide produced by a bacterium.

**6** What is one trait of the Flavr Savr Tomato?

**A** Has a better shelf life

**B** Is not a variety of vine-ripened tomato in the supermarket

**C** Was not created to have better flavor

**D** Undergoes soft rot

**Solution** The solution is (A). The Flavr Savr Tomato was genetically modified to resist rot and to ripen more slowly, which gives it a better shelf life.

**7** What is first step in isolating DNA?

**A** Generating genomic DNA fragments with restriction endonucleases

**B** Introducing recombinant DNA into an organism by any means

**C** Overexpressing proteins in *E. coli*

**D** Lysing the cells in the sample

**Solution** The solution is (D). The first step in isolating DNA is cell lysis, a process in which the cell membrane is broken.

**8** What is genomics?

**A** Genomics is the study of entire genomes, including the complete set of genes, their nucleotide sequence and organization, and their interactions within a species and with other species.

**B** Genomics is the process of finding the locations of genes on each chromosome.

**C** Genomics is an illustration that lists genes and their location on a chromosome.

**D** Genomics is a genetic marker is a gene or sequence on a chromosome that co-segregates (shows genetic linkage) with a specific trait.

**Solution** The solution is (A). Genomics is the study of entire genomes, including the complete set of genes, their nucleotide sequence and organization, and their interactions within a species and with other species.

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**********379***

**9** What is required in addition to a genetic linkage map to build a complete picture of the genome?

**A** A genetic marker

**B** A physical map

**C** Linkage analysis of chromosomes

**D** Plasmids

**Solution** The solution is (B). A physical map, which shows the arrangement of genes on the chromosome, is necessary to build a complete picture of the genome.

**10** Genetic recombination occurs by which process?

**A** Crossing over

**B** Chromosome segregation

**C** Independent assortment

**D** Sister chromatids

**Solution** The solution is (A). Genetic recombination occurs when homologous chromosomes exchange material in a process called crossing over.

**11** Individual genetic maps in a given species are —

**A** genetically similar

**B** genetically identical

**C** genetically dissimilar

**D** not useful in species analysis

**Solution** The solution is (A). Individual genetic maps in a given species are genetically similar but not identical.

**12** What procedure uses information obtained by microscopic analysis of stained chromosomes?

**A** Cytogenetic mapping

**B** Radiation hybrid mapping

**C** RFLP mapping

**D** sequence mapping

**Solution** The solution is (A). A cytogenetic map is the visual appearance of a chromosome that has been stained.

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**********380**********

**13** What is true about linkage analysis?

**A** It is used to create a physical map.

**B** It is based on the natural recombination process.

**C** It involves breaking and re-joining of DNA artificially.

**D** It requires radiation hybrid mapping.

**Solution** The solution is (B). Genes far apart on a chromosome are separated by natural recombination more frequently than genes that are close together. Linkage analysis assesses the relative order of genes based on this natural recombination frequency.

**14** What does the chain termination method of DNA sequencing use to terminate polynucleotide elongation?

**A** Labeled dideoxynucleotides

**B** Unlabeled dideoxynucleotides

**C** Labeled deoxynucleotides

**D** Unlabeled deoxynucleotides

**Solution** The solution is (A). Chain termination occurs when a dideoxynucleotide is introduced into the DNA strand. Each dideoxynucleotide is labeled so that the strand can be visualized.

**15** What sequencing technique is used to identify regions of similarity between cell types or species?

**A** Dideoxy chain termination

**B** Proteins, DNA, or RNA sequence alignment

**C** Shotgun sequencing

**D** Whole-exome sequencing

**Solution** The solution is (B). Similarity among cell types or species can be assessed by aligning the sequence of proteins, DNA, or RNA.

**16** Whole-genome sequencing can be used for advances in what field?

**A** Bioinformatics

**B** Iron industry

**C** Multimedia

**D** The medical field

**Solution** The solution is (D). Whole genome sequencing yields genetic information that can lead to medical advances.

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**********379***

**17** Sequencing an individual person's genome —

**A** is currently impossible

**B** helps identify genetic mutations associated with certain diseases

**C** will not lead to legal issues regarding discrimination and privacy

**D** will not help make informed choices about medical treatment

**Solution** The solution is (B). Sequencing an individual's genome yields information about genetic mutations associated with disease.

**18** Genomics can be used in agriculture to do what?

**A** Generate new hybrid strains

**B** Improve disease resistance

**C** Improve yield

**D** Improve yield, resistance, and generate hybrids

**Solution** The solution is (D). Genomics yields a wide range of information that can lead to improved yield, resistance to disease, and the generation of new hybrid strains.

**19** What are the uses of metagenomics?

**A** Identification of biofuels

**B** Testing for multiple drug susceptibility in a population

**C** Use in increasing agricultural yields

**D** Identifying new species more rapidly and analyzing the effect of pollutants on the environment

**Solution** The solution is (D). Metagenomics is the study of genetic material recovered from the environment. This information can be used to identify new species and, over time, to assess the effect of pollutants on the environment.

**20** Genomics can be used on a personal level to do what?

**A** Determine the risks of genetic diseases for an individual's children

**B** Increase transplant rejection

**C** Predict the career success of a person

**D** Produce antibodies for an antigen

**Solution** The solution is (A). Genomics can be used to determine whether an individual has genes that might cause genetic disease in his or her children.

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**********380**********

**21** What is the percentage of single gene defects causing disease in developed countries?

**A** 0.05

**B** 0.1

**C** 0.2

**D** 0.4

**Solution** The solution is (A). Approximately 0.05, or 5 percent, of single gene defects cause disease in persons living in developed countries.

**22** The rapid identification of new species and the analysis of the effect of pollutants on the environment is a function of what?

**A** Metagenomics

**B** Linkage analysis

**C** Genomics

**D** Shotgun sequencing

**Solution** The solution is (A). Metagenomics involves the study and analysis of genetic material obtained from the environment.

**23** The risks of genetic diseases for an individual's children can be determined through —

**A** metagenomics

**B** linkage analysis

**C** genomics

**D** shotgun sequencing

**Solution** The solution is (C). Genomics involves analyzing genes, which can determine the chances of genetic diseases appearing in an individual's children.

**24** What is a biomarker?

**A** The color coding of different genes

**B** A protein uniquely produced in a diseased state

**C** A molecule in the genome or proteome

**D** A marker that is genetically inherited

**Solution** The solution is (B). A biomarker is a protein only produced when disease is present.

**25** What is a metabolome?

**A** A provisional listing of the genome of a species

**B** A unique metabolite used to identify an individual

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**********379***

**C** A method used for protein analysis

**D** The complete set of metabolites related to the genetic makeup of an organism

**Solution** The solution is (D). A metabolome is complete set of metabolites related to the genetic makeup of an organism.

**26** How would you describe a set of proteins with altered expression levels?

**A** A group of biomarkers

**B** A protein signature

**C** The result of a defect in mRNA transcription

**D** The results of crossing over during cell replication

**Solution** The solution is (B). A protein signature is a unique set of proteins present in a disease state.

**27** What is a protein signature?

**A** A protein expressed on the cell surface

**B** A unique set of proteins present in a diseased state

**C** The path followed by a protein after it is synthesized in the nucleus

**D** The path followed by a protein in the cytoplasm

**Solution** The solution is (B). A protein signature is a unique set of proteins present in a diseased state

**28** What describes a protein that is uniquely produced in a diseased state?

**A** A genomic protein

**B** A genetic defect

**C** A chimeric molecule

**D** A biomarker

**Solution** The solution is (D). A biomarker is a protein that indicates the occurrence of a particular disease.

**29** What are the metabolites that result from the anabolic and catabolic reactions of an organism called?

**A** Genetic metabolic profile

**B** Metabolic signature

**C** Metabolome

**D** Metagenomic

**Solution** The solution is (C). Metabolome refers to the metabolites that are produced by catabolic and anabolic biochemical reactions.

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**********380**********

## CRITICAL THINKING QUESTIONS

**30** What is the process of Southern blotting?

**A** Southern blotting is used to find particular DNA sequences. Fragments are separated on gel, incubated with probes to check for sequence of interest, and transferred to nylon membrane.

**B** Southern blotting is used to find particular DNA sequences. Fragments are separated on gel, transferred to nylon membrane, and incubated with probes to check for sequence of interest.

**C** Southern blotting is used to find particular RNA sequences. Fragments are separated on gel, transferred to nylon membrane, and incubated with probes to check for sequence of interest.

**D** Southern blotting is used to find particular RNA sequences. Fragments are separated on gel, incubated with probes to check for sequence of interest, and transferred to nylon membrane.

**Solution** The solution is (B). Southern blotting is used to find particular DNA sequences. Fragments are separated on gel, transferred to nylon membrane, and incubated with probes to check for sequence of interest.

**31** A researcher wants to study cancer cells from a patient with breast cancer. Is cloning the cancer cells an option?

**A** The cancer cells should be cloned along with a biomarker for better detection and study.

**B** The cells should be screened first in order to assure their carcinogenic nature.

**C** The cancer cells, being the clones of each other already, should directly be grown in a culture media and then studied.

**D** The cancer cells should be extracted using the specific antibodies.

**Solution** The solution is (C). Cancer cells are by definition clones of each other. All the researcher needs to do is grow the patient's cell through cell culture and study them.

**32** What are the uses of genome mapping?

**A** Genome mapping is useful in identifying human disease-causing genes, developing microbes to clean up pollutants, and increasing crop yield.

**B** Genome mapping is directly required to produce recombinants, in FISH detection, and detecting the methylated parts of genetic material.

**C** Genome mapping is useful for knowing the pedigree of diseases in humans and tracing the movement of transposons in plants.

**D** Genome mapping identifies human disease-causing genes only.

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**********379***

**Solution** The solution is (A). Human genome maps help researchers in their efforts to identify human disease-causing genes and can be used in a variety of other applications, such as using live microbes to clean up pollutants or even prevent pollution. Research involving plant genome mapping may lead to producing higher crop yields or developing plants that better adapt to climate change.

**33** If you had a chance to get your genome sequenced, what are some questions you might be able to have answered about yourself?

**A** You can determine the drugs that can rectify the disease, symptoms of the disease, and its severity.

**B** You can determine the ancestry and genetic origin of diseases and their susceptibility to drugs.

**C** You can predict the symptoms of disease, the vectors to be used in gene therapy, and the causal organism of the disease.

**D** You can determine the pedigree of a disease, produce recombinants, and detect the presence of extracellular genes using FISH.

**Solution** The solution is (B). It would be possible to determine ancestry, tendency to develop some diseases that are of genetic origin, or susceptibility to drugs.

**34** What is an example of a genomic mapping method?

**A** The radiation mapping method is an example which uses radiations to break the DNA and is affected by the change in recombination frequency.

**B** Cytogenetic mapping obtains information from microscopic analysis of stained chromosomes. It can estimate the approximate distance between markers.

**C** In restriction mapping, the DNA fragments are cut by using the restriction enzymes and then stained fragments are viewed on gel.

**D** Cytogenetic mapping obtains information from microscopic analysis of stained chromosomes. It can estimate the exact base pair distance between markers.

**Solution** The solution is (B). Cytogenetic mapping uses information obtained by microscopic analysis of stained sections of the chromosome. It is possible to determine the approximate distance between genetic markers using cytogenetic mapping, but not the exact distance (number of base pairs).

**35** What are three methods of gene sequencing?

**A** Chain termination method – automated sequencers are used to generate sequences of short fragments; Shotgun sequencing method – incorporation of ddNTP during DNA replication; Next-generation sequencing – cutting DNA into random fragments, sequencing using chain termination, and assembling overlapping sequences

**B** Chain termination method – incorporation of ddNTP during DNA replication; Shotgun sequencing method – cutting DNA into random fragments, sequencing using chain

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termination, and assembling overlapping sequences; Next-generation sequencing – automated sequencers are used to generate sequences of short fragments

**C** Chain termination method – incorporation of ddNTP during DNA replication; Shotgun sequencing method – automated sequencers are used to generate sequences of short fragments; Next-generation sequencing – cutting DNA into random fragments, sequencing using chain termination, and assembling overlapping sequences

**D** Chain termination method – automated sequencers are used to generate sequences of short fragments; Shotgun sequencing method – cutting DNA into random fragments, sequencing using chain termination, and assembling overlapping sequences; Next-generation sequencing – incorporation of ddNTP during DNA replication

**Solution** The solution is (B). The basic sequencing technique used in all modern-day sequencing projects is the chain termination method (also known as the dideoxy method), which was developed by Fred Sanger in the 1970s. The chain termination method involves DNA replication of a single-stranded template with the use of a primer and a regular dideoxynucleotide (ddNTP), which is a monomer of DNA. In the shotgun sequencing method, several copies of a DNA fragment are cut randomly into many smaller pieces (somewhat like what happens to a round shot cartridge when fired from a shotgun). All of the segments are then sequenced using the chain-sequencing method. Next-generation sequencing is a group of automated techniques used for rapid DNA sequencing. These automated, low-cost sequencers can generate sequences of hundreds of thousands or millions of short fragments (25 to 500 base pairs) in the span of one day.

**36** What is the greatest challenge facing genome sequencing?

**A** The lack of resources and use of chemicals for the sequencing of the DNA fragments

**B** The ethical issues such as discrimination based on person's genetics

**C** The use of chemicals during the sequencing methods could incorporate mutations

**D** The scientific issues such as conserving the human genome sequences

**Solution** The solution is (B). The ethical issues surrounding genome sequencing are the most challenging. Humans have a responsibility to use this knowledge wisely. Otherwise, it could be easy to misuse the power of such knowledge, leading to discrimination based on a person's genetics, human genetic engineering, and other ethical concerns. This information also could lead to legal issues regarding health and privacy.

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**********379***

**37** How is shotgun sequencing performed?

**A** The DNA is cut into fragments, sequencing is done using chain termination method, fragments are analyzed to see the overlapping sequences, and the entire fragment is reformed.

**B** The DNA is cut into fragments, overlapping sequences are analyzed using computer, sequencing is done using chain termination method, and the DNA fragment is reformed.

**C** The DNA is cut into fragments, stained with fluorescent dye, and sequenced using the chain termination method; the fragments are analyzed to see the overlapping sequences; and the entire DNA fragment is reformed.

**D** The DNA is cut into fragments, sequencing is done using the chain termination method, the DNA is stained with fluorescent dye, and a computer is used to analyze and reform the entire DNA fragment.

**Solution** The solution is (A). In the shotgun sequencing method, several copies of a DNA fragment are cut randomly into many smaller pieces (somewhat like what happens to a round shot cartridge when fired from a shotgun). All of the segments are sequenced using the chain-sequencing method. Then, with the help of a computer, the fragments are analyzed to see where their sequences overlap. By matching up overlapping sequences at the end of each fragment, the entire DNA sequence can be reformed.

**38** Coumadin is a drug frequently given to prevent excessive blood clotting in stroke or heart attack patients, which could lead to another stroke or heart attack. Administration of the drug also can result in an overdose in some patients, depending on the liver function of a patient.

How could pharmacogenomics be used to assist these patients?

**A** Pharmacogenomics could provide a counteracting drug to decrease the effect of Coumadin.

**B** Pharmacogenomics could test every patient for their sensitivity to the drug.

**C** Pharmacogenomics will not be able to provide any help to patients highly sensitive to the drug.

**D** Pharmacogenomics could provide an overdose to each patient to test for the symptoms of the drug.

**Solution** The solution is (B). Pharmacogenomics allows each patient to be tested for genotype associated sensitivity to drugs, thereby identifying patients who might experience an overdose of drugs prior to administration.

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**********380**********

**39** Why is so much effort being poured into genome mapping applications?

**A** Genome mapping is necessary to know the base pair difference between the markers.

**B** The mapping would help scientists understand the role of proteins in specific organelles.

**C** The mapping technique identifies the role of transposons.

**D** Genome mapping helps identify faulty alleles, which could cause diseases.

**Solution** The solution is (D). A genetic map of the human genome for multiple individuals could identify alleles of genes susceptible to cancer causing agents. The mapping could also identify allele variations resistant to changes resulting in cancer, thereby offering the opportunity for genetic therapy for the disorders.

**40** What is the reason for studying mitochondrial genomics that is most directly important for humans?

**A** Mitochondria evolved from bacteria; therefore, their genome is important to study.

**B** Mitochondria undergo rapid mutation; and it is essential that this pattern be studied.

**C** Mitochondria contain DNA, and it is passed on from mother to the offspring, which renders it helpful in tracing genealogy.

**D** Mitochondria are the only ATP-producing organelles of the cell, thus their genome is important.

**Solution** The solution is (C). Mitochondria are intracellular organelles that contain their own DNA. Mitochondrial DNA mutates at a rapid rate and often is used to study evolutionary relationships. Another feature that makes studying the mitochondrial genome interesting is mitochondrial DNA in most multicellular organisms only is passed on from the mother. For this reason, mitochondrial genomics often is used to trace genealogy.

**41** How can proteomics complement genomics?

**A** The genes are responsible for producing proteins, which implies that proteomics complements genomics.

**B** Genomics is responsible for deciding the structure of the proteins and, thereby, the result of proteomic studies.

**C** The genome is constant, but proteome is dynamic as different tissues possess the same genes but express different genes, thereby complementing genomics.

**D** The study of genes is incomplete without the study of their respective proteins, thus they complement each other.

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**********379***

**Solution** The solution is (C). Proteomics complements genomics and is useful when scientists want to test their hypotheses that were based on genes. Even though all cells of a multicellular organism have the same set of genes, the set of proteins produced in different tissues is different and dependent on gene expression. Thus, the genome is constant, but the proteome varies and is dynamic within an organism.

**42** How could a proteomic map of the human genome help find a cure for cancer?

**A** A genetic map could help identify genes that could counteract the cause of cancer.

**B** Metabolomics can be used to study the genes producing metabolites during cancer.

**C** Proteomics detects biomarkers whose expression is affected by the disease process.

**D** The mapping helps analyze the inheritance of cancer-causing genes.

**Solution** The solution is (C). Proteomic approaches are being used to improve screening and early detection of cancer. This is achieved by identifying proteins whose expression is affected by the disease process. An individual protein is called a biomarker, whereas a set of proteins with altered expression levels is called a protein signature.

**43** What contributions have been made through the use of microbial genomics?

**A** Microbial genomics has provided various tools to study psychological behaviors of organisms.

**B** Microbial genomics has been useful in producing antibiotics, enzymes, improved vaccines, disease treatments, and advanced cleanup techniques.

**C** Microbial genomics has contributed resistance in other bacteria by horizontal and lateral gene transfer mechanisms.

**D** Microbial genomics has contributed to fighting global warming.

**Solution** The solution is (B). Microorganisms are used to create products, such as enzymes that are used in research, antibiotics, and other anti-microbial mechanisms. Microbial genomics is helping develop diagnostic tools, improved vaccines, new disease treatments, and advanced environmental cleanup techniques.

## TEST PREP FOR AP® COURSES

**44** In separating DNA for genomic analysis, it is important to consider RNA contaminating the sample during the cell lysis step of a DNA extraction, which is likely to cause what to occur?

**A** DNA separates into the supernatant.

**B** The protease destroys the DNA.

**C** RNA does not affect the DNA.

**D** DNA combines with the RNA.

**Solution** The solution is (C). DNA is unaffected by the RNA.

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**********380**********

**45** There are many techniques for investigating human genomic disorders. Western blotting looks for protein, eastern blotting looks for post-translational changes, northern blotting looks at mRNA, and Southern blotting looks at DNA.

If you were to look at sickle cell anemia, a disorder affecting hemoglobin produced in red blood cells, which technique would be the most useful in detecting a polymorphism in a sample?

**A** Northern blotting

**B** Southern blotting

**C** Western blotting

**D** Eastern blotting

**Solution** The solution is (B). The polymorphism results in change (mutation) in the sequence of a gene, so the analyses of DNA will be most useful.

**46** A population of insects was formally distinguished by a mix of colors on their thorax and legs. This population now appears to be split into two subgroups, purple legged and orange legged. Researchers hypothesize that the purple-legged group may be increasing resistance to the Bt (*Bacillus thuringiensis*) toxin.

Which idea supports this observation?

**A** Transgenesis

**B** Natural selection

**C** Hybridization

**D** Recombination

**Solution** The solution is (B). The resistance to certain environmental pressure is result of mutations that produce organisms able to survive and reproduce, transmitting the favorable trait, which in turn will increase the number of organisms carrying the trait.

**47** Which statement describes the process of molecular cloning?

**A** The foreign DNA and plasmid are cut with the same restriction enzyme, and DNA is inserted within the lacZ gene, whose product metabolizes lactose. The foreign DNA and vector are allowed to anneal. The vector is transferred to a bacterial host that is ampicillin sensitive, and those with a disrupted lacZ gene show an inability to metabolize X-gal.

**B** The foreign DNA and plasmid are denatured using high heat, and DNA is inserted within the lacZ gene, whose product metabolizes glucose. The foreign DNA and vector are allowed to anneal. The vector is transferred to a bacterial host that is ampicillin sensitive, and the disrupted lacZ gene will metabolize X-gal.

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**********379***

**C** The foreign DNA and plasmid are cut with the same restriction enzyme, and DNA is inserted randomly in the plasmid. The foreign DNA and vector are allowed to anneal. The vector is transferred to a bacterial host that is ampicillin sensitive, and the disrupted lacZ gene shows an inability to synthesize X-gal.

**D** The foreign DNA and plasmid are cut with the same restriction enzyme, and DNA is inserted within the lacZ gene, whose product metabolizes lactose. The foreign DNA and vector are allowed to anneal. The vector is transformed into a viral host that is ampicillin sensitive, and the disrupted lacZ gene shows an inability to synthesize X-gal.

**Solution** The solution is (A). The foreign DNA and plasmid are cut with the same restriction enzyme, which recognizes a particular sequence of DNA called a restriction site. The restriction site occurs only once in the plasmid, and is located within the lacZ gene, a gene necessary for metabolizing lactose. The restriction enzyme creates sticky ends, which allow the foreign DNA and cloning vector to anneal. Ligase, an enzyme, binds the annealed fragments together. The ligated cloning vector is transformed into a bacterial host strain that is ampicillin sensitive and missing the lacZ gene from its genome. Bacteria are grown in a medium containing ampicillin and X-gal, a chemical metabolized by the same pathway as lactose. The ampicillin kills bacteria without the plasmid. Plasmids lacking the foreign insert have an intact lacZ gene and are able to metabolize X-gal, releasing a dye that turns blue. Plasmids with an insert have a disrupted lacZ gene and produce white colonies.

**48** There are three methods of creating maps to evaluate genomes: cytogenetic (staining chromosomes), radiation hybrid maps (fragments with X-rays), and sequence maps (comparing DNA sequences). Which option accurately describes the three methods?

**A** Cytogenetic mapping – stained sections of chromosomes are analyzed using microscope, the distance between genetic markers can be found; Radiation hybrid mapping – breaks DNA using radiation and is affected by recombination frequency; Sequence mapping – DNA sequencing technology used to create physical maps

**B** Cytogenetic mapping – stained sections of chromosomes are analyzed using microscope, the approximate distance between genetic markers can be found; Radiation hybrid mapping – breaks DNA using radiation and is unaffected by recombination frequency; Sequence mapping – DNA sequencing technology used to create physical maps

**C** Cytogenetic mapping – stained sections of chromosomes are analyzed using microscope, the distance in base pairs between genetic markers can be found; Radiation hybrid mapping – breaks DNA using radiation and is unaffected by recombination frequency; Sequence mapping – DNA sequencing technology used to create physical maps

**D** Cytogenetic mapping – stained sections of chromosomes are analyzed using a telescope, the distance between genetic markers can be found; Radiation hybrid mapping – breaks DNA using radiation and is affected by recombination frequency; Sequence mapping – DNA sequencing technology used to create physical maps

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**********380**********

**Solution** The solution is (B). Cytogenetic mapping uses information obtained by microscopic analysis of stained sections of the chromosome. It is possible to determine the approximate distance between genetic markers using cytogenetic mapping, but not the exact distance (number of base pairs). Radiation hybrid mapping uses radiation, such as X-rays, to break the DNA into fragments. The amount of radiation can be adjusted to create smaller or larger fragments. This technique overcomes the limitation of genetic mapping and is not affected by increased or decreased recombination frequency. Sequence mapping resulting from DNA sequencing technology allowed for the creation of detailed physical maps with distances measured in terms of the number of base pairs.

**49** How many cells with different genetic variations are possible after a single round of meiosis?

**A** Two

**B** Three

**C** Four

**D** Eight

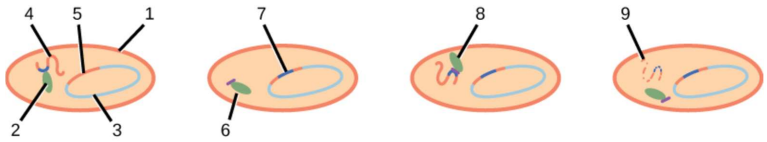
**Solution** The solution is (C). Complete meiosis produces four gametes which are genetically different due to events in meiosis I (recombination during prophase I, and the random alignment of the homologous chromosomes during metaphase I).

## SCIENCE PRACTICE CHALLENGE QUESTIONS

### 17.1 Biotechnology

**50** Prokaryotes have an adaptive strategy to identify and respond to viral infections. This strategy uses segments of the cyclic DNA called CRISPRs and genes coding for CRISPR-associated (cas) proteins. When a virus enters the cell, a strand of the viral DNA is excised by a cas protein and inserted into the bacterial DNA in a CRISPR region. When the same viral DNA is encountered subsequently, this foreign DNA is targeted by cas proteins that carry RNA markers transcribed from the inserted segment. The cas proteins cleave the viral DNA. The bacteria "remember" the infectious agent, providing a form of immunity.

**A.** Use the diagram to identify the components of a transcript-based response of bacteria to the presence of viral DNA by placing the corresponding number next to each feature of the diagram.

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**********379***

___ viral DNA

___ cellular DNA

___ excised viral DNA

___ cas protein–RNA–viral DNA complex

___ degraded viral DNA

___ cas protein

___ cas protein–RNA complex

___ cell membrane

___ stored viral DNA template

The CRISPR system was discovered in cultures of yogurt in 2002. Subsequently, researchers developed a technology based on manipulation of this system. The code for the prokaryotic CRISPR/cas system is highly conserved and is found in the human genome. DNA sequences are known that encode proteins responsible for many heritable diseases. CRISPR/cas is a technology that allows DNA to be cleaved at the boundaries of a nucleotide sequence, making the protein dysfunctional. The break in the strand is then recognized and replaced with code for the functional protein. If the editing is done with zygote-forming cells, the change is inherited. Not only the patient, but all progeny of the patient is cured. This technology is the first to easily make genomic modifications of a germ line. In the words of a prominent molecular biologist, this technology, which was recognized as the *Breakthrough of 2015* in the journal *Science*, "democratizes genetic engineering." Just as PCR became a standard tool that is widely used, any molecular biology lab is now able to apply this technology.

**B. Pose three questions**—whose pursuit would require an understanding of genetics—regarding the ethical and social issues that accompany the use of this medical technology.

**C. Explain** the value of genetic variation within a population. **Predict** a possible effect that this technology could have, if unregulated, on human genetic variation.

**Solution** Sample answer:

**A.**

4 viral DNA

3 cellular DNA

5 excised viral DNA

8 cas protein–RNA–viral DNA complex

9 degraded viral DNA

2 cas protein

6 cas Protein–RNA complex

1 cell membrane

7 stored viral DNA template

**B.** The nature of the problem elicits predictions of future events which cannot be tested now. However, the question should discriminate between those that are likely to eventually be answerable and those that will not be. For example, should the use of the technology be restricted or should the use depend on the ability to pay, are questions that will be decided without scientific reasoning. There are many possible questions that do require reasoning. Sample questions:

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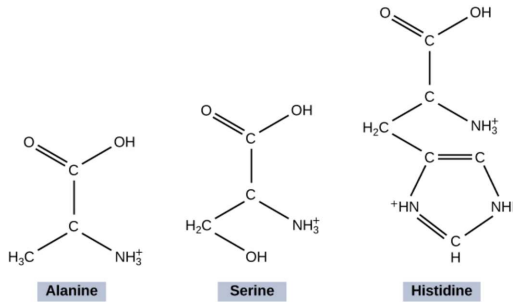
**********380**********

- How will disease be defined and differentiated from a phenotypic variation?
- What is the uncertainty associated with environmental factors that may or may not be required for expression?
- What is the likelihood of developing a disease?
- How do we weight the induction of expression due to environmental factors that may be avoided?
- If the gene in question is in a gene network, what is the relative importance of the targeted gene?
- At the time when a decision regarding the use of the technology is needed, how will expertise needed to answer these questions be accessed?

**C.** Phenotypic variation within a population increases likelihood of survival of genes within that population. Genome editing will cause a reduction in variation. If unregulated, the genome could behave as if the population were small, since effective population size is a measure of diversity. Small populations have greater risk of extinction.

**51** Gel electrophoresis of polymers and polymer fragments is an important element in many investigations. Samples of a solution are pipetted onto a gel. The gel is placed in a solution that maintains a constant pH, and an electric field is applied over the length of the gel. Separated components are placed on a substrate where they can be visualized and identified by comparison with samples of standards. Application of this method to DNA is called a Southern blot, named for the inventor of the technology. Application to RNA is called a northern blot, another demonstration that biologists have fun (there are also western, eastern, and far-eastern blots, but these techniques are *not* named for their inventor).

**A.** Consider the three amino acids shown in the figure and **explain** how when placed on a gel in an electric field the amino acids would move, how the amino acids would be separated as they moved, and which would move further.




**B.** A biologist wants to determine whether a new protocol is successful in constructing and amplifying a molecular clone of a segment of DNA introduced as a plasmid. After the

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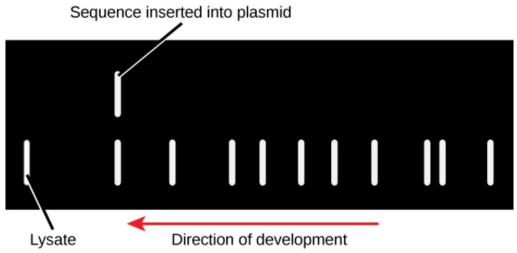
procedure is complete, the bacterial cells containing plasmid with the inserted segment are lysed, and a gel is run on which spots of the lysate and the sequence to be cloned have been pipetted. Use the data displayed in the developed gel shown in the figure to **evaluate the question** of whether or not the protocol was successful.




**C. Design a plan** to answer the question of whether the new DNA has been incorporated in the DNA of the host organism.

**Solution** Sample answer:

**A.** The electric field exerts a force on a charged molecule. Higher molecular mass molecules migrate less far, as do molecules with smaller charge and so the components will be separated and in this case it is uncertain whether histidine, with a larger charge but also a greater mass, will travel further than serine. Certainly alanine will travel further than serine. The rubric will award points for reasoning, not for correct answer.

**B.** The sequence is indicted in the run of the lysate. However, this does not mean that the sequence is incorporated into the genome.

**C.** To determine whether the sequence is heritable, the examination of lysate would be repeated after the passage of a few generations. So, the plan would be grow the cells on nutrient media, dilute, plate, grow, and repeat this sequence a few times. Then lyse the cells and run a gel.

## 17.3 Whole-Genome Sequencing

**52** Genetic engineering can be applied to heritable information to produce what is referred to as a "knockdown organism." Biotechnology also can be applied to produce non-heritable changes in a "knockdown gene." Post-transcriptional strategies target the mRNA product of a gene. One such strategy uses the conserved genes that encode RNA interference (RNAi) proteins for the regulation of level of mRNA transcription.

Some viral RNA is double stranded (dsRNA). A cell responds to the presence of double stranded RNA by attachment of the enzyme DICER which cuts dsRNA into short fragments. One strand of the fragment is transferred to the RNA induced silencing complex (RISC) which searches for mRNA with a sequence matching that of the fragment strand. When detected, this mRNA is degraded.

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**********380**********

**A.** Common in cancer cells is a mutation of the gene that codes for the protein p53, whose role is to detect and repair errors in DNA and, if repairs cannot be made, initiate apoptosis. **Create a visual representation** to **explain** how the DICER-RISC system within the cell can be used to suppress the translation of a mutated form of the gene coding for p53, potentially destroying a tumor.

**B.** Whole genome sequences provide a library of potentially expressed proteins, but they do not provide information on the functions of each protein. In an approach called reverse genetics, investigations attempt to determine the function of the gene, often by silencing the gene using RNAi technology. Assume that you have the ability to synthesize dsRNA from a DNA segment taken from an organism whose whole genome has been determined. **Design a plan** for collecting data that could be used to assign a function to the protein encoded by this sequence. (Hint—Do not worry about the number of experiments that might need to be conducted to implement your plan. An automated technique called high throughput screening robotically supports thousands of simultaneous experiments.)

**Solution** Sample answers:

**A.** Because the sequence coding for the mutant p53 is known, a dsRNA complementing this template can be constructed and introduced with a viral vector. When the dsRNA is recognized, the DICER-RISC machinery will repress the mutant. This technology was applied to this problem in 2014.

**B.** A dsRNA is constructed using the desired sequence as the template. Cells (probably using a surrogate such as yeast) are exposed. Any suspected function can be evaluated by presenting the appropriate substrate and looking for reaction products or growing the cells on nutrient media and looking for the absence of product.

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