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Unit 5 - Week 3: Genome Analysis (Part 2)

Course outline

How to access the portal

Pre-requisite Assignment

Week 1: Introduction to Functional Genomics

Week 2: Genome Analysis (Part 1)

Week 3: Genome Analysis (Part 2)

- Lecture 09: Genome Sequence Databases (unit? unit=21&lesson=22)
- Lecture 10: DNA Sequencing Methods (Part 1) (unit? unit=21&lesson=23)
- Lecture 11: DNA Sequencing Methods (Part

Assignment week 3

The due date for submitting this assignment has passed. **Due on 2019-09-18, 23:59 IST.**
As per our records you have not submitted this assignment.

1) Which one of the following statements is NOT true with regard to the cycle sequencing method, which is based on the Sanger's method of DNA sequencing? **1 point**

- DNA amplification in cycle sequencing is done by PCR using a pair of primers
- During the PCR, the growing chain will be terminated when ddNTP is incorporated into a new strand
- Dideoxy ribose doesn't contain hydroxyl group at both 2' as well as at 3' carbon in the ribose sugar
- Base sequences derived from the sequencing reaction are reverse complementary to the template sequence

No, the answer is incorrect.
Score: 0

Accepted Answers:

DNA amplification in cycle sequencing is done by PCR using a pair of primers

2) Identify the INCORRECT statement with regard to the steps involved in the next generation sequencing methods: **1 point**

- Adapters are used to create libraries
- Clusters are used to create libraries
- Every DNA fragment generated from the species is ligated
- Each cluster represents several identical copies of DNA

No, the answer is incorrect.
Score: 0

Accepted Answers:

Clusters are used to create libraries

3) Identify the option which distinguishes next-gen sequencing from the first-gen sequencing: **1 point**

2) (unit? unit=21&lesson=24)

Lecture 12: Applications of Next-Generation Sequencing (NGS) (unit? unit=21&lesson=25)

Lecture 13: Tutorial (Session 1) (unit? unit=21&lesson=26)

Lecture 14: Tutorial (Session 2) (unit? unit=21&lesson=27)

Quiz : Assignment week 3 (assessment? name=48)

Feedback For Week 3 (unit? unit=21&lesson=57)

Assignment solution - week 3 (unit? unit=21&lesson=60)

Week 4: Comparative Genomics

Text Transcripts

Live Session

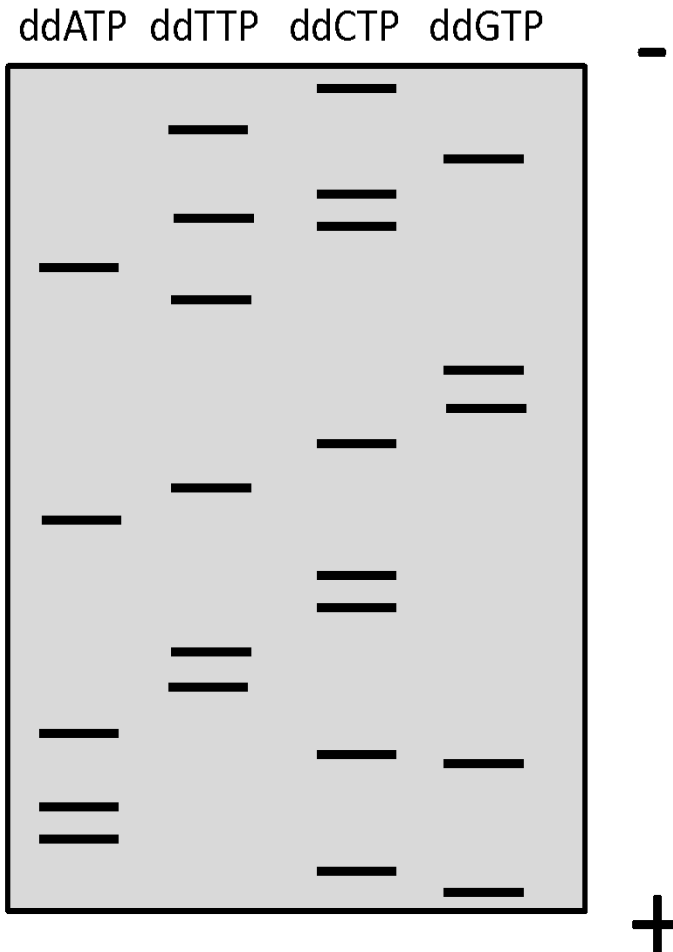
- First-gen sequencing method sequences a single DNA fragment per run while the next-gen method sequences millions of fragments per run
- First-gen sequencing method uses only the cDNA as template while Next-gen method uses genomic DNA
- First-gen sequencing method uses single strand DNA while Next gen uses double-stranded DNA as the template
- All of these

No, the answer is incorrect.
Score: 0

Accepted Answers:

First-gen sequencing method sequences a single DNA fragment per run while the next-gen method sequences millions of fragments per run

4) Shown here is a schematic of the image for a DNA sequencing gel using the Sanger method. **1 point**
Based on your understanding of the methodology, identify the option that shows the DNA sequence of the template strand



- 5'-CTGCTCATGGCTACCTTACGAACG-3'
- 5'-GACGAGTACCGATGGAATGCTTGC-3'
- 5'-GCAAGCATTCCATCGGTACTCGTC-3'
- 5'-CGTTCGTAAGGTAGCCATGAGCAG-3'

No, the answer is incorrect.

Score: 0

Accepted Answers:

5'-GACGAGTACCGATGGAATGCTTGC-3'

5) Both Maxam Gilbert method and the Sanger method were used for the sequencing purpose. **1 point**
Which one of the following statements correctly identifies the difference between these two?

- Maxam Gilbert method is a chemical based sequencing method while Sanger method is based on enzymes
- Sanger method can be used to sequence both genomic DNA and the cDNA while the Maxam Gilbert method cannot be used for cDNA
- Maxam Gilbert method can use RNA as the template while Sanger method can only use DNA as template
- None of these

No, the answer is incorrect.

Score: 0

Accepted Answers:

Maxam Gilbert method is a chemical based sequencing method while Sanger method is based on enzyme.

6) A sequencing method where the visible light, generated by the luciferin-mediated reaction, is **1 point**
collected as the raw data and the base sequences are called. The type of sequencing method being referred to

- Sanger's dideoxy method
- Maxam-Gilbert chemical method
- Pyrosequencing
- None of these

No, the answer is incorrect.

Score: 0

Accepted Answers:

Pyrosequencing

7) Which one of the following methods can be used to analyse the DNA-protein interaction? **1 point**

- Microarray
- Chromatin immunoprecipitation
- DNA fingerprinting
- in situ* hybridization

No, the answer is incorrect.

Score: 0

Accepted Answers:

Chromatin immunoprecipitation

8) Which one of the following options correctly identifies the direct outcome of "genome revolution"? **1 point**

- Identification of conserved gene sequences
- Understanding global regulation of the gene expression
- Genetic variation across species
- All of these

No, the answer is incorrect.

Score: 0

Accepted Answers:

All of these

9) Which one of the following statements is TRUE with regard to the identification of fetal genome in the maternal body fluids using a non-invasive genomic method? **1 point**

- Polymerase chain reaction with a pair of primers for a conserved gene can easily identify the fetal DNA
- Next-Gen Sequencing methods are sensitive enough to identify fetal DNA for known paternally-derived mutations
- Karyotyping of cells derived from the amniotic fluid can identify chromosomal disorders
- Chromatin immuno-precipitation to identify interaction between fetal DNA and maternal protein

No, the answer is incorrect.

Score: 0

Accepted Answers:

Next-Gen Sequencing methods are sensitive enough to identify fetal DNA for known paternally-derived mutations

10) Which one of the following options is TRUE with regard to the statement “Chromatin or DNA modifications can alter the gene function”? **1 point**

- DNA methylation can modulate gene expression
- “Open chromatin” correlates with expression of genes in that region
- Chromatin of enhancer element regions of active genes are often acetylated
- All of these

No, the answer is incorrect.

Score: 0

Accepted Answers:

All of these