Question Paper Name:	PGD BIG DATA AND PHD Computaional Biology TRACK 2 30th May 2019 Shift 1 Set1
Subject Name:	PGD BIG DATA AND PHD Computaional Biology TRACK 2
Creation Date:	2019-05-30 13:50:39
Duration:	180
Total Marks:	100
Display Marks:	Yes
Share Answer Key With Delivery Engine:	Yes
Actual Answer Key:	Yes

PGD BIG DATA AND PHD Computaional Biology TRACK 2

Group Number :	1
Group Id :	128206195
Group Maximum Duration :	0
Group Minimum Duration :	180
Revisit allowed for view? :	No
Revisit allowed for edit? :	No
Break time:	0
Group Marks:	100

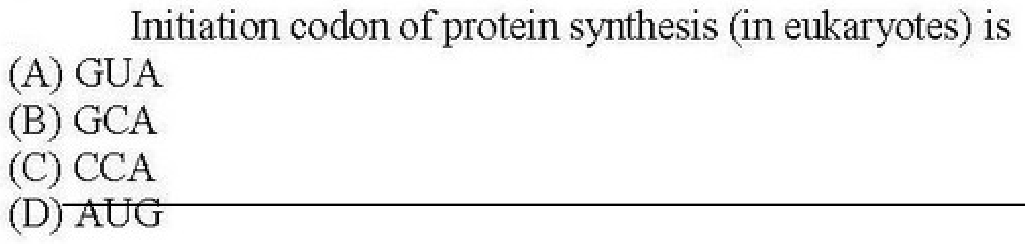
Part-A

Section Id :	128206331
Section Number :	1
Section type :	Online
Mandatory or Optional:	Mandatory
Number of Questions:	15
Number of Questions to be attempted:	15
Section Marks:	30
Display Number Panel:	Yes
Group All Questions:	No

Sub-Section Number:	1
Sub-Section Id:	128206530
Question Shuffling Allowed :	Yes

Question Number : 1 Question Id : 12820611496 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0



Initiation codon of protein synthesis (in eukaryotes) is

(A) GUA
(B) GCA
(C) CCA
(D) AUG

Options :

431. A

12820645432. B

12820645433. C

12820645434. D

Question Number : 2 Question Id : 12820611497 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

Evaluation of phylogenetic trees is done by

(A) Probability
(B) Null hypothesis
(C) Bootstrapping
(D) Chi square

Options :

12820645435. A

12820645436. B

12820645437. C

12820645438. D

Question Number : 3 Question Id : 12820611498 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

Best method to determine paternity is

(A) Protein analysis
(B) Chromosome counting
(C) Gene counting
(D) DNA finger printing

Options :

12820645439. A

12820645440. B

12820645441. C

12820645442. D

Question Number : 4 Question Id : 12820611499 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

Plasmids are vectors for gene cloning because they

(A) Self replicate in bacterial cells
(B) Replicate freely outside bacterial cells
(C) Can be multiplied in culture
(D) Can be multiplied in laboratories using enzymes

Options :

12820645443. A

12820645444. B

12820645445. C

12820645446. D

Question Number : 5 Question Id : 12820611500 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Two bacteria found to be very useful in genetic engineering experiments are
(A) Nitrobacter and Azotobacter
(B) Rhizobium and Diplococcus
(C) Nitrosomonas and Kliebsiella
(D) Escherichia and Agrobacterium

Options :
12820645447. A
12820645448. B
12820645449. C
12820645450. D

Question Number : 6 Question Id : 12820611501 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

In tissue / bacterial culture glassware and nutrients are sterilized through
(A) Water bath at 200° C
(B) Dry air oven at 200° C
(C) Dehumidifier
(D) Autoclave

Options :
12820645451. A
12820645452. B
12820645453. C
12820645454. D

Question Number : 7 Question Id : 12820611502 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

A gene sequence given to you consists of 600 nucleotides of 5'-UTR, 600 nucleotides of open reading frame and 300 nucleotides of 3'-UTR. The protein coded by this gene would consist of
(A) 200 amino acids
(B) 199 amino acids
(C) 198 amino acids
(D) 600 amino acids

Options :
12820645455. A
12820645456. B
12820645457. C
12820645458. D

Question Number : 8 Question Id : 12820611503 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

stX is used to
(A) Search protein database for a translated nucleotide query
(B) Search nucleotide database for a protein sequence query
(C) Search a translated nucleotide database for a translated nucleotide query
(D) Search protein database for a protein sequence query

Options :
12820645459. A
12820645460. B
12820645461. C
12820645462. D

Question Number : 9 Question Id : 12820611504 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following is untrue about DNA sequencing?
(A) It is now routinely carried out using the Sanger method
(B) This doesn't make use of DNA polymerases
(C) This involves synthesis of DNA chains of varying length
(D) The DNA synthesis is stopped by adding dideoxynucleotides

Options :
12820645463. A
12820645464. B
12820645465. C
12820645466. D

Question Number : 10 Question Id : 12820611505 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following is amino acid may be considered helix breaker due to its low probability to form an alpha helix?
(A) Arginine
(B) Trypotophan
(C) Lysine
(D) Proline

Options :
12820645467. A
12820645468. B
12820645469. C
12820645470. D

Question Number : 11 Question Id : 12820611506 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0


ence distance between two residues forming hydrogen bond as a part of beta strand is
(A) 4 residues
(B) 3 residues
(C) 10 residues
(D) is not fixed

Options :

12820645471. A

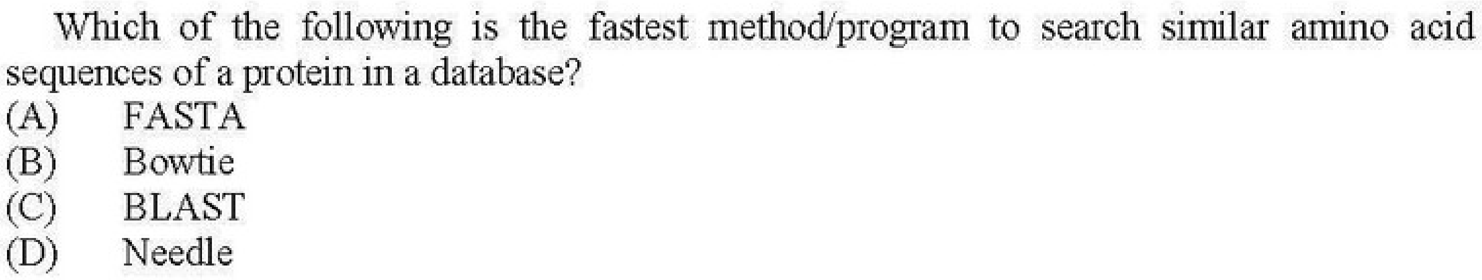
12820645472. B

12820645473. C

12820645474. D

Question Number : 12 Question Id : 12820611507 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0


Which of the following is the fastest method/program to search similar amino acid sequences of a protein in a database?
(A) FASTA
(B) Bowtie
(C) BLAST
(D) Needle

Options :

12820645475. A

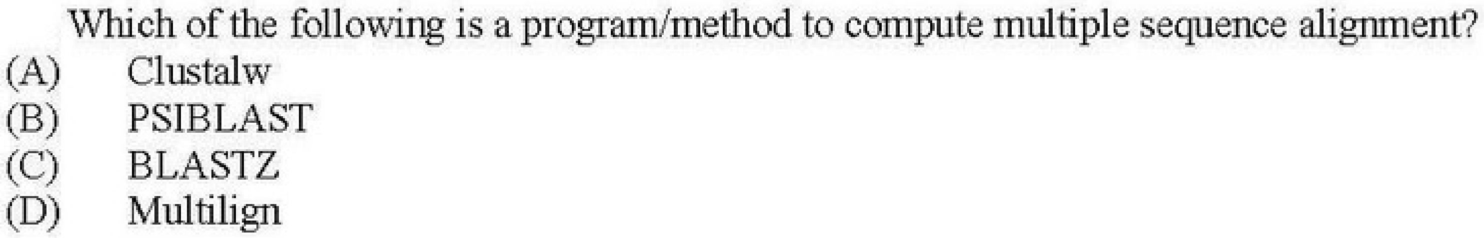
12820645476. B

12820645477. C

12820645478. D

Question Number : 13 Question Id : 12820611508 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0


Which of the following is a program/method to compute multiple sequence alignment?
(A) Clustalw
(B) PSIBLAST
(C) BLASTZ
(D) Multilign

Options :

12820645479. A

12820645480. B

12820645481. C

12820645482. D

Question Number : 14 Question Id : 12820611509 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

amino acid residues in a protein are polymerized by
(A) Peptide bond
(B) Hydrogen bond
(C) Electrostatic forces
(D) Hydrophobic forces

Options :

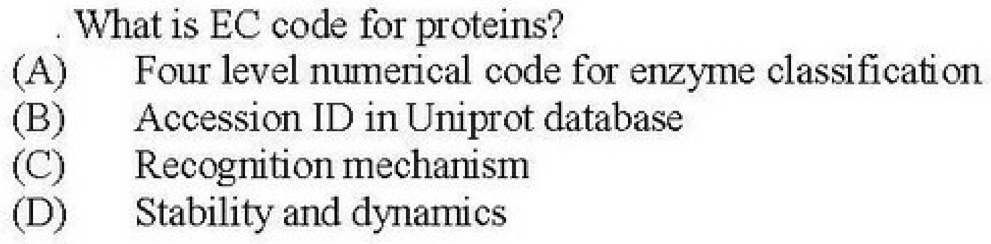
12820645483. A

12820645484. B

12820645485. C

12820645486. D

Question Number : 15 Question Id : 12820611510 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0



. What is EC code for proteins?
(A) Four level numerical code for enzyme classification
(B) Accession ID in Uniprot database
(C) Recognition mechanism
(D) Stability and dynamics

Options :

12820645487. A

12820645488. B

12820645489. C

12820645490. D

Part-B Life Sciences

Section Id :	128206332
Section Number :	2
Section type :	Online
Mandatory or Optional:	Optional
Number of Questions:	35
Number of Questions to be attempted:	35
Section Marks:	70
Display Number Panel:	Yes
Group All Questions:	No

Sub-Section Number:	1
Sub-Section Id:	128206531
Question Shuffling Allowed :	Yes

Question Number : 16 Question Id : 12820611511 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which one of the following statements about protein separation by gel filtration is correct?

(A) When a mixture of proteins is separated by gel filtration, the smallest molecular weight protein is eluted first.
(B) When a mixture of proteins is separated by gel filtration, the largest molecular weight protein is eluted first.
(C) When a mixture of proteins is separated by gel filtration, the mid-size molecular weight protein is eluted last.
(D) When a mixture of proteins is separated by gel filtration, the smallest molecular weight proteins sticks to the beads.

Options :

12820645491. A
12820645492. B
12820645493. C
12820645494. D

Question Number : 17 Question Id : 12820611512 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

In case of parasites that require multiple hosts to complete their life cycle, what does definitive host mean?

(A) It is the host that harbours the sexual stages of the parasite
(B) It is the host in which the parasite reproduces sexually
(C) It is the host in which the parasite feeds
(D) It is the host in which the parasite remains in dormant stage.

Options :

12820645495. A
12820645496. B
12820645497. C
12820645498. D

Question Number : 18 Question Id : 12820611513 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Conversion of nitrite to nitrate in soil is done by the bacteria

(A) Azotobacter
(B) Nitrosomonas
(C) Nitrobacter
(D) Pseudomonas

Options :

12820645499. A
12820645500. B
12820645501. C
12820645502. D

Question Number : 19 Question Id : 12820611514 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following vectors can carry the longest piece of foreign DNA ?

(A) plasmids
(B) bacteriophage
(C) cosmids
(D) yeast artificial chromosome

Options :

12820645503. A
12820645504. B
12820645505. C
12820645506. D

Question Number : 20 Question Id : 12820611515 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

A messenger RNA is 336 bases long including the initiation and termination codon. The number of amino acids in polypeptide translated from this is

(A) 110
(B) 333
(C) 111
(D) 600

Options :

12820645507. A
12820645508. B
12820645509. C
12820645510. D

Question Number : 21 Question Id : 12820611516 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

As you increase the n (number of measurements) in an experiment, which quantity do you expect to decrease?

(A) mean
(B) correlation
(C) standard error of the mean
(D) both b and c

Options :

12820645511. A
12820645512. B
12820645513. C
12820645514. D

Question Number : 22 Question Id : 12820611517 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

s consider three independently assorting autosomal genes in Drosophila: A,B and C. What is the probability that a female of genotype AaBBCc when crossed to a male of AAbbCc will produce an offspring of genotype AABbcc?

(A) ½
(B) ¼
(C) 1/8
(D) 1/16

Options :

12820645515. A

12820645516. B

12820645517. C

12820645518. D

Question Number : 23 Question Id : 12820611518 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

What is true for monoclonal antibodies?

(A) These are obtained from one parent & for one antigen.
(B) These are obtained from many parents & for many antigen.
(C) These are obtained from different parents & for one antigen.
(D) These are obtained from one parent & for many antigens.

Options :

12820645519. A

12820645520. B

12820645521. C

12820645522. D

Question Number : 24 Question Id : 12820611519 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

Which of the following is an amino acid found in proteins and has a negative charge at normal pH values?

(A) Arginine
(B) Lysine
(C) Asparigine
(D) Glutamic acid

Options :

12820645523. A

12820645524. B

12820645525. C

12820645526. D

Question Number : 25 Question Id : 12820611520 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

icillin resistant bacteria produce beta-lactamase which inactivates penicillin by
(A) Esterifying the carboxyl group
(B) Oxidizing S atom
(C) Hydrolyzing the side chain
(D) hydrolyzing the C-N bond

Options :
12820645527. A
12820645528. B
12820645529. C
12820645530. D

Question Number : 26 Question Id : 12820611521 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following techniques can be used to accurately measure the molecular weight of protein?
(A) NMR
(B) Size exclusion chromatography
(C) Mass spectrometry
(D) Analytical ultra centrifugation.

Options :
12820645531. A
12820645532. B
12820645533. C
12820645534. D

Question Number : 27 Question Id : 12820611522 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Introduction of foreign genes for improving genotype is
(A) Tissue culture
(B) Immunisation
(C) Biotechnology
(D) Genetic engineering

Options :
12820645535. A
12820645536. B
12820645537. C
12820645538. D

Question Number : 28 Question Id : 12820611523 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

A replication in eukaryotes commences
(A) From both ends of a chromosome simultaneously
(B) Several sites along DNA of a chromosome simultaneously
(C) From centromere to either end
(D) From one end of chromosome to the other

Options :
12820645539. A
12820645540. B
12820645541. C
12820645542. D

Question Number : 29 Question Id : 12820611524 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Amino acid binding site of tRNA is
(A) 5'end
(B) Anticodon loop
(C) DHU loop
(D) -CCA 3'end

Options :
12820645543. A
12820645544. B
12820645545. C
12820645546. D

Question Number : 30 Question Id : 12820611525 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

The alignment procedure that tries to align the entire sequence is
(A) multiple sequence alignment
(B) pair wise alignment
(C) global alignment
(D) local alignment

Options :
12820645547. A
12820645548. B
12820645549. C
12820645550. D

Question Number : 31 Question Id : 12820611526 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Haploid plant cultures are obtained from
(A) Leaves
(B) Root tip
(C) Pollen grain
(D) Buds

Options :
12820645551. A
12820645552. B
12820645553. C
12820645554. D

Question Number : 32 Question Id : 12820611527 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Viruses are
(A) obligate parasites
(B) Free living
(C) Both free living and parasitic
(D) None of these

Options :
12820645555. A
12820645556. B
12820645557. C
12820645558. D

Question Number : 33 Question Id : 12820611528 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

The primary structure of protein represents
(A) linear sequence of amino acids joined by peptide bond
(B) 3D structure of protein
(C) helical structure of protein
(D) Subunit structure of protein

Options :
12820645559. A
12820645560. B
12820645561. C
12820645562. D

Question Number : 34 Question Id : 12820611529 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

The 3 D structure of protein can be determined by
(A) NMR
(B) X ray crystallography
(C) both a and b
(D) spectroscopy

Options :
12820645563. A
12820645564. B
12820645565. C
12820645566. D

Question Number : 35 Question Id : 12820611530 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

During gel electrophoresis, where will you find the smallest segments of DNA?
(A) near the positive electrode, far away from the wells.
(B) near the negative electrode, close to the wells.
(C) near the top
(D) in the middle

Options :
12820645567. A
12820645568. B
12820645569. C
12820645570. D

Question Number : 36 Question Id : 12820611531 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

The colonies of recombinant bacteria appear white in contrast to blue colonies of non-recombinant bacteria because of
(A) Insertional inactivation of beta-galactosidase in recombinant bacteria
(B) Inactivation of glycosidase in recombinant bacteria.
(C) Recombinant bacteria containing beta-galactosidase.
(D) Insertional inactivation of alpha-galactosidase in non-recombinant bacteria.

Options :
12820645571. A
12820645572. B
12820645573. C
12820645574. D

Question Number : 37 Question Id : 12820611532 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

n advantage of discontinuous buffer system in SDS and native PAGE is
(A) confirmation of protein is conserved
(B) constantly maintains charge of proteins
(C) Assists in migration of proteins
(D) Enhance resolution of separation

Options :
12820645575. A
12820645576. B
12820645577. C
12820645578. D

Question Number : 38 Question Id : 12820611533 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Yeast one-hybrid assay is used for screening
(A) Protein-protein interactions
(B) DNA-Protein interactions
(C) DNA-DNA interactions
(D) DNA-RNA interactions

Options :
12820645579. A
12820645580. B
12820645581. C
12820645582. D

Question Number : 39 Question Id : 12820611534 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following is not a method to estimate the levels of mRNA quantitatively?
(A) 30 cycles of RT-PCR
(B) RNase protection assay
(C) RNA-seq
(D) Microarray

Options :
12820645583. A
12820645584. B
12820645585. C
12820645586. D

Question Number : 40 Question Id : 12820611535 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

SNPs generally are the cause of
(A) Genetic variation
(B) Maternal inheritance
(C) Non-mendelian inheritance
(D) Acquired resistance

12820645587. A

12820645588. B

12820645589. C

12820645590. D

Question Number : 41 Question Id : 12820611536 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following formats is used for storing sequence data and corresponding quality scores?
(A) FASTA
(B) FASTQ
(C) FASTAP
(D) FASTA-NGS

Options :

12820645591. A

12820645592. B

12820645593. C

12820645594. D

Question Number : 42 Question Id : 12820611537 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

A gene with more than one allele is termed as
(A) heterologous
(B) hybrid
(C) pleiotropic
(D) polymorphic

Options :

12820645595. A

12820645596. B

12820645597. C

12820645598. D

Question Number : 43 Question Id : 12820611538 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Cluster analysis in DNA microarray experiment refer to
(A) genes that are clustered together in the genome
(B) cluster of probes that are used to monitor gene expression
(C) genes that are likely to work in concert in the cell
(D) cluster of cDNAs printed on microarray chip

Options :

12820645599. A

12820645600. B

12820645601. C

12820645602. D

Question Number : 44 Question Id : 12820611539 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Small nucleolar RNA (snoRNA) is involved in
(A) inhibition of translation from mRNA
(B) processing of mRNA
(C) processing of pre-rRNA to mature rRNA species
(D) site-specific base modifications in rRNA

Options :
12820645603. A
12820645604. B
12820645605. C
12820645606. D

Question Number : 45 Question Id : 12820611540 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

A protein made up of two identical subunits having MW of 60 kDa, when resolved on SDS-polyacrylamide gel will show how many protein bands after proper staining and destaining?
(A) single band of 60 kDa
(B) two bands of 30 kDa each
(C) single band of 30 kDa
(D) two bands of 60 kDa each

Options :
12820645607. A
12820645608. B
12820645609. C
12820645610. D

Question Number : 46 Question Id : 12820611541 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following markers is based on mRNA?
(A) RFLP
(B) SNP
(C) SSR
(D) EST

Options :
12820645611. A
12820645612. B
12820645613. C
12820645614. D

Question Number : 47 Question Id : 12820611542 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

nment method that tries to align the entire sequence is?
(A) multiple sequence alignment
(B) pair wise alignment
(C) global alignment
(D) local alignment

Options :
12820645615. A
12820645616. B
12820645617. C
12820645618. D

Question Number : 48 Question Id : 12820611543 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Human genome contains about 21,000 genes but the number of proteins in human cell is estimated to be 250,000, which of the following explain this
(A) Alternative splicing and post translational modifications
(B) Alternative splicing and protein folding
(C) Post transcriptional silencing
(D) Multiple promoters and operons

Options :
12820645619. A
12820645620. B
12820645621. C
12820645622. D

Question Number : 49 Question Id : 12820611544 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Isoschizomers are the restriction endonucleases that have
(A) different recognition and cleavage sites.
(B) different recognition and similar cleavage sites
(C) same recognition and cleavage sites
(D) same recognition and different cleavage sites

Options :
12820645623. A
12820645624. B
12820645625. C
12820645626. D

Question Number : 50 Question Id : 12820611545 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

f the following crop genomes is the largest in size?
(A) chickpea
(B) tomato
(C) rice
(D) wheat

Options :

12820645627. A

12820645628. B

12820645629. C

12820645630. D

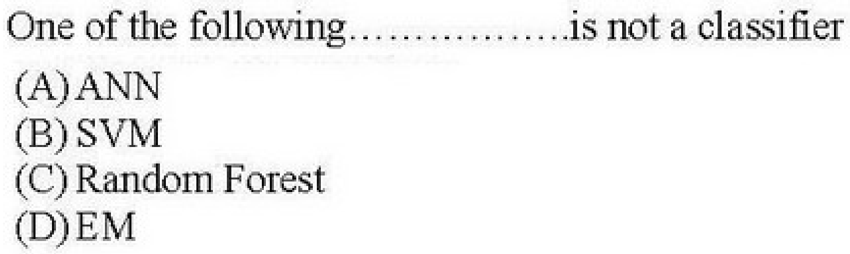
Part-B Bioinformatics

Section Id :	128206333
Section Number :	3
Section type :	Online
Mandatory or Optional:	Optional
Number of Questions:	35
Number of Questions to be attempted:	35
Section Marks:	70
Display Number Panel:	Yes
Group All Questions:	No

Sub-Section Number:	1
Sub-Section Id:	128206332
Question Shuffling Allowed :	Yes

Question Number : 51 Question Id : 12820611546 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0



One of the following.................is not a classifier
(A) ANN
(B) SVM
(C) Random Forest
(D) EM

Options :

12820645631. A

12820645632. B

12820645633. C

12820645634. D

Question Number : 52 Question Id : 12820611547 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

n "progressive alignment" is related to ....

(A) pairwise global alignment

(B) pairwise local alignment

(C) multiple alignment

(D) read alignment

Options :

12820645635. A

12820645636. B

12820645637. C

12820645638. D

Question Number : 53 Question Id : 12820611548 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

What does RPKM counts obtained in RNA sequencing experiment stand for

(A) Reads per K-Mers

(B) Reads per kilobase per million

(C) Reads per kilobase per machine

(D) Reads per kilobyte and Megabyte

Options :

12820645639. A

12820645640. B

12820645641. C

12820645642. D

Question Number : 54 Question Id : 12820611549 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

Which of the following is NOT contained in FASTQ formatted NGS data?

(A) Genomic alignments

(B) Sequence quality

(C) Read length

(D) Information about individual read

Options :

12820645643. A

12820645644. B

12820645645. C

12820645646. D

Question Number : 55 Question Id : 12820611550 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

. Which of the following is not a secondary structure of protein?

(A) Bend

(B) 3-10 helix

(C) Beta hairpin

(D) Helical Kink

647. A

12820645648. B

12820645649. C

12820645650. D

Question Number : 56 Question Id : 12820611551 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

Pathway enrichment means

(A) More genes than expected in a gene list coming from that pathway
(B) Addition of new genes to a given pathway
(C) Many pathways being activated
(D) Over-expression of all genes from that pathway in an experiment

Options :

12820645651. A

12820645652. B

12820645653. C

12820645654. D

Question Number : 57 Question Id : 12820611552 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

In a broad sense, at what threshold of sequence similarity a good homology model (ignoring loops and side chain orientations) can be developed (choose the lowest value applicable)?

(A) 10% sequence identity
(B) 30% sequence identity
(C) 80% sequence identity
(D) 100% sequence identity

Options :

12820645655. A

12820645656. B

12820645657. C

12820645658. D

Question Number : 58 Question Id : 12820611553 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical

Correct Marks : 2 Wrong Marks : 0

Bioconductor packages can be installed using

(A) BiocLite
(B) BioMart
(C) Genome browser
(D) Standard R interface

Options :

12820645659. A

12820645660. B

12820645661. C

12820645662. D

Question Number : 59 Question Id : 12820611554 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following techniques produces most accurate estimates of gene expression?
(A) Hybridization based Microarray
(B) RNA-Seq
(C) ChIP-Seq
(D) RT-PCR

Options :
12820645663. A
12820645664. B
12820645665. C
12820645666. D

Question Number : 60 Question Id : 12820611555 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

. Cross-validation of a predictive model is used to
(A) Increase the generalization of a predictive model
(B) Improve predictive performance
(C) Increase the training data
(D) Creating new features from a data

Options :
12820645667. A
12820645668. B
12820645669. C
12820645670. D

Question Number : 61 Question Id : 12820611556 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following software can be used to generate *de novo* sequence motif from ChIP-Seq data of a transcription factor?
(A) MEME
(B) DAVID
(C) Transfac
(D) JASPAR

Options :
12820645671. A
12820645672. B
12820645673. C
12820645674. D

Question Number : 62 Question Id : 12820611557 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

olecular dynamics simulations, which of the following is NOT a force field?

(A) AMBER
(B) CHARMM
(C) GROMACS
(D) OPLS

Options :
12820645675. A
12820645676. B
12820645677. C
12820645678. D

Question Number : 63 Question Id : 12820611558 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Technologies that uses single molecule real time sequencing is
(A) Illumina
(B) Nanopore
(C) Ion Torrent
(D) ABI-SOLiD

Options :
12820645679. A
12820645680. B
12820645681. C
12820645682. D

Question Number : 64 Question Id : 12820611559 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

A Phred score of 30 in DNA sequencing means probability of incorrect base call as
(A) 1 in 100
(B) 1 in 1000
(C) 1 in 10000
(D) 1 in 100000

Options :
12820645683. A
12820645684. B
12820645685. C
12820645686. D

Question Number : 65 Question Id : 12820611560 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

During genome assembly, scaffolds are obtained after
(A) assembly of reads
(B) sequencing DNA or RNA
(C) arranging contigs in order
(D) after indexing

12820645687. A
12820645688. B
12820645689. C
12820645690. D

Question Number : 66 Question Id : 12820611561 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following algorithm is NOT used to generate phylogenetic tree from molecular data?

(A) Parsimony
(B) Monogamy
(C) Neighbor-joining
(D) Maximum likelihood

Options :
12820645691. A
12820645692. B
12820645693. C
12820645694. D

Question Number : 67 Question Id : 12820611562 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

. Which of the following program can be used to compute the secondary structure of a protein from atomic coordinates?

(A) DSSP
(B) Uniprot
(C) Modeller
(D) ASAView

Options :
12820645695. A
12820645696. B
12820645697. C
12820645698. D

Question Number : 68 Question Id : 12820611563 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

ENCODE expands to
(A) Entire Compendium of DNA Elements
(B) Encyclopedia of DNA Elements
(C) Encyclopedia of Disaster Estimates
(D) Encyclopedia of Disease Estimates

Options :
12820645699. A
12820645700. B

701. C
12820645702. D

Question Number : 69 Question Id : 12820611564 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

What does quaternary structure of a protein involve?
(A) The association of two or more peptide chain
(B) The complete three-dimensional conformation
(C) Partial denaturation
(D) Random coil alternating with alpha helix

Options :
12820645703. A
12820645704. B
12820645705. C
12820645706. D

Question Number : 70 Question Id : 12820611565 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which of the following is incorrect about Oligonucleotide Design in A microarray?
(A) DNA microarrays are generated by fixing oligonucleotides onto a solid support
(B) The oligonucleotide array slide represents thousands of preselected genes from an organism
(C) The length of oligonucleotides is typically in the range of twenty-five to seventy bases long
(D) The oligonucleotides don’t react with cDNA samples

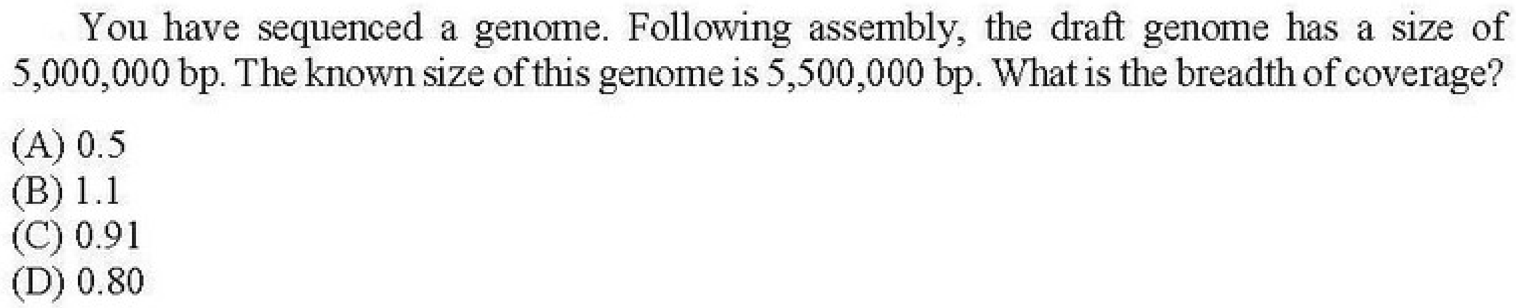
Options :
12820645707. A
12820645708. B
12820645709. C
12820645710. D

Question Number : 71 Question Id : 12820611566 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

Which file format is used for storing the sequence data of assembled genomes (draft and finished)?
(A) Sanger format
(B) FASTQ format
(C) Illumina format
(D) FASTA format

Options :
12820645711. A
12820645712. B
12820645713. C
12820645714. D

Question Number : 72 Question Id : 12820611567 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0



You have sequenced a genome. Following assembly, the draft genome has a size of 5,000,000 bp. The known size of this genome is 5,500,000 bp. What is the breadth of coverage?

(A) 0.5
(B) 1.1
(C) 0.91
(D) 0.80

Options :

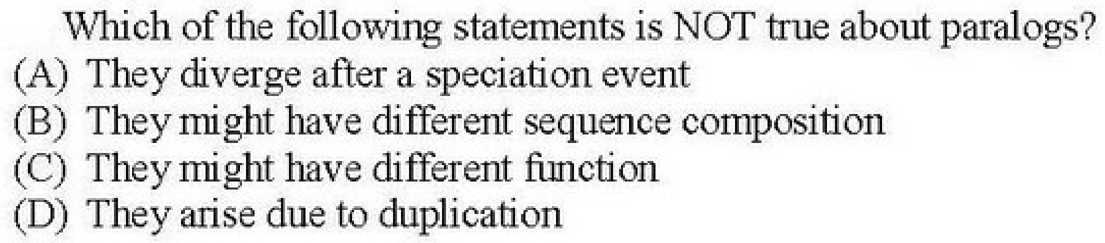
12820645715. A

12820645716. B

12820645717. C

12820645718. D

Question Number : 73 Question Id : 12820611568 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0



Which of the following statements is NOT true about paralogs?
(A) They diverge after a speciation event
(B) They might have different sequence composition
(C) They might have different function
(D) They arise due to duplication

Options :

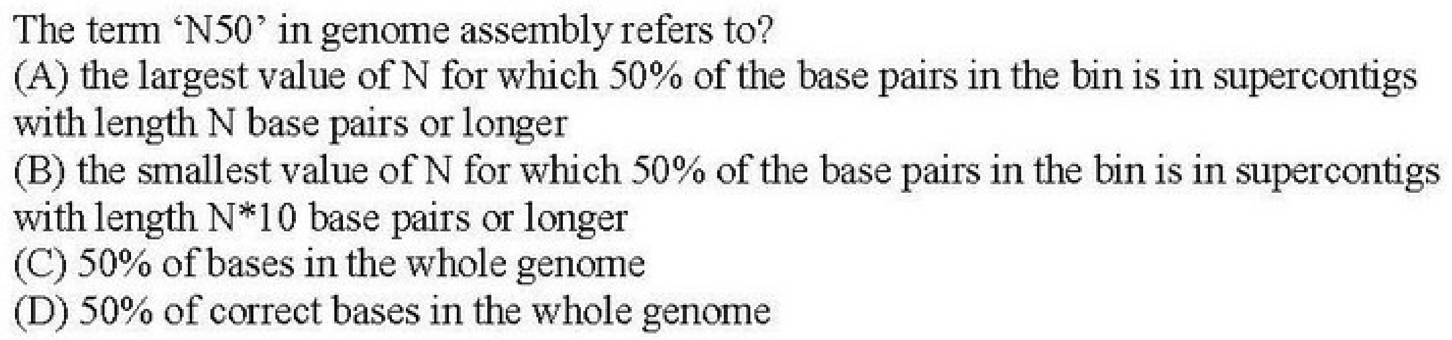
12820645719. A

12820645720. B

12820645721. C

12820645722. D

Question Number : 74 Question Id : 12820611569 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0



The term ‘N50’ in genome assembly refers to?
(A) the largest value of N for which 50% of the base pairs in the bin is in supercontigs with length N base pairs or longer
(B) the smallest value of N for which 50% of the base pairs in the bin is in supercontigs with length N*10 base pairs or longer
(C) 50% of bases in the whole genome
(D) 50% of correct bases in the whole genome

Options :

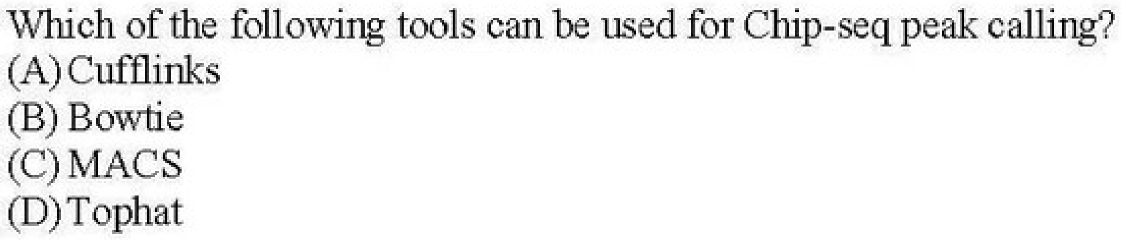
12820645723. A

12820645724. B

12820645725. C

12820645726. D

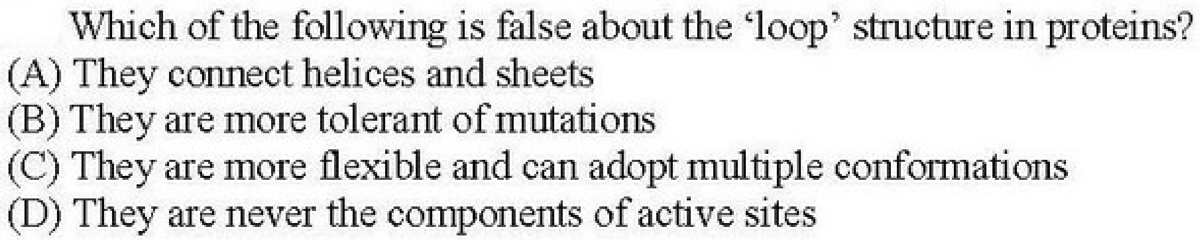
mber : 75 Question Id : 128206115 0 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0



Which of the following tools can be used for Chip-seq peak calling?
(A) Cufflinks
(B) Bowtie
(C) MACS
(D) Tophat

Options :
12820645727. A
12820645728. B
12820645729. C
12820645730. D

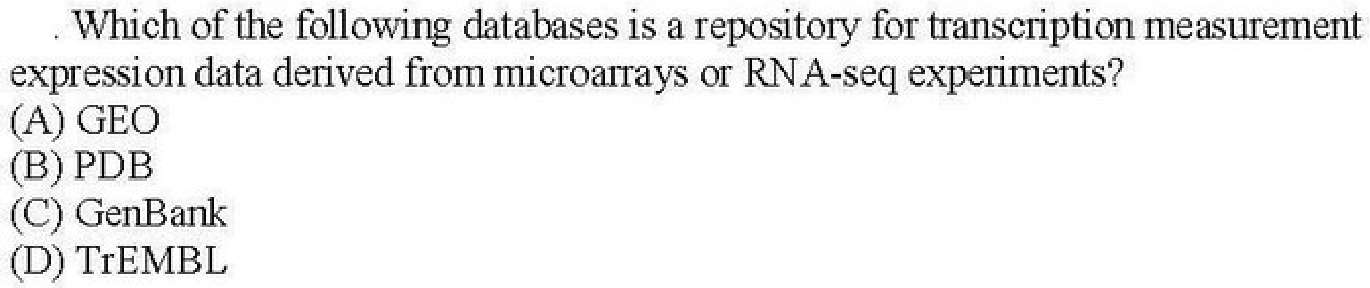
Question Number : 76 Question Id : 12820611571 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0



Which of the following is false about the 'loop' structure in proteins?
(A) They connect helices and sheets
(B) They are more tolerant of mutations
(C) They are more flexible and can adopt multiple conformations
(D) They are never the components of active sites

Options :
12820645731. A
12820645732. B
12820645733. C
12820645734. D

Question Number : 77 Question Id : 12820611572 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0



. Which of the following databases is a repository for transcription measurement expression data derived from microarrays or RNA-seq experiments?
(A) GEO
(B) PDB
(C) GenBank
(D) TrEMBL

Options :
12820645735. A
12820645736. B
12820645737. C
12820645738. D

Question Number : 78 Question Id : 12820611573 Question Type : MCQ Option Shuffling : No Display Question Number : Yes
Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

ch of the following definitions is completely correct?
(A) BLOSUM (Blocks Substitution Matrix) is a scoring matrix for sequence alignment derived from closely related global alignments in the BLOCKS database. The BLOSUM62 matrix is derived from alignments containing 62% identity, and is most commonly used
(B) PET91 (Pair Exchange table for year 1991) was developed by Jones, Taylor and Thornton and derived from sequences clustered at 85% similarity from 2621 protein families. It corrects for mutations that were poorly represented in the original Dayhoff matrix
(C) PAM (Percentage Accepted Mutation) matrix is derived from PAM1 - which estimates the rate at which 1% of amino acids are mutated. PAM250 is derived by multiplying this matrix by itself 250 times. The PAM alignments are based on stretches of local alignments forbidden to contain gaps
(D) The BLOSUM and PAM matrices can be used interchangeably, with the higher number used for scoring sequences which are less divergent. BLOSUM90 and PAM250 are used for detecting nearly identical sequences, while BLOSUM45 and PAM100 are used for weak similarities

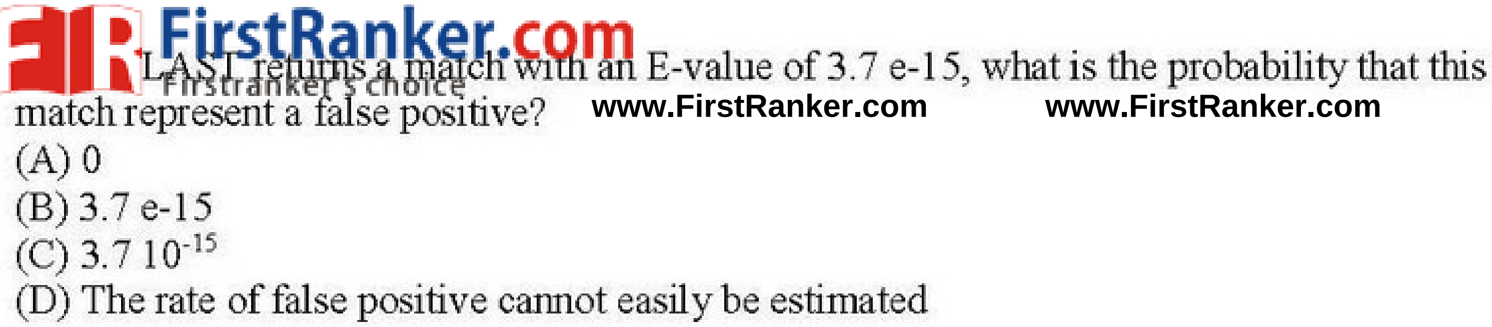
Options :
12820645739. A
12820645740. B
12820645741. C
12820645742. D

Question Number : 79 Question Id : 12820611574 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0

If you want to BLAST the non-redundant database using a new nucleotide sequence as query, which is the BEST search program to use to find its putative function?
(A) BLASTP
(B) BLASTN
(C) BLASTQ
(D) BLASTX

Options :
12820645743. A
12820645744. B
12820645745. C
12820645746. D

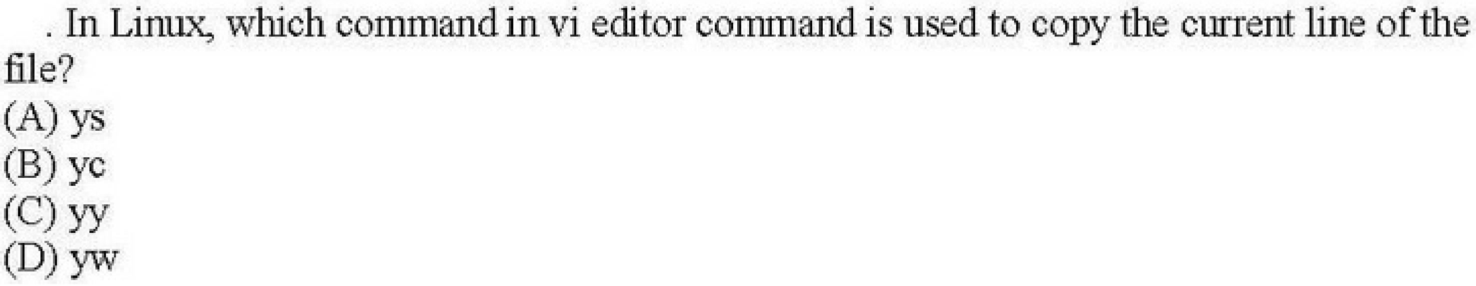
Question Number : 80 Question Id : 12820611575 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0



LAST returns a match with an E-value of 3.7 e-15, what is the probability that this match represent a false positive?
(A) 0
(B) 3.7 e-15
(C) 3.7 10^{-15}
(D) The rate of false positive cannot easily be estimated

Options :
12820645747. A
12820645748. B
12820645749. C
12820645750. D

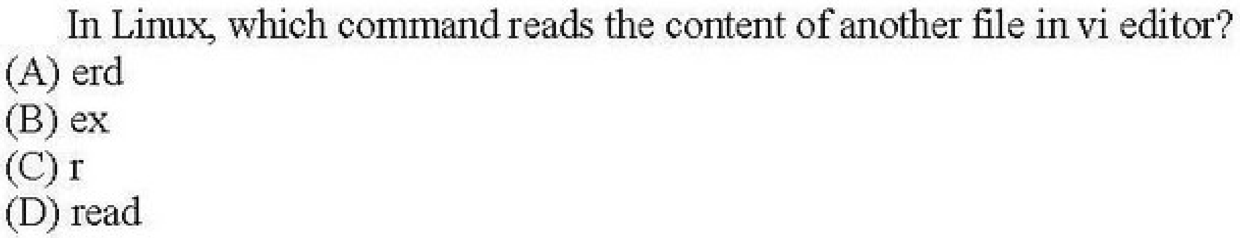
Question Number : 81 Question Id : 12820611576 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0



. In Linux, which command in vi editor command is used to copy the current line of the file?
(A) ys
(B) yc
(C) yy
(D) yw

Options :
12820645751. A
12820645752. B
12820645753. C
12820645754. D

Question Number : 82 Question Id : 12820611577 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0



In Linux, which command reads the content of another file in vi editor?
(A) erd
(B) ex
(C) r
(D) read

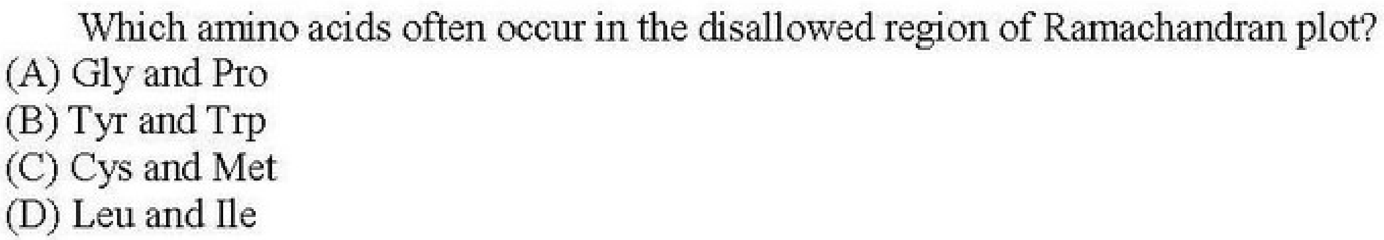
Options :
12820645755. A
12820645756. B
12820645757. C
12820645758. D

Question Number : 83 Question Id : 12820611578 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0


ch is the following is most high throughput assay for analyzing variants at whole genome level is?
(A) Genotyping
(B) Sequencing
(C) Arrays
(D) Karyotyping

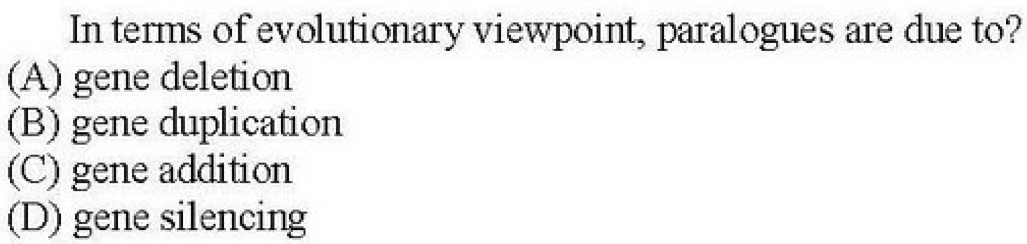
Options :
12820645759. A
12820645760. B
12820645761. C
12820645762. D

Question Number : 84 Question Id : 12820611579 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0


Which amino acids often occur in the disallowed region of Ramachandran plot?
(A) Gly and Pro
(B) Tyr and Trp
(C) Cys and Met
(D) Leu and Ile

Options :
12820645763. A
12820645764. B
12820645765. C
12820645766. D

Question Number : 85 Question Id : 12820611580 Question Type : MCQ Option Shuffling : No Display Question Number : Yes Single Line Question Option : No Option Orientation : Vertical
Correct Marks : 2 Wrong Marks : 0


In terms of evolutionary viewpoint, paralogues are due to?
(A) gene deletion
(B) gene duplication
(C) gene addition
(D) gene silencing

Options :
12820645767. A
12820645768. B
12820645769. C
12820645770. D