bif 501

note swiss port 2

limitation of ab intio 2

why sanger awaed noble prize 2

challenge of limitation 3

why bac used for sequence 3

digital revolution

fasta and BBRF formats and example 3

fragment aessmbly algorithms 5

target discovery aapproach 5

Endosymbiont hypothesis 5

RNA structure function typre and processed RNA 10

mcq gene expression .... mrna , microarry , all these

repeated questions mostly. RNA details is must. 10 marks ⍰

new questions :-

partial digest algorithm with actual values 5 marks ☺ and knuth morris algorithm 5 marks.

bif

PDGF stands

  Hmm stands

: Which rna converted into protein

: Hamming distance - ---- technology for dna similarity

: Genomic rearrangements results in change of....

: Uniprot is database of protein....

: Motif facilitate for binding....

: A drug target..... Protein

: HGP revealed that.... Disease are hereditary

: Nation spectral similarity shared peak count....

..... Is good for gapped alignment

: When sanger sequence insulin....????

  Needleman alignment published in....????

Size fragment can be ligated into BAC vector

  Programming language for modellers....

  Brute force is called....

  3D-1D bowie algorithm at el in.....

..... Help in finding global minimum

bif501

Insertions. Dels. Deletions diffrence

2. Ab initio challenges

3. Error in fragment reads

4. Y we use genome animation.

5. Define pharmacology and pharmagenomics and its application

6. What is simple score and alignment

7. What is method to score alignment how it is calculated give example.

8. Why we use shotgun sequence

9. Rna structure definition types function processing and secondary structure and prediction.

Bif501

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BIF 501

1:Write a short note on cystic fibrosis gene? 2mks

2: Limitation of Ab-Initio method? 2

3: Why we are interested to obtaining superstrings? 2

4: Explain spiceosome? 3mks

5: Explian the following function with example:

DELETE(y, L)? 3

6: Explain the digital resolution in recent time? 3

7: List the stop and start codons and their functions? 5mrks

8: Write two approaches of target discovery? 5

9: Find the prefix function of pattern using KMP Algorithm? 5

10: RNA,RNA Structure, its types with functions,Secondary structure and how we predict and RNA processing?

BIF 501

edit distance? With examples

RNA structure, types, processing,

Start and stop codon

KMP Matcher

Two target approaches

Method for four different groups sequencing

Digital resolution

Limitations of Ab initio

Challenges of AB initio

Q.1 explain RNA(definition,structure,secondary structure,prediction,types of RNA and their function etc). 10 marks.

Q.2 needleman-wunsch algorithm complete (5 marks)

Q.3 write and explain 2 approaches of target discovery (5 marks).

Q.4 explain gene expression omnibus (5 marks)

Q.5 challenges of ab initio modelling (3 marks)

Q.6 why Edman degradation strategy was failed in protein identification.(3 marks)

Q.7 longest common subsequence problem (only single strip) with example (3 marks)

Q.8 define pharmacology and pharmacogenomics and write three applications of pharmacogenomics (3 marks)

Q.9 what is primary medical database??? list four databases.(2 marks)

Q.10 how sanger method solved Edman degradation problemof protein identification (2 marks)

Q.11 differentiate b/w supervised and unsupervised machine learning (2 marks)

Mcqs

mcqs from ab initio modelling, RNA structure, chou fasman algorithm, DNAsequencing pharmacogenomics homolgy modelling, orthology paralogy,