BIF501-Bioinformatics-II   MCQs FINAL TERM (PAST PAPERS)

1. Lcs scoring mechanism is for _____ **sequence similarity analysis**

2. Physiological base approach _____ **disease centric**

3. An association rule has two parts _____ **if and then**

4. Transfer of gene among organism is called _____ **horizontal gene transfer**

5. Eco R1 break down DNA at _____ **GAATTC**

6. Programming language used for modeler _____ **Python**

7. It is to compute the prefix function _____ **O(m)**

8. Prob used by sequencing in hybridization have size _____ 8-32

9. Which is correct _____ homology vs paralogy + orthology

10. _____ helps in finding global alignment _____ Needleman wunsch

11. Brute force algorithm use every possible ……….. to find the solution _____ l mer

12. LCS scoring award 1 for _____ **match**

13. …….. programming approach does not require prior sequence alignment_____ **dynamic** programming

14. Brute force is a _____ motif finding problem

15. DNA array is also known as _____ DNA chip

16. GCG stand for _____ **Genetics Computer Group**

17. Gene mapping is determining the ······ on chromosome _____ **location**

18. MS2 genom has _____ amino acid _____129

19. Method use fr lesd validation_____ virtual screening

20. Use for embryonic development _____ *Homeobox* **genes**

21. concerned with the effect of genetic factors on reactions to drugs _____ Pharmacogenetics

22. Sequence in EMBL formate start with _____ SQ

23. an ordered sequence of symbols _____ pattern

24. deletion in alignment in Edit graph shows _____ east (horizontal arrow)

25. how many methods for lead validation? _____ 5

26. Chou fasman algorithm helps to find _____ 2ndary structure of protein

27. Plant mitochondria contain genes _____ 150 – 200kb

28. Brut force is an ……. Pattern finding algorithm _____ **Approximation algorithm**

29. Which identify the structure with minimum free energy _____ **Ab initio**

30. Length of each line for FASTA algorithm should be _____ **shorter than 80 or (60)**

31. Genome rearrangement results in a change of _____ **gene ordering**

32. Human genome consist of repeats _____ 20 %

33. Responsible for protein function _____ protein structure

34. ······ pattern matches with *k* mismatches or differences _____ **approximate**

35. We look for molecule which need to be selected as target and those molecule that cause disease
_____ target discovery

36. GEO for _____ gene expression omnibus

37. Intron start from5 end is ········ ans 3´ end is ········ _____ GT , AG

38. SINE are ········ bp long _____80 – 300

39. Needle man publicsh in _____ 1970

40. Chou fasman algorithm was 1st used in _____ 1974 – 1978

41. The notion of spectral similarity with shared peaks count _____ P1, P2-S1 and S2

42. Human genome project _____ 1988

43. TCGGGATTTCC is in drosophila for activate _____ immunity

44. BLOSUM 6 is good for _____ un gaped alignment

45. Disease that are hereditary _____ 3000 – 4000

46. Computational technique use for protein not present in database _____ Denovo

47. Motif are found in _____**promoter**

Objective:

1. Waardenburg syndrome is a genetic disorder found in _____ Human
2. Fourth step of homology modeling is _____ Loop modeling
3. The notion of spectral similarity with shared peaks counts is _____ P1,P2-S1, S2
4. Number of methods for target validation are _____ 5
5. 3D 1D algorithm was proposed by bowie et al in _____ 1991
6. AG and GT are _____ Exon flanking dinucleotide
7. Paralogs genes originated from _____ Rare gene duplication
8. ORF stands for _____ Open reading frame
9. PAM stands for _____ Point accepted mutation
10. GEO stands for _____ Gene Expression Omnibus
11. _____ % of sequence is unique enough to differentiate people.   0.01%
12. In Chou Fasman algorithm, Alpha helix is formed from 4 contagious amino acids having propensity over _____ 1 .
13. methods for lead validation _____ Genome sequencing and screening
14. MS2 has _____ codons? 49
15. TIGR stand for what _____ The institute of genome research
16. Bypass is a type of _____ Branch and Bound algorithm.
17. Simple motif search lgorithm based on _____ Next vertex
18. Systic fibrosis gene is found on the chromosome No. _____ 7
19. Genome rearrangement results in change of gene _____ Order
20. Consensus score is define as _____ Score(s DNA)
21. Next vertex algorithm provides an output _____ Next subtree
22. Median string problem is one of the way to find _____ Motif
23. Restriction enzyme breaks DNA molecules at _____ specific location
24. Motifs facilitates for binding _____ Transcription factor
25. Regulatory motif are generally found _____ Promoter region of DNA.
26. Gel electrophoresis is used to measure _____ of restriction fragments. ___Size___