

**STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI 600 086**  
(For candidates admitted from the academic year 2004-2005 & thereafter)

**SUBJECT CODE: BT/MO/IB64**

**B.Sc. DEGREE EXAMINATION, APRIL 2009**  
**BRANCH V(a) – PLANT BIOLOGY AND PLANT BIOTECHNOLOGY**  
**SIXTH SEMESTER**

**COURSE : MAJOR – OPTIONAL**  
**PAPER : INTRODUCTION TO BIOINFORMATICS**  
**TIME : 3 HOURS** **MAX. MARKS: 100**

**SECTION –A**

**ANSWER ALL QUESTIONS**

**( 18 x 1 = 18 )**

**I. FILL IN THE BLANKS**

1. Identifying \_\_\_\_\_ is the simple first step in gene finding.
2. One method of Optical mapping is \_\_\_\_\_.
3. The DNA sequence of BamH1 is \_\_\_\_\_.
4. \_\_\_\_\_ is a structural database.
5. BLOSUM Substitution Scoring Matrix was created by \_\_\_\_\_ in 1992.
6. \_\_\_\_\_ and \_\_\_\_\_ are the stop codons.

**II. EXPAND THE FOLLOWING**

7. FISH
8. BLAST
9. EMBL
10. DDBJ
11. STS
12. ESTs

**III. STATE WHETHER TRUE OR FALSE:**

13. Contig maps are low –resolution physical maps.
14. DOCK is a programme used for visualizing interacting molecules.
15. All proteins have a motif.
16. A number with the PAM1 matrix refers evolutionary distance of 1.
17. Needleman – Wunsch Method is a method of Local alignment of sequences.
18. The functional part of the protein is the small portions called as the active site.

