**Assignment – II**

**Deadline: 25-08-20**

1. The enzymes BamH I and Bal II recognise different sequences but leave the same sticky ends:

BamH I: ----------G|G A T C C ------

Bal II: ----------A|G A T C T ------

(i)Will the two enzymes result in the same number of fragments in a random DNA sequence? Give reasons.

(ii)What’s the advantage of having such a pair of REs? Explain with example.

1. Both cloning and PCR can be used for making copies of DNA. What is the advantage or limitation of one over the other?
2. What is role of (i) primer, (ii) Taq polymerase, and (iii) ddNTPs in sequencing by PCR?
3. An unknown DNA sequence is cloned in a vector. How would you design primers for sequencing the insert sequence?
4. What is the major advantage of RNA sequencing by NGS approach compared to cDNA sequencing?