Question 1: X-ray diffraction data helps measure _____.

    Phi and angles
    C-Alpha atoms
    Protein structure
✅ Atomic positions

Question 2: In GenBank, specific gene can be searched by using?

    Sequence ID
    Name
    Species
✅ All of the given

Question 3: The putative ORF can be translated into a protein sequence, which is then used to search against a protein database.

    TRUE
✅ FALSE

Question 4: The scoring of gaps in a MSA (Multiple Sequence Alignment) has to be performed in a different manner from scoring gaps in a pair-wise alignment?

✅ TRUE
    FALSE

Question 5: The _____ tool compares nucleotide sequence against DNA database.

✅ blastn
    blastp
    blastx
    tblastn

Question 6: Nussinov-Jacobson (NJ) Algorithm is a dynamic Programming (DP) strategy to predict _____.

    Stabilizing energies
    Destabilizing energies
✅ Optimal RNA 2' structures
    Optimal RNA 3' structures

Question 7: Name any two frequently used scoring matrices

    BLAST & FASTA