

Activity 2: Identification of an Unknown Biological Sequence Using BLAST

Tool Used: NCBI BLAST

Sequence Analyzed: Sequence 3 (Protein Sequence)

Step 1: Observation of the Given Sequence

The given sequence contains amino acid characters such as M, G, L, F, W, I and V, indicating that it is a protein sequence.

Prediction: The given sequence is a Protein sequence.

Step 2: Selection of BLAST Program

Since the sequence is a protein sequence, BLASTp was used for analysis on the NCBI BLAST platform.

Step 3: BLAST Analysis

The protein sequence was pasted into the BLASTp query box and searched using default parameters against the NCBI protein database.

Step 4: Identification of the Best Match

The top BLAST hit showed high similarity with a membrane-associated protein from Escherichia coli. The result showed high percentage identity and an E-value of 0.0, indicating a strong match.

Step 5: Alignment Verification

The alignment showed large matching regions with minimal gaps, confirming the reliability of the BLAST result.

Step 6: Identification of Biological Function

The identified protein plays an important role in membrane structure and transport-related biological processes.

Step 7: Classification and Interpretation

The sequence is a protein from a prokaryotic organism and appears to be conserved across related bacterial species.

Step 8: Final Conclusion

The given unknown sequence is identified as a membrane-associated protein from Escherichia coli. BLAST analysis revealed a high percentage identity with an E-value of 0.0, indicating a strong and reliable match.