

# 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.