

Protocol: Molecular Diagnosis Using BLAST (Starting from a FASTA File)

This protocol guides students through **sequence identification** using **BLAST** (Basic Local Alignment Search Tool) to diagnose unknown sequences (e.g., pathogens, genes).

Step 1: Prepare Your Sequence

Input: A FASTA file (query.fasta) containing your unknown sequence.

Example:

```
>Unknown_Sequence_1
```

```
ATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGC...
```

Step 2: Choose a BLAST Method

Option A: Online BLAST (NCBI Web Service, No Installation Required)

◆ Best for quick, small-scale analysis

1. Go to <https://blast.ncbi.nlm.nih.gov/>
2. Upload query.fasta or paste the sequence.
3. Select the appropriate BLAST program:
 - **BLASTn** (for DNA vs. DNA)
 - **BLASTp** (for protein vs. protein)
4. Choose a database (e.g., nr for nucleotides, RefSeq for curated sequences).
5. Click **BLAST** and wait for results.