

Computational Analysis of Unknown Sequence by Bioinformatics Tools

DNA Analysis

The screenshot shows the National Library of Medicine BLAST search interface. The search results for the query sequence MJ82KMHV034 are displayed. The search parameters include:

- Job Title: RBD
- Program: BLASTN
- Database: core_nt
- Query ID: IclQuery_669787
- Description: None
- Molecule type: dna
- Query Length: 1960
- Other reports: Distance tree of results, MSA viewer

The results table lists two significant alignments:

Descriptor	Scientific Name	Max Score	Total Score	Cover	E value	Per cent	Avg Len	Assessor
Streptomyces laevigatus	Streptomyces laevigatus	3621	3625	100%	0.0	100.00%	803264	
Streptomyces sp. NCI_3025	Streptomyces sp. NCI_3025	2167	2279	100%	0.0	85.79%	803064	

RNA Analysis

The RNAfold WebServer interface displays the results for the minimum free energy prediction of the RNA sequence. It shows two predicted RNA structures with colored base-pairing probabilities. The color scale indicates the probability of base pairing, ranging from green (low probability) to red (high probability).

Protein Analysis

Number of amino acids: 336 Theoretical pI: 5.19
Molecular weight: 35934.81

Sub Cellular Localization

The TargetP-2.0 analysis tool interface shows the results for a single protein sequence. The summary table indicates a Non-Plant localization with a score of 0.8917. The detailed protein information table includes columns for Protein type, Other, Signal peptide, and Mitochondrial transfer peptide.

Protein type	Other	Signal peptide	Mitochondrial transfer peptide
Unpredicted	0.8917	None	None

The Results of the k-NN Prediction tool interface shows the top 10 nearest neighbors for the protein. The table lists the neighbor ID, name, and E-value.

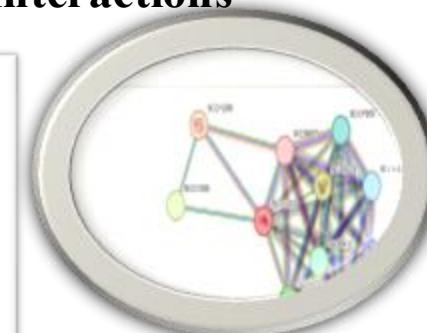
Rank	Neighbor	E-value
1	NP_001456.1	0.000000
2	NP_001457.1	0.000000
3	NP_001458.1	0.000000
4	NP_001459.1	0.000000
5	NP_001460.1	0.000000
6	NP_001461.1	0.000000
7	NP_001462.1	0.000000
8	NP_001463.1	0.000000
9	NP_001464.1	0.000000
10	NP_001465.1	0.000000

Phylogenetics Analysis

The phylogenetic tree diagram illustrates the evolutionary relationships between various protein sequences. The tree is rooted at the bottom and branches upwards, with each node labeled with a protein identifier and its source species.

- RP_901040.1 MULTISPICES cytochrome P450 [unclassified Stepmyces]
- NP_001459.1
- NP_001460.1
- NP_001461.1 cytochrome P450 [Stepmyces sp. NPSC064C]
- NP_001462.1
- NP_001463.1 cytochrome P450 [Stepmyces sp. NPDC064C]

Protein Protein Interactions



TOOLS

NCBI BLAST
ORF Finder
ExPASy ProtParam
InterPro
RNAfold
STRING
Clustal Omega
MEGA Web