

nucleotide ► nucleotide

protein ► protein

translated nucleotide ► protein

protein ► translated nucleotide

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By

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Question No.1

The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches.

Basic Programs of Blast:

1. Blastn

Nucleotide-nucleotide BLAST (blastn) – This program, given a DNA query, returns the most similar DNA sequences from the DNA database that the user specifies.

Uses:

Mapping oligonucleotides, cDNAs, and PCR products to a genome; screening repetitive elements; cross-species sequence exploration; annotating genomic DNA; clustering sequencing reads; vector clipping.

2.Blastp

Protein-protein BLAST (blastp) – This program, given a protein query, returns the most similar protein sequences from the protein database that the user specifies. [?]

Position-Specific Iterative BLAST (PSI- BLAST) (blastpgp) – This program is used to find distant relatives of a protein.

Uses:

Identifying common regions between proteins; collecting related proteins for phylogenetic analyses.

3.Blastx

Nucleotide 6-frame translation-protein (blastx) -This program compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database.

Uses:

Finding protein-coding genes in genomic DNA; determining if a cDNA corresponds to a known protein.

4.tblastx

Nucleotide 6-frame translation-nucleotide 6-frame translation (tblastx) -The purpose of tblastx is to find very distant relationships between nucleotide sequences.

Uses:

Cross-species gene prediction at the genome or transcript level; searching for genes missed by traditional methods or not yet in protein databases.

5.tblastn

Protein-nucleotide 6-frame translation (tblastn) -This program compares a protein query against the all six reading frames of a nucleotide sequence database.

Uses:

Identifying transcripts, potentially from multiple organisms, similar to a given protein; mapping a protein to genomic DNA.

Question No.2

tblastx will be used to search a nucleotide sequence to another nucleotide sequence encoded for similar protein.

Regards:

VU Expert Zoologists: