

18-12-2021

EXPERIMENT NO: 03

AIM OF THE EXPERIMENT: To perform pair-wise alignment of sequences (BLAST) and interpret the output.

THEORY:

Basic Local Alignment Search Tool (BLAST) is an online algorithm that is used to find similar sequences available in publicly available databases for a particular query sequence. Using BLAST one can find homologous sequences or may identify a new gene.

BLAST is available as an open access tool maintained by NCBI based on the query sequence and the target database. BLAST is classified as follows -

① BLAST-n (Nucleotide BLAST):

Here the query sequence as well as target database are nucleotide.

② BLAST-p (Protein BLAST):

Here the query sequence as well as target database are protein sequence.

③ BLAST-x :

Here the query sequence is a nucleotide sequence which is first translated into an amino acid sequence and the target database is protein sequence database.

④ t-BLAST-n :

Query is a protein sequence which is aligned with nucleotide sequence databases following translation of the latter.

MATERIALS: Computer, Internet, Copy etc.

PROCEDURE:

- ① Using google chrome browser the NCBI BLAST website was opened.
- ② We select BLAST-x and provide the following sequence as query which was copied and pasted.

BLAST parameters:

- ① Genetic code type selected 'standard'
- ② Database was selected to be 'Non-redundant protein sequence.'
- ③ Other parameters were kept as default.
- ④ 'BLAST' was hit/clicked.

RESULTS:

Sequence identity and similarity:

- ① Length of query sequence: 276
- ② Types of the query: DNA.

Our query sequence is 100% similar with accession number 0912534A of somatoliberin precursor of Homo sapiens.

The query coverage is 72% of the above accession number.

Percent identity is 100%

Length of aligned: 103

Number of Matches: 1