

BLAST is used to generate alignment between query and protein sequence within a database. There are five different BLAST searches. Different suffix represents different outcome for each search. Suffix P refers to protein, N refers to nucleotide, X refers to a DNA query that translated into six protein sequences, and T refers to translating. BLASTP compares a protein query to a database query. BLASTN compares both strands of DNA query against a DNA database. BLASTX translate a DNA sequence six protein sequence using all reading frames. TBLASTN is used to translate every DNA sequence into six protein sequence and then compare the protein query against each of those translated proteins. TBLASTX translates DNA from both a query and a database into six potential protein, then perform protein database search.

Before generating outcome, there are few optional parameter that are important to know. Limiting organism section is important because it help to improve efficiency of BLAST search and results are easier to interpret since database grows fast in size. Select appropriate scoring matrix is also important since it indicate the the local alignment boundaries increasing or decreasing the length of the optimal local alignment reduces the total alignment score. Word size determines the length of exact match so that we will have more accurate result. A grid that provides scores for the substitution of every nucleotide for every other. They are used to score the substitution of one residue for another in a protein alignment. Gap penalty is a method of scoring alignment of two or more sequence. The gap allow algorithm to match more term.

Max score is the highest alignment score for match amino acid and penalties for mismatches and gaps. Total score is the sum of alignment scores of all segments from the same subject sequence. Query coverage is the percentage of the sequence aligned to a sequence in database. E value describe the random background noise. Max indent is the highest percent identity for a set of aligned segments to the same subject sequence.