

Using tBLASTx to Identify a gene by using its DNA Sequence (DNA-DNA BLAST)

-tBLASTx is a gene prediction tool.

-This tool converts a **nucleotide query sequence** into **protein sequence** in all 6 reading frames.

-Then **compare** this to an NCBI nucleotide database which has been translated on all six reading frames.

Translated BLAST: tblastx

blastn blastp blastx tblastn **tblastx**

TBLASTX search translated nucleotide databases using a translated nucleotide query. [more...](#) [Reset page](#) [Bookmark](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) Query subrange [From](#) [To](#)

```
GGCATGAAAGTCAGGGCAGAGCCATCTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCAAC
CTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGT
GAACGTGGATGAAGTTGGTGGTGGCCCTGGGCAAGTTGGTATCAAGTTACAAGACAGGTTTAAGGAG
ACCAATAGAAACTGGGCATGTGGAGACAGAGAAGACTCTTGGGTTCTGATAGGCACTGACTCTCTGTC
CTATTGGTCTATTTCCACCCTTAGGCTGCTGGTGGTCTACCCTGGACCCAGAGGTTCTTTGAGTCCT
```

Or, upload file Dosya seçilmedi [Genetic code](#) [Job Title](#)

Align two or more sequences [Enter a descriptive title for your BLAST search](#)

Choose Search Set

Database [Organism](#) Exclude [Exclude](#) [+](#)

[Optional](#) Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [Exclude](#)

[Optional](#) Models (XM/XP) Uncultured/environmental sample sequences

[Optional](#) Sequences from type material

[Optional](#) [Entrez Query](#) [YouTube](#) [Create custom database](#)

[Optional](#) Enter an Entrez query to limit search [Entrez Query](#)

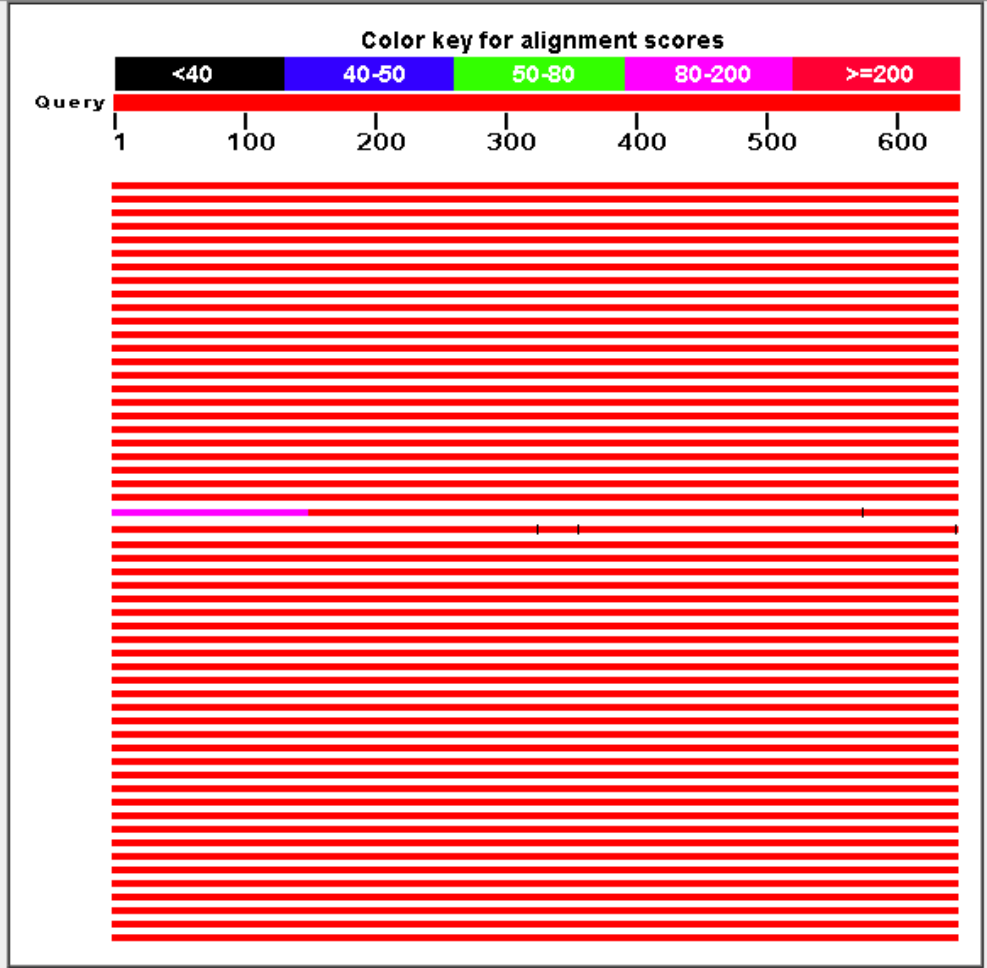
Search database **Nucleotide collection (nr/nt)** using **Tblastx** (Search translated nucleotide databases using a translated nucleotide query)

Show results in a new window

[+ Algorithm parameters](#)

Distribution of 947 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments



Alignments

Download GenBank Graphics Sort by: E value Next Previous Descriptions

Homo sapiens hemoglobin (HBB) gene, promoter region, exons 1, 2 and partial cds

Sequence ID: [gb|DQ659148.1](#) Length: 646 Number of Matches: 7

Range 1: 2 to 646 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Positives	Gaps	Frame
517 bits(1123)	2e-143	215/215(100%)	215/215(100%)	0/215(0%)	-1/-1

Query 646 NHSSVSHSKLYPVTSP... 467

Sbjct 646 NHSSVSHSKLYPVTSP... 467

Query 466 ALEVVQVSQAITK... 287

Sbjct 466 ALEVVQVSQAITK... 287

Query 286 Q*AERVSAYQPK... 107

Sbjct 286 Q*AERVSAYQPK... 107

Query 106 PQESGAPWCLFE... 2

Sbjct 106 PQESGAPWCLFE... 2

Range 2: 2 to 646 GenBank Graphics Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps	Frame
500 bits(1087)	2e-138	215/215(100%)	215/215(100%)	0/215(0%)	+2/+2

Query 2 A*KSGQSHLLLT... 181

Sbjct 2 A*KSGQSHLLLT... 181

Query 182 YQGYKTGLRRP... 361

Sbjct 182 YQGYKTGLRRP... 361

Query 362 STPDAMGNPKV... 541

Sbjct 362 STPDAMGNPKV... 541

Query 542 DP*CFLSPSFL... 646

Sbjct 542 DP*CFLSPSFL... 646

Related Information

- [Gene](#) - associated gene details
- [GEO Profiles](#) - microarray expression data
- [Map Viewer](#) - aligned genomic context

Using tBLASTn (Translated BLAST/protein-DNA BLAST)

- Search **translated nucleotide** database using a **protein** query
- TBLASTN operates by translating database nucleotide sequences to hypothetical amino acid sequences in all six reading frames and then aligning the hypothetical amino acid sequences to the query.
- It takes your protein, translates the DNA databases in all 6 frames, and searches the protein against the (now translated) databases.

- Search;
 - Protein ID: Q9BDJ6.1/FASTA
- tBLASTn
- ESTs
- Exclude Bos taurus

In general, the way to remember things is this:

- 't' at the front stands for 'translated': the query sequence will be translated in 6 frames.
- 'x' at the back means 'protein': whatever the sequence database *is*, it will be translated into protein for the search.
- 'n' at the back means 'DNA': the database being searched is a nucleotide database.

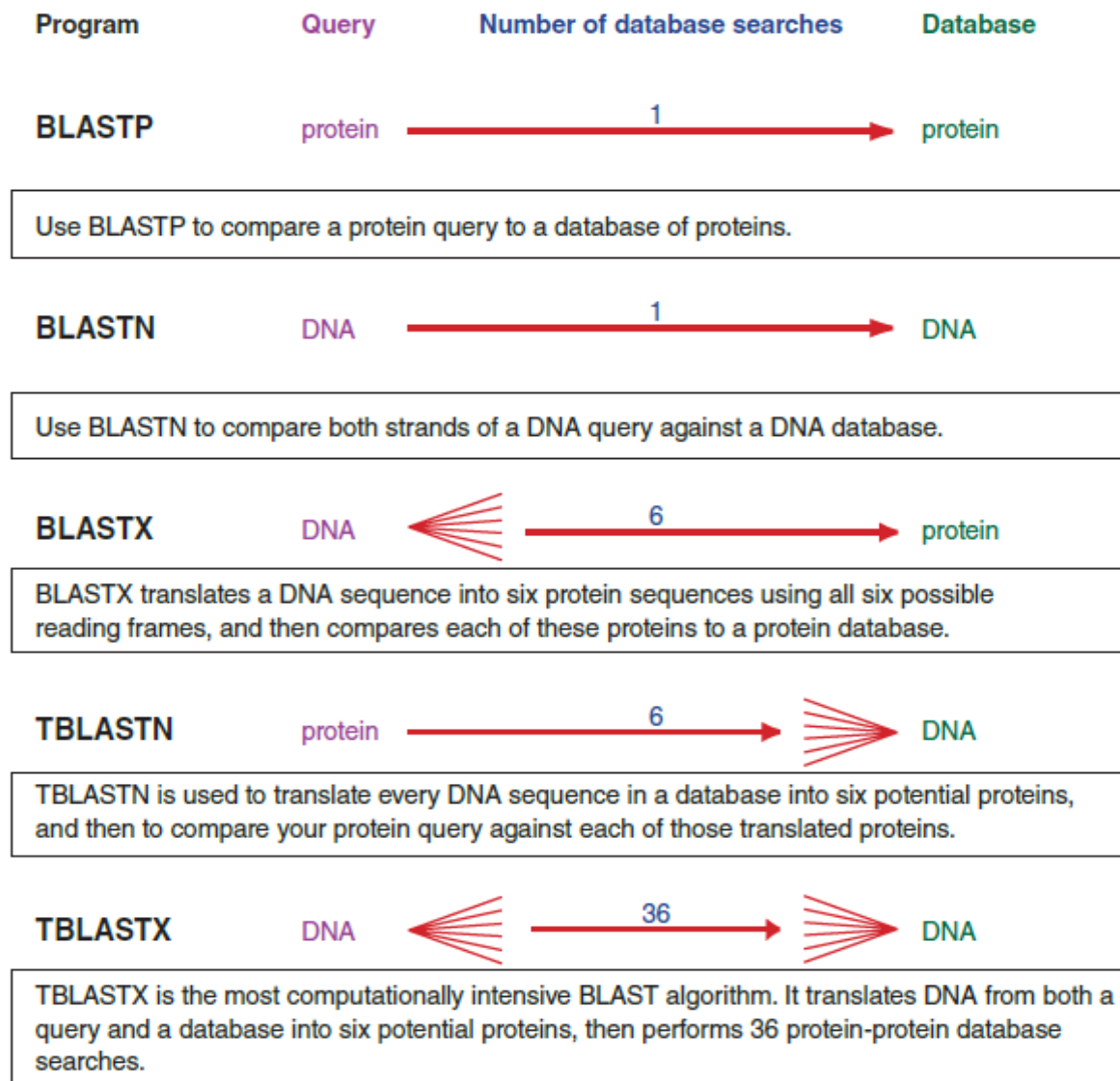


Figure: Overview of the five main BLAST algorithms. `P` refers to protein (as in BLASTP), `N` refers to nucleotide, and `X` refers to a DNA query that is dynamically translated into six protein sequences. The prefix `T` refers to “translating,” in which a DNA database is dynamically translated into six proteins. (Figure adopted from; Bioinformatics and Functional Genomics, 3rd Edition, Jonathan Pevsner, pg.124.)

- The BLASTP program compares an amino acid query sequence against a protein sequence database.
- The BLASTN program is used to compare a nucleotide query sequence against a nucleotide sequence database.
- The program BLASTX compares a nucleotide query sequence translated in all reading frames against a protein sequence database. If you have a DNA sequence and you want to know what protein (if any) it encodes, you can perform a BLASTX search. This automatically translates the DNA into six potential proteins. The BLASTX program then compares each of the six translated protein sequences to all the members of a protein database.
- The program TBLASTN compares a protein query sequence against a nucleotide sequence database dynamically translated in all reading frames. One might use this program to ask whether a DNA database encodes a protein that matches your protein query of interest. Does a query with beta globin yield any matches in a database of genomic DNA from the genome sequencing project of a particular organism?
- The program TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database. The TBLASTX program is computationally intensive. Consider a situation in which you have a DNA sequence with no obvious database matches and you want to know if it encodes a protein with distant, statistically significant database matches in a database of expressed sequence tags.
- A BLASTX search would be more sensitive than BLASTN, and therefore useful to reveal genes that encode proteins homologous to your query. (Bioinformatics and Functional Genomics, 3rd Edition, Jonathan Pevsner)