All BLAST algorithms are available on the web site of ncbi at: https://blast.ncbi.nlm.nih.gov/Blast.cgi
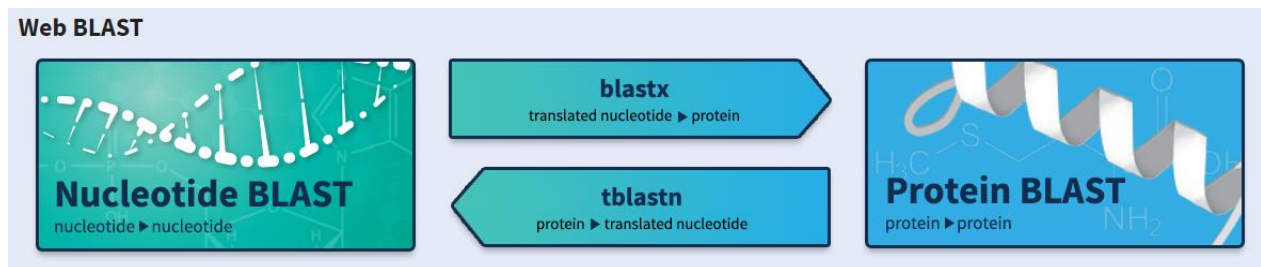


Fig 1: Main BLAST programs.

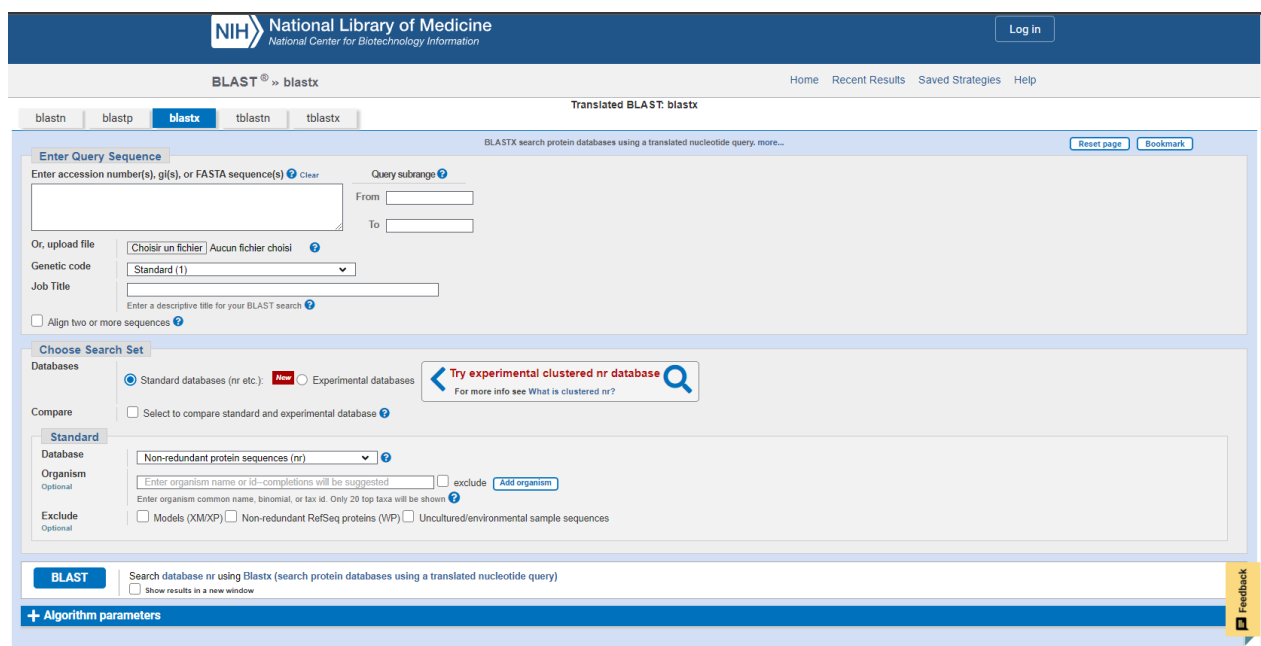To use, BLASTx (nucleotide against protein), one must double-click.



Fig 2: BLAST sequence submission interface.

By switching from one tab (i.e. 'blastx', on the figure) to another, one can access the other BLAST programs.

Many databases are proposed. By default, nt nucleotides collections as nucleotide database and nr as protein database. New experimental databases are present and can be relevant, depending on use cases. Some of these databases are smaller and can reduce BLAST processing duration.

BLAST searches can also be restricted to given taxa making it faster. Some other can be excluded from search.

Advanced parameters can be used to adjust searches.

All parameters are described in the corresponding window to get more detailed information.

Once a search is successfully finished, we get a new page with results. If homologous sequences are found, they will be sorted, in increased order of e-value, by default. Many filters are present to focus on part of these results.

 Multiple sequences alignments or a distance-based tree can be obtained from BLAST outputs.


A detailed "how to" is available at https://github.com/stirera/d-chimer_v1?tab=readme-ov-file#6-appendix--install-blast-programs-and-databases to get blast programs and databases for a command line usage.


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Let's illustrate with a use case:

>set3_133_k141_72529_flag_1_multi_11.0000_len_1871
TTTTTTTTATTTTTTTTAAATTTCCCTCCCCCCTGCGCGCCTTTGGGGTTTTCTCGCGCGCGTGGGTGTCTGCTGGTGG
GGGGTCCCGTGGGCCCGCGCCCCCCCTTTGGGTTCGCCCGCGGCCGCCGAGGGCGTTGCACCAGGGCAGAGGGT
CGCACTCCTCGCTGACGCTCGGAGTGCTTAGTGACCTTAAGAGGTAGACACCGACCAGTGAGACTCCCACGGCCTT
GTTTATTTGAAACCGAGCTTGAAGCTCACCTTTATTTCAGGGTTTGGGGTGGGGAGCCAGGGGTAGATAGGTGTGT
CTGTGAGGTACTTTCTGGGGGGCCTGTCGAAGGCCTGGCAGGCCTCGAACTCAGTGTTCCATCCGTGGTATCCTTG
TATGGGAGTAGGTTTGTTTGGTGGAAATAGGAACACTTCGTTTATTGCGGGAAGGATAACAGGGGGTTTACGTGG
AGATTCGCCTGGGTCTTGGCGAGTTGGAGCGCGAACTGCTGGAGTTGGAGCTGGAGTGCTCGCTGCTCTCGGAGC
TTTCGCTGGAGGAGCTCCCTCGTCGTCTCCGCCGGGTCCTCCTCCGAGGAGAGGCTCGGCGTCTGGGTCTCTTCGA
ACGAGTACCGGGGTCTTTTGACCGGTGAACCTGAGCCGCTTTCGACAGCGCCGTCTTCTCGTTGGTATTCTGAGGG
TAGAAAGAGGAGGGGTGCCCTGAGGGTTGAAGCAACATACTCGCCAGGTATTGGTTGCTTGAGCAGACGTCTGA
GAGTTGTCTCAGTAAAGAGGCCTCTTCTCTGGTCGAAGTTGTGGAGGACCCACGGGGGCGTGACGAGCTGCGGGT
CAACGACTTGTACTTCGCGAGGCTGTCGACGGGGTCCGGATACTTGGTTGTCTTTGCACGGGTTTCTGATGATCTG
AGAGTGGACAGTGTTACCTCCCCACATGAACCTGAAGGAGTACTTGGCCACTAGCTGGCTGTTTTTGTTATCGTCTC
TGTACTGCCAGGGCCCGCAGGTTACTATGTCATGGAATACGTCAGTCTGGTATCTTAGCATGACATACCACTTTGTC
CTCTCGTGCAGGGGGATGTAGCCCCCTCCGTCTATCCATTTGCCCCTGCCAAAATTTCTGTTGTAGACTACGAAGCC
TGCAGTGTCGTCTTTCTTGTCTACGAGGGGCGGCTTGGTGTAGGGACACCTGATGAGAACTTTGCCTTCTTTGCTGA
GGTCGCCCCACTGTATTTGAGTCTCTAGGTAGTCTGCATACCCGTTTAGGAGGGCCCACAGGGGCATGTCTTTGAT
CTCCCAGTGGCACTCTGGTTTTTTGAACTTGTTGTCTGCTTTAGTGTGGTACTGGAACCATACCATGTTACCCTCGGC
CTTGTCTAAGAAGGGATTGTATACTATGTCTCTGTAGGCAGTAAAGAATTCAATGTTGGATCTGCCATCTGAGAGG

AATATGGGGCTGTAAAATCCCAGGTAGTAGTCTAGCATGTGAGTGTTGCCTGCATATTGAGCTGTGCTGTCTCCAT
ATAGGTCATTGGGGCCTGTCGCCAGAGCGAAGTTGTTATCTCTCATCGTTTTAATTGTTGATTTTATTTTGTCAGGGT
GATAGGTGGCAAAAAGAAACAGGCTGTCTCTTGTGTCAGTGAAGCTGTTTTTCCAACTATTAAACTGGTCCTTAGTA
GGTTTTGTGGGAAAGGGCTCAGTGTTATAGGTAGGTGAAGTGGCATCAGTTTGAGCCTTCTTTGCTTTGTCTGCAT
CTATGTGGGCTCTCACCATGCTGTTAGTTATGAAGGTTTGCCAGTAGTGGCCAGATATTTTTTTAGTGAATAGTTCG
TTATATAATTCTTTTAAGTTGTTTTTATTGGGCTTATCATAG

- Copy paste the DNA sequence into the appropriate window.
- Choose a database conveniently, here standar nr database.
- Launch the BLASTx search with the "BLAST" labelled blue button.



After the BLASTx search completed, a new window with results is brought. Generally the closest homologous sequence is at top; here the sequence with accession 'UGV43885.1'.

Many options are possible. Results are downloadable in many csv format for example or aligned sequences in fasta format among others.