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The .gov means it's official.

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[Main Content](#) [Main Navigation](#)**BLAST** [®][Home](#)[Recent Results](#)[Saved Strategies](#)[Help](#)

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

[Learn more](#)

News

BLAST+ 2.13.0 is here!

Starting with this release, we are including the blastn_vdb and tblastn_vdb executables in the BLAST+ distribution.

Thu, 17 March 2022

[More BLAST news...](#)

Web BLAST

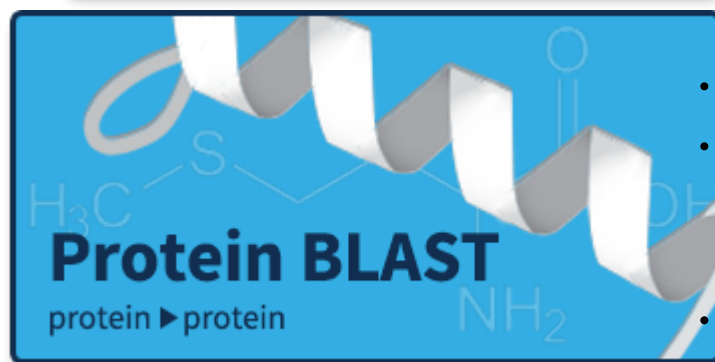
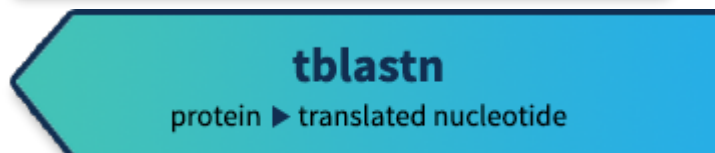
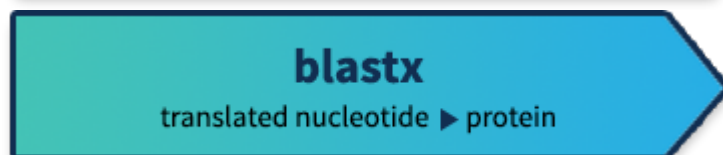


BLAST Genomes

Enter organism common name, scientific name, or tax id.

- [Human](#)
- [Mouse](#)
- [Rat](#)
- [Microbes](#)

Standalone and API BLAST



Download BLAST

[Get BLAST databases and executables](#)

- [Use BLAST API](#)
- [Call BLAST from your application](#)
- [Use BLAST in the cloud](#)
- [Start an instance at a cloud provider](#)

Specialized searches

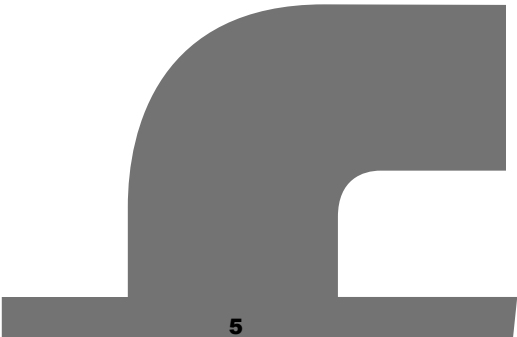
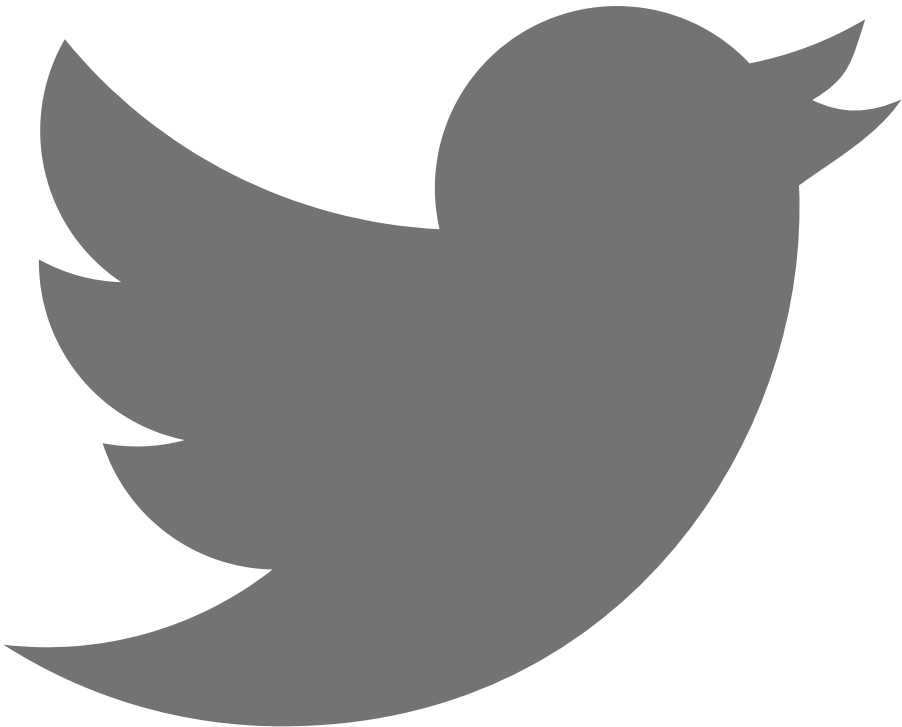
- [SmartBLAST](#)
- [Find proteins highly similar to your query](#)
- [Primer-BLAST](#)

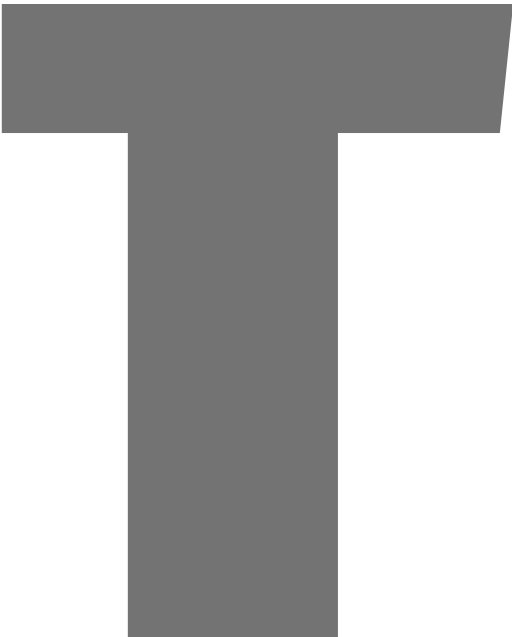
[Design primers specific to your PCR template](#)

- [Global Align](#)
- [Compare two sequences across their entire span \(Needleman-Wunsch\)](#)
- [CD-search](#)
- [Find conserved domains in your sequence](#)
- [IgBLAST](#)
- [Search immunoglobulins and T cell receptor sequences](#)
- [VecScreen](#)
- [Search sequences for vector contamination](#)
- [CDART](#)
- [Find sequences with similar conserved domain architecture](#)

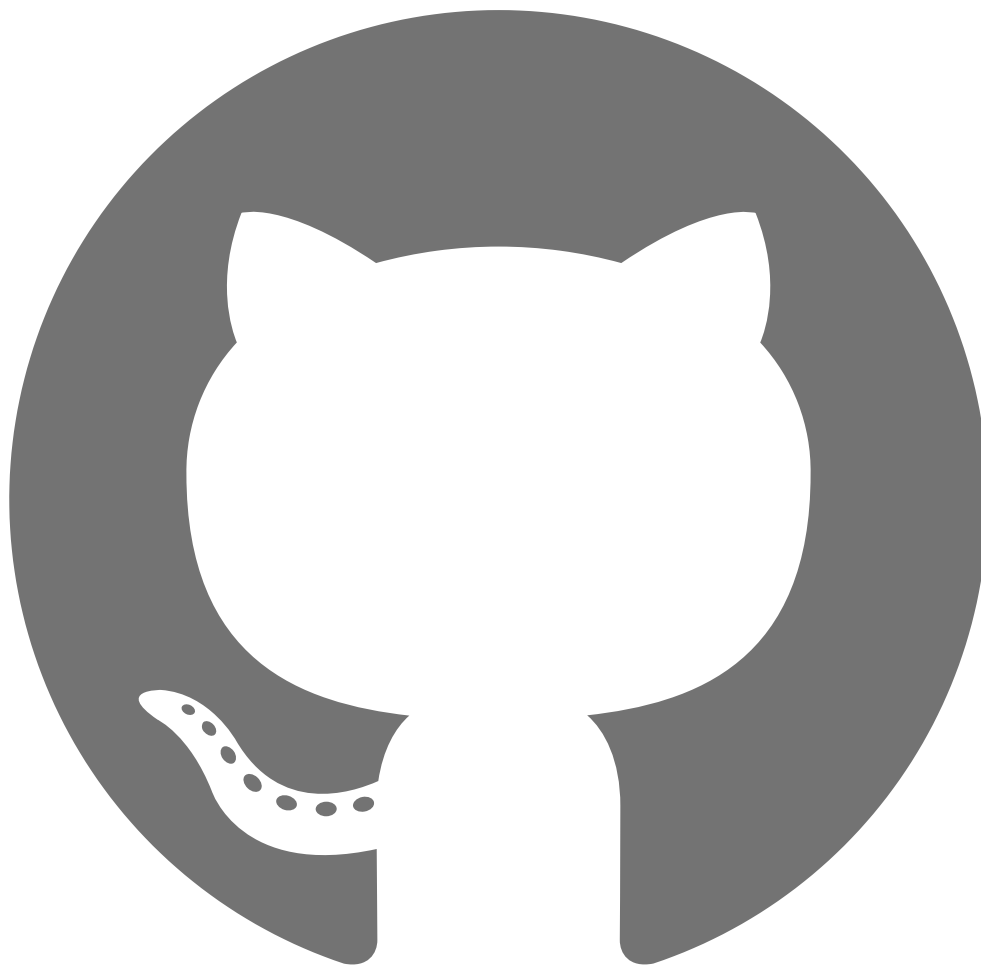
- [Multiple Alignment](#)
[Align sequences using domain and protein constraints](#)
- [MOLE-BLAST](#)
[Establish taxonomy for uncultured or environmental sequences](#)

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