BLAST

Process

The Basic Local Alignment Search
Tool (BLAST) finds regions of local
similarity between nucleotide
sequences.

Algorithm

The program compares nucleotide sequences to sequence in a database and calculates the statistical significance of the matches.
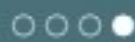
Blast Output Visualisation

BLAST finds similar sequences, by locating short matches between the two sequences. This process of finding similar sequences is called seeding.

Get Started!

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Password

Foeget password!

Sign in

It's first time here? Register

First name

Last name

Email

Password 👁

Confirm password
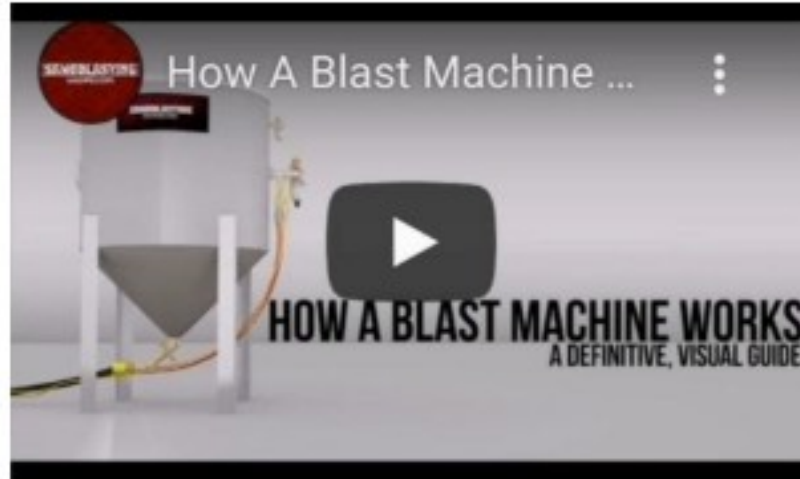
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☰   🔬 **BLASTn**

What is BLAST?

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..

Search

What is BLAST?

Basic Local Alignment Search Tool

The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families

Nucleotide BLAST
nucleotide ▶ nucleotide

Search

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Article Name   15 seen

Writer

Articels Name   15 seen

Wrirer

BLASTn

Job Title

Enter accession number(s), gi(s), or
FASTA sequence(s)

Search

BLASTn

75.0

25.0

● Miss match
● Match

Sequence1: ATAGG--GTTGA

| | | | | | | | | |

Sequence2: ATAGGTAGTTGA