Intended Users:	Information Professionals	Researchers



Basic Logical Alignment Tool (BLAST)

Description: BLAST is product of NLM's National Center for Biotechnology Information. This resource finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and provides statistical information that helps identify biologically meaningful similarities. In other words, BLAST looks at bits of DNA, RNA, or proteins and calculates how similar they are to one another. BLAST offers specialized searches that find, compare immunologically important genes and proteins, design PCR primers, screen for vector contamination, and identify conserved domains. BLAST is available on the web or as a standalone program. Access BLAST on the cloud to run high volume searches or download BLAST+ executables for greater security or for use with proprietary data.

Popular uses of this product:

Information Professionals	Researchers
• Help researchers find guides and tutorials on using BLAST. • Advise researchers to create an account to save search strategies on BLAST and other NLM products. • Advise researchers to use open-source formats such as .txt, or .csv files.	• Search and compare nucleotide and protein sequence information to identify query sequences and find related sequences in the database. • Search and align sequences to assembled genome sequences. • Use specialized search functions to find vector contamination, design PCR primers, find conserved domains, compare sequences, or establish taxonomy.

Key Points:

1. BLAST is a powerful tool that researchers can use to find and compare biological DNA, RNA, and protein sequences.
2. BLAST is well documented so there are numerous resources to help patrons if they run into issues or need help with queries.

Potential Predicaments:

1. Searches often take significant computing power and may take additional time to complete. Using the API, cloud, or the downloadable version may help depending on the researcher's needs and server capabilities.
2. Use copy/paste and plain text files, when possible, to avoid transcription and formatting errors.

Teaching Examples:

1. BLAST has a Quick Start Guide that provides step by step instructions to get started with BLAST. (Note: this guide does not appear on the BLAST homepage. The guide will start users on the NCBI homepage.)

Real Life Examples:

1. A researcher is studying variation in the sequence of a gene and uses Primer-BLAST to design primers to amplify the gene region of interest from biological samples.

2. A researcher is studying a protein of unknown function from an uncharacterized bacterium. They use protein-protein BLAST to identify related proteins in other bacteria to help assign a function to the uncharacterized protein.
3. A researcher studying genetic diseases uses different BLAST features to compare affected protein sequences.

More Information:

YouTube BLAST Tutorials How to BLAST Guide BLAST FAQ