

DNA SEQUENCING TO IDENTIFY SPECIES

Follow-up to Wild Yeast Isolation Project

November 14, 2018

A COMMON PART OF THE GENOME OF ALL ORGANISMS

Different DNA is (mostly) what makes organisms different, so there are not many parts of the genome that are similar enough to compare between species, but different enough to be unique for each species.

The “rDNA” sequences are among the few that can work.

The next slide will show you an example for a small bit of rDNA sequence and some vertebrate species

RDNA SEQUENCE ALIGNMENTS FOR VERTEBRATES



Human

GGAAGGATCATTAAACG-GAGCCC

Chimpanzee

GGAAGGATCATTAAACG-GAGCCG

Orangutan

GGAAGGATCATTAAACG-GAGCGA

Gorilla

GGAAGGATCATT-ACG-GAGCGA

Gibbon

GGAAGGATCATTAAACG-GGACGG

Rat

GGAAGGATCATTAAACG-GAGAAG

Guinea pig

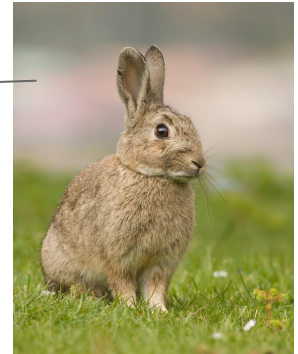
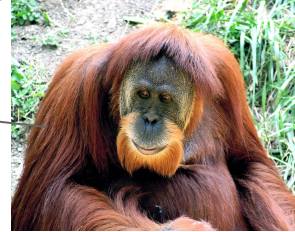
GGAAGGATCATTAAACG-GACGAT

Rabbit

GGAAGGATCATTAAACGAGACCGG

Armadillo

GGAAGGATCATTAAACGAGAGGAG



NOW YOU USE rDNA SEQUENCES TO IDENTIFY YEAST!

- Choose a sequence file from this Google Drive folder (choose any class folder you want):

https://drive.google.com/drive/folders/1yQ4PBbAAN36AOTlDgcj_0YKfufdHG-70?usp=sharing

- Point your browser to <https://blast.ncbi.nlm.nih.gov/Blast.cgi>
- click on “Nucleotide BLAST”
- paste the sequence in the “Enter Query Sequence” field
- click the “BLAST” button about half-way down the screen
- Scroll down to list of “hits”
- Enter species in Google Form and submit:

https://docs.google.com/forms/d/e/1FAIpQLSddnb4lPu0t1Zb-o31L6EnP0G5Fo3SaRtI24FKvDnZKc25imw/viewform?usp=sf_link

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

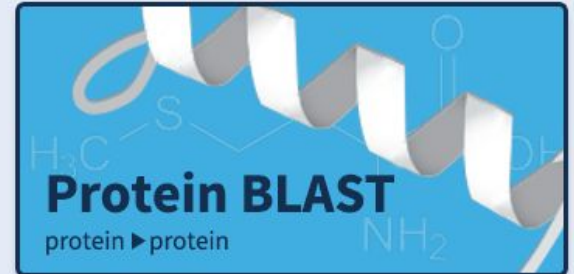
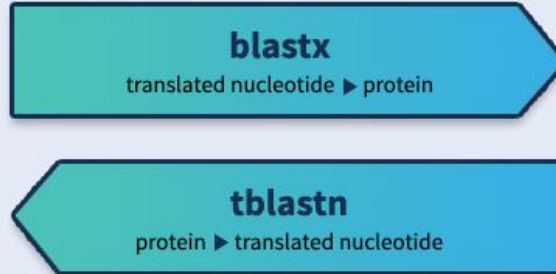
[Learn how to use BLAST](#)

See our collection of webinars and tutorials designed to help you.

Wed, 17 Oct 2018 15:00:00 EST

[More BLAST news...](#)

Web BLAST



[Click here!](#)

Enter Query Sequence

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

Clear

Query subrange ?

From

To

Paste here

Or, upload file

Choose File No file chosen ?

Job Title

Enter a descriptive title for your BLAST search ?

☐ Align two or more sequences ?

Choose Search Set

Database

☐ Human genomic + transcript ☐ Mouse genomic + transcript ☒ Others (nr etc.):

Nucleotide collection (nr/nt) ?

Organism

Optional

☐ Exclude +

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown ?

Exclude

Optional

☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Limit to

Optional

☐ Sequences from type material

Entrez Query

Optional

[YouTube](#) [Create custom database](#)

Enter an Entrez query to limit search ?

Program Selection

Optimize for

- ☐ Highly similar sequences (megablast)
☐ More dissimilar sequences (discontiguous megablast)
☒ Somewhat similar sequences (blastn)

Choose a BLAST algorithm ?

Then click here

BLAST

Search database Nucleotide collection (nr/nt) using Blastn (Optimize for somewhat similar sequences)

☐ Show results in a new window