

**COVID-19 is an emerging,  
rapidly evolving situation.**

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[SARS-CoV-2 data \(NCBI\)](#)

[Prevention and treatment information \(HHS\)](#)

# BLAST<sup>®</sup> » blastn suite

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## Standard Nucleotide BLAST

- 
- [blastn](#)
- [blastp](#)
- [blastx](#)
- [tblastn](#)
- [tblastx](#)

BLASTN programs search nucleotide databases using a nucleotide query. [more...](#)

[Reset page](#)[Bookmark](#)

Enter Query Sequence

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

[? Help](#)[Clear](#)

CCTTAGGCAACCTGGTGGTCCCCGCTCCCGGGAGGTCACCATATTGATG

Query subrange

[? Help](#)

Query subrangeFrom

Query subrangeTo

Or, upload file

[Choose File](#)

No file chosen

[? Help](#)

Genetic code

Standard (1)



Job Title

Nucleotide Sequence

Enter a descriptive title for your BLAST search

[? Help](#)

☐ Align two or more sequences

[? Help](#)

New columns added to the Description TableNew

Click 'Select Columns' or 'Manage Columns'.

Enter Subject Sequence

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

[? Help](#)

[Clear](#)

Subject subrange

[? Help](#)Subject subrangeFrom Subject subrangeTo 

Or, upload file

 No file chosen[? Help](#)

## Choose Search Set

Database

☒ Standard databases (nr etc.): ☐ rRNA/ITS databases ☐ Genomic + transcript databases ☐ Betacoronavirus[Targeted Loci Project Information](#)◆ Database sequences non-default value  [? Help](#)

Limit by

☐ Organism ☐ BioProjectID ☐ WGS Project

Organism

Optional

 

exclude

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

[? Help](#)

Exclude

Optional

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

Limit to

Optional

☐ Sequences from type material

Entrez Query

Optional

 [Create custom database](#)

Enter an Entrez query to limit search

[? Help](#)

## Program Selection

Optimize for

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

Choose a BLAST algorithm

[? Help](#)

Algorithm

☐ Algorithm Quick BLASTP (Accelerated protein-protein BLAST)☐ Algorithm blastp (protein-protein BLAST)☐ Algorithm PSI-BLAST (Position-Specific Iterated BLAST)☐ Algorithm PHI-BLAST (Pattern Hit Initiated BLAST)

Enter a PHI pattern

[? Help](#)☐ Algorithm DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

[? Help](#)

## BLAST

Search database Reference RNA sequences (refseq\_rna) using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

Note: Parameter values that differ from the default are highlighted in yellow and marked with ♦ sign

## Algorithm parameters + −

Restore default search parameters

## General Parameters

Max target sequences

♦Max target sequences non-default value 100 ▼

Select the maximum number of aligned sequences to display

[? Help](#)

Short queries

☒ Automatically adjust parameters for short input sequences

[? Help](#)

Expect threshold

♦Expect threshold non-default value 0.05

[? Help](#)

Word size

♦Word size non-default value 28 ▼

[? Help](#)

Max matches in a query range

♦Max matches in a query range non-default value 0

[? Help](#)

## Scoring Parameters

Matrix

♦Matrix non-default value PAM30 ▼

[? Help](#)

Match/Mismatch Scores

♦Match/Mismatch Scores non-default value 1,-2 ▼

[? Help](#)

Gap Costs

♦Gap Costs non-default value Linear ▼

[? Help](#)

Compositional adjustments

♦Compositional adjustments non-default value No adjustment ▼

[? Help](#)

## Filters and Masking

Filter

♦Low complexity regions filter non-default value ☒ Low complexity regions filter

[? Help](#)

♦Species-specific repeats filter non-default value ☐

Species-specific repeats filter for:

Homo sapiens (Human) ▼

[? Help](#)

Mask

♦Mask for lookup table only non-default value ☒ Mask for lookup table only

[? Help](#)

♦Mask lower case letters non-default value ☐

Mask lower case letters

[? Help](#)

## Discontiguous Word Options

Template length

♦Template length non-default value None ▼

[? Help](#)

Template type

♦Template type non-default value Coding ▼

[? Help](#)

## PSI/PHI/DELTA BLAST

PSSM ♦PSSM non-default value

PSSM is uploaded... [Clear](#)

Upload PSSM Optional

 No file chosen[? Help](#)

PSI-BLAST Threshold

[? Help](#)

DELTA-BLAST Threshold

◆DELTA-BLAST Threshold non-default value

[? Help](#)

Pseudocount

◆Pseudocount non-default value

[? Help](#)

Search database Reference RNA sequences (refseq\_rna) using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window7  28  11  Linear  Linear  Linear Linear  Linear  Existence: 5 Extension: 2 Reference RNA sequences (refseq\_rna)  Human genomic plus transcript (Human G+T) Betacoronavirus Genbank  16S ribosomal RNA sequences (Bacteria and Archaea)  

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