

NCBI/BLAST/blastn suite

Standard Nucleotide BLAST

blastnblasttblasttblastx

Enter Query Sequence

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

Reset pageBookmark

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

Clear

taatggctcacaaggcgacgacgggtagcggcctgagaggggtgacggccacactgggactgagacagggcca
gactcctacgggagggcagcagtggggaatattgcacaatggggcgaagcctgatgcagcgacggcggtagggat
gacggccttcgggttgtaacctcttccagtaggggaagaagcgaaagtgaacgtacctgcagaagaagcaccggcctaa
ctacgtgccagcagccggcggtataactgtaggggtcgagcggtatccggaattattgggcgtaagagctcgtaggcgg
ttgtcgcgctctgctg

Query subrange

From

To

Or, upload file

Choose FileNo 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

Enter organism name or id--completions will be suggested

☐ 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

Entrez Query

Optional

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

BLAST

Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

+ Algorithm parameters