

NCBI BLAST/ blastn suite

### Align Sequences Nucleotide BLAST

blastn blastp blastx tblastn tblastx

Enter Query Sequence

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

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Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) [Query subrange](#)

ACACCACGAG  
ACGTTGTACACCCGAACTCCGTACGCTAACCTTTTGACCCAGCCGCCCAAGCTCGGAT  
ACATCATTCG  
CGTCAACTCGTAMCACTAGCCTTCGGGG

From   
To

Or, upload file [Choose File](#) No file chosen

Job Title

Enter a descriptive title for your BLAST search

☒ Align two or more sequences

Enter Subject Sequence

Enter accession number, gi, or FASTA sequence [Clear](#) [Subject subrange](#)

GTCGTGAGATGTTGGTTAAGTCCCCGAACGCGCAACCTTGATCTAGTTGCCATCAT  
TTAGTTGGGCACTTAAGTGACTCCCGTCACAAACCGGAGCAAGTCGGGATCACGTC  
AAATCATCATCCCTTATCACTCGGCTACACACGTGCTACAAGTGGAGATACAAACGG  
TTGCCAACTCCGAGAGGAGCTAATCCGATAAAGCTGTTCTCAGTTCCGATTCAGGCT  
GCAACTCGGCTACATGAAGCTCGAATCCCTAGTATCCCGCATCAGC

From   
To

Or, upload file [Choose File](#) No file chosen

Program Selection

Optimize for

☒ Highly similar sequences (megablast)

☐ More dissimilar sequences (discontiguous megablast)

☐ Somewhat similar sequences (blastn)

[Choose a BLAST algorithm](#)

**BLAST** Search nucleotide sequence using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

[Algorithm parameters](#) **Note: Parameter values that differ from the default are highlighted in yellow and marked with † sign**