

SequenceServer, BLAST search made easy!

<http://www.sequenceserver.com>

<http://dx.doi.org/10.1101/033142>

SequenceServer is not a new alignment
tool

How do we use BLAST?

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](#)

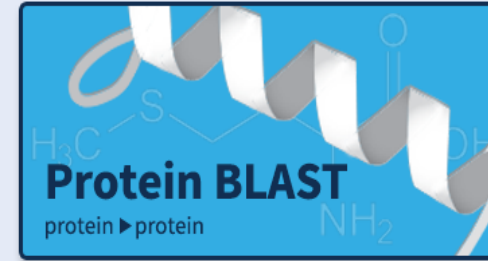
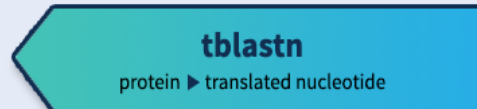
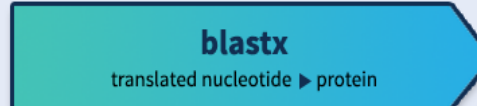
BLAST+ 2.5.0 released

NEWS

The new version offers support for HTTPS, accession.version as the primary sequence identifier, support for composition-based statistics with RPSTBLASTN, and a new taxonomic organism report.

Fri, 23 Sep 2016 17:00:00 EST [More BLAST news...](#)

Web BLAST



```
C:\ Command Prompt
C:\Documents and Settings\surya>cd C:\blast-2.2.25+
C:\blast-2.2.25+>makeblastdb -in db/nuclic.fasta -dbtype nucl -out db/nuclic

Building a new DB, current time: 05/02/2012 13:53:38
New DB name:      db/nuclic
New DB title:     db/nuclic.fasta
Sequence type:    Nucleotide
Keep Linkouts:    T
Keep MBits:       T
Maximum file size: 1073741824B
Adding sequences from FASTA; added 3 sequences in 0.00236433 seconds.

C:\blast-2.2.25+>blastn -query db/test.txt -db db/nuclic -out db/output.txt
C:\blast-2.2.25+>_
```

```
Command Prompt
C:\Documents and Settings\surya>cd C:\blast-2.2.25+
C:\blast-2.2.25+>makeblastdb -in db/nuclic.fasta -dbtype nucl -out db/nuclic

Building a new DB, current time: 05/02/2012 13:53:38
New DB name:   db/nuclic
New DB title:  db/nuclic.fasta
Sequence type: Nucleotide
Keep Linkouts: T
Keep MBits: T
Maximum file size: 1073741824B
Adding sequences from FASTA; added 1 sequences in 0.00236433 seconds.
C:\blast-2.2.25+>blastn -query db/test.txt -db db/nuclic -out db/output.txt
C:\blast-2.2.25+>_
```

.. goals

- Demonstrate SequenceServer
- Encourage adoption
- Collect suggestions and reviews for future improvement

.. existing issues

User Interface

The screenshot displays the BLASTN web interface. At the top, there are tabs for different BLAST programs: **blastn**, **blastp**, **blastx**, **tblastn**, and **tblastx**. The main heading is "BLASTN programs search nucleotide databases".

The interface is divided into several sections:

- Enter Query Sequence**: This section contains a large text input field for "Enter accession number(s), gi(s), or FASTA sequence(s)". To the right of this field is a "Clear" link. Further right is a "Query subrange" section with "From" and "To" input fields. Below the main input field is a section for "Or, upload file" with a "Browse..." button and the text "No file selected.". Below that is a "Job Title" field containing "Nucleotide Sequence (1114 letters)" and a prompt "Enter a descriptive title for your BLAST search". At the bottom of this section is a checkbox for "Align two or more sequences".
- Choose Search Set**: This section contains several options for database selection. It starts with radio buttons for "Human genomic + transcript", "Mouse genomic + transcript", and "Others (nr etc.):". Below these is a dropdown menu currently showing "Nucleotide collection (nr/nt)". To the right of the dropdown is an "Exclude" button with a "+" icon. Below the dropdown is a text input field for "Enter organism name or id--completions will be suggested" and a prompt "Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown". There are also checkboxes for "Models (XM/XP)", "Uncultured/environmental sample sequences", and "Sequences from type material". At the bottom of this section is an "Entrez Query" field with a prompt "Enter an Entrez query to limit search" and a link to "Create custom database".
- Program Selection**: This section contains a section for "Optimize for" with three radio buttons: "Highly similar sequences (megablast)", "More dissimilar sequences (discontiguous megablast)", and "Somewhat similar sequences (blastn)". Below these is a prompt "Choose a BLAST algorithm".

.. existing issues

Cannot use private databases

Choose Search Set

Database	<input type="radio"/> Human genomic + transcript <input type="radio"/> Mouse genomic + transcript <input checked="" type="radio"/> Others (nr etc.):
	<div>Nucleotide collection (nr/nt) </div>
Organism Optional	<div>Enter organism name or id--completions will be suggested <input type="checkbox"/> Exclude </div> <div>Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown </div>
Exclude Optional	<input type="checkbox"/> Models (XM/XP) <input type="checkbox"/> Uncultured/environmental sample sequences
Limit to Optional	<input type="checkbox"/> Sequences from type material
Entrez Query Optional	<div><input type="text"/></div> <div>Enter an Entrez query to limit search </div>

[Create custom database](#)

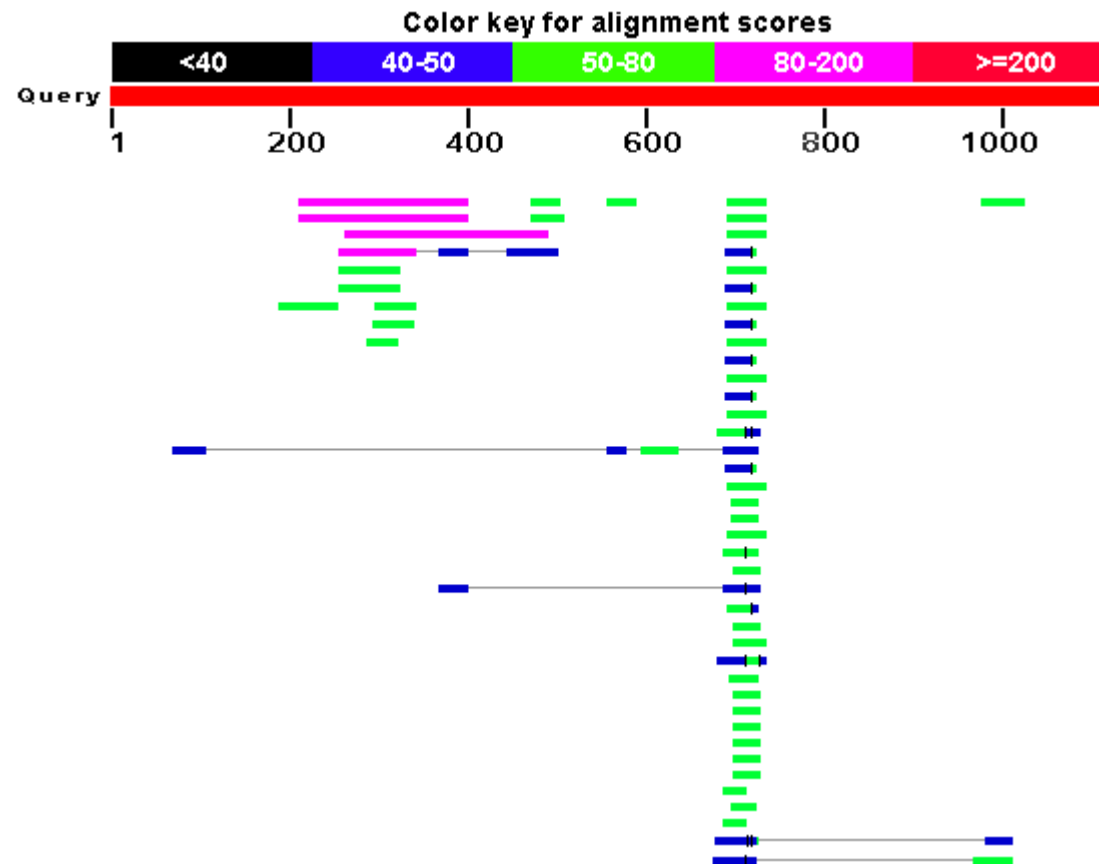
.. existing issues

Difficult to customize report

Formatting options		Reformat
Show	Alignment as HTML <input type="checkbox"/> Old View	Reset form to defaults
Alignment View	Pairwise	
Display	<input checked="" type="checkbox"/> Graphical Overview <input type="checkbox"/> NCBI-gi <input type="checkbox"/> CDS feature	
Masking	Character: Lower Case Color: Grey	
Limit results	Descriptions: 100 Graphical overview: 100 Line length: 60	
Organism <small>Type common name, binomial, taxid, or group name. Only 20 top taxa will be shown.</small>		
<input type="text" value="Enter organism name or id--completions will be suggested"/> <input type="checkbox"/> Exclude <input type="button" value="+"/>		
Entrez query: <input type="text"/>		
Expect Min: <input type="text"/> Expect Max: <input type="text"/>		
Percent Identity Min: <input type="text"/> Percent Identity Max: <input type="text"/>		

.. existing issues

Unintuitive visualizations

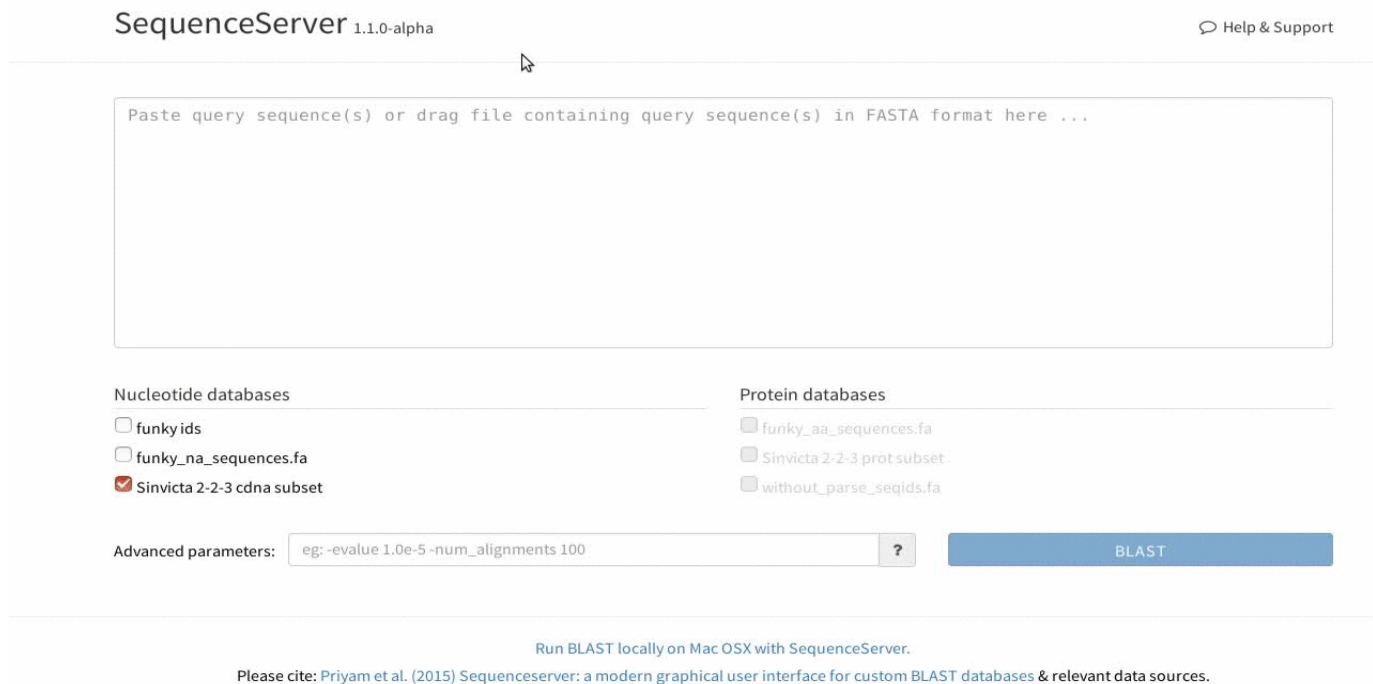


SequenceServer

40,000+ downloads, 30+ citations

.. bespoke interface

Clutter free, streamlined, intelligent interface



SequenceServer 1.1.0-alpha [Help & Support](#)

Paste query sequence(s) or drag file containing query sequence(s) in FASTA format here ...

Nucleotide databases

- ☐ funky ids
- ☐ funky_na_sequences.fa
- ☒ Sinivicta 2-2-3 cdna subset

Protein databases

- ☐ funky_aa_sequences.fa
- ☐ Sinivicta 2-2-3 prot subset
- ☐ without_parse_seqsids.fa

Advanced parameters: ? [BLAST](#)

Run BLAST locally on Mac OSX with SequenceServer.
Please cite: Priyam et al. (2015) Sequenceserver: a modern graphical user interface for custom BLAST databases & relevant data sources.

.. host anyway you like

Can be setup for personal or public use;
share with collaborators

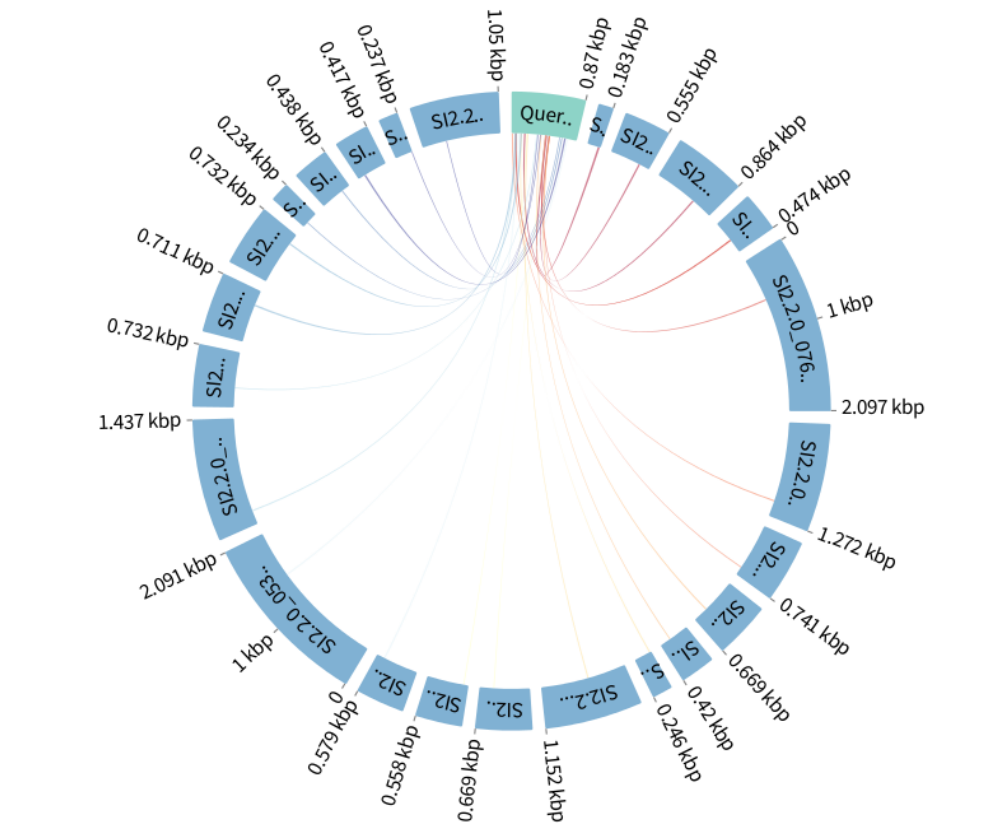
<http://localhost:4567>

<http://www.antgenomes.org/sequenceserver/>

<http://reefgenomics.org/blast/>

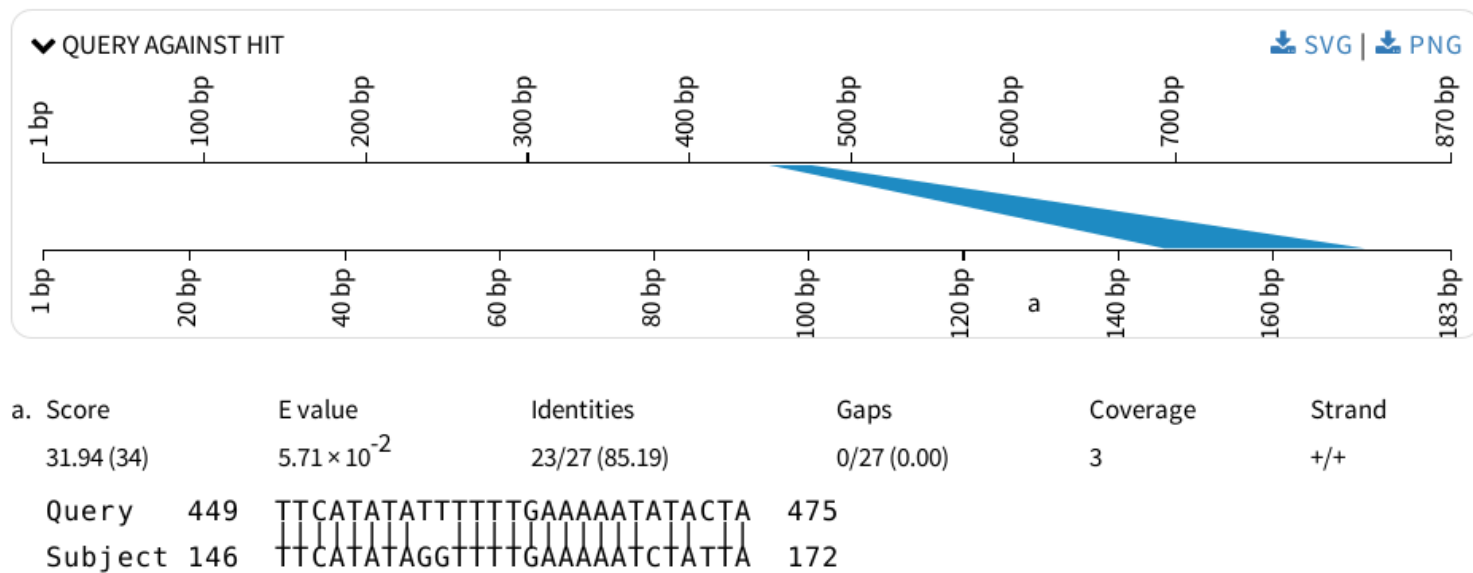
.. visualizations

Export graphics



.. visualizations

Export graphics



.. customized reports

Download FASTA files, reports

BLASTN: 1 query, 1 database

[Query= Query_1](#)

Download FASTA, XML, TSV

[FASTA of all hits](#)

[FASTA of 2 selected hit\(s\)](#)

[Alignment of all hits](#)

[Alignment of 2 selected hit\(s\)](#)

[Standard tabular report](#)

[Full tabular report](#)

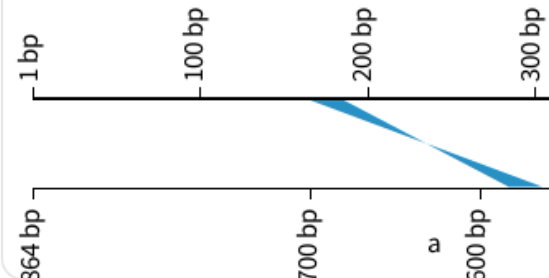
[Full XML report](#)

Query 490 TAGATTACATAATTTTAT
Subject 402 TACATTACATAAATTTCA

▼ SI2.2.0_05000 Si_gnF.scaffold04017[8473..9

☒ Select | [Sequence](#) | [FASTA](#) | [Align](#)

▼ QUERY AGAINST HIT



a.	Score	E value	Iden
	30.14 (32)	1.99×10^{-1}	19/2
Query	166	CTGTACAAATTTTGC	
Subject	583	CTTTACAAATTTTAC	

.. and many more

- Link with other databases
- Support other search programs
- All features of BLAST+ supported
- Guided setup (takes less than 15 minutes)
- Free for research

Demonstration

<http://128.199.192.58:4567/>

<http://128.199.192.58:4568/>

ACAAATCAATGATCTTTtGTAGaCCATTGATTTGTTTTCTTATAAAAAaTAAAAaTGCTTTTTATGACATTAAAtCTTTTTTTtATGACATTAGATTTTTACACACAAATAAGTCGCACA
AAACAAAGTTTTTACGAACATTTAAAAATAAtTTTTTtGCTTTTAATAAATAATATACGACGTCTACAATGCGATTGTAAAATAGCAGCAgAGGTGCATATGATGAACGACTATGTTCCAC
AACCACAGCTCATATATAACATGATTTtGTTTGCCGAATTcATACACGCATTACAACACACATTGAATTCAATAATAATATCAAATTCACATTCAAAGCTTTCAAGTTAGACAAAAGTTA
AAAAAaTTAATATGTAACATATTTCTCAAAATTACGTAGAGAATATACGAGTAAATCTGTACAAATTTTTGCTACaTGCAAAACTAAAATTCAGTTTTTAtAAAAATACGATAAACACTAA
TGACTAGTAACATCCTACAGTGTCATAGAACGAAATAATTATAACAGTTATTTTTAGAAATTCAACGCGAATTATACAAGATATCATGACTCTAGATATATTCTACCACCACCGTCTTTT
CCTTATTATTTGAGTTGTATTTTTTTTTtCCAAATTATACAATAGTTGTTTCAAAGGAATATATATTGTATAGTTTTTgTAATTGACGCAATTTAAAGATTTTCATATATTTTTTGAAAAAT
ATACTACATATGACTTGAATTAGATTACAtAATTTtAtaaTTtTTTTTTTTTTtAAGaTTTAAAAATaTTACTAATTGGGTTTTTtGGTATAAGTTTTTtCATTGAACAGCATTTAATG
CCGTTTTtACCTGTTTTtGAAAAGGTAAATTTCTTTAGATATATACAGTTTGTAAATaTTAGGTATTTTATAAACAGTGTGTATATTTCTTACAATATAAAAGACACAATTGCAAACTAGC
ATGATTGTAAACAATTGCTAAACGGATCAATATAAATTAATAATTGTAATATTAAGTATCAAACCGATAATTTTTATTTATTGTTTCATTGTTTGTCTTTATTTTGTATTTGTAAATAAT
GAAATACTGAACTTATGCAGATAAATACTGGAAAGTCAAGAACGCATTCTATGAACAATTTAATAGCTTTAAACACAATAATCAGAATACCAGACTCACACAGCATCTTACTTTATTTA
CAAATCACATTTATCTGATTTcGAAAGATTTATATTTCTATGAATTCTAAGAAAGATTGTACGTTTTTAAATAGAGATAAGCAAACGTTCTTACTAATAAATACGAAGATAAAAAATTAT
ACATATATAGTTCTTAGTACAAATACAAATAATTCTCATGCTTCTAATAAGGGAAGATACACATGTGAGGTAACCGATTTTCATTGAATTTTTAACTTATACTATATACCTCTCACTTAT
TCATAGTATAAACTAACTTGTTCTATACGCAGTAGTTAATGAGAGGTGACTGTTACGAATTTTTCATACGCTGTATGTATTcAGTTTCCTAAGCCTGAGCAAACATTGTcGAGCAGACAA
CGTTAGGTAACATTACGATGTTGAACATGTGACGCGACACCAGTTCAAATCTTGCTTTTT

.. summary

Feature	NCBI wwwBlast	SequenceServer
Private databases	✗	✓
Publishable Graphics	✗	✓
Personal/Public setup	✗	✓
Clutter free UI	✗	✓
BLAST	✓	✓
Support other programs	✗	✓

Thank you!

Questions?