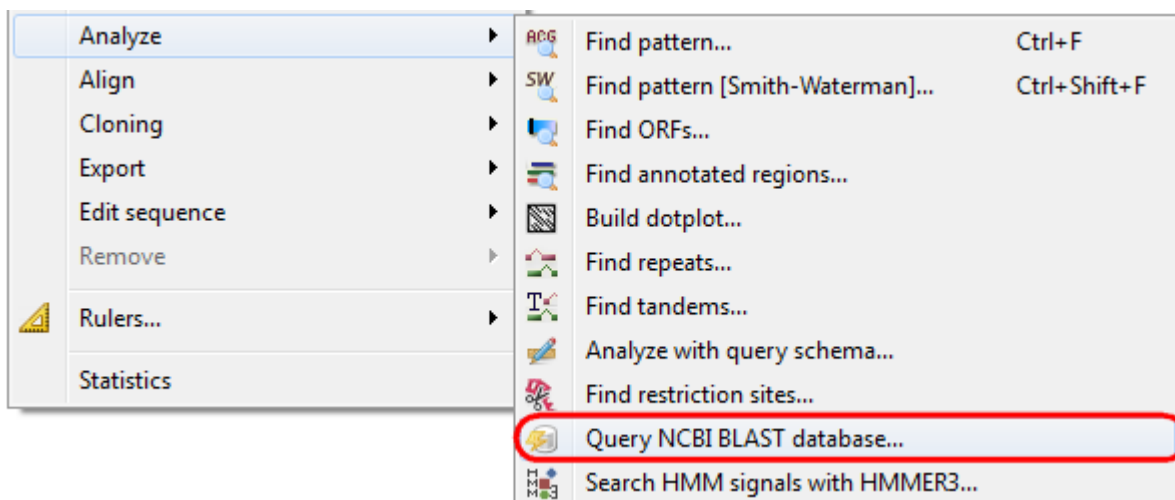


# Remote BLAST

The *Remote BLAST* plugin provides a capability to annotate sequences with information stored in the [NCBI BLAST](#) remote database.

To perform a remote database search open a *Sequence View*, select a sequence region to analyze and click the *Analyze Query NCBI BLAST database* context menu item. If a region is not selected the whole sequence will be analyzed.



The following dialog will appear where you can choose the search options:

**Search Through a Remote Database**

General options    Advanced options

Select the search type: blastn ☐ Search for short, nearly exact matches

Expectation value: 10.000000 ☐ Megablast

Max hits: 20

The database: Nucleotide collection - nr

The database description:

Basic Local Alignment Search Tool, or BLAST, is an algorithm for comparing primary biological sequence information, such as the amino-acid sequences of different proteins or the nucleotides of DNA sequences. A BLAST search enables a researcher to compare a query sequence with a library or database of sequences, and identify library sequences that resemble the query sequence above a certain threshold.

▼ Save annotation(s) to

☐ Existing table

☒ Create new table C:/Users/yalgaer/MyDocument.gb

▼ Annotation parameters

Group name <auto>

Search timeout 8 min

Search Cancel Help

General options are:

*Select the search type* — in the remote databases the *blastn* search is used for nucleotide sequences, *blastp* and *cdd* searches are used for amino sequences.

UGENE also provides a way to use *blastp* and *cdd* searches for nucleotide sequences. This is achieved by translating the nucleotide sequence into the amino sequences.

When a sequence is translated the translation table from the active *Sequence View* is used. Finally, all 6 translations are used to query the remote database with the selected *blastp* or *cdd* search.

*Expectation value* — this option specifies the statistical significance threshold for reporting matches against database sequences. Lower expect thresholds are more stringent, leading to fewer chance matches being reported.

*Max hits* — the maximum number of hits that will be shown (not equal to number of annotations). The maximum available number is 5000.

*Database* — the target database.

*Search for short, nearly exact matches* — automatically adjusts the word size and other parameters to improve results for short queries.

*Megablast* — select this option to compare query with closely related sequences. It works best if the target percent identity is 95% or more, but it is very fast.

You can see the description of the annotation saving parameters [here](#).

*Search timeout* — the remote task terminated if the timeout is reached.



There is a little difference in default values of parameters between [NCBI Nucleotide BLAST](#) web interface and UGENE:

- The web interface uses the *megablast* option by default: the search is fast, but only highly similar sequences are found.
- UGENE ignores the option by default: the search may take more time, but all somewhat similar sequences are found.

Check the *Megablast* option, if you want exactly the same results to be found in UGENE as you had in the NCBI web interface.

Also there is *Advanced options* tab:

The view of the *Advanced options* tab depends on the selected search. For the *blastn* search it looks like on the picture above.

*Word size* — the size of the subsequence parameter for the initiated search.

*Gap costs* — costs to create and extend a gap in an alignment. Increasing the Gap costs will result in alignments which decrease the number of Gaps introduced.

*Match scores* — reward and penalty for matching and mismatching bases.

*Entrez query* — a BLAST search can be limited to the result of an *Entrez query* against the database chosen. This restricts the search to a subset of entries from that database fitting the requirement of the *Entrez query*. Examples are given below:

*protease NOT hiv1[organism]* — this will limit a BLAST search to all proteases, except those in HIV 1.

*1000:2000[slen]* — this limits the search to entries with lengths between 1000 to 2000 bases for nucleotide entries, or 1000 to 2000 residues for protein entries.

*Mus musculus[organism] AND biomol\_mrna[properties]* — this limits the search to mouse mRNA entries in the database. For common organisms, one can also select from the pulldown menu.

*10000:100000[mlwt]* — this is yet another example usage, which limits the search to protein sequences with calculated molecular weight between 10 kD to 100 kD.

*src specimen voucher[properties]* — this limits the search to entries that are annotated with a /specimen\_voucher qualifier on the source feature.

*all[filter] NOT envirommental sample[filter] NOT metagenomes[orgn]* — this excludes sequences from metagenome studies and uncultured sequences from anonymous environmental sample studies.

For help in constructing *Entrez queries* see the [Entrez Help document](#).

*Filters* — filters for regions of low compositional complexity and repeat elements of the human's genome.

*Masks for lookup table only* — this option masks only for purposes of constructing the lookup table used by BLAST so that no hits are found based upon low-complexity sequence or repeats (if repeat filter is checked).

*Mask lower case letters* — with this option selected you can cut and paste a FASTA sequence in upper case characters and denote areas you would like filtered with lower case.

*Filter by* — filters results by accession, by definition of annotations or by id.

*Select result by* — selects results by EValue or by score.

When the *blastp* search is selected in the general options, the view of the *Advanced options* tab is the following:

Search Through a Remote Database

General options   Advanced options

Word size: 3   Gap costs: 11 1

Entrez query:

Matrix: BLOSUM62   Service: plain

Filters

- ☒ Low complexity filter
- ☐ Human repeats filter

Masks

- ☐ Mask for lookup table only
- ☐ Mask lower case letters

Filter results

Filter by

- ☐ accession
- ☐ def (filter by definition of annotations)
- ☐ id

Select result by

- ☒ EValue
- ☐ Score

Search   Cancel   Help

As you can see there is no *Match scores* option, but there are *Matrix* and *Service* options.

*Matrix* — key element in evaluating the quality of a pair-wise sequence alignment is the “substitution matrix”, which assigns a score for aligning any possible pair of residues.

*Service* — blastp service which needs to be performed: plain, psi or phi.

The *Advanced options* tab is not available when the *cdd* search is selected.

- [Exporting BLAST Results to Alignment](#)
- [Fetching Sequences from Remote Database](#)