BLAST/BLAST+

The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance of matches. BLAST can be used to infer functional and evolutionary relationships between sequences as well as help identify members of gene families.

BLAST+ is a new version of the BLAST package from the NCBI.

From UGENE you can use the following tools of the old BLAST package:

- **blastall** — the old program developed and distributed by the NCBI for running BLAST searches.
- **formatdb** — formats protein or nucleotide source databases before these databases can be searched by **blastall**.

And the following tools of the new BLAST+ package:

- **blastn** — searches a nucleotide database using a nucleotide query.
- **blastp** — searches a protein database using a protein query.
- **blastx** — searches a protein database using a translated nucleotide query.
- **tblastn** — compares a protein query against a translated nucleotide database (the all six reading frames).
- **tblastx** — translates the query nucleotide sequence in all six possible frames and compares it against the six-frame translations of a nucleotide sequence database.
- **makeblastdb** — — formats protein or nucleotide source databases before these databases can be searched by other *BLAST+* tools.

BLAST home page: http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Web&PAGE_TYPE=BlastHome

To make *BLAST* (or *BLAST+*) tools available from UGENE:

1. Install the required verion of *BLAST* (or *BLAST+*) on your system.
2. Set the paths to the executables, you are going to use, on the *External tools* tab of UGENE *Application Settings* dialog.

After you've finished this configuration you can access the tools from the *Tools BLAST* submenu of the main menu.

- Creating Database
- Making Request to Database
- Fetching Sequences from Local BLAST Database