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.

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.
- 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+ tools available from UGENE:

- 1. Install the required version of 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