

# Local BLAST+ Search Element

Finds annotations for DNA sequence in a local BLAST database.

BLAST+ is a newer version of the BLAST package and is recommended to use by the NCBI.



BLAST+ is used as an external tool from UGENE and it must be installed on your system. To learn more about the external tools, please, read main [UGENE User Manual](#).

## Parameters in GUI

| Parameter           | Description                                                                                                | Default value   |
|---------------------|------------------------------------------------------------------------------------------------------------|-----------------|
| Search type         | Selects the type of the BLAST searches.                                                                    | blastn          |
| Database path       | Path to the database files.                                                                                |                 |
| Database name       | Base name for BLAST DB files.                                                                              |                 |
| Tool path           | Path to the BLAST executable.                                                                              | default         |
| Temporary directory | Directory for temporary files.                                                                             | default         |
| Expected value      | Expectation threshold value.                                                                               | 10              |
| Culling limit       | If the query range of a hit is enveloped by that of at least this many higher-scoring hits, delete the hit | 0               |
| Annotate as         | Name of the result annotations.                                                                            | blast_result    |
| Gapped alignment    | Perform gapped alignment.                                                                                  | use             |
| Gap costs           | Cost to create and extend a gap in an alignment.                                                           | 2 2             |
| Match scores        | Reward and penalty for matching and mismatching bases.                                                     | 1 -3            |
| BLAST output        | Location of BLAST output file.                                                                             |                 |
| BLAST output type   | Type of BLAST output file.                                                                                 | XML (-outfmt 5) |

## Parameters in Workflow File

Type: blast-plus

| Parameter   | Parameter in the GUI | Type                                                                                                                                                                  |
|-------------|----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| blast-type  | Search type          | <i>string</i><br>Available values are: <ul style="list-style-type: none"><li>• blastn</li><li>• blastp</li><li>• blastx</li><li>• tblastn</li><li>• tblastx</li></ul> |
| db-path     | Database path        | <i>string</i>                                                                                                                                                         |
| db-name     | Database name        | <i>string</i>                                                                                                                                                         |
| tool-path   | Tool path            | <i>string</i>                                                                                                                                                         |
| temp-dir    | Temporary directory  | <i>string</i>                                                                                                                                                         |
| e-val       | Expected value       | <i>numeric</i>                                                                                                                                                        |
| max-hits    | Culling limit        | <i>numeric</i>                                                                                                                                                        |
| result-name | Annotate as          | <i>string</i>                                                                                                                                                         |

|                     |                          |                |
|---------------------|--------------------------|----------------|
| <b>gapped-aln</b>   | <b>Gapped alignment</b>  | <i>boolean</i> |
| <b>gap-costs</b>    | <b>Gap costs</b>         | <i>string</i>  |
| <b>match-scores</b> | <b>Match scores</b>      | <i>string</i>  |
| <b>blast-output</b> | <b>BLAST output</b>      | <i>string</i>  |
| <b>type-output</b>  | <b>BLAST output type</b> | <i>string</i>  |

## Input/Output Ports

The element has 1 *input port*:

**Name in GUI:** *Input sequence*

**Name in Workflow File:** in-sequence

**Slots:**

| Slot In GUI     | Slot in Workflow File | Type            |
|-----------------|-----------------------|-----------------|
| <b>Sequence</b> | <b>sequence</b>       | <i>sequence</i> |

And 1 *output port*:

**Name in GUI:** *Annotations*

**Name in Workflow File:** out-annotations

**Slots:**

| Slot In GUI               | Slot in Workflow File | Type                    |
|---------------------------|-----------------------|-------------------------|
| <b>Set of annotations</b> | <b>annotations</b>    | <i>annotation-table</i> |