

Local BLAST Search Element

Finds annotations for the supplied DNA sequence in local BLAST database.



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
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 (-m 7)

Parameters in Workflow File

Type: blast

Parameter	Parameter in the GUI	Type
blast-type	Search type	<i>string</i> Available values are: • blastn • blastp • blastx • tblastn • tblastx
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>
result-name	Annotate as	<i>string</i>
gapped-aln	Gapped alignment	<i>boolean</i>
gap-costs	Gap costs	<i>string</i>
match-scores	Match scores	<i>string</i>

blast-output	BLAST output	<i>string</i>
type-output	BLAST output type	<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
Sequence	sequence	<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
Set of annotations	annotations	<i>annotation-table</i>