

Local BLAST+ Search Element

Finds annotations for DNA sequence in a local BLAST database.

Element type: blast-plus



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

Parameter	Description	Default value	Parameter in Workflow File	Type
Search type	Selects the type of the BLAST searches.	blastn	blast-type	<i>string</i> Available values are: • blastn • blastp • blastx • tblastn • tblastx
Database path	Path to the database files.		db-path	<i>string</i>
Database name	Base name for BLAST DB files.		db-name	<i>string</i>
Tool path	Path to the BLAST executable.	default	tool-path	<i>string</i>
Temporary directory	Directory for temporary files.	default	temp-dir	<i>string</i>
Expected value	Expectation threshold value.	10	e-val	<i>numeric</i>
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	max-hits	<i>numeric</i>
Annotate as	Name of the result annotations.	blast_result	result-name	<i>string</i>
Gapped alignment	Perform gapped alignment.	use	gapped-aln	<i>boolean</i>
Gap costs	Cost to create and extend a gap in an alignment.	2 2	gap-costs	<i>string</i>
Match scores	Reward and penalty for matching and mismatching bases.	1 -3	match-scores	<i>string</i>
BLAST output	Location of BLAST output file.		blast-output	<i>string</i>
BLAST output type	Type of BLAST output file.	XML (-outfmt 5)	type-output	<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>