

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	string Available values are: <ul style="list-style-type: none">• blastn• blastp• blastx• tblastn• tblastx
Database path	Path to the database files.		db-path	string
Database name	Base name for BLAST DB files.		db-name	string
Tool path	Path to the BLAST executable.	default	tool-path	string
Temporary directory	Directory for temporary files.	default	temp-dir	string
Expected value	Expectation threshold value.	10	e-val	numeric
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	numeric
Annotate as	Name of the result annotations.	blast_result	result-name	string
Gapped alignment	Perform gapped alignment.	use	gapped-aln	boolean
Gap costs	Cost to create and extend a gap in an alignment.	2 2	gap-costs	string
Match scores	Reward and penalty for matching and mismatching bases.	1 -3	match-scores	string
BLAST output	Location of BLAST output file.		blast-output	string
BLAST output type	Type of BLAST output file.	XML (-outfmt 5)	type-output	string

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	sequence

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>