

Remote BLAST Element

Finds annotations for the supplied DNA sequence in the NCBI remote database.

Element type: **blast**

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Database	Selects the database to search through. Available databases are blastn, blastp and cdd.	ncbi-blastn	db	<i>string</i> Available values are: • ncbi-blastn • ncbi-blastp • ncbi-cdd
Database	Select the database to search through.		db	<i>string</i>
Expected value	This parameter specifies the statistical significance threshold of reporting matches against the database sequences.	10	e-val	<i>string</i>
Results limit	The maximum number of results.	10	hits	<i>numeric</i>
Megablast	Use megablast.	False	megablast	<i>boolean</i>
Short sequence	Optimizes search for short sequences.	False	short-sequence	<i>boolean</i>
Entrez query	Enter an Entrez query to limit search.		entrez-query	<i>string</i>
Annotate as	Name of the result annotations.		result-name	<i>string</i>
BLAST output	Location of the BLAST output file. This parameter insignificant for cdd search.		blast-output	<i>string</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>

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>