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

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**	*annotation-table*