

# 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
<b>Database</b>	Selects the database to search through. Available databases are blastn, blastp and cdd.	ncbi-blastn	<b>db</b>	<i>string</i> Available values are: <ul style="list-style-type: none"><li>• ncbi-blastn</li><li>• ncbi-blastp</li><li>• ncbi-cdd</li></ul>
<b>Database</b>	Select the database to search through.		<b>db</b>	<i>string</i>
<b>Expected value</b>	This parameter specifies the statistical significance threshold of reporting matches against the database sequences.	10	<b>e-val</b>	<i>string</i>
<b>Results limit</b>	The maximum number of results.	10	<b>hits</b>	<i>numeric</i>
<b>Megablast</b>	Use megablast.	False	<b>megablast</b>	<i>boolean</i>
<b>Short sequence</b>	Optimizes search for short sequences.	False	<b>short-sequence</b>	<i>boolean</i>
<b>Entrez query</b>	Enter an Entrez query to limit search.		<b>entrez-query</b>	<i>string</i>
<b>Annotate as</b>	Name of the result annotations.		<b>result-name</b>	<i>string</i>
<b>BLAST output</b>	Location of the BLAST output file. This parameter insignificant for cdd search.		<b>blast-output</b>	<i>string</i>
<b>Gap costs</b>	Cost to create and extend a gap in an alignment.	2 2	<b>gap-costs</b>	<i>string</i>
<b>Match scores</b>	Reward and penalty for matching and mismatching bases.	1 -3	<b>match-scores</b>	<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
<b>Sequence</b>	<b>sequence</b>	<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
<b>Set of annotations</b>	<b>annotations</b>	<i>annotation-table</i>