

# Gene-by-gene approach report

Output a table of genes found in a reference sequence.

## Parameters in GUI

Parameter	Description	Default value
<b>Output file</b>	File to store a report.	
<b>Annotation name</b>	Annotation name used to compare genes and reference genomes..	blast-result
<b>Existing file</b>	If a target report already exists you should specify how to handle that. Merge two table in one. Overwrite or Rename existing file..	Merge
<b>Identity cutoff</b>	Identity between gene sequence length and annotation length in per cent. BLAST identity (if specified) is checked after	90.0000%

## Parameters in Workflow File

**Type:** genebygene-report-id

Parameter	Parameter in the GUI	Type
<b>output-file</b>	<b>Output file</b>	<i>string</i>
<b>annotation_name</b>	<b>Annotation name</b>	<i>string</i>
<b>existing</b>	<b>Existing file</b>	<i>string</i>
<b>identity</b>	<b>Identity cutoff</b>	<i>numeric</i>

## Input/Output Ports

The element has 1 *input port*.

**Name in GUI:** Gene by gene report data

**Name in Workflow File:** in-data

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Input annotations</b>	<b>gene-ann</b>	<i>ann-table-list</i>
<b>Input sequences</b>	<b>gene-seq</b>	<i>seq</i>