# Gene-by-gene approach report

Output a table of genes found in a reference sequence.

## Parameters in GUI

| Parameter | Description | Default value |
|---|---|---|
| **Output file** | File to store a report. | |
| **Annotation name** | Annotation name used to compare genes and reference genomes.. | blast-result |
| **Existing file** | If a target report already exists you should specify how to handle that. Merge two table in one. Overwrite or Rename existing file.. | Merge |
| **Identity cutoff** | 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 |
|-----------|---------------------|------|
| **output-file** | **Output file** | *string* |
| **annotation_name** | **Annotation name** | *string* |
| **existing** | **Existing file** | *string* |
| **identity** | **Identity cutoff** | *numeric* |

## 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 |
|---|---|---|
| **Input annotations** | **gene-ann** | *ann-table-list* |
| **Input sequences** | **gene-seq** | *seq* |