

Importing Annotations from CSV

It is possible to import annotations for a sequence from an annotations table stored in the CSV format.

To import annotations from a CSV file, right-click on a *Project View* and select *Import Import annotations from CSV*. The following dialog box will appear:

U Import Annotations from CSV

File to read

Results

Result file

File format **Genbank**

☒ Add result file to project

Column separator value: [,], hex: [2c], length: 1

File parsing

☒ Column separator , **Guess**

☐ Script **Edit**

First lines to skip **Do not skip**

Skip all lines starts with the text #

☐ Interpret multiple separators like a single separator (try when separator is a whitespace character)

☒ Remove quotes

Default annotation name **misc_feature**

Results preview **Preview**

Raw file preview:

Run Cancel Help

Basically you need to specify the file to read annotations table from (*required*):

File to read

And the format of and the path to the file to write the annotations table into (*required*):

Results

Result file ...

File format

Check *Add result file to project* to link the annotations to the currently opened sequence.

☒ Add result file to project

To use a separator to split the table, check the *Column separator* item and specify the separator symbols. Also you can press *Guess* to try to detect the separator from the input file.

File parsing

☒ Column separator

Alternatively, you can press *Edit* and edit the script which will specify the separator for each parsed line. It is possible to use line number in the script.

Script Editor

Used script

Script text

```
//The script parses input line
// and returns an array of parsed elements as the result
var line; //input line
var lineNum; //parsed line number

var firstColumn = [lineNum];
var otherColumns = line.split(" ");
result =firstColumn.concat(otherColumns);
```

Line: 1

Using the arrows, you exclude the necessary number of lines at the beginning of the document from parsing. You can also skip all lines that start with the specified text.

First lines to skip

By pressing *Preview* one can bring up the view of the current annotations table (which is produced from the input file with the specified parameters values). The input file contents will also be shown at the bottom part of the dialog.

Results preview Preview

[ignored]	[ignored]	[ignored]	[ignored]
a1	10	20	pp
a1	19	40	ppe

Raw file preview:

```

name,start,end,qual1
a1,10,20,pp
a1,19,40,ppe

```

The preview table headline indicates the types of the information contained in the corresponding columns. By default the values are *[ignored]*. To specify a column role, click on the corresponding headline element:

U Select the Role of the Column ? X

Column role

☐ Annotation start position
☐ Add offset

☐ Annotation end position
☒ Inclusive

☐ Annotation length

☐ Complement strand mark
☐ Mark value

☐ Annotation name

☐ Annotation group

☐ Qualifier

☒ Ignore this column

OK
Cancel
Help

The annotation start and end positions must be specified. It is possible to add an offset to every read start position by checking the *Add offset* checkbox, and to shorten annotations by one from the end by unchecking the *Inclusive* checkbox.

When all the roles are specified, press *Run*. With the *Add to project* checkbox specified and a *Sequence View* opened, on success you will see the *Sequence View* with annotations linked:

