

# Package: victortools (via r-universe)

June 9, 2026

**Title** Manipulate the Output File from the Victor

**Version** 0.1

**URL** <https://github.com/sdhutchins/victortools>

**BugReports** <https://github.com/sdhutchins/victortools/issues>

**Description** This package will parse the output from the Victor, clean data, summarize data, and perform some basic stats functions that may be relevant for data analysis.

**Depends** R (>= 3.4.0)

**Imports** tidyverse, ggthemes, readxl, stats

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.0

**Date** 2018-10-02

**Suggests** testthat

**Config/pak/sysreqs**

cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev make libharfbuzz-dev libicu-dev libjpeg-dev libpng-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev libssl-dev libx11-dev zlib1g-dev

**Repository** <https://sdhutchins.r-universe.dev>

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add_metadata	<i>Add Metadata</i>
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### Description

Adds additional metadata to the metadata list

### Usage

```
add_metadata(metadata, title, data)
```

### Arguments

metadata	The input metadata list
title	The title or descriptor of the metadata
data	The output file from the Victor run

### Value

An updated list of metadata is returned

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ap1_cols	<i>API Expression Test columns</i>
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### Description

Use these columns when testing AP1 expression.

**Control** control well

**10 ng/ul PMA** experiemental well

### Usage

```
ap1_cols
```

### Format

An object of class character of length 2.

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cre_cols	<i>CRE Expression Test columns</i>
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**Description**

Use these columns when testing CRE expression.

**Control** control well

**10 uM Forskolin** experiemental well

**Usage**

cre\_cols

**Format**

An object of class character of length 2.

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expression_barplot	<i>Expression Barplot</i>
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**Description**

A barplot of expression data.

**Usage**

```
expression_barplot(assay_data)
```

**Arguments**

assay\_data      The assay data frame.

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get_assay_data	<i>Get Assay Data</i>
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**Description**

Retrieves and cleans assay results from Victor output file

**Usage**

```
get_assay_data(file)
```

**Arguments**

file	The output file from the Victor run
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**Value**

A dataframe of the assay results is returned

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get_metadata	<i>Get Metadata</i>
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**Description**

Retrieves metadata from Victor output file

**Usage**

```
get_metadata(file)
```

**Arguments**

file	The output file from the Victor run
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**Value**

A list of metadata is returned

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`import_victor_file`      *Import Victor File*

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**Description**

Imports and manipulates the victor file

**Usage**

`import_victor_file(filename)`

**Arguments**

`filename`      The output file from the Victor run

**Value**

Returns a list of assay and metadata from a Victor file

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`nfkb_cols`      *NFkB Expression Test columns*

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**Description**

Use these columns when testing NFkB expression.

**Control** control well

**10 ng/ul TNFa** experiemental well

**Usage**

`nfkb_cols`

**Format**

An object of class character of length 2.

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select_data	<i>Select Data</i>
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**Description**

Selects columns and rows from assay data to analyze

**Usage**

```
select_data(data, columns, rows)
```

**Arguments**

data	The assay data object.
columns	The rows to select.
rows	The rows to select.

**Value**

Returns a subsetting data object.

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sre_cols	<i>SRE Expression Test columns</i>
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**Description**

SRE Expression Test columns

**Usage**

```
sre_cols
```

**Format**

An object of class character of length 4.

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