

# Package ‘Toolsets’

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**Type** Package

**Title** Toolsets

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**Description** Toolsets

**License** GPL (>= 2)

**Depends** R (>= 3.0)

**LazyData** true

**Encoding** UTF-8

**RoxygenNote** 6.1.1

## R topics documented:

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example.function	<i>description of the example function</i>
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## Description

description of the example function

## Usage

```
example.function(param1 = NULL)
```

## Arguments

param1	param1
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**Value**

the return object

**Examples**

```
example.function()
```

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plot.violin	<i>draw violin plot</i>
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**Description**

draw violin plot

**Usage**

```
## S3 method for class 'violin'
plot(exprData, cellAnno, genes, use, direction = "h",
      showGroup = T, groupOrder = NULL)
```

**Arguments**

exprData	the expression matrix to be used
cellAnno	the annotation of the cells
genes	genes wanted to show
use	the group selected in the cellAnno
direction	direction of the violin plot
showGroup	whether to show the group names
groupOrder	the order of the group

**Value**

a ggplot violin object

**Examples**

```
options(repr.plot.width=4, repr.plot.height=9)
plot.violin(exprData=seuset@data, cellAnno=all_tsne_2, genes=key_genes, use="final", direction = "h")

all_tsne_3 <- subset(all_tsne_2, final %in% c('ctrl:c4','kif7:c4','ctrl:c6','kif7:c6'))
options(repr.plot.width=4, repr.plot.height=4)
plot.violin(exprData=seuset@data, cellAnno=all_tsne_3, genes=key_genes, use="final", direction = "h",
            groupOrder = c('ctrl:c4','kif7:c4','ctrl:c6','kif7:c6'))
```

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`toC_get_genes_of_GO_by_keyWords`*Get the genes of interested GO terms by some key words*

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**Description**

Get the genes of interested GO terms by some key words

**Usage**

```
toC_get_genes_of_GO_by_keyWords(organism = "hs", keyWords = "axon",  
  returnAll = F)
```

**Arguments**

<code>organism</code>	organism (hs and mm)
<code>keyWords</code>	keyWords (for grey function, e.g. cell cycle DNA replication)
<code>returnAll</code>	if return all the GO terms

**Value**

a list with the GO terms and genes

**Examples**

```
tmpList <- toC_get_genes_of_GO_by_keyWords(organism = "hs", keyWords = "axon", returnAll = F)  
tmpList <- toC_get_genes_of_GO_by_keyWords(organism = "hs",  
  keyWords = "cell cycle|DNA replication|cell division|segregation")
```

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