

Package ‘facsDorit’

April 14, 2020

Version 1.28.0

Date 2006-06-08

Title DKFZ FACS example data

Author Florian Hahne <f.hahne@dfkz-heidelberg.de>

Depends R (>= 1.9.1), prada (>= 1.0.5)

Maintainer Florian Hahne <f.hahne@dfkz-heidelberg.de>

Description FACS example data for cell-based assays. This data is used in the examples and vignettes of the package prada.

License GPL-2

URL <http://www.dkfz.de/mga>

biocViews ExperimentData, MicrotitrePlateAssayData

git_url <https://git.bioconductor.org/packages/facsDorit>

git_branch RELEASE_3_10

git_last_commit f3cb404

git_last_commit_date 2019-10-29

Date/Publication 2020-04-14

R topics documented:

| | |
|---|----------|
| Apoptosis and MAP-Kinase example data | 1 |
| Index | 3 |

Apoptosis and MAP-Kinase example data
FACS data for cell-based apoptosis assay

Description

Set of FCS 3.0 files containing FACS data for each well of a 96 well microtitre plate

Format

map and apoptosis are directories, each containing 96 FCS 3.0 files derived from a FACS experiment to characterize effectors of the MAP-Kinase and apoptotic pathways, respectively. The files may be imported using function readFCS (for single files) or function readCytoSet (for all files in the directory).

Source

Mamatha Sauermann (apoptosis), Meher Majety (MAP-Kinase), both at DKFZ Heidelberg

See Also

[readFCS](#), [readCytoSet](#)

Examples

```
apo <- readFCS(system.file("extdata", "apoptosis",
                          "test2933T3.A01", package="facsDorit"))
apo
exprs(apo[1:3,])
description(apo)[3:6]

map <- readFCS(system.file("extdata", "map",
                          "060304MAPK_controls.A01", package="facsDorit"))
map
exprs(map[1:3,])
description(map)[3:6]
```

Index

Apoptosis and MAP-Kinase example data,
[1](#)

facsdorit (Apoptosis and MAP-Kinase
example data), [1](#)

readCytoSet, [2](#)

readFCS, [2](#)