

Package ‘facsDorit’

October 17, 2019

Version 1.26.0

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_9

git_last_commit b446230

git_last_commit_date 2019-05-02

Date/Publication 2019-10-17

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](#)