

Package ‘facsDorit’

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Title DKFZ FACS example data

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

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

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

biocViews ExperimentData, MicrotitrePlateAssayData

NeedsCompilation no

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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 Saueremann (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]
```

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