

# Package ‘facsDorit’

October 18, 2017

**Version** 1.18.0

**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

**NeedsCompilation** no

## R topics documented:

Apoptosis and MAP-Kinase example data . . . . .	1
<b>Index</b>	<b>3</b>

---

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](#)