

# 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.

**License** GPL-2

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

**biocViews** ExperimentData, MicrotitrePlateAssayData

**git\_url** <https://git.bioconductor.org/packages/facsDorit>

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

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### 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]
```

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