

# Package ‘faahKO’

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**Version** 1.10.0

**Date** 2012-07-31

**Title** Saghatelian et al. (2004) FAAH knockout LC/MS data

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**Depends** xcms

**ZipData** no

**Description** Positive ionization mode data in NetCDF file format.  
Centroided subset from 200-600 m/z and 2500-4500 seconds. Data originally reported in "Assignment of Endogenous Substrates to Enzymes by Global Metabolite Profiling" *Biochemistry*; 2004; 43(45). Also includes detected peaks in an xcmsSet.

**biocViews** ExperimentData, MassSpectrometryData

**License** LGPL

**URL** <http://dx.doi.org/10.1021/bi0480335>

**NeedsCompilation** no

## R topics documented:

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faahko *FAAH knockout LC/MS data xcmsSet*

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## Description

xcmsSet object containing quantitated LC/MS peaks from the spinal cords of 6 wild-type and 6 FAAH knockout mice. The data is a subset of the original data from 200-600 m/z and 2500-4500 seconds. It was collected in positive ionization mode.

**Usage**

```
data(faahko)
```

**Format**

The format is:

```
Formal class 'xcmsSet' [package "xcms"] with 8 slots
..@ peaks      : num [1:4776, 1:11] 200 201 205 206 207 ...
..@ groups     : logi[0 , 0 ]
..@ groupidx   : list()
..@ sampnames  : chr [1:12] "ko15" "ko16" "ko18" "ko19" ...
..@ sampclass  : Factor w/ 2 levels "KO","WT": 1 1 1 1 1 1 2 2 2 ...
..@ rt         :List of 2
.. ..$ raw     :List of 12
.. ..$ corrected:List of 12
..@ filepaths  : chr [1:12] ...
..@ profinfo   :List of 2
.. ..$ method  : chr "bin"
.. ..$ step    : num 0.1
```

**Details**

The corresponding raw NetCDF files are located in the `cdf` subdirectory of this package.

**Source**

<http://dx.doi.org/10.1021/bi0480335>

**References**

Saghatelian A, Trauger SA, Want EJ, Hawkins EG, Siuzdak G, Cravatt BF. Assignment of endogenous substrates to enzymes by global metabolite profiling. *Biochemistry*. 2004 Nov 16;43(45):14332-9.

**See Also**

[xcmsSet](#), [xcmsRaw](#)

**Examples**

```
## The directory with the NetCDF LC/MS files
cdfpath <- file.path(find.package("faahKO"), "cdf")
cdfpath
list.files(cdfpath, recursive = TRUE)

if (require(xcms)) {

## xcmsSet Summary
show(faahko)
```

```
## Access raw data file
ko15 <- xcmsRaw(filepaths(faahko)[1], profmethod = "bin", profstep = 0.1)
ko15

}
```

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\*Topic **datasets**

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