

# Package ‘faahKO’

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**Version** 1.34.0

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

**Author** Colin A. Smith <csmith@scripps.edu>

**Maintainer** Steffen Neumann <sneumann@ipb-halle.de>

**Depends** R (>= 2.10), xcms (>= 3.4.0)

**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>

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

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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 "K0","WT": 1 1 1 1 1 1 2 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

}
```

faahko3

*FAAH knockout LC/MS data XCMSnExp***Description**

XCMSnExp 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(faahko3)
```

**Format**

The format is:

```
MSn experiment data ("XCMSnExp")
Object size in memory: 4.59 Mb
- - - Spectra data - - -
  MS level(s): 1
  Number of spectra: 15336
  MSn retention times: 41:32 - 75:14 minutes
- - - Processing information - - -
Data loaded [Tue Mar 24 13:28:38 2020]
  MSnbase version: 2.13.2
- - - Meta data - - -
phenoData
  rowNames: 1 2 ... 12 (12 total)
  varLabels: sample_name sample_group
  varMetadata: labelDescription
```

```
Loaded from:
  [1] ko15.CDF... [12] wt22.CDF
  Use 'fileNames(.)' to see all files.
protocolData: none
featureData
  featureNames: F01.S0001 F01.S0002 ... F12.S1278 (15336 total)
  fvarLabels: fileIdx spIdx ... spectrum (33 total)
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
- - - xcms preprocessing - - -
Chromatographic peak detection:
  method: centWave
  5627 peaks identified in 12 samples.
  On average 469 chromatographic peaks per sample.
Alignment/retention time adjustment:
  method: peak groups
Correspondence:
  method: chromatographic peak density
  206 features identified.
  Median mz range of features: 0.10001
  Median rt range of features: 28.965
  325 filled peaks (on average 27.08333 per sample).
```

## 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

[OnDiskMSnExp](#), [XCMSnExp](#)

## Examples

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

data(faahko3)
```

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```
## XCMSnExp Summary  
show(faahko3)
```

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