Package ‘faahKO’

September 23, 2012

Version 1.2.11

Date 2012-07-31

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

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

Maintainer Colin A. Smith <`csmith@scripps.edu`>

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`

R topics documented:

faahko 1

Index **4**

`faahko` *FAAH knockout LC/MS data xcmsSet*

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 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
```

```
    }
```

Index

∗Topic **datasets**
    `faahko`, 1

`faahKO` *(`faahko`)*, 1
`faahko`, 1

`xcmsRaw`, *2*
`xcmsSet`, *2*