

faahKO

April 2, 2010

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](#)