

Package ‘PtH2O2lipids’

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Title P. tricornutum HPLC-ESI-MS Lipid Data from van Creveld et al. (2015)

Version 1.2.0

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Depends R (>= 3.3), xcms, CAMERA, LOBSTAHS, methods, utils

Suggests gplots, RColorBrewer, cluster, vegan, clustsig

Description Annotated HPLC-ESI-MS lipid data in positive ionization mode from an experiment in which cultures of the marine diatom *Phaeodactylum tricornutum* were treated with various concentrations of hydrogen peroxide (H2O2) to induce oxidative stress. The experiment is described in Graff van Creveld, et al., 2015, "Early perturbation in mitochondria redox homeostasis in response to environmental stress predicts cell fate in diatoms," ISME Journal 9:385-395. PtH2O2lipids consists of two objects: A CAMERA xsAnnotate object (ptH2O2lipids\$xsAnnotate) and LOBSTAHS LOBSet object (ptH2O2lipids\$xsAnnotate\$LOBSet). The LOBSet includes putative compound assignments from the default LOBSTAHS database. Isomer annotation is recorded in three other LOBSet slots.

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URL <http://dx.doi.org/10.1038/ismej.2014.136>,
<https://github.com/vanmooylipidomics/PtH2O2lipids>,
<http://www.whoi.edu/page.do?pid=133616&tid=282&cid=192529>

BugReports <https://github.com/vanmooylipidomics/PtH2O2lipids/issues/new>

biocViews ReproducibleResearch, CellCulture, MassSpectrometryData, Phaeodactylum_tricornutum_data

NeedsCompilation no

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Details

ptH2O2lipids\$LOBSet includes compound identifications assigned from the default LOBSTAHS positive mode database. ptH2O2lipids\$LOBSet also includes in the slots iso_C3r, iso_C3f, and iso_C3c the various possible isomers identified for each compound. Note that all other slots in the ptH2O2lipids object can be accessed using the accessor functions described for the "LOBSet-class" object class.

The dataset contains peaks from 16 samples that span three H2O2 treatments (0, 30 and 150 μ M) and three timepoints (+4, +8, and +24 hours) in duplicate. The dataset contains only one replicate sample for the 0 and 150 μ M treatments at +4h.

The mzXML files and Thermo .raw files from which these objects are derived can be accessed at <https://github.com/vanmooylipidomics/PtH2O2lipids/tree/master/mzXML> and <http://www.whoii.edu/page.do?pid=133616&tid=282&cid=192529>, respectively.

Users should note that the LOBSet in this package does not include any PUA (polyunsaturated aldehyde) identifications.

Source

<http://www.nature.com/ismej/journal/v9/n2/full/ismej2014136a.html>

References

Collins, J.R., B.R. Edwards, H.F. Fredricks, and B.A.S. Van Mooy. 2016. LOBSTAHS: An adduct-based lipidomics strategy for discovery and identification of oxidative stress biomarkers. *Analytical Chemistry*.

Graff van Creveld, et al., 2015, "Early perturbation in mitochondria redox homeostasis in response to environmental stress predicts cell fate in diatoms", *ISME Journal* 9:385-395

See Also

[LOBSet-class](#), [LOBSet](#), [doLOBscreen](#), [getLOBpeaklist](#), [xcmsSet](#), [xsAnnotate](#)

Examples

```
## generate the object in ptH2O2lipids$LOBSet using ptH2O2lipids$xsAnnotate as
## input
library(PtH2O2lipids)

## yields output identical to ptH2O2lipids$LOBSet
myPtH2O2LOBSet = doLOBscreen(ptH2O2lipids$xsAnnotate, polarity = "positive",
database = NULL, remove.iso = TRUE, rt.restrict = TRUE, rt.windows = NULL,
exclude.oddFA = TRUE, match.ppm = 2.5)

## access xsAnnotate object
ptH2O2lipids$xsAnnotate

## access xcmsSet
ptH2O2lipids$xsAnnotate@xcmsSet
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