

# Package ‘PtH2O2lipids’

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

**Version** 1.32.0

**Date** 2016-07-06

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

**Suggests** gplots, RColorBrewer, cluster, vegan

**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 (H<sub>2</sub>O<sub>2</sub>) 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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## Description

Positive ionization mode HPLC-ESI-MS lipid data 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. `ptH2O2lipids$LOBSet` was generated from `ptH2O2lipids$xsAnnotate` using the `LOBSTAHS` function [doLOBscreen](#).

## Usage

```
data(ptH2O2lipids)
```

## Format

A list object containing the lipid data in two forms:

`ptH2O2lipids$LOBSet` A 1.2 MB object of formal class "`LOBSet`" containing screened peak data to which compound assignments and isomer identifications have been made. The structure of `ptH2O2lipids$LOBSet` is:

```
Formal class 'LOBSet' [package "LOBSTAHS"] with 9 slots
 ..@ peakdata          : 'data.frame': 2056 obs. of 54 variables
 ..@ iso_C3r           : List of 2056
 ..@ iso_C3f           : List of 2056
 ..@ iso_C3c           : List of 2056
 ..@ LOBscreen_diagnostics: 'data.frame': 6 obs. of 4 variables:
 ..@ LOBisoID_diagnostics : 'data.frame': 3 obs. of 2 variables:
 ..@ LOBscreen_settings  : List of 6
 .. ..$ database         : chr "default"
 .. ..$ remove.iso       : logi TRUE
 .. ..$ rt.restrict      : logi TRUE
 .. ..$ rt.windows       : chr "default"
 .. ..$ exclude.oddFA    : logi TRUE
 .. ..$ match.ppm        : num 2.5
 ..@ polarity           : Factor w/ 1 level "positive": 1
 ..@ samplenames        : chr [1:16] "0uM_24h_Orbi_0468" "0uM_24h_Orbi_0473" "0uM_4h_Orbi_0476"
```

ptH2O2lipids\$xsAnnotate An 80 MB object of formal class "xsAnnotate" containing 18,314 peakgroups in 5,080 pseudospectra. This is the object from which ptH2O2lipids\$LOBSet was created using doLOBscreen. It includes annotation of possible isotope peaks from findIsotopes. The xcmsSet from which the xsAnnotate object was created (64.5 MB) can be accessed at ptH2O2lipids\$xsAnnotate@xcmsSet.

## 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  $\mu\text{M}$ ) and three timepoints (+4, +8, and +24 hours) in duplicate. The dataset contains only one replicate sample for the 0 and 150  $\mu\text{M}$  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.who.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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