# Package 'tartare'

April 14, 2020

**Type** Package

**Title** Raw ground spectra recorded on Thermo Fisher Scientific mass
spectrometers

**Version** 1.0.0

**Depends** R (>= 3.6), AnnotationHub (>= 2.16), ExperimentHub (>= 1.0)

**Imports** utils

**Suggests** BiocStyle, knitr, testthat, tools

**Description** provides raw files (size=278MBytes) recorded on different Liquid
Chromatography Mass Spectrometry (LC-MS) instruments. All included MS
instruments are manufactured by Thermo Fisher Scientific and belong to the
Orbitrap Tribrid or Q Exactive Orbitrap family of instruments. Despite their
common origin and shared hardware components (e.g. Orbitrap mass analyser),
the above instruments tend to write data in different ``dialects'' in a shared
binary file format (.raw). The intention behind tartare is to provide complex
but slim real-world files that can be used to make code robust with respect
to this diversity. In other words, it is intended for enhanced unit testing.
The package is considered to be used with the
rawDiag package (Trachsel, 2018 <doi:10.1021/acs.jproteome.8b00173>) and the
Spectra MsBackends.

**URL** https://github.com/cpanse/tartare

**BugReports** https://github.com/cpanse/tartare/issues

**Encoding** UTF-8

**NeedsCompilation** no

**biocViews** ExperimentData, MassSpectrometryData, ExperimentHub

**RoxygenNote** 6.1.1

**License** GPL-3

**VignetteBuilder** knitr

**Collate** tartare.R zzz.R

**git_url** https://git.bioconductor.org/packages/tartare

**git_branch** RELEASE_3_10

**git_last_commit** 16343af

**git_last_commit_date** 2019-10-29

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# R topics documented:

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getFilename                    *downloads files from aws storage and returns local filepath*

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### Description

calls the query method of an ExperimentHub object query and returns the local filenames. Of note: for proprietary reasons, a file.link is set to the cached files. It seems that the New RawfileReader .Net library is only accepting files ending with raw. The overall file size is 285MB.

### Usage

```
getFilename(eh, query = c("tartare"))
```

### Arguments

eh              ExperimentHub object.

query           a query string, e.g., c('tartar','20190710_003_PierceHeLaProteinDigestStd.raw')

### Value

returns file(s) contained in the tartare package.

### Author(s)

Christian Panse <cp@fgcz.ethz.ch>, 2019-10

### See Also

• browseVignettes('tartare')

• query

### Examples

```
library(ExperimentHub)
eh <- ExperimentHub()
query(eh, c('tartare'))

## Not run:
(files <- getFilename(eh))
library(MsBackendRawFileReader)

be <- lapply(files, function(f){
```

```
if (grepl("mzXML$", f))
    backendInitialize(MsBackendMzR(), files = f)
else
    backendInitialize(MsBackendRawFileReader(), files = f, extra=FALSE)
})

## End(Not run)

## Not run:
hfx.filename <- .query(eh, c('tartar', '20190710_003_PierceHeLaProteinDigestStd.raw'))
x <- .cnew ("Rawfile", hfx.filename)
x$GetInfoValues()

## End(Not run)
```

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