

Package ‘adductData’

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Title Data from untargeted MS of modifications to Cys34 of serum albumin

Version 1.20.0

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Description mzXML files from Grigoryan et al 2016 (Anal Chem).

Depends R (>= 3.6)

Imports ExperimentHub (>= 1.9.0), AnnotationHub (>= 2.13.10), stats (>= 3.5.0), utils (>= 3.5.0), methods (>= 3.5.0), datasets (>= 3.5.0)

Suggests knitr (>= 1.15.1), rmarkdown (>= 1.5)

License Artistic-2.0

LazyData false

LazyLoad false

Encoding UTF-8

RoxygenNote 6.1.0

biocViews ExperimentData,MassSpectrometryData,ExperimentHub

VignetteBuilder knitr

git_url <https://git.bioconductor.org/packages/adductData>

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|------------|---|
| adductData | <i>Adduct data from Grigoryan et al 2016. This package contains 2 mzXML files from Grigoryan et al that were used to perform adductomics.</i> |
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Description

Adduct data from Grigoryan et al 2016. This package contains 2 mzXML files from Grigoryan et al that were used to perform adductomics.

Value

2 mzXML files and processed data

Source

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5555296/>

Examples

```
## Not run:  
hub <- ExperimentHub::ExperimentHub()  
x <- AnnotationHub::query(hub, c("adductData"))  
## download resource  
data = x[[1]]  
  
## End(Not run)
```

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* **utilities**

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