

# Package ‘adductData’

December 19, 2024

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

**Version** 1.22.0

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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>

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** 337b703

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

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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/PMC555296/>

**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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