## Package 'msPurityData'

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Type Package	
<b>Title</b> Fragmentation spectral libraries and data to test the msPurity package	
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<b>Description</b> Fragmentation spectral libraries and data to test the msPurity package	
License GPL (>= 2)	
LazyData TRUE	
VignetteBuilder knitr	
RoxygenNote 5.0.1	
Suggests knitr	
biocViews ExperimentData, MassSpectrometryData	
NeedsCompilation no	
git_url https://git.bioconductor.org/packages/msPurityData	
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## **Description**

This data package contains test data to be used with package msPurity, see folders lcms and dims. This contains LC-MS, LC-MS/MS and DI-MS datasets in mzML format. There are also various .csv files and .rds files representing model outputs from the msPurity package. The LC-MS, LC-MS/MS and DI-MS datasets have been reduced in size by reducing the number of scans and m/z range.

The data package also contains a fragmentation spectral library created by msp2db (https://msp2db.readthedocs.io/en/late with data from MassBank, GNPS, LipidBlast and HMDB. This is the default spectral library that is used with the spectral\_matching with msPurity. The library data is from MoNA (http://mona.fiehnlab.ucdavis.edu/downloaded on 5th November 2018.

The dataset also contains data relating to the msPurity publication.

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