Package 'synapterdata'

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Type Package

Title Data accompanying the synapter package

Version 1.0.1

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Description Data independant acquisition of UPS1 protein mix in an E. coli background obtained on a Waters Synapt G2 instrument.

Depends R (>= 2.10), synapter (>= 0.99.6)

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R topics documented:

`synapterdata-package` *Data accompanying the synapter package*

Description

Data independant acquisition of UPS1 protein mix in an *E. coli* background obtained on a Waters Synapt G2 instrument.

Details

See the synapter package for details.

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```
getHDMSeFinalPeptide    PLGS csv data and fasta files
getMaster               Get _master_ HDMSe data
ups25a                  Synapter spiked-in example data.
```

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References

Shliaha P.V., Gatto L., Bond N.J. and Lilley K.S. Synapter: Improving qualitative and quantitative performance for label free proteomics, in prep.

Shliaha, P.V., Bond N.J., Gatto L. and Lilley K.S. The Effects of Ion Mobility Separation on Data Independent Acquisition in Proteomics Studies., in prep.

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getHDMSeFinalPeptide *PLGS csv data and fasta files*

Description

The PLGS HDMSe final peptide, MSe final peptide and MSe Pep3D output files are provided as gzipped csv files and their repective full paths can be obtained with `getHDMSeFinalPeptide`, `getMSeFinalPeptide` and `getMSePep3D`. These can then be used directly in the respective `synpater` functions and methods, as `read.csv` automatically uncompressed the files.

The fasta database file is also available in as a gnuzip archive. Fasta file are however not automatically handled in gzipped format. `getFasta` first decompresses the file in a temporary directory and returns the full path to that uncompressed file.

Usage

```
getHDMSeFinalPeptide()
getMSeFinalPeptide()
getMSePep3D()
getFasta()
```

Examples

```
getHDMSeFinalPeptide()
```

getMaster *Get* master *HDMSe data*

Description

TODO A concise (1-5 lines) description of what the function does.

Usage

```
getMaster()
loadMaster()
```

Details

TODO If necessary, more details than the description above

Author(s)

Laurent Gatto <lg390@cam.ac.uk>

References

Bond N. J., Shliaha P.V., Gatto L. and Lilley K.S., in prep.

See the `synapter` vignette from the `synapter` package, available with `ysnapterGuide()` for a description of the underlying concepts and detailed description of the pipeline.

See Also

`ups25a` and `getHDMSeFinalPeptide`

Examples

```
loadMaster()
master
```

ups25a `Synapter` *spiked-in example data.*

Description

Objects of class `Synapter`, implented in the `synapter` package. The 6 instances represent triplicate run of the Universal Proteomics Standard (UPS1) 48 protein mix in an E. coli background, spiked in at 25 and 50 femtomoles.

Usage

```
data(ups25c)
```

Details

Each instance has been created with the `synergise` function. The respective MSe final petptide and MSe Pep3D final are also provided in the package (see `getMSeFinalPeptide` and `getMSePep3D`). The identification peptides is a master HDMSe file (see `getMaster`). The code generating the instances is available in the `synergise.R` R file, in the `scripts` package directory.

Source

Bond N. J., Shliaha P.V., Gatto L. and Lilley K.S., in prep.

References

See the `synapter` vignette from the `synapter` package, available with `ysnapterGuide()` for a description of the underlying concepts and detailed description of the pipeline.

Examples

```
library(synapter)
data(ups25a)
performance(ups25a)
```

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