Package 'plantGlycoMS'

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Type Package

Title A package for processing plant glycosylation MS data

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Description A package for processing plant glycosylation MS data.

License GPL-2

LazyLoad yes

Imports protViz

RoxygenNote 6.0.1

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

`glycoChainSaw` *glycoChainSaw*

Description

This function takes in the results of an in silico digest with chainsaw in tsv format, optionally adds the mass for carbamidomethylation of cysteines (+57) as a fixed modification, optionally adds the mass for oxidation of methionine (+16) as a variable modification, and optionally returns a list of only peptides with a glycosylation site.

Usage

```
glycoChainSaw(digest.N, digest.n, carbamidomethylation = TRUE,
  methionineOxidation = TRUE, glycoOnly = TRUE)
```

Arguments

digest.N	a chainsaw in silico digest with all glycosylation sites having a capital n (N).
digest.n	a chainsaw in silico digest with all glycosylation sites having a lower case n.
carbamidomethylation	if TRUE, 57 Da is added to the peptide mass for every cysteine present, default=TRUE
methionineOxidation	if TRUE, 16 Da is added to the peptide mass for every methionine present,and a new row is added to the table so that every methionine containing peptide has a value for oxidized and not oxidized, default=TRUE
glycoOnly	if TRUE, return a dataframe containing only data for peptide with glycosylation sites, default=TRUE

Value

A data.frame with modified in silico digest results

PreferredDeltaMasses *PreferredDeltaMasses*

Description

this function is used to make a vector of glycan masses with "N!P[ST] * " pasted in front of the glycan masses which can be pasted into a MyriMatch configuration file.

Usage

```
PreferredDeltaMasses(input)
```

Arguments

input	A vector of glycan masses (from the pGlycoFilter function)

Value

A vector of glycan masses with "N!P[ST] * " pasted in front of the glycan masses

spectrumTable *spectrumTable*

Description

This function calculates the monoisotopic precursor mass from the precursor mz.

Usage

```
spectrumTable(input)
```

Arguments

input	The name of the csv file containing precursor m/z values. For the MiMB workflow, use the precursor m/z column of the spectrum table obtained from an msaccess search (proteowizard).

Value

This function returns a data.frame including the input and additionally the monoisotopic precursor masses.

Index