

Package ‘PTMods’

April 4, 2026

Type Package

Version 0.99.3

Title Managing Post-Translational Modifications in R

Description An interface to the community supported database for amino acid/protein modifications using mass spectrometry.

Depends R (>= 4.5.0), methods

Suggests xml2, testthat, knitr, BiocStyle, Biostrings

Enhances PSMATCH

License GPL-3

VignetteBuilder knitr

biocViews Proteomics, MassSpectrometry

BugReports <https://github.com/RforMassSpectrometry/PTMods/issues>

URL <https://github.com/RforMassSpectrometry/PTMods>

RoxygenNote 7.3.3

Encoding UTF-8

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

git_branch devel

git_last_commit 19e3a93

git_last_commit_date 2026-03-23

Repository Bioconductor 3.23

Date/Publication 2026-04-03

Author Laurent Gatto [aut] (ORCID: <<https://orcid.org/0000-0002-1520-2268>>),
Sebastian Gibb [aut] (ORCID: <<https://orcid.org/0000-0001-7406-4443>>),
Guillaume Deflandre [cre] (ORCID:
<<https://orcid.org/0009-0008-1257-2416>>)

Maintainer Guillaume Deflandre <guillaume.deflandre@uclouvain.be>

Contents

PTMods-package	2
addFixedModifications	3
addModifications	4
addVariableModifications	6
aminoacids	7
combineModifications	8
convertAnnotation	8
elements	10
getCanonicalSequence	11
modifications	11
Index	13

PTMods-package	<i>Managing amino acid modifications for mass spectrometry in R.</i>
----------------	--

Description

The ‘PTMods’ package focuses on handling post-translational modifications (PTMs). It distributes PTMs from the Unimod database and allows to convert PTM annotations between multiple formats.

Author(s)

Maintainer: Guillaume Deflandre <guillaume.deflandre@uclouvain.be> ([ORCID](#))

Authors:

- Laurent Gatto <laurent.gatto@uclouvain.be> ([ORCID](#))
- Sebastian Gibb <mail@sebastiangibb.de> ([ORCID](#))

References

<https://github.com/RforMassSpectrometry/PTMods/>

See Also

Useful links:

- <https://github.com/RforMassSpectrometry/PTMods>
- Report bugs at <https://github.com/RforMassSpectrometry/PTMods/issues>

addFixedModifications *Add fixed modifications*

Description

Applies fixed modifications to peptide sequences.

The annotation style of modifications already present in 'sequences' is preserved as-is. The annotation style of newly applied modifications matches the style supplied in 'fixedModifications': numeric values produce deltaMass notation (e.g. '[+79.966331]'), while character values are used verbatim (e.g. '[Phospho]' or '[UNIMOD:21]').

Usage

```
addFixedModifications(sequences, fixedModifications = NULL)
```

Arguments

sequences Character vector. Peptide sequences that may have modifications or not.

fixedModifications Named 'numeric' or 'character'. If a 'character' is given, values must be in UniMod name or UniMod ID format (e.g. "Phospho", "UNIMOD:21"). The annotation style of the values is preserved in the output. Specifies which fixed modifications are applied to which amino acids.

Value

A named list of character strings with all fixed modifications applied to the corresponding amino acids, one element per input sequence.

Author(s)

Guillaume Deflandre <guillaume.deflandre@uclouvain.be>

Examples

```
addFixedModifications("ATCK", fixedModifications = c(Nterm = 304, C = 57.02146))
addFixedModifications("ATSK", fixedModifications = c(A = -42, S = 79.966331))
addFixedModifications("ATK", fixedModifications = c(T = "Phospho", A = 42))
addFixedModifications("A[+42]TK", fixedModifications = c(T = "Phospho"))
addFixedModifications("AT[+79.966]AK", fixedModifications = c(A = 42))
addFixedModifications("ATA[+79.966]K", fixedModifications = c(A = 42))
```

addModifications *Add fixed and variable modifications to peptide sequences*

Description

A convenience wrapper around [addFixedModifications()] and [addVariableModifications()] that applies both fixed and variable modifications in a single call. Fixed modifications are applied first, followed by the enumeration of all possible combinations of variable modifications. Optionally, the annotation style of the output can be converted via [convertAnnotation()].

Usage

```
addModifications(
    sequences,
    fixedModifications = NULL,
    variableModifications = NULL,
    convertToStyle = NULL,
    ...
)
```

Arguments

sequences 'character'. Peptide sequences with or without existing modification annotations. Modifications must be enclosed in square brackets (e.g. "AT[+79.966]K", "[+304]-ATK").

fixedModifications Named 'numeric' or 'character', or 'NULL'. Fixed modifications to be applied unconditionally to the specified amino acids or termini. Names correspond to single-letter amino acid codes, "Nterm", or "Cterm". If 'character', values must be in UniMod name or UniMod ID format (e.g. "Phospho", "UNIMOD:21"). See [addFixedModifications()] for full details. Set to 'NULL' to skip.

variableModifications Named 'numeric' or 'character', or 'NULL'. Variable modifications to enumerate over the specified amino acids. Names correspond to single-letter amino acid codes. If 'character', values must be in UniMod name or UniMod ID format. See [addVariableModifications()] for full details. Set to 'NULL' to skip.

convertToStyle 'character(1)'. Controls the annotation format of modifications in the returned sequences. One of:

- 'NULL' (default) Same as input modification style.
- 'deltaMass' Delta mass notation, e.g. '[+79.966]'.
- 'unimodId' UniMod ID notation, e.g. '[UNIMOD:21]'.
- 'name' UniMod name notation, e.g. '[Phospho]'.

Conversion is performed by [convertAnnotation()].

... Additional arguments passed to the underlying modification functions. Currently supported:

- ‘**maxMods**’ Forwarded to [addVariableModifications()]. A ‘numeric(1)’ specifying the maximum number of variable modifications that may be applied simultaneously. Defaults to ‘Inf’.

Value

A ‘character’ vector of peptidoforms. The length is greater than or equal to ‘length(sequences)’, as each input sequence may expand into multiple peptidoforms corresponding to all combinations of variable modifications.

Author(s)

Guillaume Deflandre <guillaume.deflandre@uclouvain.be>

See Also

- * [addFixedModifications](#) for applying fixed modifications.
- * [addVariableModifications](#) for enumerating variable modification combinations.
- * [convertAnnotation](#) for converting between modification annotation styles.

Examples

```
## Fixed modifications only
addModifications(
  c("ATCK", "PEPCK"),
  fixedModifications = c(C = 57.02146)
)

## Variable modifications only
addModifications(
  c("ATSK", "PEPTSK"),
  variableModifications = c(S = 79.966331, T = 79.966331),
  maxMods = 2
)

## Both fixed and variable modifications
addModifications(
  "ATCSK",
  fixedModifications = c(C = 57.02146),
  variableModifications = c(S = 79.966331, T = 79.966331),
  maxMods = 1
)

## Return annotations in UniMod name style
addModifications(
  "ATSK",
  variableModifications = c(S = 79.966331, T = 79.966331),
  convertToStyle = "name"
)
```

```
## N-terminal fixed modification with variable modifications
addModifications(
  "ATSK",
  fixedModifications = c(Nterm = 304),
  variableModifications = c(S = 79.966331)
)
```

```
addVariableModifications
  Add variable modifications
```

Description

Generates all possible combinations of variable modifications for peptide sequences.

The annotation style of modifications already present in ‘sequences’ is preserved as-is. The annotation style of newly applied modifications matches the style supplied in ‘variableModifications’: numeric values produce deltaMass notation (e.g. ‘[+79.966331]’), while character values are used verbatim (e.g. ‘[Phospho]’ or ‘[UNIMOD:21]’).

Usage

```
addVariableModifications(
  sequences,
  variableModifications = NULL,
  maxMods = Inf
)
```

Arguments

sequences	Character vector. Peptide sequences that may have modifications or not.
variableModifications	Named ‘numeric’ or ‘character’. If a ‘character’ is given, values must be in UniMod name or UniMod ID format (e.g. ‘Phospho’, ‘UNIMOD:21’). The annotation style of the values is preserved in the output. Specifies which variable modifications are used on which amino acids.
maxMods	Numeric. Indicates how many modifications can be applied at once.

Value

A named list of character vectors with all possible combinations of modifications, one element per input sequence.

Author(s)

Guillaume Deflandre <guillaume.deflandre@uclouvain.be>

Examples

```
addVariableModifications("APGHKA", variableModifications = c(A = 4, K = 5, S = 8), maxMods = 2)
addVariableModifications("APGHKA", variableModifications = c(A = 4, K = 5, S = 8), maxMods = 3)
addVariableModifications(c("ATK", "PAK"), variableModifications = c(T = "Phospho", A = "UNIMOD:1"))
addVariableModifications("A[+10]KT[-5]", variableModifications = c(A = -20, T = "Phospho"))
```

aminoacids

Amminoacids data set.

Description

‘data.frame’ of aminoacids from the unimod database.

Usage

```
data("aminoacids")
```

Format

A ‘data.frame’ with 11 columns (OneLetter, ThreeLetter, FullName, AvgMass, MonoMass, H, C, N, O S, Se) for the aminoacids. The H/C/N/O/S/Se columns contain the number of elements that build the aminoacid.

Details

It was created as follows:

```
““ PTMods:::.createDataSets() ““
```

Source

Taken from the unimod database: <http://www.unimod.org/xml/unimod.xml>.

Examples

```
data(aminoacids)
head(aminoacids)
```

combineModifications *Combines consecutive modifications on amino acids in peptide sequences.*

Description

Combines consecutive modifications on amino acids in peptide sequences.

Usage

```
combineModifications(sequences)
```

Arguments

sequences ‘character’. A character vector of peptide sequences with modifications in any format accepted by ‘convertAnnotation’. Multiple modifications per amino acid are allowed.

Value

A character vector of the same length as ‘sequences’ with consecutive modifications on each amino acid summed into a single modification. This summed modifications is written in delta mass format.

Author(s)

Guillaume Deflandre <guillaume.deflandre@uclouvain.be>

Examples

```
combineModifications("AT[+10][-5]K")
combineModifications("[+10][-5]-ATK")
combineModifications("AT[Phospho][UNIMOD:1]K")
combineModifications("EM[+15.9949][-10]EK[+42][-8]")
combineModifications(c("AT[+10][-5]K", "EM[+15.9949][-10]EK"))
```

convertAnnotation *Convert sequences from one annotation style to another*

Description

Converts modifications between different annotation formats for multiple sequences at once. See the details and examples sections for more information. The annotation styles are inferred from the ‘modifications’ dataframe (see ‘?modifications’).

Usage

```
convertAnnotation(
  x,
  convertToStyle = c("deltaMass", "unimodId", "name"),
  massTolerance = 0.01
)
```

Arguments

x Character vector with peptide sequences in ProForma format

convertToStyle Character string specifying target format. Options: "deltaMass", "unimodId", "name"

massTolerance Numeric mass tolerance in Daltons for matching modifications (default: 0.01). Used when converting from deltaMass.

Details

The function handles three main conversion scenarios:

- Name to deltaMass: "M[Oxidation]PEPTIDE" -> "M[+15.994915]PEPTIDE" - Name to unimodId: "M[Oxidation]PEPTIDE" -> "M[UNIMOD:35]PEPTIDE" - deltaMass to name: "M[+15.995]PEPTIDE" -> "M[Oxidation]PEPTIDE" - deltaMass to unimodId: "M[+15.995]PEPTIDE" -> "M[UNIMOD:35]PEPTIDE"
- unimodId to name: "M[UNIMOD:35]PEPTIDE" -> "M[Oxidation]PEPTIDE" - unimodId to deltaMass: "M[UNIMOD:35]PEPTIDE" -> "M[+15.994915]PEPTIDE"

Value

Character vector with the sequences in the target annotation format

Author(s)

Guillaume Deflandre <guillaume.deflandre@uclouvain.be>

Examples

```
# Convert sequence from name to delta mass
convertAnnotation("M[Oxidation]PEPTIDE", convertToStyle = "deltaMass")
# Result: "M[+15.994915]PEPTIDE"

# Name to Unimod ID
convertAnnotation("M[Oxidation]PEPTIDE", convertToStyle = "unimodId")
# Result: "M[UNIMOD:35]PEPTIDE"

# Delta mass to name
convertAnnotation("M[+15.995]PEPTIDE", convertToStyle = "name")
# Result: "M[Oxidation]PEPTIDE"

# Multiple modifications
convertAnnotation("M[Oxidation]EVNES[Phospho]PEK", convertToStyle = "deltaMass")
# Result: "M[+15.994915]EVNES[+79.966331]PEK"
```

```
# Convert multiple sequences from name to delta mass
sequences <- c("M[Oxidation]PEPTIDE", "EVNES[Phospho]PEK", "PEPTIDE")
convertAnnotation(sequences, convertToStyle = "deltaMass")
# Result: c("M[+15.994915]PEPTIDE", "EVNES[+79.966331]PEK", "PEPTIDE")

# Convert from delta mass to name
sequences <- c("M[+15.995]PEPTIDE", "S[+79.966]EQUENCE")
convertAnnotation(sequences, convertToStyle = "name")
# Result: c("M[Oxidation]PEPTIDE", "S[Phospho]EQUENCE")

# Convert to Unimod IDs
sequences <- c("M[Oxidation]PEPTIDE", "C[Carbamidomethyl]PEPTIDE")
convertAnnotation(sequences, convertToStyle = "unimodId")
# Result: c("M[UNIMOD:35]PEPTIDE", "C[UNIMOD:4]PEPTIDE")
```

elements

Elements data set.

Description

‘data.frame’ of chemical elements from the unimod database.

Usage

```
data("elements")
```

Format

A ‘data.frame’ with 4 columns (Name, FullName, AvgMass, MonoMass) for the chemical elements.

Details

It was created as follows:

```
““ PTMods:::.createDataSets() ““
```

Source

Taken from the unimod database: <http://www.unimod.org/xml/unimod.xml>.

Examples

```
data(elements)
head(elements)
```

getCanonicalSequence *Get canonical sequence from any peptidofom*

Description

Remove any modifications annotation on a sequence. Annotation from any type (so long as they are specified within brackets "[..]") are removed.

Usage

```
getCanonicalSequence(x)
```

Arguments

x 'character', ProForma sequence.

Value

'character', a 'character' vector with sequences cleaned of all modifications.

Examples

```
getCanonicalSequence(  
  c(  
    "EM[-15.9949]EVEES[+79.9663]PEK",  
    "EK[Acetyl]EVEES[UNIMOD:21]PEK"  
  )  
)
```

modifications *Modifications data set.*

Description

'data.frame' of modifications from the unimod database.

Usage

```
data("modifications")
```

Format

A 'data.frame' with 15 columns (Id (created by Name:(Position-)Site(:NeutralLoss) because unimod id is not unique), UnimodId, Name, Description, AvgMass, MonoMass, Site, Position, Classification, SpecGroup, NeutralLoss, LastModification, Approved, Hidden) for the modifications.

Details

It was created as follows:

```
““ PTMods:::.createDataSets() ““
```

Source

Taken from the unimod database: <http://www.unimod.org/xml/unimod.xml>.

Examples

```
data(modifications)  
head(modifications)
```

Index

* **datasets**

- aminoacids, [7](#)
- elements, [10](#)
- modifications, [11](#)

* **package**

- PTMods-package, [2](#)
- .convertAnnotation (convertAnnotation),
[8](#)

- addFixedModifications, [3](#), [5](#)
- addModifications, [4](#)
- addVariableModifications, [5](#), [6](#)
- aminoacids, [7](#)

- combineModifications, [8](#)
- convertAnnotation, [5](#), [8](#)

- elements, [10](#)

- getCanonicalSequence, [11](#)

- modifications, [11](#)

- PTMods (PTMods-package), [2](#)
- PTMods-package, [2](#)