

Package ‘proteasy’

August 26, 2024

Type Package

Title Protease Mapping

Version 1.6.0

Description Retrieval of experimentally derived protease- and cleavage data derived from the MEROPS database. Proteasy contains functions for mapping peptide termini to known sites where a protease cleaves. This package also makes it possible to quickly look up known substrates based on a list of (potential) proteases, or vice versa - look up proteases based on a list of substrates.

biocViews Proteomics, BiomedicalInformatics, FunctionalGenomics

URL <https://github.com/martinry/proteasy>

BugReports <https://github.com/martinry/proteasy/issues>

Depends R (>= 4.2.0)

Imports data.table, stringr, ensemblDb, AnnotationFilter,
EnsDb.Hsapiens.v86, EnsDb.Mmusculus.v79, EnsDb.Rnorvegicus.v79,
Rapi, methods, utils

Suggests BiocStyle, knitr, rmarkdown, igraph, ComplexHeatmap, viridis,

License GPL-3

LazyData false

VignetteBuilder knitr

Encoding UTF-8

RoxygenNote 7.2.0

Collate 'Classes.R' 'Generics.R' 'Methods.R' 'browseProtease.R'
'helper-functions.R' 'findProtease.R' 'proteasy-package.R'
'searchProtease.R' 'searchSubstrate.R' 'zzz.R'

PackageStatus Deprecated

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

git_branch RELEASE_3_19

git_last_commit cab3cc0

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-08-25

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proteasy-package	<i>Protease Mapping</i>
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Description

Retrieval of experimentally derived protease- and cleavage data derived from the MEROPS database. Proteasy contains a function, [findProtease](#) for mapping peptide termini to known sites where a protease cleaves. This package also makes it possible to quickly look up known substrates based on a list of (potential) proteases ([searchProtease](#)), or vice versa - look up proteases based on a list of substrates ([searchSubstrate](#)).

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browseProtease	<i>Browse Protease on MEROPS</i>
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Description

Opens relevant MEROPS (<https://www.ebi.ac.uk/merops/>) page with information on specified protease.

Usage

browseProtease(p, keytype)

Arguments

p a single protease
 keytype UniprotID (default) or MEROPS.

Value

utils::browseURL

Examples

```
if (interactive()) {
  # The following function calls opens in browser
  browseProtease("P07339", keytype = "UniprotID")
  browseProtease("A01.009", keytype = "MEROPS")
}
```

cleavages	<i>Access resulting object from 'findProteases' function.</i>
-----------	---

Description

'cleavages' returns a 'data.table' with the corresponding details derived from MEROPS.

Usage

```
## S4 method for signature 'Cleavages'
cleavages(x)
```

Arguments

x A 'data.table' object.

Value

A 'data.table' object.

Examples

```
protein <- c("P02671", "P02671", "P68871", "P01011")
peptide <- c("FEEVSGNVSPGTR", "FVSETESR", "LLVVYPW", "ITLLSAL")
res <- findProtease(protein = protein, peptide = peptide,
  organism = "Homo sapiens")
cleavages(res)
```

findProtease	<i>Find Proteases</i>
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Description

Given a vector of peptides and proteins, finds known proteases acting on cleavage sites.

Usage

```
findProtease(protein, peptide, organism, start_pos, end_pos)
```

Arguments

protein	a vector of UniProt Accession IDs.
peptide	a vector of amino acid sequences corresponding to the proteins.
organism	name of organism.
start_pos	(optional) numeric vector of N-terminus positions in protein sequence.
end_pos	(optional) numeric vector of C-terminus positions in protein sequence.

Value

S4 object Cleavages

Examples

```
protein <- c("P02671", "P02671", "P68871", "P01011")
peptide <- c("FEEVSGNVSPGTR", "FVSETESR", "LLVVYPW", "ITLLSAL")
res <- findProtease(protein = protein,
                    peptide = peptide,
                    organism = "Homo sapiens")
```

proteases	<i>Access resulting object from 'findProteases' function.</i>
-----------	---

Description

'proteases' returns a 'data.table' with the corresponding details derived from MEROPS.

Usage

```
## S4 method for signature 'Cleavages'
proteases(x)
```

Arguments

x A 'data.table' object.

Value

A 'data.table' object.

Examples

```
protein <- c("P02671", "P02671", "P68871", "P01011")
peptide <- c("FEEVSGNVSPGTR", "FVSETESR", "LLVVYPW", "ITLLSAL")
res <- findProtease(protein = protein, peptide = peptide,
  organism = "Homo sapiens")
proteases(res)
```

searchProtease	<i>Show Cleaving Data for a Peptidase or Inhibitor by Uniprot accession</i>
----------------	---

Description

Given a vector of proteins, finds which substrates they cleave.

Usage

```
searchProtease(protein, organism = "Homo sapiens", summarize = FALSE)
```

Arguments

protein a vector of corresponding UniProt Accession IDs.
 organism name of organism.
 summarize if false (default), provides a detailed table of all associated cleaving events, otherwise outputs a summarized table and only includes reviewed (Uniprot) entries.

Value

data.table, character

Examples

```
protein <- c("P98073", "P00734")
searchProtease(protein = protein)
```

searchSubstrate	<i>Show Cleaving Data for a Substrate by Uniprot accession</i>
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Description

Given a vector of proteins, finds known proteases acting on cleavage sites.

Usage

```
searchSubstrate(protein, summarize = FALSE)
```

Arguments

protein	a vector of corresponding UniProt Accession IDs.
summarize	if false (default), provides a detailed table of all associated cleaving events, otherwise outputs a summarized table and only includes reviewed (Uniprot) entries.

Value

data.table, character

Examples

```
protein <- c("P05067", "P68871")
searchSubstrate(protein = protein)
```

substrates	<i>Access resulting object from 'findProteases' function.</i>
------------	---

Description

'substrates' returns a 'data.table' with the corresponding details derived from MEROPS.

Usage

```
## S4 method for signature 'Cleavages'
substrates(x)
```

Arguments

x	A 'data.table' object.
---	------------------------

Value

A 'data.table' object.

Examples

```
protein <- c("P02671", "P02671", "P68871", "P01011")
peptide <- c("FEEVSGNVSPGTR", "FVSETESR", "LLVVYPW", "ITLLSAL")
res <- findProtease(protein = protein, peptide = peptide,
organism = "Homo sapiens")
substrates(res)
```

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