

# Package ‘proteasy’

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**Type** Package

**Title** Protease Mapping

**Version** 1.2.0

**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'

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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`).

### Author(s)

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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")
}
```

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cleavages	<i>Access resulting object from 'findProteases' function.</i>
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**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)
```

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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")
```

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proteases	<i>Access resulting object from 'findProteases' function.</i>
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**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)
```

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

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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>
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**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.
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**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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