

# Package ‘cleaver’

August 13, 2025

**Version** 1.47.0

**Title** Cleavage of Polypeptide Sequences

**Maintainer** Sebastian Gibb <mail@sebastiangibb.de>

**Depends** R (>= 3.0.0), methods, Biostrings (>= 1.29.8)

**Imports** S4Vectors, IRanges

**Suggests** testthat (>= 0.8), knitr, BiocStyle (>= 0.0.14), rmarkdown,  
BRAIN, UniProt.ws (>= 2.36.5)

**Description** In-silico cleavage of polypeptide sequences. The cleavage  
rules are taken from:  
[http://web.expasy.org/peptide\\_cutter/peptidecutter\\_enzymes.html](http://web.expasy.org/peptide_cutter/peptidecutter_enzymes.html)

**License** GPL (>= 3)

**URL** <https://github.com/sgibb/cleaver/>

**BugReports** <https://github.com/sgibb/cleaver/issues/>

**LazyLoad** yes

**VignetteBuilder** knitr

**biocViews** Proteomics

**git\_url** <https://git.bioconductor.org/packages/cleaver>

**git\_branch** devel

**git\_last\_commit** c2fe2f8

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-08-13

**Author** Sebastian Gibb [aut, cre] (ORCID:  
<<https://orcid.org/0000-0001-7406-4443>>)

## Contents

|                           |          |
|---------------------------|----------|
| cleaver-package . . . . . | 2        |
| cleave-methods . . . . .  | 2        |
| <b>Index</b>              | <b>9</b> |

---

cleaver-package

*Cleavage of polypeptide sequences*

---

## Description

This package cleaves polypeptide sequences. It provides three functions: [cleave](#), [cleavageRanges](#) and [cleavageSites](#).

## Details

The cleavage rules are taken from: [https://web.expasy.org/peptide\\_cutter/peptidecutter\\_enzymes.html](https://web.expasy.org/peptide_cutter/peptidecutter_enzymes.html)

Package: cleaver  
License: GPL (>= 3)  
URL: <https://github.com/sgibb/cleaver/>

## Author(s)

Sebastian Gibb <[mail@sebastiangibb.de](mailto:mail@sebastiangibb.de)>

## References

<https://github.com/sgibb/cleaver/>

Gasteiger E., Hoogland C., Gattiker A., Duvaud S., Wilkins M.R., Appel R.D., Bairoch A.; "Protein Identification and Analysis Tools on the ExPASy Server". (In) John M. Walker (ed): The Proteomics Protocols Handbook, Humana Press (2005).

[https://web.expasy.org/peptide\\_cutter/peptidecutter\\_enzymes.html](https://web.expasy.org/peptide_cutter/peptidecutter_enzymes.html)

## See Also

[cleave](#), [cleavageRanges](#) and [cleavageSites](#).

---

cleave-methods

*Cleavage of polypeptide sequences*

---

## Description

This functions cleave polypeptide sequences. Use [cleavageSites](#) to find the cleavage sites, [cleavageRanges](#) to find the cleavage ranges and [cleave](#) to get the cleavage products.

## Usage

```
## S4 method for signature 'character'
cleave(x, enzym = "trypsin", missedCleavages = 0,
       custom = NULL, unique = TRUE)

## S4 method for signature 'AAString'
cleave(x, enzym = "trypsin", missedCleavages = 0,
       custom = NULL, unique = TRUE)

## S4 method for signature 'AAStringSet'
cleave(x, enzym = "trypsin", missedCleavages = 0,
       custom = NULL, unique = TRUE)

## S4 method for signature 'character'
cleavageRanges(x, enzym = "trypsin", missedCleavages = 0,
               custom = NULL)

## S4 method for signature 'AAString'
cleavageRanges(x, enzym = "trypsin", missedCleavages = 0,
               custom = NULL)

## S4 method for signature 'AAStringSet'
cleavageRanges(x, enzym = "trypsin", missedCleavages = 0,
               custom = NULL)

## S4 method for signature 'character'
cleavageSites(x, enzym = "trypsin", custom = NULL)

## S4 method for signature 'AAString'
cleavageSites(x, enzym = "trypsin", custom = NULL)

## S4 method for signature 'AAStringSet'
cleavageSites(x, enzym = "trypsin", custom = NULL)
```

## Arguments

|                 |                                                                                                                                                                                                                                                                                                                             |
|-----------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x               | polypeptide sequences.                                                                                                                                                                                                                                                                                                      |
| enzym           | character, cleavage rule.                                                                                                                                                                                                                                                                                                   |
| missedCleavages | numeric, number of missed cleavages.                                                                                                                                                                                                                                                                                        |
| custom          | character, of length 1 or 2. Could be used to define own cleavage rules. The first element would be the pattern and the optional second element would be an exception (non-cleavage) pattern. Perl-like regular expressions are supported, see <a href="#">gregexpr</a> for details. If custom is set the enzym is ignored. |
| unique          | logical, if TRUE all duplicated cleavage products per peptide are removed.                                                                                                                                                                                                                                                  |

## Details

The cleavage rules are taken from: [https://web.expasy.org/peptide\\_cutter/peptidecutter\\_enzymes.html](https://web.expasy.org/peptide_cutter/peptidecutter_enzymes.html)

Cleavage rules (cleavage between P1 and P1'):

| Rule name                  | P4              | P3              | P2        | P1                | P1'           |
|----------------------------|-----------------|-----------------|-----------|-------------------|---------------|
| arg-c proteinase           | -               | -               | -         | R                 | -             |
| asp-n endopeptidase        | -               | -               | -         | -                 | D             |
| bnps-skatole-c             | -               | -               | -         | W                 | -             |
| caspase1                   | F,W,Y,L         | -               | H,A,T     | D                 | not P,E,D,Q,K |
| caspase2                   | D               | V               | A         | D                 | not P,E,D,Q,K |
| caspase3                   | D               | M               | Q         | D                 | not P,E,D,Q,K |
| caspase4                   | L               | E               | V         | D                 | not P,E,D,Q,K |
| caspase5                   | L,W             | E               | H         | D                 | -             |
| caspase6                   | V               | E               | H,I       | D                 | not P,E,D,Q,K |
| caspase7                   | D               | E               | V         | D                 | not P,E,D,Q,K |
| caspase8                   | I,L             | E               | T         | D                 | not P,E,D,Q,K |
| caspase9                   | L               | E               | H         | D                 | -             |
| caspase10                  | I               | E               | A         | D                 | -             |
| chymotrypsin-high          | -               | -               | -         | F,Y               | not P         |
|                            | -               | -               | -         | W                 | not M,P       |
| chymotrypsin-low           | -               | -               | -         | F,L,Y             | not P         |
|                            | -               | -               | -         | W                 | not M,P       |
|                            | -               | -               | -         | M                 | not P,Y       |
|                            | -               | -               | -         | H                 | not D,M,P,W   |
| clostripain                | -               | -               | -         | R                 | -             |
| cnbr                       | -               | -               | -         | M                 | -             |
| enterokinase               | D,E             | D,E             | D,E       | K                 | -             |
| factor xa                  | A,F,G,I,L,T,V,M | D,E             | G         | R                 | -             |
| formic acid                | -               | -               | -         | D                 | -             |
| glutamyl endopeptidase     | -               | -               | -         | E                 | -             |
| granzyme-b                 | I               | E               | P         | D                 | -             |
| hydroxylamine              | -               | -               | -         | N                 | G             |
| iodosobenzoic acid         | -               | -               | -         | W                 | -             |
| lysc                       | -               | -               | -         | K                 | -             |
| lysn                       | -               | -               | -         | -                 | K             |
| lysarginase                | -               | -               | -         | -                 | K,R           |
| neutrophil elastase        | -               | -               | -         | A,V               | -             |
| ntcb                       | -               | -               | -         | -                 | C             |
| pepsin1.3                  | -               | not H,K,R       | not P     | not R             | F,L           |
| pepsin                     | -               | not H,K,R       | not P     | not R             | F,L,W,Y       |
|                            | -               | not H,K,R       | not P     | F,L,W,Y           | -             |
|                            | -               | not H,K,R       | not P     | F,L               | -             |
| proline endopeptidase      | -               | -               | not H,K,R | P                 | not P         |
| proteinase k               | -               | -               | -         | A,E,F,I,L,T,V,W,Y | -             |
| staphylococcal peptidase i | -               | -               | not E     | E                 | -             |
| thermolysin                | -               | -               | -         | not D,E           | A,F,I,L,M,V   |
| thrombin                   | -               | -               | G         | R                 | G             |
|                            | A,F,G,I,L,T,V,M | A,F,G,I,L,T,V,W | P         | R                 | not D,E       |
| trypsin                    | -               | -               | -         | K,R               | not P         |
|                            | -               | -               | W         | K                 | P             |
|                            | -               | -               | M         | R                 | P             |
| trypsin-high               | -               | -               | -         | K,R               | not P         |
|                            | -               | -               | W         | K                 | P             |
|                            | -               | -               | M         | R                 | P             |
| trypsin-low                | -               | -               | -         | K,R               | not P         |
|                            | -               | -               | W         | K                 | P             |

|                |   |   |   |     |   |
|----------------|---|---|---|-----|---|
|                | - | - | M | R   | P |
| trypsin-simple | - | - | - | K,R | - |

Exceptions:

| Rule name    | Enzyme name | P4 | P3  | P2 | P1 | P1' | P2' |
|--------------|-------------|----|-----|----|----|-----|-----|
| trypsin      | -           | -  | C,D | K  | D  | -   | -   |
|              |             | -  | -   | C  | K  | H,Y | -   |
|              |             | -  | -   | C  | R  | K   | -   |
|              |             | -  | -   | R  | R  | H,R | -   |
| trypsin-high | -           | -  | C,D | K  | D  | -   | -   |
|              |             | -  | -   | C  | K  | H,Y | -   |
|              |             | -  | -   | C  | R  | K   | -   |
|              |             | -  | -   | R  | R  | H,R | -   |

| Rule name              | Enzyme name                                                    |
|------------------------|----------------------------------------------------------------|
| arg-c proteinase       | Arg-C proteinase                                               |
| asp-n endopeptidase    | Asp-N endopeptidase                                            |
| bnps-skatole-c         | BNPS-Skatole                                                   |
| caspase1               | Caspase 1                                                      |
| caspase2               | Caspase 2                                                      |
| caspase3               | Caspase 3                                                      |
| caspase4               | Caspase 4                                                      |
| caspase5               | Caspase 5                                                      |
| caspase6               | Caspase 6                                                      |
| caspase7               | Caspase 7                                                      |
| caspase8               | Caspase 8                                                      |
| caspase9               | Caspase 9                                                      |
| caspase10              | Caspase 10                                                     |
| chymotrypsin-high      | Chymotrypsin-high specificity (C-term to [FYW], not before P)  |
| chymotrypsin-low       | Chymotrypsin-low specificity (C-term to [FYWML], not before P) |
| clostripain            | Clostripain (Clostridiopeptidase B)                            |
| cnbr                   | CNBr                                                           |
| enterokinase           | Enterokinase                                                   |
| factor xa              | Factor Xa                                                      |
| formic acid            | Formic acid                                                    |
| glutamyl endopeptidase | Glutamyl endopeptidase                                         |
| granzyme-b             | Granzyme B                                                     |
| hydroxylamine          | Hydroxylamine                                                  |
| iodosobenzoic acid     | Iodosobenzoic acid                                             |
| lysc                   | LysC                                                           |
| lysn                   | LysN                                                           |
| lysarginase            | LysargiNase                                                    |
| neutrophil elastase    | Neutrophil elastase                                            |
| ntcb                   | NTCB (2-nitro-5-thiocyanobenzoic acid)                         |
| pepsin1.3              | Pepsin (pH == 1.3)                                             |
| pepsin                 | Pepsin (pH > 2)                                                |
| proline endopeptidase  | Proline-endopeptidase                                          |
| proteinase k           | Proteinase K                                                   |

|                            |                                                                                    |
|----------------------------|------------------------------------------------------------------------------------|
| staphylococcal peptidase i | Staphylococcal Peptidase I                                                         |
| thermolysin                | Thermolysin                                                                        |
| thrombin                   | Thrombin                                                                           |
| trypsin                    | Trypsin                                                                            |
| trypsin-high               | Trypsin, higher specificity as defined in PeptideMass, identical to <i>trypsin</i> |
| trypsin-low                | Trypsin, C-term to K/R if C-term is not P, as defined in PeptideMass               |
| trypsin-simple             | Trypsin, C-term to K/R, even before P, as defined in PeptideMass                   |

## Value

**cleave** If *x* is a character it returns a list of the same length as *x*. Each element contains a character vector with the corresponding cleavage products of the polypeptides. If *x* is an [AAString](#) or an [AAStringSet](#) an [AAStringSet](#) or an [AAStringSetList](#) instance of the same length as *x* is returned. Each element contains an [AAString](#) or an [AAStringSet](#) instance with the corresponding cleavage products of the polypeptides.

**cleavageRanges** If *x* is a character it returns a list of the same length as *x*. Each element contains a two-column matrix with the start and end positions of the peptides. If *x* is an [AAString](#) or an [AAStringSet](#) instance an [IRanges](#) or an [IRangesList](#) of the same length as *x* is returned.

**cleavageSites** Returns a list of the same length as *x*. Each element contains an integer vector with the cleavage positions.

Overview:

| Input                       | cleave                          | cleavageRanges              | cleavageSites   |
|-----------------------------|---------------------------------|-----------------------------|-----------------|
| character                   | list of character               | list of matrix              | list of integer |
| <a href="#">AAString</a>    | <a href="#">AAStringSet</a>     | <a href="#">IRanges</a>     | list of integer |
| <a href="#">AAStringSet</a> | <a href="#">AAStringSetList</a> | <a href="#">IRangesList</a> | list of integer |

## Author(s)

Sebastian Gibb <[mail@sebastiangibb.de](mailto:mail@sebastiangibb.de)>

## References

Gasteiger E., Hoogland C., Gattiker A., Duvaud S., Wilkins M.R., Appel R.D., Bairoch A.; "Protein Identification and Analysis Tools on the ExPASy Server". (In) John M. Walker (ed): The Proteomics Protocols Handbook, Humana Press (2005).

[https://web.expasy.org/peptide\\_cutter/peptidecutter\\_enzymes.html](https://web.expasy.org/peptide_cutter/peptidecutter_enzymes.html)

PeptideMass [https://web.expasy.org/peptide\\_mass/peptide-mass-doc.html#table1](https://web.expasy.org/peptide_mass/peptide-mass-doc.html#table1)

## See Also

[AAString](#), [AAStringSet](#), [AAStringSetList](#), [IRanges](#), [IRangesList](#)

## Examples

```
library("cleaver")

## Gastric juice peptide 1 (UniProtKB/Swiss-Prot: GAJU_HUMAN/P01358)
gaju <- "LAAGKVEDSD"
```

```

cleave(gaju, "trypsin")
# $LAAGKVEDSD
# [1] "LAAGK" "VEDSD"

cleavageRanges(gaju, "trypsin")
# $LAAGKVEDSD
#      start end
# [1,]      1  5
# [2,]      6 10

cleavageSites(gaju, "trypsin")
# $LAAGKVEDSD
# [1] 5

cleave(gaju, "trypsin", missedCleavages=1)
# $LAAGKVEDSD
# [1] "LAAGKVEDSD"

cleavageRanges(gaju, "trypsin", missedCleavages=1)
# $LAAGKVEDSD
#      start end
# [1,]      1 10

cleave(gaju, "trypsin", missedCleavages=0:1)
# $LAAGKVEDSD
# [1] "LAAGK" "VEDSD" "LAAGKVEDSD"

cleavageRanges(gaju, "trypsin", missedCleavages=0:1)
# $LAAGKVEDSD
#      start end
# [1,]      1  5
# [2,]      6 10
# [3,]      1 10

cleave(gaju, "pepsin")
# $LAAGKVEDSD
# [1] "LAAGKVEDSD"
# (no cleavage)

## use AAStringSet
gaju <- AAStringSet("LAAGKVEDSD")

cleave(gaju)
# AAStringSetList of length 1
# [1] "LAAGKVEDSD" LAAGK VEDSD

## Beta-enolase (UniProtKB/Swiss-Prot: ENOB_THUAL/P86978)
enob <- "SITKIKAREILD"

cleave(enob, "trypsin")
# $SITKIKAREILD
# [1] "SITK" "IK" "AR" "EILD"

```

```

cleave(enob, "trypsin", missedCleavages=2)
# $SITKIKAREILD
# [1] "SITKIKAR" "IKAREILD"

cleave(enob, "trypsin", missedCleavages=0:2)
# $SITKIKAREILD
# [1] "SITK"      "IK"        "AR"        "EILD"      "SITKIK"    "IKAR"
# [7] "AREILD"    "SITKIKAR" "IKAREILD"

## define own cleavage rule: cleave at K
cleave(enob, custom="K")
# $SITKIKAREILD
# [1] "SITK"      "IK"        "AREILD"

cleavageRanges(enob, custom="K")
# $SITKIKAREILD
#      start end
# [1,]      1  4
# [2,]      5  6
# [3,]      7 12

## define own cleavage rule: cleave at K but not if followed by A
cleave(enob, custom=c("K", "K(?=A)"))
# $SITKIKAREILD
# [1] "SITK"      "IKAREILD"

cleavageRanges(enob, custom=c("K", "K(?=A)"))
# $SITKIKAREILD
#      start end
# [1,]      1  4
# [2,]      5 12

cleavageSites(enob, custom=c("K", "K(?=A)"))
# $SITKIKAREILD
# [1] 4

```

# Index

## \* **methods**

cleave-methods, [2](#)

## \* **package**

cleaver-package, [2](#)

AAString, [6](#)

AAStringSet, [6](#)

AAStringSetList, [6](#)

cleavageRanges, [2](#)

cleavageRanges (cleave-methods), [2](#)

cleavageRanges, AAString-method  
(cleave-methods), [2](#)

cleavageRanges, AAStringSet-method  
(cleave-methods), [2](#)

cleavageRanges, character-method  
(cleave-methods), [2](#)

cleavageSites, [2](#)

cleavageSites (cleave-methods), [2](#)

cleavageSites, AAString-method  
(cleave-methods), [2](#)

cleavageSites, AAStringSet-method  
(cleave-methods), [2](#)

cleavageSites, character-method  
(cleave-methods), [2](#)

cleave, [2](#)

cleave (cleave-methods), [2](#)

cleave, AAString-method  
(cleave-methods), [2](#)

cleave, AAStringSet-method  
(cleave-methods), [2](#)

cleave, character-method  
(cleave-methods), [2](#)

cleave-methods, [2](#)

cleaver-package, [2](#)

gregexpr, [3](#)

IRanges, [6](#)

IRangesList, [6](#)