Package ‘cleaver’

January 14, 2017

Version 1.12.0
Date 2015-02-02
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), BRAIN, UniProt.ws (>= 2.1.4)
Description In-silico cleavage of polypeptide sequences. The cleavage rules are taken from:
License GPL (>= 3)
URL https://github.com/sgibb/cleaver/
BugReports https://github.com/sgibb/cleaver/issues/
LazyLoad yes
VignetteBuilder knitr
biocViews Proteomics
NeedsCompilation no
Author Sebastian Gibb [aut, cre]

R topics documented:

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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: http://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>

References

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

See Also

cleave, cleavageRanges and cleavageSites.

cleave  

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

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

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

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

## 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 `gregexpr` 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: http://web.expasy.org/peptide_cutter/peptidescutter_enzymes.html

Cleavage rules (cleavage between P1 and P1'):

<table>
<thead>
<tr>
<th>Rule name</th>
<th>P4</th>
<th>P3</th>
<th>P2</th>
<th>P1</th>
<th>P1'</th>
</tr>
</thead>
<tbody>
<tr>
<td>arg-c proteinase</td>
<td></td>
<td></td>
<td></td>
<td>R</td>
<td></td>
</tr>
<tr>
<td>asp-n endopeptidase</td>
<td></td>
<td></td>
<td></td>
<td>-</td>
<td>D</td>
</tr>
<tr>
<td>bnps-skatole-c</td>
<td></td>
<td></td>
<td>W</td>
<td></td>
<td></td>
</tr>
<tr>
<td>caspase2</td>
<td>D</td>
<td>V</td>
<td>A</td>
<td>D</td>
<td>not P.E,D.Q.</td>
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<tr>
<td>Enzyme name</td>
<td>P4</td>
<td>P3</td>
<td>P2</td>
<td>P1</td>
<td>P1'</td>
</tr>
<tr>
<td>-----------------------------</td>
<td>----</td>
<td>----</td>
<td>----</td>
<td>----</td>
<td>-----</td>
</tr>
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<td>cleave</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>D</td>
</tr>
<tr>
<td>caspase3</td>
<td>D</td>
<td>M</td>
<td>Q</td>
<td>D</td>
<td></td>
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<tr>
<td>caspase4</td>
<td>L</td>
<td>E</td>
<td>V</td>
<td>D</td>
<td></td>
</tr>
<tr>
<td>caspase5</td>
<td>L,W</td>
<td>E</td>
<td>H</td>
<td>D</td>
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<tr>
<td>caspase6</td>
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<td>E</td>
<td>H,I</td>
<td>D</td>
<td></td>
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<td>D</td>
<td>E</td>
<td>V</td>
<td>D</td>
<td></td>
</tr>
<tr>
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<td>I,L</td>
<td>E</td>
<td>T</td>
<td>D</td>
<td></td>
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<tr>
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<td>E</td>
<td>H</td>
<td>D</td>
<td></td>
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<tr>
<td>caspase10</td>
<td>I</td>
<td>E</td>
<td>A</td>
<td>D</td>
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<td>chymotrypsin-high</td>
<td>F</td>
<td>Y</td>
<td></td>
<td></td>
<td></td>
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<td>chymotrypsin-low</td>
<td>W</td>
<td></td>
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<tr>
<td>clostripain</td>
<td>R</td>
<td></td>
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<td></td>
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<tr>
<td>cnbr</td>
<td>M</td>
<td></td>
<td></td>
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<tr>
<td>enterokinase</td>
<td>D,E</td>
<td>D,E</td>
<td>D,E</td>
<td>K</td>
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</tr>
<tr>
<td>formic acid</td>
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<tr>
<td>glutamyl endopeptidase</td>
<td>I</td>
<td>E</td>
<td>P</td>
<td>D</td>
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<td>granzyme-b</td>
<td>N</td>
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<tr>
<td>hydroxylamine</td>
<td>W</td>
<td></td>
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<td>iodosobenzoic acid</td>
<td>K</td>
<td></td>
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<tr>
<td>lysozyme</td>
<td>A,V</td>
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<td></td>
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<tr>
<td>neutrophil elastase</td>
<td>C</td>
<td></td>
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<tr>
<td>pepsin1.3</td>
<td>F,L,W</td>
<td>Y</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>pepsin</td>
<td>F,L,W</td>
<td>Y</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>proteinase k</td>
<td>A,F,G,I,L,T,V,W</td>
<td>E</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>staphylococcal peptidase i</td>
<td>E</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>thermolysin</td>
<td>A,F,G,I,L,M,V</td>
<td>G</td>
<td></td>
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<td></td>
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<tr>
<td>trypsin</td>
<td>K,R</td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>trypsin</td>
<td>M</td>
<td></td>
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Exceptions:

<table>
<thead>
<tr>
<th>Rule name</th>
<th>Enzyme name</th>
</tr>
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<tbody>
<tr>
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</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Rule name</th>
<th>Enzyme name</th>
</tr>
</thead>
<tbody>
<tr>
<td>trypsin</td>
<td></td>
</tr>
</tbody>
</table>
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 [FY], not before P)
chymotrypsin-low | Chymotrypsin-low specificity (C-term to [FYWM], 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
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

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 AAStringSet 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:
Author(s)
Sebastian Gibb <mail@sebastiangibb.de>

References

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)
# cleave

```r
# $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
# [["LAAGKVEDSD"]]

## 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
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