Package 'pepDat'

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Type Package

Title Peptide microarray data package

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Description Provides sample files and data for the vignettes of pepStat and Pviz as well as peptide collections for HIV and SIV.

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Depends R(>= 3.0.0)

Imports GenomicRanges

Suggests knitr

biocViews MicroarrayData

VignetteBuilder knitr

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pep_hxb2 *Reference peptide dataset for HIV enveloppe*

Description

A peptide dataset created from the multiple alignment of the reference sequence hxb2 and the seven subtypes A, B, C, D, M, CRF01, CRF02

Usage

```
data(pep_hxb2)
```

Format

A GRanges object. One row per peptide.

Details

- peptides: The rownames are 15mers from the envelope of 7 subtypes of HIV-1.
- seqnames: An information regarding the genomic location of the peptide.
- ranges: The start and end coordinate of the peptide based on the coordinates of the reference hxb2.
- aligned: The aligned column represents the peptide as it is aligned in the multiple alignment.
- trimmed: The trimmed column represents the part of hxb2's sequence aligned with the peptide.
- zSums: The sum of the zScale of each amino-acid of the 15mer.
- clade: A list of the subtypes which contain this peptide.

Note

The alignments used to create this collections are available in the extdata/alignments folder, as well as the raw sequences on fasta format.

References

http://www.hiv.lanl.gov/content/sequence/HIV/REVIEWS/HXB2.html

pep_hxb2JPT *Peptide collection for HXB2 and JPT clades*

Description

Peptide collection for HXB2 and JPT clades

Usage

```
data(pep_hxb2JPT)
```

Format

A GRanges object. One row per peptide.

pep_m239smE543 *Peptide collection for SIV enveloppe*

Description

Peptide collection for SIV enveloppe

Usage

```
data(pep_m239smE543)
```

Format

A GRanges object. One row per peptide.

pep_mac239 *Reference peptide dataset for SIV enveloppe*

Description

A peptide dataset created from the multiple alignment of the reference sequence mac239 from LANL database, our mac239 and E660 subtypes.

Usage

```
data(pep_mac239)
```

Format

A GRanges object. One row per peptide.

Details

- peptides: The rownames are 15mers from the envelope of mac239 and E660.
- seqnames: An information regarding the genomic location of the peptide.
- ranges: The start and end coordinate of the peptide based on the coordinates of the reference mac239.
- aligned: The aligned column represents the peptide as it is aligned in the multiple alignment.
- peptideNb:Number of the corresponding mac239 peptide.
- zSums: The sum of the zScale of each amino-acid of the 15mer.
- clade: A list of the subtypes which contain this peptide.

Note

The alignments used to create this collections are available in the extdata/alignments folder, as well as the raw sequences on fasta format.

References

http://www.hiv.lanl.gov/content/sequence/HIV/REVIEWS/SIV_NUMBERING2001/SivNumbering.html

restab *Summary tables from pepStat*

Description

This is the result tables of a peptide microarray analysis using pepStat. It summarizes the antibody binding prediction for each peptide, depending on the group. restab_aggregate has one row per peptide. Peptides that belong to more than one clade have a single entry. restab has one row per peptide per clade. Each clade has been normalized separately.

Format

A data.frame containing 1964 rows and 9 variables for restab. 1423 rows and 9 variables for restab_aggregate.

- peptide: Peptide sequences
- position: The position of peptides on the reference sequence HXB2.
- space: The location of the peptide. Here, gp160, the evelope of HIV.
- start: The start coordinate of the peptide on the reference sequence.
- end: The end coordinate of the peptide on the reference sequence.
- widt: The length of the peptides.
- clade: The virus subtypes that the peptide belongs to.
- group1: Frequency of antibody binding events in the subjects of group1 for that peptide.
- group2: Frequency of antibody binding events in the subjects of group2 for that peptide.

Note

For more information, see ?pepStat::restab.

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