Package ‘pepDat’

April 2, 2026

Type Package

Title Peptide microarray data package

Version 1.30.0

Author Renan Sauteraud, Raphael Gottardo

Maintainer Renan Sauteraud `<rsautera@fhcrc.org>`

Date 2021-11-21

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

License Artistic-2.0

Depends R(>= 3.0.0)

Imports GenomicRanges

Suggests knitr

biocViews MicroarrayData

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/pepDat

git_branch RELEASE_3_22

git_last_commit b268acd

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-04-02

Contents

`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`.

Index