

# Package ‘pepDat’

May 30, 2024

**Type** Package

**Title** Peptide microarray data package

**Version** 1.24.0

**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\_19

**git\_last\_commit** 9783660

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-05-30

## Contents

pep_hxb2 . . . . .	2
pep_hxb2JPT . . . . .	3
pep_m239smE543 . . . . .	3
pep_mac239 . . . . .	3
restab . . . . .	4

<b>Index</b>	<b>6</b>
--------------	----------

---

pep\_hxb2

*Reference peptide dataset for HIV envelope*

---

### **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	<i>Peptide collection for HXB2 and JPT clades</i>
-------------	---

---

**Description**

Peptide collection for HXB2 and JPT clades

**Usage**

```
data(pep_hxb2JPT)
```

**Format**

A GRanges object. One row per peptide.

---

pep_m239smE543	<i>Peptide collection for SIV envelope</i>
----------------	--

---

**Description**

Peptide collection for SIV envelope

**Usage**

```
data(pep_m239smE543)
```

**Format**

A GRanges object. One row per peptide.

---

pep_mac239	<i>Reference peptide dataset for SIV envelope</i>
------------	---

---

**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](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 envelope of HIV.
- start: The start coordinate of the peptide on the reference sequence.
- end: The end coordinate of the peptide on the reference sequence.
- width: 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.

*restab*

5

**Note**

For more information, see `?pepStat::restab`.

# Index

pep\_hxb2, [2](#)

pep\_hxb2JPT, [3](#)

pep\_m239smE543, [3](#)

pep\_mac239, [3](#)

restab, [4](#)

restab\_aggregate (restab), [4](#)