

Package ‘SCLCBam’

September 17, 2019

Type Package

Title Sequence data from chromosome 4 of a small-cell lung tumor

Version 1.16.0

Date 2015-02-18

Author Thomas Kuilman

Maintainer Oscar Krijgsman <o.krijgsman@nki.nl>

Depends R(>= 2.10)

Suggests BiocStyle

Description Whole-exome sequencing data from a murine small-cell lung tumor; only contains data of chromosome 4.

License GPL-2

biocViews SequencingData, LungCancerData

git_url <https://git.bioconductor.org/packages/SCLCBam>

git_branch RELEASE_3_9

git_last_commit 9903b74

git_last_commit_date 2019-05-02

Date/Publication 2019-09-17

R topics documented:

getPathBamFolder	1
Index	3

getPathBamFolder	<i>SCLCBam: Sequence data from chromosome 4 of a small-cell lung tumor</i>
------------------	--

Description

Sequence reads from chromosome 4 of a whole-exome sequencing approach on a small-cell lung tumor.

Usage

```
getPathBamFolder()
```

Details

The `getPathBamFolder()` function returns the full path name to the folder containing the `.bam` file.

Value

Returns the full path name of the folder containing the `.bam` file.

Author(s)

Thomas Kuilman (t.kuilman@nki.nl)

References

The dataset was downloaded from the European Nucleotide Archive using the accession number PRJEB6954 using sample accession number SAMEA2697779, and reads on chromosome 4 were extracted. The full `.bam` file containing data for all chromosomes can be downloaded from here <http://www.ebi.ac.uk/ena/data/view/SAMEA2697779>

Examples

```
getPathBamFolder()
```

Index

`getPathBamFolder`, [1](#)

`SCLCBam (getPathBamFolder)`, [1](#)