

# Package ‘crisprViz’

April 17, 2025

**Title** Visualization Functions for CRISPR gRNAs

**Version** 1.11.0

**Description** Provides functionalities to visualize and contextualize CRISPR guide RNAs (gRNAs) on genomic tracks across nucleases and applications. Works in conjunction with the `crisprBase` and `crisprDesign` Bioconductor packages. Plots are produced using the Gviz framework.

**Depends** R (>= 4.2.0), `crisprBase` (>= 0.99.15), `crisprDesign` (>= 0.99.77)

**Imports** `BiocGenerics`, `Biocstrings`, `BSgenome`, `GenomeInfoDb`, `GenomicFeatures`, `GenomicRanges`, `grDevices`, `Gviz`, `IRanges`, `methods`, `S4Vectors`, `txdbmaker`

**Suggests** `AnnotationHub`, `BiocStyle`, `BSgenome.Hsapiens.UCSC.hg38`, `knitr`, `rmarkdown`, `rtracklayer`, `testthat`, `utils`

**biocViews** CRISPR, FunctionalGenomics, GeneTarget

**License** MIT + file LICENSE

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

**VignetteBuilder** knitr

**BugReports** <https://github.com/crisprVerse/crisprViz/issues>

**URL** <https://github.com/crisprVerse/crisprViz>

**git\_url** <https://git.bioconductor.org/packages/crisprViz>

**git\_branch** devel

**git\_last\_commit** ac1fc76

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-04-17

**Author** Jean-Philippe Fortin [aut, cre],  
Luke Hoberecht [aut]

**Maintainer** Jean-Philippe Fortin <fortin946@gmail.com>

## Contents

|                       |   |
|-----------------------|---|
| cage                  | 2 |
| cas12aGuideSet        | 2 |
| cas9GuideSet          | 3 |
| dnase                 | 3 |
| gpr21GeneModel        | 3 |
| gpr21GuideSet         | 4 |
| krasGeneModel         | 4 |
| krasGuideSet          | 4 |
| ltn1GeneModel         | 5 |
| mmp7GeneModel         | 5 |
| mmp7GuideSet          | 5 |
| plotGuideSet          | 6 |
| plotMultipleGuideSets | 8 |
| repeats               | 9 |

|              |           |
|--------------|-----------|
| <b>Index</b> | <b>11</b> |
|--------------|-----------|

---

|      |                                                |
|------|------------------------------------------------|
| cage | <i>CAGE peak annotation from AnnotationHub</i> |
|------|------------------------------------------------|

---

### Description

A sample of CAGE peak annotation from AnnotationHub (ascension number AH5084), lifted over to hg38.

### Usage

```
data(cage, package="crisprViz")
```

### Format

A [GRanges](#) object.

---

|                |                                                        |
|----------------|--------------------------------------------------------|
| cas12aGuideSet | <i>Example GuideSet targeting the human LTN1 gene.</i> |
|----------------|--------------------------------------------------------|

---

### Description

An example [GuideSet](#) object targeting the CDS of the human LTN1 gene. Generated using the As-Cas12a CRISPR nuclease, the genome sequence from the BSgenome.Hsapiens.UCSC.hg38 package, and the gene model from txdb\_human in the crisprDesignData package (Ensembl release 104).

### Usage

```
data(cas12aGuideSet, package="crisprViz")
```

### Format

A [GuideSet](#) object.

---

|              |                                                        |
|--------------|--------------------------------------------------------|
| cas9GuideSet | <i>Example GuideSet targeting the human LTN1 gene.</i> |
|--------------|--------------------------------------------------------|

---

**Description**

An example [GuideSet](#) object targeting the CDS of the human LTN1 gene. Generated using the Sp-Cas9 CRISPR nuclease, the genome sequence from the `BSgenome.Hsapiens.UCSC.hg38` package, and the gene model from `txdb_human` in the `crisprDesignData` package (Ensembl release 104).

**Usage**

```
data(cas9GuideSet, package="crisprViz")
```

**Format**

A [GuideSet](#) object.

---

|       |                                                                  |
|-------|------------------------------------------------------------------|
| dnase | <i>DNase I hypersensitive site annotation from AnnotationHub</i> |
|-------|------------------------------------------------------------------|

---

**Description**

A sample of DNase I hypersensitive site annotation from AnnotationHub (ascension number AH30743), lifted over to hg38.

**Usage**

```
data(dnase, package="crisprViz")
```

**Format**

A [GRanges](#) object.

---

|                |                                                               |
|----------------|---------------------------------------------------------------|
| gpr21GeneModel | <i>CompressedGRangesList describing the human GPR21 gene.</i> |
|----------------|---------------------------------------------------------------|

---

**Description**

A [CompressedGRangesList](#) object describing the gene model of the human GPR21 gene. Coordinates were subset from `txdb_human` in the `crisprDesignData` package (Ensembl release 104).

**Usage**

```
data(gpr21GeneModel, package="crisprViz")
```

**Format**

A [CompressedGRangesList](#) object.

---

|               |                                                         |
|---------------|---------------------------------------------------------|
| gpr21GuideSet | <i>Example GuideSet targeting the human GPR21 gene.</i> |
|---------------|---------------------------------------------------------|

---

### Description

An example [GuideSet](#) object targeting a section of the CDS of the human GPR21 gene. Generated using the BE4max CRISPR nuclease, the genome sequence from the BSgenome.Hsapiens.UCSC.hg38 package, and the gene model from txdb\_human in the crisprDesignData package (Ensembl release 104).

### Usage

```
data(gpr21GuideSet, package="crisprViz")
```

### Format

A [GuideSet](#) object.

---

|               |                                                              |
|---------------|--------------------------------------------------------------|
| krasGeneModel | <i>CompressedGRangesList describing the human KRAS gene.</i> |
|---------------|--------------------------------------------------------------|

---

### Description

A [CompressedGRangesList](#) object describing the gene model of the human KRAS gene. Coordinates were subset from txdb\_human in the crisprDesignData package (Ensembl release 104).

### Usage

```
data(krasGeneModel, package="crisprViz")
```

### Format

A [CompressedGRangesList](#) object.

---

|              |                                                        |
|--------------|--------------------------------------------------------|
| krasGuideSet | <i>Example GuideSet targeting the human KRAS gene.</i> |
|--------------|--------------------------------------------------------|

---

### Description

An example [GuideSet](#) object targeting the CDS of the human KRAS gene. Generated using the Sp-Cas9 CRISPR nuclease, the genome sequence from the BSgenome.Hsapiens.UCSC.hg38 package, and the gene model from txdb\_human in the crisprDesignData package (Ensembl release 104).

### Usage

```
data(krasGuideSet, package="crisprViz")
```

### Format

A [GuideSet](#) object.

---

|               |                                                              |
|---------------|--------------------------------------------------------------|
| ltn1GeneModel | <i>CompressedGRangesList describing the human LTN1 gene.</i> |
|---------------|--------------------------------------------------------------|

---

**Description**

A [CompressedGRangesList](#) object describing the gene model of the human LTN1 gene. Coordinates were subset from txdb\_human in the crisprDesignData package (Ensembl release 104).

**Usage**

```
data(ltn1GeneModel, package="crisprViz")
```

**Format**

A [CompressedGRangesList](#) object.

---

|               |                                                              |
|---------------|--------------------------------------------------------------|
| mmp7GeneModel | <i>CompressedGRangesList describing the human MMP7 gene.</i> |
|---------------|--------------------------------------------------------------|

---

**Description**

A [CompressedGRangesList](#) object describing the gene model of the human MMP7 gene. Coordinates were subset from txdb\_human in the crisprDesignData package (Ensembl release 104).

**Usage**

```
data(mmp7GeneModel, package="crisprViz")
```

**Format**

A [CompressedGRangesList](#) object.

---

|              |                                                        |
|--------------|--------------------------------------------------------|
| mmp7GuideSet | <i>Example GuideSet targeting the human MMP7 gene.</i> |
|--------------|--------------------------------------------------------|

---

**Description**

An example [GuideSet](#) object targeting the promoter region of the human MMP7 gene. Generated using the SpCas9 CRISPR nuclease, the genome sequence from the BSgenome.Hsapiens.UCSC.hg38 package, and the gene model from tss\_human in the crisprDesignData package (Ensembl release 104).

**Usage**

```
data(mmp7GuideSet, package="crisprViz")
```

**Format**

A [GuideSet](#) object.

plotGuideSet

*Plotting a GuideSet and other genomic annotations***Description**

Function to plot guide targets stored in a [GuideSet](#) object in a gene browser view supported by Gviz. Target gene isoforms and other genomic annotation, along with the target chromosome ideogram and sequence, may also be added, permitting a comprehensive visualization of the genomic context around the target protospacer sequences.

**Usage**

```
plotGuideSet(
  x,
  geneModel = NULL,
  targetGene = NULL,
  annotations = list(),
  from = NULL,
  to = NULL,
  extend.left = 0,
  extend.right = 0,
  margin = 1,
  includeIdeogram = TRUE,
  bands = NULL,
  guideStacking = "squish",
  bsgenome = NULL,
  pamSiteOnly = FALSE,
  showGuideLabels = TRUE,
  onTargetScore = NULL,
  includeSNPTrack = TRUE,
  gcWindow = NULL
)
```

**Arguments**

|                           |                                                                                                                                                                                                                                                                                                                                                                                                        |
|---------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x                         | A <a href="#">GuideSet</a> object.                                                                                                                                                                                                                                                                                                                                                                     |
| geneModel                 | A <a href="#">TxDb</a> object or a <a href="#">GRangesList</a> object obtained using <a href="#">TxDb2GRangesList</a> .                                                                                                                                                                                                                                                                                |
| targetGene                | String specifying the gene symbol or Ensembl ID of the gene to plot.                                                                                                                                                                                                                                                                                                                                   |
| annotations               | A named (optional) list of genomic annotations as <a href="#">GRanges</a> to plot. Provided names are displayed as track titles.                                                                                                                                                                                                                                                                       |
| from, to                  | Numeric value giving the genomic coordinate range to plot; see <a href="#">plotTracks</a> .                                                                                                                                                                                                                                                                                                            |
| extend.left, extend.right | Numeric value giving the length in bases to extend the plotting range; see <a href="#">plotTracks</a> .                                                                                                                                                                                                                                                                                                |
| margin                    | A numeric value that sets the margin of the plotting range with respect to the range of x. The value is a ratio of the width of x considered as a single range, with a value of 1 (default) extending the plotting window by the same distance as that between <code>min(start(x))</code> and <code>max(end(x))</code> . Only works for the respective side of the plot if either from or to are NULL. |

|                 |                                                                                                                                                                                                                          |
|-----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| includeIdeogram | Logical; whether to include an <a href="#">IdeogramTrack</a> in the plot.                                                                                                                                                |
| bands           | A data.frame of cytoband information for the target genome required for ideogram plotting; see <a href="#">IdeogramTrack</a> .                                                                                           |
| guideStacking   | Character string specifying how to stack guides. Options are squish, dense, hide (see <a href="#">GeneRegionTrack</a> ), or NA to have each guide occupy a separate track.                                               |
| bsgenome        | A <a href="#">BSgenome</a> object; used to generate <a href="#">SequenceTrack</a> and GC content <a href="#">DataTrack</a> .                                                                                             |
| pamSiteOnly     | Whether to plot only the PAM site in representing guides, or plot the full guide and PAM sequence (default).                                                                                                             |
| showGuideLabels | Logical; whether to show labels for individual guides.                                                                                                                                                                   |
| onTargetScore   | Optional column name in mcols(x) of on-target scores. Applies a color scheme to the guide track based on on-target scores, with light gray corresponding to 0 and dark blue corresponding to 1.                          |
| includeSNPTrack | Logical; whether to include an <a href="#">AnnotationTrack</a> for SNPs if such annotation exists in x.                                                                                                                  |
| gcWindow        | If not NULL, a numeric value specifying the distance from a given base for which to establish a window for calculating GC content at that base. These values are then added to the plot in a <a href="#">DataTrack</a> . |

**Value**

A Gviz plot; see [plotTracks](#).

**Author(s)**

Luke Hoberecht

**See Also**

[plotMultipleGuideSets](#) for plotting multiple GuideSet objects together.

**Examples**

```
if (interactive()){
  data(krasGuideSet, package="crisprViz")
  data(krasGeneModel, package="crisprViz")
  plotGuideSet(krasGuideSet[1:4],
               geneModel=krasGeneModel,
               targetGene="KRAS")
}
```

---

plotMultipleGuideSets *Plotting a GuideSet and other genomic annotation*


---

## Description

Function to plot guide targets stored in multiple [GuideSet](#) objects in a gene browser view supported by Gviz. Target gene isoforms and other genomic annotation, along with the target chromosome ideogram and sequence, may also be added, permitting a comprehensive visualization of the genomic context targeted by spacers in [GuideSet](#) objects.

## Usage

```
plotMultipleGuideSets(
  x,
  geneModel = NULL,
  targetGene = NULL,
  annotations = list(),
  from = NULL,
  to = NULL,
  extend.left = 0,
  extend.right = 0,
  margin = 1,
  includeIdeogram = TRUE,
  bands = NULL,
  bsgenome = NULL,
  onTargetScores = NULL,
  includeSNPTrack = TRUE,
  gcWindow = NULL
)
```

## Arguments

|                           |                                                                                                                                                                                                                                                                                                                                                                                                        |
|---------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x                         | A named (optional) list of <a href="#">GuideSet</a> objects. List names are displayed as track titles.                                                                                                                                                                                                                                                                                                 |
| geneModel                 | A <a href="#">TxDb</a> object or a <a href="#">GRangesList</a> object obtained using <a href="#">TxDb2GRangesList</a> .                                                                                                                                                                                                                                                                                |
| targetGene                | A character string giving the gene symbol or Ensembl ID of the gene to plot.                                                                                                                                                                                                                                                                                                                           |
| annotations               | A named (optional) list of genomic annotations as <a href="#">GRanges</a> to plot. Provided names are displayed as track titles.                                                                                                                                                                                                                                                                       |
| from, to                  | Numeric value giving the genomic coordinate range to plot; see <a href="#">plotTracks</a> .                                                                                                                                                                                                                                                                                                            |
| extend.left, extend.right | Numeric value giving the length in bases to extend the plotting range; see <a href="#">plotTracks</a> .                                                                                                                                                                                                                                                                                                |
| margin                    | A numeric value that sets the margin of the plotting range with respect to the range of x. The value is a ratio of the width of x considered as a single range, with a value of 1 (default) extending the plotting window by the same distance as that between <code>min(start(x))</code> and <code>max(end(x))</code> . Only works for the respective side of the plot if either from or to are NULL. |
| includeIdeogram           | Logical; whether to include an <a href="#">IdeogramTrack</a> in the plot.                                                                                                                                                                                                                                                                                                                              |

|                 |                                                                                                                                                                                                                          |
|-----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| bands           | A data.frame of cytoband information for the target genome required for ideogram plotting; see <a href="#">IdeogramTrack</a> .                                                                                           |
| bsgenome        | A <a href="#">BSgenome</a> object; used to generate <a href="#">SequenceTrack</a> and GC content <a href="#">DataTrack</a> .                                                                                             |
| onTargetScores  | Optional list of column names for each element in x of on-target scores. Applies a color scheme to the guide track based on on-target scores, with light gray corresponding to 0 and dark blue corresponding to 1.       |
| includeSNPTrack | Logical; whether to include an <a href="#">AnnotationTrack</a> for SNPs if such annotation exists in x.                                                                                                                  |
| gcWindow        | If not NULL, a numeric value specifying the distance from a given base for which to establish a window for calculating GC content at that base. These values are then added to the plot in a <a href="#">DataTrack</a> . |

**Value**

A Gviz plot; see [plotTracks](#).

**Author(s)**

Luke Hoberecht, Jean-Philippe Fortin

**See Also**

[plotGuideSet](#)

**Examples**

```
if (interactive()){
  library(BSgenome.Hsapiens.UCSC.hg38)
  data(cas9GuideSet, package="crisprViz")
  data(cas12aGuideSet, package="crisprViz")
  data(ltn1GeneModel, package="crisprViz")
  plotMultipleGuideSets(list(SpCas9=cas9GuideSet, AsCas12a=cas12aGuideSet),
                        geneModel=ltn1GeneModel,
                        targetGene="LTN1",
                        bsgenome=BSgenome.Hsapiens.UCSC.hg38,
                        margin=0.2,
                        gcWindow=10)
}
```

---

repeats

---

*Subset of repeat elements for hg38.*


---

**Description**

A [GRanges](#) object describing a subset of repeat elements for the hg38 genome. Coordinates were subset from `gr.repeats.hg38` in the `crisprDesignData` package.

**Usage**

```
data(repeats, package="crisprViz")
```

**Format**

A [GRanges](#) object.

# Index

## \* datasets

- cage, [2](#)
- cas12aGuideSet, [2](#)
- cas9GuideSet, [3](#)
- dnase, [3](#)
- gpr21GeneModel, [3](#)
- gpr21GuideSet, [4](#)
- krasGeneModel, [4](#)
- krasGuideSet, [4](#)
- ltn1GeneModel, [5](#)
- mmp7GeneModel, [5](#)
- mmp7GuideSet, [5](#)
- repeats, [9](#)

AnnotationTrack, [7, 9](#)

BSgenome, [7, 9](#)

cage, [2](#)  
cas12aGuideSet, [2](#)  
cas9GuideSet, [3](#)  
CompressedGRangesList, [3–5](#)

DataTrack, [7, 9](#)  
dnase, [3](#)

GeneRegionTrack, [7](#)  
gpr21GeneModel, [3](#)  
gpr21GuideSet, [4](#)  
GRanges, [2, 3, 6, 8–10](#)  
GRangesList, [6, 8](#)  
GuideSet, [2–6, 8](#)

IdeogramTrack, [7–9](#)

krasGeneModel, [4](#)  
krasGuideSet, [4](#)

ltn1GeneModel, [5](#)

mmp7GeneModel, [5](#)  
mmp7GuideSet, [5](#)

plotGuideSet, [6, 9](#)  
plotMultipleGuideSets, [7, 8](#)

plotTracks, [6–9](#)

repeats, [9](#)

SequenceTrack, [7, 9](#)

TxDb, [6, 8](#)  
TxDb2GRangesList, [6, 8](#)