

# Package ‘crisprViz’

November 25, 2024

**Title** Visualization Functions for CRISPR gRNAs

**Version** 1.9.0

**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`, `Biostrings`, `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`

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**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>

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

### 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>
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---

**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>
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---

**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`*Example GuideSet targeting the human MMP7 gene.*

---

**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 <code>mcols(x)</code> 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 <code>data.frame</code> 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.

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