Package ‘crisprScore’

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Title On-Target and Off-Target Scoring Algorithms for CRISPR gRNAs
Depends R (>= 4.1), crisprScoreData (>= 1.1.3)
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Description Provides R wrappers of several on-target and off-target scoring methods for CRISPR guide RNAs (gRNAs). The following nucleases are supported: SpCas9, AsCas12a, enAsCas12a, and Rfx-Cas13d (CasRx). The available on-target cutting efficiency scoring methods are RuleSet1, Azimuth, DeepHF, DeepCpf1, enPAM+GB, and CRISPRscan. Both the CFD and MIT scoring methods are available for off-target specificity prediction. The package also provides a Lindel-derived score to predict the probability of a gRNA to produce indels inducing a frameshift for the Cas9 nuclease. Note that DeepHF, DeepCpf1 and enPAM+GB are not available on Windows machines.
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getAzimuthScores

Calculate on-target sgRNA activity scores for Cas9 using Azimuth

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas9-induced knockout using the Azimuth scoring method. The Azimuth algorithm is an improvement upon the commonly-used 'Rule Set 2', also developed by the Doench lab.

Usage

getAzimuthScores(sequences, fork = FALSE)
getCasRxRFScores

Arguments

sequences Character vector of 30bp sequences needed for Azimuth scoring, see details below.
fork Set to TRUE to preserve changes to the R configuration within the session.

Details

The input sequences for Azimuth scoring require 4 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (23 nucleotides) and 3 nucleotides downstream of the protospacer sequence, for a total of 30 nucleotides: [4nt][20nt-spacer][NGG][3nt]. Note that a canonical PAM sequence (NGG) is required for Azimuth.

Value

getAzimuthScores returns a data.frame with sequence and score columns. The Azimuth score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

Author(s)

Jean-Philippe Fortin

References


Examples

if (interactive()){
  flank5 <- "ACCT" #4bp
  spacer <- "ATCGATGCTGATGCTAGATA" #20bp
  pam <- "AGG" #3bp
  flank3 <- "TTG" #3bp
  input <- paste0(flank5, spacer, pam, flank3)
  results <- getAzimuthScores(input)
}

getCasRxRFScores  Calculate on-target sgRNA activity scores for CasRx using CasRx-RF

Description

Calculate on-target sgRNA activity scores for CasRx (RfxCas13d) using the CasRx-RF algorithm.
Usage

getCasRxFscores(
  mrnaSequence,
  directRepeat = "aacccctaccaactggcgggtttgaaac",
  binaries = NULL,
  sort = FALSE,
  verbose = TRUE
)

Arguments

mrnaSequence  A DNAStringSet representing the mRNA sequence for which to extract spacer sequences and calculate scores.
directRepeat  String specifying the direct repeat used in the CasRx construct.
binaries      Named list of paths for binaries needed for CasRx-RF. Names of the list must be "RNAfold", "RNAhybrid", and "RNAplfold". Each list element is a string specifying the path of the binary. If NULL (default), binaries must be available on the PATH.
sort          Should spacers be sorted by score? FALSE by default.
verbose       Should messages be printed to console? TRUE by default.

Details

The function first extracts all 23mer spacer sequences targeting the mRNA sequence, and scores them for on-target activity.

Value

A data.frame with the following columns:

- ID  Character vector specifying spacer ID.
- spacer  23-mer spacer sequence.
- pfs_site  coordinate of the protospacer flanking sequence (PFS).
- protospacer  23-mer protospacer sequence (reverse complement of the spacer sequence).
- PFS  PFS nucleotide.
- score  Raw score (not standardized).
- standardizedScore  Score standardized between 0 and 1.
- quartile  Quartile score (1 to 4, with 4 being the best quartile.

A score closer to 1 indicates higher predicted on-target activity.

Author(s)

Jean-Philippe Fortin
getCFDScores

References

Examples
if (interactive()){
  fasta <- file.path(system.file(package="crisprScore"),
    "casrxf/test.fa")
  mrnaSequence <- Biostrings::readDNAStringSet(filepath=fasta,
    format="fasta",
    use.names=TRUE)
  results <- getCasRxFScores(mrnaSequence)
}

getCFDScores  Calculate CFD off-target specificity scores

Description
Calculate cutting frequency determination (CFD) off-target specificity scores for CRISPR/Cas9 or CRISPR/CasRX.

Usage
getCFDScores(spacers, protospacers, pams, nuclease = c("SpCas9", "CasRx"))

Arguments
spacers Character vector of 20bp spacer sequences. Must be in 5’ to 3’ direction. For SpCas9, must be of length 20bp. For CasRx, must be at most of length 27bp.
protospacers Character vector of 20bp protospacer sequences (target sequences). Must be in 5’ to 3’ direction.
pams Character vector of PAM sequences.
nuclease String specifying the nuclease. Either "SpCas9" (default) or "CasRx".

Value
getCFDScores returns a data.frame with spacer, protospacer, and score columns. The CFD score takes on a value between 0 and 1. For a given pair (on-target, off-target), a higher CFD score indicates a higher likelihood for the nuclease to cut at the off-target. Non-canonical PAM sequences are taken into account by the CFD algorithm.

Author(s)
Jean-Philippe Fortin
getCrispraiScores

Calculate on-target sgRNA activity scores for CRISPRa and CRISPRi

Description

Use the Weissman lab scoring method (library design v2) to calculate on-target sgRNA activity scores for Cas9-based CRISPR activation (CRISPRa) and CRISPR inactivation (CRISPRi) gene perturbation studies. The algorithm incorporates chromatin features, transcription start site, and sequence to predict gRNA activity scores. Only sgRNAs designed for the human genome (hg38 build) using Cas9 are supported at the moment, and only spacers of length 19 are supported at the moment.

Usage

gETCHPRaiScores(
  tss_df,
  sgrna_df,
  verbose = FALSE,
  modality = c("CRISPRa", "CRISPRi"),
  fastaFile = NULL,
  chromatinFiles = NULL
)

Arguments

tss_df A data.frame specifying coordinates of transcription start site (TSS) of the targeted promoter regions. Must have the following columns: gene_symbol, promoter, transcripts, position, strand, and chr. See details section below for more information.

Examples

# Calculating MIT scores for two off-targets with respect to # one spacer sequence:
spacers <- "AGGTGTAGTGTGTGTGATAA"
protospacer1 <- "CGGTGTAGTGTGTGTGATAA"
protospacer2 <- "CGGTGTCGTGTGTGTGATAA"
results <- getCFDScores(spacers=spacers,
  protospacers=c(protospacer1, protospacer2),
  pams=c("AGG", "CGG")
)
**getCrispraiScores**

sgrna_df A data.frame specifying coordinates and spacer sequences of the sgRNAs to score. Must have the following columns: grna_id, tss_id, pam_site, strand, and spacer_19mer. See details section below for more information.

verbose Should messages be printed to the console? TRUE by default.

modality Which mode of perturbation is being used? Must be a string specifying either CRISPRa or CRISPRi.

fastaFile String specifying fasta file of the hg38 genome.

chromatinFiles Named character vector of length 3 specifying BigWig files containing chromatin accessibility data.

Details
tss_df details: This must be a data.frame that contains the following columns: * tss_id: string specifying name of the TSS. * gene_symbol: string specifying sHGNC/HUGO gene identifier. * promoter: string specifying promoter ID (e.g. "P1" or "P2"). * transcripts: Ensembl transcript identifier. * position: start position of TSS in hg38 coordinates. * strand: strand of the gene/TSS. Must be either + or -. * chr: string specifying chromosome (e.g. "chr1").
sgrna_df details: This must be a data.frame that contains the following columns: * grna_id: string specifying a unique sgRNA identifier. * tss_id: string specifying name of the TSS. * pam_site: genomic coordinate of the N in the NGG PAM sequence. * strand: strand fo the sgRNA. Must be either + or -. * spacer_19mer: string specifying sgRNA 19mer spacer sequence.

Value

getCrispraiScores returns a data.frame with grna_id and score columns. The Weissman score takes on a value between 0 and 1. A higher score indicates higher sgRNA efficiency.

Author(s)
Pirunthan Perampalam, Jean-Philippe Fortin

References


Examples

```r
## Not run:
results <- getCrispraiScores(tss_df=tssExampleCrispra,
                               sgrna_df=sgrnaExampleCrispra,
                               modality="CRISPRa")
results <- getCrispraiScores(tss_df=tssExampleCrispri,
                               sgrna_df=sgrnaExampleCrispri,
                               modality="CRISPRi")
## End(Not run)
```
**getCRISPRaterScores**

*Calculate on-target sgRNA activity scores for Cas9 using CRISPRater*

**Description**

Calculate on-target sgRNA activity scores for CRISPR/Cas9-induced knockout using the DeepHF scoring method. Both U6 and T7 promoters are supported. Three different versions of the SpCas9 nuclease are supported: wildtype (WT-SpCas9), high-fidelity Cas9 (SpCas9-HF1) and enhanced Cas9 (eSpCas9). Currently not supported on Windows machines.

**Usage**

```r
getCRISPRaterScores(sequences)
```

**Arguments**

- `sequences` Character vector of 20bp protospacer sequences.

**Details**

Input sequences for CRISPRater scoring must be 20 spacer sequences.

**Value**

`getCRISPRaterScores` returns a data.frame with `sequence` and `score` columns. The CRISPRater score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

**Author(s)**

Jean-Philippe Fortin

**References**


**Examples**

```r
spacer <- "ATCGATGCTGATGCTAGATA" #20bp
results <- getCRISPRaterScores(spacer)
```
getCRISPRscanScores

**Description**

Calculate on-target sgRNA activity scores for Cas9 using CRISPRscan. The method is also known as the Moreno-Mateos score. The CRISPRscan algorithm was trained using in vitro transcription of sgRNAs using a T7 promoter, and might therefore be suboptimal to predict sgRNA activity when expressed from U6 promoter.

**Usage**

```
getCRISPRscanScores(sequences)
```

**Arguments**

- `sequences`: Character vector of 35bp sequences needed for CRISPRscan scoring, see details below.

**Details**

The input sequences for Rule Set 1 scoring require 6 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (23 nucleotides) and 6 nucleotides downstream of the protospacer sequence, for a total of 35 nucleotides: [6nt][20nt-spacer][NGG][6nt]. Note that a canonical PAM sequence (NGG) is required for CRISPRscan.

**Value**

`getCRISPRscanScores` returns a data.frame with `sequence` and `score` columns. The CRISPRscan score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

**Author(s)**

Jean-Philippe Fortin

**References**


**Examples**

```r
flank5 <- "ACCTGG" #6bp
spacer <- "ATCGATGCTAGCTAGATA" #20bp
pam <- "AGG" #3bp
flank3 <- "TTGAGC" #6bp
input <- paste0(flank5, spacer, pam, flank3)
results <- getCRISPRscanScores(input)
```
**getDeepCpf1Scores**

*Calculate on-target sgRNA activity scores for Cas12a using DeepCpf1*

**Description**

Calculate on-target sgRNA activity scores for CRISPR/Cas12a-induced knockout using the DeepCpf1 scoring method. Currently not supported on Windows machines.

**Usage**

getDeepCpf1Scores(sequences, convertPAM = TRUE, fork = FALSE)

**Arguments**

- **sequences**: Character vector of 34bp sequences needed for DeepCpf1 scoring, see details below.
- **convertPAM**: Should non-canonical PAM sequences be converted to TTTC? TRUE by default.
- **fork**: Set to TRUE to preserve changes to the R configuration within the session.

**Details**

The input sequences for DeepCpf1 scoring require 4 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (4bp PAM sequence + 23bp spacer sequence) and 3 nucleotides downstream of the protospacer sequence, for a total of 34 nucleotides. If convertPAM is set to TRUE, any non-canonical PAM sequence will be convert to TTTC for scoring purposes.

**Value**

getDeepCpf1Scores returns a data.frame with sequence and score columns. The DeepCpf1 score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

**Author(s)**

Jean-Philippe Fortin

**References**


**Examples**

```r
if (interactive()){
  flank5 <- "ACC" #3bp
  pam <- "TTTT" #4bp
  spacer <- "AATCGATGCTGATGCTAGATATT" #23bp
  flank3 <- "AAGT" #4bp
  input <- paste0(flank5, pam, spacer, flank3)
}```
getDeepHFScores

```
results <- getDeepCpf1Scores(input)
```

---

**getDeepHFScores**  
*Calculate on-target sgRNA activity scores for Cas9 using DeepHF*

**Description**

Calculate on-target sgRNA activity scores for CRISPR/Cas9-induced knockout using the DeepHF scoring method. Both U6 and T7 promoters are supported. Three different versions of the SpCas9 nuclease are supported: wildtype (WT-SpCas9), high-fidelity Cas9 (SpCas9-HF1) and enhanced Cas9 (eSpCas9). Currently not supported on Windows machines.

**Usage**

```
getDeepHFScores(
  sequences,
  enzyme = c("WT", "ESP", "HF"),
  promoter = c("U6", "T7"),
  fork = FALSE
)
```

**Arguments**

- **sequences**: Character vector of 23bp protospacer sequences.
- **enzyme**: Character string specifying the Cas9 variant. Wildtype Cas9 (WT) by default, see details below.
- **promoter**: Character string specifying promoter used for expressing sgRNAs for wildtype Cas9 (must be either "U6" or "T7"). "U6" by default.
- **fork**: Set to TRUE to preserve changes to the R configuration within the session.

**Details**

Input sequences for DeepHF scoring must be 23bp protospacer sequences (20bp spacer sequences + 3bp PAM sequences). Only canonical PAM sequences (NGG) are allowed. Users can specify for which Cas9 they wish to score sgRNAs by using the argument enzyme: "WT" for Wildtype Cas9 (WT-SpCas9), "HF" for high-fidelity Cas9 (SpCas9-HF), or "ESP" for enhanced Cas9 (eSpCas9). For wildtype Cas9, users can also specify the promoter used for expressing sgRNAs using the argument promoter ("U6" by default).

**Value**

*getDeepHFScores* returns a data.frame with sequence and score columns. The DeepHF score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.
getDeepSpCas9Scores

Author(s)
Jean-Philippe Fortin

References

Examples

```r
if (interactive()){
  spacer <- "ATCGATGCTGATGCTAGATA" #20bp
  pam <- "AGG" #3bp
  input <- paste0(spacer, pam)

  # Wildtype Cas9 using U6 promoter:
  results <- getDeepHFScores(input)

  # Wildtype Cas9 using T7 promoter:
  results <- getDeepHFScores(input, promoter="T7")

  #' High-fidelity Cas9:
  results <- getDeepHFScores(input, enzyme="HF")

  #' Enhanced Cas9:
  results <- getDeepHFScores(input, enzyme="ESP")
}
```

getDeepSpCas9Scores Calculate on-target sgRNA activity scores for SpCas9 using DeepSpCas9

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas9-induced knockout using the DeepSpCas9 scoring method.

Usage

getDeepSpCas9Scores(sequences, fork = FALSE)

Arguments

- **sequences**: Character vector of 30bp sequences needed for DeepSpCas9 scoring, see details below.
- **fork**: Set to TRUE to preserve changes to the R configuration within the session.
getEnPAMGBScores

Details
The input sequences for DeepSpCas9 scoring require 4 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (20bp spacer sequence + 3bp PAM sequence) and 3 nucleotides downstream of the protospacer sequence, for a total of 30 nucleotides.

Value

`getDeepSpCas9Scores` returns a data.frame with `sequence` and `score` columns. The `getDeepSpCas9Scores` score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

Author(s)

Jean-Philippe Fortin

References


Examples

```r
if (interactive()){
  flank5 <- "ACCG" #4bp
  spacer <- "AATCGATGCTGATGCTAGAT" #20bp
  pam <- "AGG" #3bp
  flank3 <- "AAT" #3bp
  input <- paste0(flank5, spacer, pam, flank3)
  results <- getDeepSpCas9Scores(input)
}
```

getEnPAMGBScores

Calculate on-target sgRNA activity scores for enCas12a using enPAM+GB

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas12a-induced knockout using the enPAM+GB scoring method. Currently not supported on Windows machines.

Usage

`getEnPAMGBScores(sequences, fork = FALSE)`

Arguments

- `sequences` Character vector of 34bp sequences needed for enPAM+GB scoring, see details below.
- `fork` Set to TRUE to preserve changes to the R configuration within the session.
getLindelScores

Details
The input sequences for enPAM+GB scoring require 4 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (4bp PAM sequence + 23bp spacer sequence) and 3 nucleotides downstream of the protospacer sequence, for a total of 34 nucleotides. Both canonical and non-canonical PAM sequences can be provided.

Value
getEnPAMGBScores returns a data.frame with sequence and score columns.

Author(s)
Jean-Philippe Fortin

References

Examples

```r
if (interactive()){  
  flank5 <- "CATG" #4bp  
  pam <- "TTTT" #4bp  
  spacer <- "TTTGGACCGATCGATAATCAC" #23bp  
  flank3 <- "ATT" #3bp  
  input <- paste0(flank5, pam, spacer, flank3)  
  results <- getEnPAMGBScores(input)  
}
```

getLindelScores

```
getLindelScores(sequences, fork = FALSE)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sequences</td>
<td>Character vector of 65bp sequences needed for Lindel scoring, see details below.</td>
</tr>
<tr>
<td>fork</td>
<td>Set to TRUE to preserve changes to the R configuration within the session.</td>
</tr>
</tbody>
</table>
getMITScores

Details

The input sequences for Lindel scoring require 13 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (23 nucleotides) and 29 nucleotides downstream of the protospacer sequence, for a total of 65 nucleotides. Note that only canonical PAM sequences (NGG) are accepted by Lindel.

Value

A data.frame with predicted frameshift ratio (between 0 and 1). A higher ratio indicates a greater chance of a frameshift indel introduced by CRISPR/Cas9-induced double-strand breaks.

Author(s)

Jean-Philippe Fortin

References


Examples

if (interactive()){
  flank5 <- "ACCTTTTAATCGA" #13bp
  spacer <- "TGCTGATGCTAGATATTAAG" #20bp
  pam <- "TGG" #3bp
  flank3 <- "CTTTTAATCGATGCTGATGCTAGATATTA" #29bp
  input <- paste0(flank5, spacer, pam, flank3)
  results <- getLindelScores(input)
}

generateMITScores

Calculate MIT off-target specificity scores for CRISPR/Cas9

Description

Calculate MIT off-target specificity scores for CRISPR/Cas9.

Usage

generateMITScores(spacers, protospacers, pams, includeDistance = TRUE)
getRuleSet1Scores

Arguments

- spacers   Character vector of 20bp spacer sequences.
- protospacers Character vector of 20bp protospacer sequences for off-targets.
- pams   Character vector of 3nt PAM sequences.
- includeDistance Should distance between mismatches be considered during scoring? TRUE by default.

Value

getMITScores returns a data.frame with spacer, protospacer, and score columns. The MIT score takes on a value between 0 and 1. For a given pair (on-target, off-target), a higher MIT score indicates a higher likelihood for the Cas9 nuclease to cut at the off-target. Non-canonical PAM sequences are taken into account by the MIT algorithm.

Author(s)

Jean-Philippe Fortin

References


Examples

```r
# Calculating MIT scores for two off-targets with respect to # one spacer sequence:
spacers <- c("AGGTGTAGTGTGTGTGATAA")
protospacers <- c("CGGTGTAGTGTGTGTGATAA", "CGGTGTCGTGTGTGTGATAA")
pams <- c("AGG", "CGG")
results <- getMITScores(spacers=spacers,
protospacers=protospacers,pams=pams)
```

getRuleSet1Scores

Calculate on-target sgRNA activity scores for Cas9 using Rule Set 1

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas9-induced knockout using the Rule Set 1 scoring method. The Rule Set 1 algorithm was an early on-target efficiency method developed by the Doench lab.
getRuleSet3Scores

Usage

getRuleSet1Scores(sequences)

Arguments

sequences Character vector of 30bp sequences needed for Rule Set 1 scoring, see details below.

Details

The input sequences for Rule Set 1 scoring require 4 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (23 nucleotides) and 3 nucleotides downstream of the protospacer sequence, for a total of 30 nucleotides: [4nt][20nt-spacer][NGG][3nt]. Note that a canonical PAM sequence (NGG) is required for Rule Set 1.

Value

getRuleSet1Scores returns a data.frame with sequence and score columns. The Rule Set 1 score takes on a value between 0 and 1. A higher score indicates higher knockout efficiency.

Author(s)

Jean-Philippe Fortin

References


Examples

flank5 <- "ACCT" #4bp
spacer <- "ATCGATGCTGATGCTAGATA" #20bp
pam <- "AGG" #3bp
flank3 <- "TTG" #3bp
input <- paste0(flank5, spacer, pam, flank3)
results <- getRuleSet1Scores(input)

getRuleSet3Scores Calculate on-target sgRNA activity scores for SpCas9 using Rule Set 3

Description

Calculate on-target sgRNA activity scores for CRISPR/Cas9-induced knockout using the Rule Set 3 scoring method.
Usage

getRuleSet3Scores(
    sequences,
    tracrRNA = c("Hsu2013", "Chen2013"),
    mode = c("sequence", "target")
)

Arguments

sequences Character vector of 30bp sequences needed for Rule Set 3 scoring, see details below.
tracrRNA String specifying which tracrRNA is used. Must be either "Hsu2013" (default) or "Chen2013".
mode String specifying which prediction mode is used. Must be either "sequence" (default) or "target".

Details

The input sequences for Rule Set 3 scoring require 4 nucleotides upstream of the protospacer sequence, the protospacer sequence itself (20bp spacer sequence + 3bp PAM sequence ) and 3 nucleotides downstream of the protospacer sequence, for a total of 30 nucleotides.

Value

getRuleSet3Scores returns a data.frame with sequence and score columns. The getRuleSet3Scores score is similar to a Z-score. A higher score indicates higher knockout efficiency.

Author(s)

Jean-Philippe Fortin

References

doi: https://doi.org/10.1101/2022.06.27.497780

Examples

if (interactive()){
    flank5 <- "ACCG" #4bp
    spacer <- "AATCGATGCTGATGCTAGAT" #20bp
    pam <- "AGG" #3bp
    flank3 <- "AAT" #3bp
    input <- paste0(flank5, spacer, pam, flank3)
    results <- getRuleSet3Scores(input)
    }

scoringMethodsInfo  

**data.frame detailing available scoring methods**

**Description**

data.frame detailing available scoring methods with information needed to extract nucleotide sequences needed by each scoring algorithm.

**Usage**

data(scoringMethodsInfo)

**Format**

A data frame with 6 columns:

- **method**  name of the scoring method
- **nuclease**  nuclease compatible with the scoring method
- **left**  upstream offset (relative to PAM site) to extract nucleotide sequence needed for scoring
- **right**  downstream offset (relative to PAM site) to extract nucleotide sequence needed for scoring
- **type**  type of the scoring algorithm (on-target or off-target)
- **label**  proper case-sensitive method name for labeling
- **len**  length of the nucleotide sequence needed for scoring

sgrnaExampleCrispra  

**Example CRISPRa gRNAs data.frame for the getCrispraiScores function**

**Description**

Example CRISPRa gRNAs data.frame for the getCrispraiScores function. The targeted TSSs are described in the object tssExampleCrispra.

**Usage**

data(sgrnaExampleCrispra)

**Format**

A data.frame with 5 columns:

- **grna_id**  String specifying gRNA unique identifier.
- **tss_id**  String specifying the targeted TSS id.
- **pam_site**  Genomic coordinate specifying the first nucleotide of PAM sequence.
- **strand**  Strand of the gRNA strand. Must be "+" or "+-".
- **spacer_19mer**  String specifying the nucleotide sequence of the 19mer spacer sequence.


Example CRISPRi gRNAs data.frame for the getCrispraiScores function.

**Description**

Example CRISPRi gRNAs data.frame for the getCrispraiScores function. The targeted TSSs are described in the object tssExampleCrispra.

**Usage**

data(sgrnaExampleCrispri)

**Format**

A data.frame with 5 columns:

- **grna_id**: String specifying gRNA unique identifier.
- **tss_id**: String specifying the targeted TSS id.
- **pam_site**: Genomic coordinate specifying the first nucleotide of PAM sequence.
- **strand**: Strand of the gRNA strand. Must be "+" or "-".
- **spacer_19mer**: String specifying the nucleotide sequence of the 19mer spacer sequence.

Example TSS data.frame for the getCrispraiScores function.

**Description**

Example TSS data for gRNAs stored in sgrnaExampleCrispra.

**Usage**

data(tssExampleCrispra)

**Format**

A data.frame with 7 columns:

- **tss_id**: String specifying the targeted TSS id.
- **gene_symbol**: String specifying gene symbol.
- **promoter**: String specifying the promoter suffix to add to the gene symbol columns to obtain the unique TSS id.
- **transcripts**: Ensembl IDs of the targeted transcript.
- **position**: Integer specifying genomic coordinate of the TSS.
- **strand**: Strand of TSS. Must be "+" or "-".
- **chr**: String specifying the chromosome name.
Example TSS data.frame for the getCrizpraiScores function

Description

Example TSS data for gRNAs stored in sgrnaExampleCrispri.

Usage

data(tssExampleCrispri)

Format

A data.frame with 7 columns:

- **tss_id**  String specifying the targeted TSS id.
- **gene_symbol**  String specifying gene symbol.
- **promoter**  String specifying the promoter suffix to add to the gene symbol columns to obtain the unique TSS id.
- **transcripts**  Ensembl IDs of the targeted transcript.
- **position**  Integer specifying genomic coordinate of the TSS.
- **strand**  Strand of TSS. Must be "+" or "-".
- **chr**  String specifying the chromosome name.
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