# Package 'crisprScoreData'

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**Version** 1.12.0

**Date** 2022-10-12

**Title** Pre-trained models for the crisprScore package

**Depends** ExperimentHub

**Imports** AnnotationHub, utils

**Suggests** BiocStyle, knitr, rmarkdown, testthat

**biocViews** ExperimentHub, Homo_sapiens_Data

**Description** Provides an interface to access pre-trained models for on-target and off-target gRNA activity prediction algorithms implemented in the crisprScore package. Pre-trained model data are stored in the ExperimentHub database. Users should consider using the crisprScore package directly to use and load the pre-trained models.

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**VignetteBuilder** knitr

**BugReports** https://github.com/crisprVerse/crisprScoreData

**URL** https://github.com/crisprVerse/crisprScoreData/issues

**git_url** https://git.bioconductor.org/packages/crisprScoreData

**git_branch** RELEASE_3_21

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`crisprScoreData` *Pretrained models for several crisprScore prediction algorithms*

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## Description

Pretrained models for DeepHF and Lindel on-target prediction algorithms for Cas9 gRNA performance to be used by crisprScore package. Data were obtained using the script `inst/scripts/make-data.R`.

## Usage

```
DeepWt.hdf5(metadata=FALSE)
DeepWt_T7.hdf5(metadata=FALSE)
DeepWt_U6.hdf5(metadata=FALSE)
hf_rnn_model.hdf5(metadata=FALSE)
esp_rnn_model.hdf5(metadata=FALSE)
Model_weights.pkl(metadata=FALSE)
CRISPRa_model.pkl(metadata=FALSE)
CRISPRi_model.pkl(metadata=FALSE)
RFcombined.rds(metadata=FALSE)
```

## Arguments

| | |
|---|---|
| `metadata` | `logical` value indicating whether metadata only should be returned or if the resource should be loaded. Default behavior(metadata=FALSE) loads the data. |

## Format

character

## Value

These accessor functions return characters specifying path of the files

## References

Wang, D., Zhang, C., Wang, B. et al. Optimized CRISPR guide RNA design for two high-fidelity Cas9 variants by deep learning. Nat Commun 10, 4284 (2019). https://doi.org/10.1038/s41467-019-12281-8

Wei Chen, Aaron McKenna, Jacob Schreiber, Maximilian Haeussler, Yi Yin, Vikram Agarwal, William Stafford Noble, Jay Shendure, Massively parallel profiling and predictive modeling of the outcomes of CRISPR/Cas9-mediated double-strand break repair, Nucleic Acids Research, Volume 47, Issue 15, 05 September 2019, Pages 7989–8003, https://doi.org/10.1093/nar/gkz487.

## Examples

```
DeepWt.hdf5()
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