

# Package ‘crisprScoreData’

August 1, 2024

**Version** 1.8.0

**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\_19

**git\_last\_commit** 2dfb8bb

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-08-01

**Author** Jean-Philippe Fortin [aut, cre, cph]

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

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crisprScoreData	<i>Pretrained models for several crisprScore prediction algorithms</i>
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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

<code>metadata</code>	logical value indicating whether metadata only should be returned or if the resource should be loaded. Default behavior( <code>metadata=FALSE</code> ) loads the data.
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### 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>.

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### **Examples**

DeepWt.hdf5()

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