

# Package ‘scanMiRData’

October 10, 2024

**Type** Package

**Title** miRNA Affinity models for the scanMiR package

**Version** 1.11.0

**Depends** R (>= 4.0)

**Date** 2023-07-03

**Imports** scanMiR, utils

**Suggests** knitr, rmarkdown, BiocStyle

**Description** This package contains companion data to the scanMiR package. It contains `KdModel` (miRNA 12-mer binding affinity models) collections corresponding to all human, mouse and rat mirbase miRNAs. See the scanMiR package for details.

**BiocType** ExperimentData

**License** GPL-3

**VignetteBuilder** knitr

**RoxygenNote** 7.1.1

**biocViews** miRNAData, ExperimentData, Homo\_sapiens\_Data, Mus\_musculus\_Data, Rattus\_norvegicus\_Data

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

**git\_branch** devel

**git\_last\_commit** 4bb67d3

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

**Repository** Bioconductor 3.20

**Date/Publication** 2024-10-10

**Author** Pierre-Luc Germain [cre, aut] (<<https://orcid.org/0000-0003-3418-4218>>),  
Michael Soutschek [aut],  
Fridolin Gross [aut]

**Maintainer** Pierre-Luc Germain <pierre-luc.germain@hest.ethz.ch>

## Contents

getKdModels . . . . .	2
KdModels-hsa . . . . .	2
KdModels-mmu . . . . .	3
KdModels-rno . . . . .	3

**Index****4**


---

getKdModels	<i>getKdModels</i>
-------------	--------------------

---

**Description**

Returns a collection of miRNA KdModels for the requested species. *Note that by default, low-confidence miRNAs are not returned (see ‘categories’).*

**Usage**

```
getKdModels(species = c("hsa", "mmu", "rno"), categories = NULL)
```

**Arguments**

species	Either "hsa" (human), "mmu" (mouse) or "rno" (rat)
categories	The categories of miRNAs to return. Any combination of "Low-confidence", "Poorly conserved", "Conserved across mammals", "Conserved across vertebrates". If NULL (default), all categories are returned. miRNAs with NA as conservation are not returned unless ‘categories==NULL’.

**Value**

An object of class [KdModelList](#)

**Examples**

```
mods <- getKdModels("rno")
summary(mods)
```

---

KdModels-hsa	<i>KdModelList for human miRNAs</i>
--------------	-------------------------------------

---

**Description**

A list of binding affinity models ([KdModel](#)) for human ('hsa'), mouse ('mmu'), or rat ('rno') miR-base 21.1 miRNAs. These represent the miRNA 12-mer binding affinities predicted using the CNN from McGeary, Lin et al. (2019).

**Value**

a [KdModelList](#) list.

---

`KdModels-mmu`*KdModelList for mouse miRNAs*

---

**Description**

A list of binding affinity models ([KdModel](#)) for mouse miRbase 21.1 miRNAs. These represent the miRNA 12-mer binding affinities predicted using the CNN from McGeary, Lin et al. (2019).

**Value**

a [KdModelList](#) list.

---

`KdModels-rno`*KdModelList for rat miRNAs*

---

**Description**

A list of binding affinity models ([KdModel](#)) for rat miRbase 21.1 miRNAs. These represent the miRNA 12-mer binding affinities predicted using the CNN from McGeary, Lin et al. (2019).

**Value**

a [KdModelList](#) list.

# Index

[getKdModels](#), 2

[hsa \(KdModels-hsa\)](#), 2

[KdModel](#), 2, 3

[KdModellist](#), 2, 3

[KdModels-hsa](#), 2

[KdModels-hsa \(KdModels-hsa\)](#), 2

[KdModels-mmu](#), 3

[KdModels-mmu \(KdModels-mmu\)](#), 3

[KdModels-rno](#), 3

[KdModels-rno \(KdModels-rno\)](#), 3

[mmu \(KdModels-mmu\)](#), 3

[rno \(KdModels-rno\)](#), 3