# Package 'TargetScoreData'

November 10, 2026

**Title** TargetScoreData

**Version** 1.48.0

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**Description** Precompiled and processed miRNA-overexpression fold-changes from 84 Gene Expression Omnibus (GEO) series corresponding to 6 platforms, 77 human cells or tissues, and 113 distinct miRNAs. Accompanied with the data, we also included in this package the sequence feature scores from TargetScanHuman 6.1 including the context+ score and the probabilities of conserved targeting for each miRNA-mRNA interaction. Thus, the user can use these static sequence-based scores together with user-supplied tissue/cell-specific fold-change due to miRNA overexpression to predict miRNA targets using the package TargetScore (download separately)

**biocViews** ExperimentData, RNASeqData, miRNAData

**License** GPL-2

**Suggests** TargetScore, gplots

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

**git_branch** RELEASE_3_23

**git_last_commit** 8de45d0

**git_last_commit_date** 2026-04-28

**Repository** Bioconductor 3.23

**Date/Publication** 2026-11-10

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TargetScoreData-package

*Processed human microRNA perturbation data from GEO, and sequence information from TargetScan, and targetScore from TargetScore*

## Description

To automate the pipeline of calculating targetScore using `targetScore`, we compiled, processed and generated miRNA-overexpression fold-changes from 84 Gene Expression Omnibus (GEO) series corresponding to 6 platforms, 77 human cells or tissues, and 113 distinct miRNAs. To our knowledge, this is by far the largest miRNA-pertubation data compendium. Accompanied with the data, we also included in this package the sequence feature scores from TargetScanHuman 6.1 including the context+ score and the probabilities of conserved targeting for each miRNA-mRNA interaction. Thus, the user can use these static sequence-based scores together with user-supplied tissue/cell-specific fold-change due to miRNA overexpression to predict miRNA targets using `targetScore`.

## Details

| | |
|---|---|
| Package: | TargetScoreData |
| Type: | Package |
| Version: | 0.99.4 |
| Date: | 2013-07-13 |
| License: | GPL-2 |

`get_TargetScanHuman_contextScore`: TargetScan context score for all of the predicted sites (including conserved and nonconserved sites) downloaded from TargetScan 6 website (http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_61)

`get_TargetScanHuman_PCT`: TargetScan PCT for all of the predicted sites (including conserved and nonconserved sites) downloaded from TargetScan 6 website (http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_61)

`get_miRNA_family_info`: Get miRNA family information obtained TargetScanHuman 6

`get_precomputed_targetScores`: Pre-calculated targetScores for 112 miRNAs using logFC and sequence scores from TargetScan context score and PCT from the RData files above.

`get_precomputed_logFC`: We combined all of the logFC data columns into a single N x M matrix for all of the N = 19177 RefSeq mRNAs (NM_* obtained from UCSC) and M = 286 datasets. Missing data (logFC) for some genes across studies were imputed using `impute` from `impute.knn`.

`get_miRNA_transfection_data`: Get log fold-changes (logFC) from each study organized in a list with each item corresponding to a miRNA. Notably, some miRNAs (e.g., hsa-miR-1) appear more than once in the list corresponding to different studies.

`get_validated_targets`: Get validated targets of human miRNA obtained from mirTarBase v3.5

## Author(s)

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## References

miRTarBase: a database curates experimentally validated microRNA-target interactions. (2011). miRTarBase: a database curates experimentally validated microRNA-target interactions., 39(Database issue), D163-9. doi:10.1093/nar/gkq1107

Friedman, R. C., Farh, K. K.-H., Burge, C. B., & Bartel, D. P. (2009). Most mammalian mRNAs are conserved targets of microRNAs. Genome Research, 19(1), 92-105. doi:10.1101/gr.082701.108

Garcia, D. M., Baek, D., Shin, C., Bell, G. W., Grimson, A., & Bartel, D. P. (2011). Weak seed-pairing stability and high target-site abundance decrease the proficiency of lsy-6 and other microRNAs. Nature structural & molecular biology, 18(10), 1139-1146. doi:10.1038/nsmb.2115

Please follow the GEO series number to find the references for each microRNA-transfection dataset.

## See Also

get_TargetScanHuman_contextScore, get_TargetScanHuman_PCT, get_validated_targets, get_miRNA_family_info, get_precomputed_targetScores, get_precomputed_logFC, get_miRNA_transfection_data

## Examples

```
ls("package:TargetScoreData")
```

---

# get_miRNA_family_info *MicroRNA family information*

---

## Description

Get human miRNA family information obtained frin TargetScanHuman 6 website

## Usage

```
get_miRNA_family_info(datapath = system.file("extdata/miR_Family_Info.txt", package = "TargetScoreDat
```

## Arguments

| | |
|---|---|
| datapath | data path |

---

`get_miRNA_transfection_data` *get_miRNA_transfection_data*

---

## Description

Get log fold-changes (logFC) from each study organized in a list with each item corresponding to a miRNA. Notably, some miRNAs (e.g., hsa-miR-1) appear more than once in the list corresponding to different studies.

## Usage

```
get_miRNA_transfection_data(datapath = system.file("extdata/miRNA_transfection_data.RData", package =
```

## Arguments

| | |
|---|---|
| `datapath` | data path |

---

`get_precomputed_logFC` *get_precomputed_logFC*

---

## Description

We combined all of the logFC data columns into a single N x M matrix for all of the N = 19177 RefSeq mRNAs (NM_* obtained from UCSC) and M = 286 datasets. Missing data (logFC) for some genes across studies were imputed using `impute` from `impute.knn`.

## Usage

```
get_precomputed_logFC(datapath = system.file("extdata/logFC.RData", package = "TargetScoreData"))
```

## Arguments

| | |
|---|---|
| `datapath` | data path |

## get_precomputed_targetScores *get_precomputed_targetScores*

### Description

Pre-calculated targetScores for 112 miRNAs using logFC and sequence scores from TargetScan context score and PCT from the RData files above.

### Usage

```
get_precomputed_targetScores(datapath = system.file("extdata/targetScores.RData", package = "TargetSc
```

### Arguments

| | |
|---|---|
| datapath | data path |

## get_TargetScanHuman_contextScore *get_TargetScanHuman_contextScore*

### Description

TargetScan context score for all of the predicted sites (including conserved and nonconserved sites) downloaded from TargetScan 6 website (http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_61)

### Usage

```
get_TargetScanHuman_contextScore(datapath = system.file("extdata/TargetScanHuman_contextScore.RData"
```

### Arguments

| | |
|---|---|
| datapath | data path |

get_TargetScanHuman_PCT *get_TargetScanHuman_PCT*

## Description

TargetScan PCT for all of the predicted sites (including conserved and nonconserved sites) downloaded from TargetScan 6 website (http://www.targetscan.org/cgi-bin/targetscan/data_download.cgi?db=vert_61)

## Usage

```
get_TargetScanHuman_PCT(datapath = system.file("extdata/TargetScanHuman_PCT.RData", package = "Target
```

## Arguments

| | |
|---|---|
| datapath | data path |

get_validated_targets *get_validated_targets*

## Description

Get validated targets of human miRNA obtained from mirTarBase v3.5

## Usage

```
get_validated_targets(datapath = system.file("extdata/hsa_MTI.xls", package = "TargetScoreData"))
```

## Arguments

| | |
|---|---|
| datapath | data path |

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