

# Package ‘TargetScoreData’

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**Title** TargetScoreData

**Version** 1.41.0

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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

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TargetScoreData-package

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

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## 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-perturbation 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](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](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 microR-  
NAs. *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 from TargetScanHuman 6 website

### Usage

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

### 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 = "TargetScoreData"))
```

**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](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](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 = "TargetScoreData"))
```

### **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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