

# Package ‘miRNATarget’

November 6, 2025

**Title** gene target tabale of miRNA for human/mouse used for MiRaGE package

**Version** 1.49.0

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**Description** gene target tabale of miRNA for human/mouse used for MiRaGE package

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**Depends** R (>= 2.10), Biobase

**License** GPL

**biocViews** ExperimentData, Homo\_sapiens\_Data

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

**git\_branch** devel

**git\_last\_commit** 8e138de

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2025-11-06

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|         |                                                                                       |
|---------|---------------------------------------------------------------------------------------|
| conv_id | <i>miRNA conservation table of mouse/human, based upon TargetScan-Mouse/Human 6.1</i> |
|---------|---------------------------------------------------------------------------------------|

---

**Description**

This miRNA conservation table is for MiRaGE package. Actual name of data files is HS\_conv\_id for human and MM\_conv\_id for mouse, but name of loaded data frame is "conv\_id".

**Usage**

data(MM\_conv\_id)

**Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is two.

**Details**

The first column includes miRNA names based upon miRBase Release 18 and the second column includes integers which describe miRNA conservation. 2 stands for broadly conserved (in MiRaGE, it corresponds to "conserved"), 1 stands for conserved (in MiRaGE, broadly conserved and conserved correspond to "weakly conserved"), 0 stands for others (in MiRaGE, "all" corresponds to all miRNAs).

**Note**

How to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about TargetScan, access to <http://www.targetscan.org/>

## Examples

```
data(MM_conv_id)
```

---

|            |                                          |
|------------|------------------------------------------|
| HS_conv_id | <i>miRNA conservation table of human</i> |
|------------|------------------------------------------|

---

## Description

This miRNA conservation table of human is for MiRaGE package, based upon TargetScanHuman 6.1

## Usage

```
data(HS_conv_id)
```

## Format

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is two.

## Details

The first column includes miRNA names based upon miRBase Release 18 and the second column includes integers which describe miRNA conservation. 2 stands for broadly conserved (in MiRaGE, it corresponds to "conserved"), 1 stands for conserved (in MiRaGE, broadly conserved and conserved correspond to "weakly conserved"), 0 stands for others (in MiRaGE, "all" corresponds to all miRNAs). Please note that the name of object loaded is not "HS\_conv\_id" but "conv\_id", because of the requirements by MiRaGE package.

## Note

How to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about TargetScanHuman, access to [http://www.targetscan.org/vert\\_61/](http://www.targetscan.org/vert_61/)

## Examples

```
data(HS_conv_id)
```

---

`HS_refseq_to_affy_hc_g110`*Conversion table between RefSeq and affy\_hc\_g110 for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hc\_g110 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hc_g110)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hc\_g110. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hc\_g110" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hc_g110)
```

---

`HS_refseq_to_affy_hg_focus`*Conversion table between RefSeq and affy\_hg\_focus for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hg\_focus is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hg_focus)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_focus. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_focus" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hg_focus)
```

---

`HS_refseq_to_affy_hg_u133a`*Conversion table between RefSeq and affy\_hg\_u133a for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hg\_u133a is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hg_u133a)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u133a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u133a" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hg_u133a)
```

---

`HS_refseq_to_affy_hg_u133a_2`*Conversion table between RefSeq and affy\_hg\_u133a\_2 for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hg\_u133a\_2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hg_u133a_2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u133a\_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u133a\_2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hg_u133a_2)
```

---

`HS_refseq_to_affy_hg_u133b`*Conversion table between RefSeq and affy\_hg\_u133b for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hg\_u133b is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hg_u133b)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u133b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u133b" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hg_u133b)
```

---

`HS_refseq_to_affy_hg_u133_plus_2`*Conversion table between RefSeq and affy\_hg\_u133\_plus\_2 for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hg\_u133\_plus\_2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hg_u133_plus_2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u133\_plus\_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u133\_plus\_2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hg_u133_plus_2)
```

---

HS\_refseq\_to\_affy\_hg\_u95a

*Conversion table between RefSeq and affy\_hg\_u95a for human*

---

## Description

This gene id conversion table between RefSeq and affy\_hg\_u95a is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_affy_hg_u95a)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95a" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_affy_hg_u95a)
```

---

`HS_refseq_to_affy_hg_u95av2`*Conversion table between RefSeq and affy\_hg\_u95av2 for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hg\_u95av2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hg_u95av2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95av2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95av2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hg_u95av2)
```

---

`HS_refseq_to_affy_hg_u95b`*Conversion table between RefSeq and affy\_hg\_u95b for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hg\_u95b is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hg_u95b)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95b" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hg_u95b)
```

---

`HS_refseq_to_affy_hg_u95c`*Conversion table between RefSeq and affy\_hg\_u95c for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hg\_u95c is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hg_u95c)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95c. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95c" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hg_u95c)
```

---

`HS_refseq_to_affy_hg_u95d`*Conversion table between RefSeq and affy\_hg\_u95d for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hg\_u95d is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hg_u95d)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95d. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95d" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hg_u95d)
```

---

`HS_refseq_to_affy_hg_u95e`*Conversion table between RefSeq and affy\_hg\_u95e for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hg\_u95e is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hg_u95e)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hg\_u95e. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hg\_u95e" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hg_u95e)
```

---

`HS_refseq_to_affy_huex_1_0_st_v2`*Conversion table between RefSeq and affy\_huex\_1\_0\_st\_v2 for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_huex\_1\_0\_st\_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_huex_1_0_st_v2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_huex\_1\_0\_st\_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_huex\_1\_0\_st\_v2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_huex_1_0_st_v2)
```

---

`HS_refseq_to_affy_hugeneffl`*Conversion table between RefSeq and affy\_hugeneffl for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_hugeneffl is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_hugeneffl)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_hugeneffl. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hugeneffl" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_hugeneffl)
```

---

HS\_refseq\_to\_affy\_hugene\_1\_0\_st\_v1

*Conversion table between RefSeq and affy\_hugene\_1\_0\_st\_v1 for human*

---

## Description

This gene id conversion table between RefSeq and affy\_hugene\_1\_0\_st\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_affy_hugene_1_0_st_v1)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding affy\_hugene\_1\_0\_st\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_hugene\_1\_0\_st\_v1" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_affy_hugene_1_0_st_v1)
```

---

`HS_refseq_to_affy_u133_x3p`*Conversion table between RefSeq and affy\_u133\_x3p for human*

---

**Description**

This gene id conversion table between RefSeq and affy\_u133\_x3p is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_affy_u133_x3p)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_u133\_x3p. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_affy\_u133\_x3p" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_affy_u133_x3p)
```

---

`HS_refseq_to_agilent_cgh_44b`*Conversion table between RefSeq and agilent\_cgh\_44b for human*

---

**Description**

This gene id conversion table between RefSeq and agilent\_cgh\_44b is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_agilent_cgh_44b)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding agilent\_cgh\_44b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_agilent\_cgh\_44b" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_agilent_cgh_44b)
```

---

`HS_refseq_to_agilent_wholegenome`*Conversion table between RefSeq and agilent\_wholegenome for human*

---

**Description**

This gene id conversion table between RefSeq and agilent\_wholegenome is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_agilent_wholegenome)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding agilent\_wholegenome. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_agilent\_wholegenome" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_agilent_wholegenome)
```

---

`HS_refseq_to_canonical_transcript_stable_id`*Conversion table between RefSeq and canonical\_transcript\_stable\_id  
for human*

---

**Description**

This gene id conversion table between RefSeq and canonical\_transcript\_stable\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_canonical_transcript_stable_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding canonical\_transcript\_stable\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_canonical\_transcript\_stable\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_canonical_transcript_stable_id)
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| HS_refseq_to_ccds | <i>Conversion table between RefSeq and ccds for human</i> |
|-------------------|-----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and ccds is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_ccds)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ccds. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ccds" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_ccds)
```

---

|                       |                                                               |
|-----------------------|---------------------------------------------------------------|
| HS_refseq_to_codelink | <i>Conversion table between RefSeq and codelink for human</i> |
|-----------------------|---------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and codelink is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_codelink)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding codelink. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_codelink" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_codelink)
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| HS_refseq_to_embl | <i>Conversion table between RefSeq and embl for human</i> |
|-------------------|-----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and embl is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_embl)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding embl. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_embl" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_embl)
```

---

HS\_refseq\_to\_ensembl\_gene\_id

*Conversion table between RefSeq and ensembl\_gene\_id for human*

---

**Description**

This gene id conversion table between RefSeq and ensembl\_gene\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_ensembl_gene_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_gene\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ensembl\_gene\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_ensembl_gene_id)
```

---

`HS_refseq_to_ensembl_peptide_id`*Conversion table between RefSeq and ensembl\_peptide\_id for human*

---

**Description**

This gene id conversion table between RefSeq and ensembl\_peptide\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_ensembl_peptide_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_peptide\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ensembl\_peptide\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_ensembl_peptide_id)
```

---

`HS_refseq_to_ensembl_transcript_id`*Conversion table between RefSeq and ensembl\_transcript\_id for human*

---

**Description**

This gene id conversion table between RefSeq and ensembl\_transcript\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_ensembl_transcript_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_transcript\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ensembl\_transcript\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_ensembl_transcript_id)
```

---

HS\_refseq\_to\_entrezgene

*Conversion table between RefSeq and entrezgene for human*

---

## Description

This gene id conversion table between RefSeq and entrezgene is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_entrezgene)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding entrezgene. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_entrezgene" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_entrezgene)
```

---

HS\_refseq\_to\_hgnc\_id    *Conversion table between RefSeq and hgnc\_id for human*

---

**Description**

This gene id conversion table between RefSeq and hgnc\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_hgnc_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding hgnc\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_hgnc\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_hgnc_id)
```

---

HS\_refseq\_to\_hgnc\_symbol  
                                  *Conversion table between RefSeq and hgnc\_symbol for human*

---

**Description**

This gene id conversion table between RefSeq and hgnc\_symbol is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_hgnc_symbol)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding hgnc\_symbol. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_hgnc\_symbol" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_hgnc_symbol)
```

---

```
HS_refseq_to_hgnc_transcript_name
```

*Conversion table between RefSeq and hgnc\_transcript\_name for human*

---

**Description**

This gene id conversion table between RefSeq and hgnc\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_hgnc_transcript_name)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding hgnc\_transcript\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_hgnc\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_hgnc_transcript_name)
```

---

```
HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k
```

*Conversion table between RefSeq and  
HS\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k for human*

---

**Description**

This gene id conversion table between RefSeq and HS\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_efg\_agilent\_sureprint. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

---

|                                                                                                    |
|----------------------------------------------------------------------------------------------------|
| HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1                                         |
| <i>Conversion table between RefSeq and HS_refseq_to_efg_agilent_wholegenome_4x44k_v1 for human</i> |

---

## Description

This gene id conversion table between RefSeq and HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

---

HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2  
*Conversion table between RefSeq and  
 HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2 for human*

---

## Description

This gene id conversion table between RefSeq and HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

---

HS\_refseq\_to\_HS\_refseq\_to\_ensembl\_exon\_id

*Conversion table between RefSeq and HS\_refseq\_to\_ensembl\_exon\_id  
for human*

---

## Description

This gene id conversion table between RefSeq and HS\_refseq\_to\_ensembl\_exon\_id is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_HS_refseq_to_ensembl_exon_id)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_ensembl\_exon\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_ensembl\_exon\_id" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_HS_refseq_to_ensembl_exon_id)
```

---

|                                                                                                    |
|----------------------------------------------------------------------------------------------------|
| HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name                                         |
| <i>Conversion table between RefSeq and HS_refseq_to_uniprot_genename_transcript_name for human</i> |

---

## Description

This gene id conversion table between RefSeq and HS\_refseq\_to\_uniprot\_genename\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_uniprot\_genename\_tr. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_genename\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name)
```

---

HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_sptreml

*Conversion table between RefSeq and HS\_refseq\_to\_uniprot\_sptreml  
for human*

---

## Description

This gene id conversion table between RefSeq and HS\_refseq\_to\_uniprot\_sptreml is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_sptreml)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_uniprot\_sptreml. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_sptreml" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_HS_refseq_to_uniprot_sptreml)
```

---

|                                                                                     |
|-------------------------------------------------------------------------------------|
| HS_refseq_to_HS_refseq_to_uniprot_swissprot                                         |
| <i>Conversion table between RefSeq and HS_refseq_to_uniprot_swissprot for human</i> |

---

## Description

This gene id conversion table between RefSeq and HS\_refseq\_to\_uniprot\_swissprot is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_uniprot\_swissprot. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_swissprot" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot)
```

---

HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_swissprot\_accession  
*Conversion table between RefSeq and  
 HS\_refseq\_to\_uniprot\_swissprot\_accession for human*

---

## Description

This gene id conversion table between RefSeq and HS\_refseq\_to\_uniprot\_swissprot\_accession is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot_accession)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_uniprot\_swissprot\_accession. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_swissprot\_accession" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot_accession)
```

---

`HS_refseq_to_HS_refseq_to_wikigene_id`*Conversion table between RefSeq and HS\_refseq\_to\_wikigene\_id for human*

---

**Description**

This gene id conversion table between RefSeq and HS\_refseq\_to\_wikigene\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_HS_refseq_to_wikigene_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding HS\_refseq\_to\_wikigene\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_HS\_refseq\_to\_wikigene\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_HS_refseq_to_wikigene_id)
```

---

`HS_refseq_to_illumina_humanht_12`*Conversion table between RefSeq and illumina\_humanht\_12 for human*

---

**Description**

This gene id conversion table between RefSeq and illumina\_humanht\_12 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_illumina_humanht_12)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_humanht\_12. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_illumina\_humanht\_12" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_illumina_humanht_12)
```

---

`HS_refseq_to_illumina_humanwg_6_v1`*Conversion table between RefSeq and illumina\_humanwg\_6\_v1 for human*

---

**Description**

This gene id conversion table between RefSeq and illumina\_humanwg\_6\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_illumina_humanwg_6_v1)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_humanwg\_6\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_illumina\_humanwg\_6\_v1" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_illumina_humanwg_6_v1)
```

---

`HS_refseq_to_illumina_humanwg_6_v2`*Conversion table between RefSeq and illumina\_humanwg\_6\_v2 for human*

---

**Description**

This gene id conversion table between RefSeq and illumina\_humanwg\_6\_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_illumina_humanwg_6_v2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_humanwg\_6\_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_illumina\_humanwg\_6\_v2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_illumina_humanwg_6_v2)
```

---

`HS_refseq_to_illumina_humanwg_6_v3`*Conversion table between RefSeq and illumina\_humanwg\_6\_v3 for human*

---

**Description**

This gene id conversion table between RefSeq and illumina\_humanwg\_6\_v3 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_illumina_humanwg_6_v3)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_humanwg\_6\_v3. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_illumina\_humanwg\_6\_v3" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_illumina_humanwg_6_v3)
```

---

HS\_refseq\_to\_interpro *Conversion table between RefSeq and interpro for human*

---

### Description

This gene id conversion table between RefSeq and interpro is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_interpro)
```

### Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### Details

The first column includes RefSeq gene id and the second column includes corresponding interpro. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_interpro" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

### Examples

```
data(HS_refseq_to_interpro)
```

---

HS\_refseq\_to\_ipi *Conversion table between RefSeq and ipi for human*

---

### Description

This gene id conversion table between RefSeq and ipi is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_ipi)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ipi. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ipi" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_ipi)
```

---

|                     |                                                             |
|---------------------|-------------------------------------------------------------|
| HS_refseq_to_merops | <i>Conversion table between RefSeq and merops for human</i> |
|---------------------|-------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and merops is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_merops)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding merops. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_merops" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_merops)
```

---

|                  |                                                          |
|------------------|----------------------------------------------------------|
| HS_refseq_to_pdb | <i>Conversion table between RefSeq and pdb for human</i> |
|------------------|----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and pdb is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_pdb)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding pdb. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_pdb" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_pdb)
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| HS_refseq_to_pfam | <i>Conversion table between RefSeq and pfam for human</i> |
|-------------------|-----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and pfam is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_pfam)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding pfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_pfam" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_pfam)
```

---

|                               |                                                                       |
|-------------------------------|-----------------------------------------------------------------------|
| HS_refseq_to_phalanx_onearray | <i>Conversion table between RefSeq and phalanx_onearray for human</i> |
|-------------------------------|-----------------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and phalanx\_onearray is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_phalanx_onearray)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding phalanx\_onearray. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_phalanx\_onearray" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_phalanx_onearray)
```

---

```
HS_refseq_to_protein_id
```

*Conversion table between RefSeq and protein\_id for human*

---

**Description**

This gene id conversion table between RefSeq and protein\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_protein_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding protein\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_protein\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_protein_id)
```

---

```
HS_refseq_to_refseq_dna
```

*Conversion table between RefSeq and refseq\_dna for human*

---

**Description**

This gene id conversion table between RefSeq and refseq\_dna is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_refseq_dna)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding refseq\_dna. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_refseq\_dna" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_refseq_dna)
```

---

HS\_refseq\_to\_refseq\_genomic

*Conversion table between RefSeq and refseq\_genomic for human*

---

## Description

This gene id conversion table between RefSeq and refseq\_genomic is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(HS_refseq_to_refseq_genomic)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding refseq\_genomic. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_refseq\_genomic" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(HS_refseq_to_refseq_genomic)
```

---

`HS_refseq_to_refseq_peptide`*Conversion table between RefSeq and refseq\_peptide for human*

---

**Description**

This gene id conversion table between RefSeq and refseq\_peptide is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_refseq_peptide)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding refseq\_peptide. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_refseq\_peptide" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_refseq_peptide)
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| HS_refseq_to_rfam | <i>Conversion table between RefSeq and rfam for human</i> |
|-------------------|-----------------------------------------------------------|

---

### Description

This gene id conversion table between RefSeq and rfam is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(HS_refseq_to_rfam)
```

### Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### Details

The first column includes RefSeq gene id and the second column includes corresponding rfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_rfam" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

### Examples

```
data(HS_refseq_to_rfam)
```

---

|                             |                                                                     |
|-----------------------------|---------------------------------------------------------------------|
| HS_refseq_to_rfam_gene_name | <i>Conversion table between RefSeq and rfam_gene_name for human</i> |
|-----------------------------|---------------------------------------------------------------------|

---

### Description

This gene id conversion table between RefSeq and rfam\_gene\_name is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_rfam_gene_name)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding rfam\_gene\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_rfam\_gene\_name" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_rfam_gene_name)
```

---

HS\_refseq\_to\_rfam\_transcript\_name

*Conversion table between RefSeq and rfam\_transcript\_name for human*

---

**Description**

This gene id conversion table between RefSeq and rfam\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_rfam_transcript_name)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding rfam\_transcript\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_rfam\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_rfam_transcript_name)
```

---

|                    |                                                            |
|--------------------|------------------------------------------------------------|
| HS_refseq_to_smart | <i>Conversion table between RefSeq and smart for human</i> |
|--------------------|------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and smart is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_smart)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding smart. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_smart" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_smart)
```

---

HS\_refseq\_to\_tigrfam    *Conversion table between RefSeq and tigrfam for human*

---

**Description**

This gene id conversion table between RefSeq and tigrfam is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_tigrfam)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding tigrfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_tigrfam" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_tigrfam)
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| HS_refseq_to_ucsc | <i>Conversion table between RefSeq and ucsc for human</i> |
|-------------------|-----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and ucsc is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_ucsc)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ucsc. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_ucsc" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_ucsc)
```

---

|                      |                                                              |
|----------------------|--------------------------------------------------------------|
| HS_refseq_to_unigene | <i>Conversion table between RefSeq and unigene for human</i> |
|----------------------|--------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and unigene is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_unigene)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding unigene. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_unigene" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_unigene)
```

---

HS\_refseq\_to\_uniprot\_genename

*Conversion table between RefSeq and uniprot\_genename for human*

---

**Description**

This gene id conversion table between RefSeq and uniprot\_genename is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_uniprot_genename)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding uniprot\_genename. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_uniprot\_genename" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_uniprot_genename)
```

---

```
HS_refseq_to_wikigene_name
```

*Conversion table between RefSeq and wikigene\_name for human*

---

**Description**

This gene id conversion table between RefSeq and wikigene\_name is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(HS_refseq_to_wikigene_name)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding wikigene\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS\_refseq\_to\_wikigene\_name" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(HS_refseq_to_wikigene_name)
```

---

id\_conv*Conversion table between refseq and various gene id/probe id*

---

**Description**

This gene id conversion table between RefSeq and gene id/probe id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_wikigene_name)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding gene id. It can be made out of getBM function in biomaRt package. Actual names of data file is HS\_refseq\_to\_[gene id/probe id] for human and MM\_refseq\_to\_[gene id/probe id] for mouse. [gene id/probe id] stands for various gene id / probe id, but loaded data frame has the name "id\_conv".

**Note**

How to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_wikigene_name)
```

---

|            |                                          |
|------------|------------------------------------------|
| MM_conv_id | <i>miRNA conservation table of mouse</i> |
|------------|------------------------------------------|

---

**Description**

This miRNA conservation table of mouse is for MiRaGE package, based upon TargetScanMouse 6.1

**Usage**

```
data(MM_conv_id)
```

**Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is two.

**Details**

The first column includes miRNA names based upon miRBase Release 18 and the second column includes integers which describe miRNA conservation. 2 stands for broadly conserved (in MiRaGE, it corresponds to "conserved"), 1 stands for conserved (in MiRaGE, broadly conserved and conserved correspond to "weakly conserved"), 0 stands for others (in MiRaGE, "all" corresponds to all miRNAs). Please note that the name of object loaded is not "MM\_conv\_id" but "conv\_id", because of the requirements by MiRaGE package.

**Note**

How to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about TargetScanMouse, access to [http://www.targetscan.org/mmu\\_61/](http://www.targetscan.org/mmu_61/)

**Examples**

```
data(MM_conv_id)
```

---

`MM_refseq_to_affy_mg_u74a`*Conversion table between RefSeq and affy\_mg\_u74a for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_mg\_u74a is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_mg_u74a)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74a" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_mg_u74a)
```

---

`MM_refseq_to_affy_mg_u74av2`*Conversion table between RefSeq and affy\_mg\_u74av2 for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_mg\_u74av2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_mg_u74av2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74av2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74av2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_mg_u74av2)
```

---

`MM_refseq_to_affy_mg_u74b`*Conversion table between RefSeq and affy\_mg\_u74b for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_mg\_u74b is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_mg_u74b)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74b" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_mg_u74b)
```

---

`MM_refseq_to_affy_mg_u74bv2`*Conversion table between RefSeq and affy\_mg\_u74bv2 for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_mg\_u74bv2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_mg_u74bv2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74bv2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74bv2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_mg_u74bv2)
```

---

`MM_refseq_to_affy_mg_u74c`*Conversion table between RefSeq and affy\_mg\_u74c for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_mg\_u74c is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_mg_u74c)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74c. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74c" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_mg_u74c)
```

---

`MM_refseq_to_affy_mg_u74cv2`*Conversion table between RefSeq and affy\_mg\_u74cv2 for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_mg\_u74cv2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_mg_u74cv2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mg\_u74cv2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mg\_u74cv2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_mg_u74cv2)
```

---

`MM_refseq_to_affy_moe430a`*Conversion table between RefSeq and affy\_moe430a for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_moe430a is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_moe430a)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_moe430a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_moe430a" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_moe430a)
```

---

`MM_refseq_to_affy_moe430b`*Conversion table between RefSeq and affy\_moe430b for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_moe430b is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_moe430b)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_moe430b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_moe430b" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_moe430b)
```

---

`MM_refseq_to_affy_moex_1_0_st_v1`*Conversion table between RefSeq and affy\_moex\_1\_0\_st\_v1 for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_moex\_1\_0\_st\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_moex_1_0_st_v1)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_moex\_1\_0\_st\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_moex\_1\_0\_st\_v1" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_moex_1_0_st_v1)
```

---

MM\_refseq\_to\_affy\_mogene\_1\_0\_st\_v1

*Conversion table between RefSeq and affy\_mogene\_1\_0\_st\_v1 for mouse*

---

## Description

This gene id conversion table between RefSeq and affy\_mogene\_1\_0\_st\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_affy_mogene_1_0_st_v1)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding affy\_mogene\_1\_0\_st\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mogene\_1\_0\_st\_v1" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(MM_refseq_to_affy_mogene_1_0_st_v1)
```

---

`MM_refseq_to_affy_mouse430a_2`*Conversion table between RefSeq and affy\_mouse430a\_2 for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_mouse430a\_2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_mouse430a_2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mouse430a\_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mouse430a\_2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_mouse430a_2)
```

---

`MM_refseq_to_affy_mouse430_2`*Conversion table between RefSeq and affy\_mouse430\_2 for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_mouse430\_2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_mouse430_2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mouse430\_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mouse430\_2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_mouse430_2)
```

---

`MM_refseq_to_affy_mu11ksuba`*Conversion table between RefSeq and affy\_mu11ksuba for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_mu11ksuba is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_mu11ksuba)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mu11ksuba. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mu11ksuba" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_mu11ksuba)
```

---

`MM_refseq_to_affy_mu11ksubb`*Conversion table between RefSeq and affy\_mu11ksubb for mouse*

---

**Description**

This gene id conversion table between RefSeq and affy\_mu11ksubb is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_affy_mu11ksubb)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding affy\_mu11ksubb. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_affy\_mu11ksubb" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_affy_mu11ksubb)
```

---

`MM_refseq_to_agilent_wholegenome`*Conversion table between RefSeq and agilent\_wholegenome for mouse*

---

**Description**

This gene id conversion table between RefSeq and agilent\_wholegenome is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_agilent_wholegenome)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding agilent\_wholegenome. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_agilent\_wholegenome" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_agilent_wholegenome)
```

---

`MM_refseq_to_canonical_transcript_stable_id`*Conversion table between RefSeq and canonical\_transcript\_stable\_id  
for mouse*

---

**Description**

This gene id conversion table between RefSeq and canonical\_transcript\_stable\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_canonical_transcript_stable_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding canonical\_transcript\_stable\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_canonical\_transcript\_stable\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_canonical_transcript_stable_id)
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| MM_refseq_to_ccds | <i>Conversion table between RefSeq and ccds for mouse</i> |
|-------------------|-----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and ccds is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_ccds)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ccds. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ccds" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_ccds)
```

---

|                       |                                                               |
|-----------------------|---------------------------------------------------------------|
| MM_refseq_to_codelink | <i>Conversion table between RefSeq and codelink for mouse</i> |
|-----------------------|---------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and codelink is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_codelink)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding codelink. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_codelink" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_codelink)
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| MM_refseq_to_embl | <i>Conversion table between RefSeq and embl for mouse</i> |
|-------------------|-----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and embl is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_embl)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding embl. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_embl" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_embl)
```

---

```
MM_refseq_to_ensembl_gene_id
```

*Conversion table between RefSeq and ensembl\_gene\_id for mouse*

---

**Description**

This gene id conversion table between RefSeq and ensembl\_gene\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_ensembl_gene_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_gene\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ensembl\_gene\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_ensembl_gene_id)
```

---

`MM_refseq_to_ensembl_peptide_id`*Conversion table between RefSeq and ensembl\_peptide\_id for mouse*

---

**Description**

This gene id conversion table between RefSeq and ensembl\_peptide\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_ensembl_peptide_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_peptide\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ensembl\_peptide\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_ensembl_peptide_id)
```

---

`MM_refseq_to_ensembl_transcript_id`*Conversion table between RefSeq and ensembl\_transcript\_id for mouse*

---

**Description**

This gene id conversion table between RefSeq and ensembl\_transcript\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_ensembl_transcript_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ensembl\_transcript\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ensembl\_transcript\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_ensembl_transcript_id)
```

---

`MM_refseq_to_entrezgene`*Conversion table between RefSeq and entrezgene for mouse*

---

**Description**

This gene id conversion table between RefSeq and entrezgene is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_entrezgene)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding entrezgene. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_entrezgene" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_entrezgene)
```

---

|                     |                                                             |
|---------------------|-------------------------------------------------------------|
| MM_refseq_to_fantom | <i>Conversion table between RefSeq and fantom for mouse</i> |
|---------------------|-------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and fantom is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_fantom)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding fantom. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_fantom" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_fantom)
```

---

|                                    |                                                                            |
|------------------------------------|----------------------------------------------------------------------------|
| MM_refseq_to_illumina_mousewg_6_v1 | <i>Conversion table between RefSeq and illumina_mousewg_6_v1 for mouse</i> |
|------------------------------------|----------------------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and illumina\_mousewg\_6\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_illumina_mousewg_6_v1)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_mousewg\_6\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_illumina\_mousewg\_6\_v1" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_illumina_mousewg_6_v1)
```

---

```
MM_refseq_to_illumina_mousewg_6_v2
```

*Conversion table between RefSeq and illumina\_mousewg\_6\_v2 for mouse*

---

**Description**

This gene id conversion table between RefSeq and illumina\_mousewg\_6\_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_illumina_mousewg_6_v2)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding illumina\_mousewg\_6\_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_illumina\_mousewg\_6\_v2" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_illumina_mousewg_6_v2)
```

---

MM\_refseq\_to\_interpro *Conversion table between RefSeq and interpro for mouse*

---

**Description**

This gene id conversion table between RefSeq and interpro is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_interpro)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding interpro. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_interpro" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_interpro)
```

---

|                  |                                                          |
|------------------|----------------------------------------------------------|
| MM_refseq_to_ipi | <i>Conversion table between RefSeq and ipi for mouse</i> |
|------------------|----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and ipi is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_ipi)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ipi. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ipi" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_ipi)
```

---

|                     |                                                             |
|---------------------|-------------------------------------------------------------|
| MM_refseq_to_merops | <i>Conversion table between RefSeq and merops for mouse</i> |
|---------------------|-------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and merops is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_merops)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding merops. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_merops" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_merops)
```

---

|                     |                                                             |
|---------------------|-------------------------------------------------------------|
| MM_refseq_to_mgi_id | <i>Conversion table between RefSeq and mgi_id for mouse</i> |
|---------------------|-------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and mgi\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_mgi_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding mgi\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_mgi\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_mgi_id)
```

---

```
MM_refseq_to_mgi_symbol
```

*Conversion table between RefSeq and mgi\_symbol for mouse*

---

**Description**

This gene id conversion table between RefSeq and mgi\_symbol is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_mgi_symbol)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding mgi\_symbol. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_mgi\_symbol" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_mgi_symbol)
```

---

```
MM_refseq_to_mgi_transcript_name
```

*Conversion table between RefSeq and mgi\_transcript\_name for mouse*

---

**Description**

This gene id conversion table between RefSeq and mgi\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_mgi_transcript_name)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding mgi\_transcript\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_mgi\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_mgi_transcript_name)
```

---

MM\_refseq\_to\_MM\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k  
*Conversion table between RefSeq and  
 MM\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k for mouse*

---

## Description

This gene id conversion table between RefSeq and MM\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

---

MM\_refseq\_to\_MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1  
*Conversion table between RefSeq and  
MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1 for mouse*

---

## Description

This gene id conversion table between RefSeq and MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v1" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

---

MM\_refseq\_to\_MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2  
*Conversion table between RefSeq and  
 MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2 for mouse*

---

## Description

This gene id conversion table between RefSeq and MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

---

MM\_refseq\_to\_MM\_refseq\_to\_ensembl\_exon\_id  
*Conversion table between RefSeq and  
MM\_refseq\_to\_ensembl\_exon\_id for mouse*

---

## Description

This gene id conversion table between RefSeq and MM\_refseq\_to\_ensembl\_exon\_id is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_MM_refseq_to_ensembl_exon_id)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_ensembl\_exon\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_ensembl\_exon\_id" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(MM_refseq_to_MM_refseq_to_ensembl_exon_id)
```

---

MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_genename\_transcript\_name  
*Conversion table between RefSeq and  
 MM\_refseq\_to\_uniprot\_genename\_transcript\_name for mouse*

---

## Description

This gene id conversion table between RefSeq and MM\_refseq\_to\_uniprot\_genename\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_uniprot\_genename\_. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_genename\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name)
```

---

MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_sptrembl  
*Conversion table between RefSeq and  
MM\_refseq\_to\_uniprot\_sptrembl for mouse*

---

## Description

This gene id conversion table between RefSeq and MM\_refseq\_to\_uniprot\_sptrembl is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_sptrembl)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_uniprot\_sptrembl. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_sptrembl" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(MM_refseq_to_MM_refseq_to_uniprot_sptrembl)
```

---

MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_swissprot  
*Conversion table between RefSeq and  
MM\_refseq\_to\_uniprot\_swissprot for mouse*

---

### Description

This gene id conversion table between RefSeq and MM\_refseq\_to\_uniprot\_swissprot is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot)
```

### Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### Details

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_uniprot\_swissprot. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_swissprot" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

### Examples

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot)
```

---

MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_swissprot\_accession  
*Conversion table between RefSeq and  
MM\_refseq\_to\_uniprot\_swissprot\_accession for mouse*

---

## Description

This gene id conversion table between RefSeq and MM\_refseq\_to\_uniprot\_swissprot\_accession is for MiRaGE package, based upon BioMart Gene ID Converter

## Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession)
```

## Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

## Details

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_uniprot\_swissprot\_a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_swissprot\_accession" but "id\_conv", because of the requirements by MiRaGE package.

## Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

## References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

## Examples

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession)
```

---

`MM_refseq_to_MM_refseq_to_wikigene_id`*Conversion table between RefSeq and MM\_refseq\_to\_wikigene\_id for mouse*

---

**Description**

This gene id conversion table between RefSeq and MM\_refseq\_to\_wikigene\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_MM_refseq_to_wikigene_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding MM\_refseq\_to\_wikigene\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_MM\_refseq\_to\_wikigene\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_MM_refseq_to_wikigene_id)
```

---

|                  |                                                          |
|------------------|----------------------------------------------------------|
| MM_refseq_to_pdb | <i>Conversion table between RefSeq and pdb for mouse</i> |
|------------------|----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and pdb is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_pdb)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding pdb. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_pdb" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_pdb)
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| MM_refseq_to_pfam | <i>Conversion table between RefSeq and pfam for mouse</i> |
|-------------------|-----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and pfam is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_pfam)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding pfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_pfam" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_pfam)
```

---

```
MM_refseq_to_phalanx_onearray
```

*Conversion table between RefSeq and phalanx\_onearray for mouse*

---

**Description**

This gene id conversion table between RefSeq and phalanx\_onearray is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_phalanx_onearray)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding phalanx\_onearray. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_phalanx\_onearray" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_phalanx_onearray)
```

---

```
MM_refseq_to_protein_id
```

*Conversion table between RefSeq and protein\_id for mouse*

---

**Description**

This gene id conversion table between RefSeq and protein\_id is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_protein_id)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding protein\_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_protein\_id" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_protein_id)
```

---

`MM_refseq_to_refseq_dna`*Conversion table between RefSeq and refseq\_dna for mouse*

---

**Description**

This gene id conversion table between RefSeq and refseq\_dna is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_refseq_dna)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding refseq\_dna. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_refseq\_dna" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_refseq_dna)
```

---

`MM_refseq_to_refseq_peptide`*Conversion table between RefSeq and refseq\_peptide for mouse*

---

**Description**

This gene id conversion table between RefSeq and refseq\_peptide is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_refseq_peptide)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding refseq\_peptide. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_refseq\_peptide" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_refseq_peptide)
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| MM_refseq_to_rfam | <i>Conversion table between RefSeq and rfam for mouse</i> |
|-------------------|-----------------------------------------------------------|

---

### Description

This gene id conversion table between RefSeq and rfam is for MiRaGE package, based upon BioMart Gene ID Converter

### Usage

```
data(MM_refseq_to_rfam)
```

### Format

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

### Details

The first column includes RefSeq gene id and the second column includes corresponding rfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_rfam" but "id\_conv", because of the requirements by MiRaGE package.

### Note

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

### References

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

### Examples

```
data(MM_refseq_to_rfam)
```

---

|                             |                                                                     |
|-----------------------------|---------------------------------------------------------------------|
| MM_refseq_to_rfam_gene_name | <i>Conversion table between RefSeq and rfam_gene_name for mouse</i> |
|-----------------------------|---------------------------------------------------------------------|

---

### Description

This gene id conversion table between RefSeq and rfam\_gene\_name is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_rfam_gene_name)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding rfam\_gene\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_rfam\_gene\_name" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_rfam_gene_name)
```

---

MM\_refseq\_to\_rfam\_transcript\_name

*Conversion table between RefSeq and rfam\_transcript\_name for mouse*

---

**Description**

This gene id conversion table between RefSeq and rfam\_transcript\_name is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_rfam_transcript_name)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding rfam\_transcript\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_rfam\_transcript\_name" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_rfam_transcript_name)
```

---

|                    |                                                            |
|--------------------|------------------------------------------------------------|
| MM_refseq_to_smart | <i>Conversion table between RefSeq and smart for mouse</i> |
|--------------------|------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and smart is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_smart)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding smart. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_smart" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_smart)
```

---

MM\_refseq\_to\_tigrfam    *Conversion table between RefSeq and tigrfam for mouse*

---

**Description**

This gene id conversion table between RefSeq and tigrfam is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_tigrfam)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding tigrfam. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_tigrfam" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_tigrfam)
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| MM_refseq_to_ucsc | <i>Conversion table between RefSeq and ucsc for mouse</i> |
|-------------------|-----------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and ucsc is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_ucsc)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding ucsc. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_ucsc" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_ucsc)
```

---

|                      |                                                              |
|----------------------|--------------------------------------------------------------|
| MM_refseq_to_unigene | <i>Conversion table between RefSeq and unigene for mouse</i> |
|----------------------|--------------------------------------------------------------|

---

**Description**

This gene id conversion table between RefSeq and unigene is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_unigene)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding unigene. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_unigene" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_unigene)
```

---

MM\_refseq\_to\_uniprot\_genename

*Conversion table between RefSeq and uniprot\_genename for mouse*

---

**Description**

This gene id conversion table between RefSeq and uniprot\_genename is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_uniprot_genename)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding uniprot\_genename. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_uniprot\_genename" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_uniprot_genename)
```

---

```
MM_refseq_to_wikigene_name
```

*Conversion table between RefSeq and wikigene\_name for mouse*

---

**Description**

This gene id conversion table between RefSeq and wikigene\_name is for MiRaGE package, based upon BioMart Gene ID Converter

**Usage**

```
data(MM_refseq_to_wikigene_name)
```

**Format**

The data set is a data frame. The number of rows is the number of gene id. The number of column is two.

**Details**

The first column includes RefSeq gene id and the second column includes corresponding wikigene\_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM\_refseq\_to\_wikigene\_name" but "id\_conv", because of the requirements by MiRaGE package.

**Note**

For more details on how to generate this table, please see functions in MiRaGE package and vignette.

**References**

For more details about BioMart Gene ID Converter, access to <http://www.ensembl.org/biomart/martview/>

**Examples**

```
data(MM_refseq_to_wikigene_name)
```

---

|      |                                |
|------|--------------------------------|
| TBL2 | <i>Target gene table miRNA</i> |
|------|--------------------------------|

---

**Description**

This target gene table of miRNA is for MiRaGE package. Actual name of data file is either TBL2\_MM (for mouse) or TBL2\_HS (for human), but name of data frame loaded is "TBL2"

**Usage**

```
data(TBL2_MM)
```

**Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is the number of RefSeq gene id.

**Details**

This target gene table is generated by simple seed match between 3' UTR RefSeq gene and 5' UTR of miRNAs. 3' UTR RefSeq gene sequence is taken from genome table. miRNA mature sequences are taken from miRBase Release 18. Row names are miRNA names and column names are RefSeq gene id.

**Note**

How to generate this table, please see functions in MiRaGE package and vignette.

**References**

M, Yoshizawa, Y-h. Taguchi and J. Yasuda, Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method, Int. J. Mol. Sci. 2011, 12(12), 9265-9276

**Examples**

```
data(TBL2_MM)
```

---

TBL2\_HS

*Target gene table miRNA of human*

---

**Description**

This target gene table miRNA of human is for MiRaGE package

**Usage**

```
data(TBL2_HS)
```

**Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is the number of RefSeq gene id.

**Details**

This target gene table is generated by simple seed match between 3' UTR RefSeq gene and 5' UTR of miRNAs. 3' UTR RefSeq gene sequence is taken from genome table, from hg19 genome sequence. miRNA mature sequences are taken from miRBase Release 18. Row names are miRNA names and column names are RefSeq gene id.

**Note**

How to generate this table, please see functions in MiRaGE package and vignette.

**References**

M, Yoshizawa, Y-h. Taguchi and J. Yasuda, Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method, Int. J. Mol. Sci. 2011, 12(12), 9265-9276

**Examples**

```
data(TBL2_HS)
```

---

TBL2\_MM

*Target gene table miRNA of mouse*

---

**Description**

This target gene table miRNA of mouse is for MiRaGE package

**Usage**

```
data(TBL2_MM)
```

**Format**

The data set is a data frame. The number of rows is the number of miRNAs. The number of column is the number of RefSeq gene id.

**Details**

This target gene table is generated by simple seed match between 3' UTR RefSeq gene and 5' UTR of miRNAs. 3' UTR RefSeq gene sequence is taken from genome table, from mm9 genome sequence. miRNA mature sequences are taken from miRBase Release 18. Row names are miRNA names and column names are RefSeq gene id.

**Note**

How to generate this table, please see functions in MiRaGE package and vignette.

**References**

M, Yoshizawa, Y-h. Taguchi and J. Yasuda, Inference of Gene Regulation via miRNAs During ES Cell Differentiation Using MiRaGE Method, Int. J. Mol. Sci. 2011, 12(12), 9265-9276

**Examples**

```
data(TBL2_MM)
```

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