# Package 'miRNATarget'

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Title gene target tabale of miRNA for human/mouse used for MiRaGE package
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biocViews ExperimentData,

# R topics documented:

conv_id
HS_conv_id
HS_refseq_to_affy_hc_g110
HS_refseq_to_affy_hg_focus
HS_refseq_to_affy_hg_u133a
HS_refseq_to_affy_hg_u133a_2
HS_refseq_to_affy_hg_u133b
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HS_refseq_to_affy_u133_x3p
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HS_refseq_to_agilent_wholegenome
HS_refseq_to_canonical_transcript_stable_id
HS_refseq_to_ccds
HS_refseq_to_codelink
HS_refseq_to_embl

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# 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.

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#### **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

miRNA conservation table of human

## **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/

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## **Examples**

```
data(HS\_conv\_id)
```

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 Mi-RaGE 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/

```
data(HS_refseq_to_affy_hc_g110)
```

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

#### **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 Mi-RaGE 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**

$$HS\_refseq\_to\_affy\_hg\_u133a$$

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

```
data(HS refseq to affy hg u133a)
```

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#### **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 Mi-RaGE 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

#### **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 Mi-RaGE package.

# Note

#### References

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

# **Examples**

$$data(HS\_refseq\_to\_affy\_hg\_u133a\_2)$$

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 Mi-RaGE 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/

```
data(HS\_refseq\_to\_affy\_hg\_u133b)
```

#### **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

#### **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**

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

```
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 Mi-RaGE 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 Mi-RaGE package.

# Note

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#### References

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

# **Examples**

$$data(HS\_refseq\_to\_affy\_hg\_u95av2)$$

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 Mi-RaGE 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/

```
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

#### **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 Mi-RaGE 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

```
data(HS refseq to affy hg u95d)
```

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#### **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 Mi-RaGE 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 Mi-RaGE package.

# Note

#### 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

#### **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/

```
data(HS refseq to affy huex 1 0 st v2)
```

Conversion table between RefSeq and affy\_hugenefl for human

# **Description**

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

## Usage

```
data(HS_refseq_to_affy_hugenefl)
```

# **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\_hugenefl. 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\_hugenefl" but "id\_conv", because of the requirements by Mi-RaGE 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 hugenefl)
```

```
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

```
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 Mi-RaGE package.

# Note

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#### References

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

# **Examples**

$$data(HS\_refseq\_to\_affy\_u133\_x3p)$$

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/

```
data(HS refseq to agilent cgh 44b)
```

```
HS_refseq_to_agilent_wholegenome

Conversion table between RefSeq and agilent_wholegenome for hu-
man
```

#### **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

HS\_refseq\_to\_ccds 19

## 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)
```

 $HS\_refseq\_to\_ccds$ 

Conversion table between RefSeq and ccds for human

## **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 Conversion table between RefSeq and codelink for human

# **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/

```
{\rm data}({\rm HS\_refseq\_to\_codelink})
```

HS\_refseq\_to\_embl 21

 $HS\_refseq\_to\_embl$ 

Conversion table between RefSeq and embl for human

#### **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

```
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

#### 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)
```

```
\begin{tabular}{ll} HS\_refseq\_to\_ensembl\_transcript\_id\\ & \textit{Conversion table between RefSeq and ensembl\_transcript\_id for human } \\ \end{tabular}
```

#### **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/

```
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**

```
{\rm data}({\rm 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

```
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**

```
{\rm data}({\rm 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 Mi-RaGE package.

# Note

#### 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/

```
data(HS_refseq_to_hgnc_transcript_name)
```

```
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)
```

#### **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/

```
data(HS\_refseq\_to\_illumina\_humanwg\_6\_v3)
```

30 HS\_refseq\_to\_ipi

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

```
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 Conversion table between RefSeq and merops for human

# 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

32 HS\_refseq\_to\_pdb

#### 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

Conversion table between RefSeq and pdb for human

# **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/

```
data(HS\_refseq\_to\_pdb)
```

HS\_refseq\_to\_pfam 33

 $HS\_refseq\_to\_pfam$ 

Conversion table between RefSeq and pfam for human

#### **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
```

Conversion table between RefSeq and phalanx\_onearray for human

#### **Description**

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

```
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

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#### 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 ref-seq\_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/

```
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 ref-seq\_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

```
data(HS refseq to refseq peptide)
```

HS\_refseq\_to\_rfam 37

#### **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 ref-seq\_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

Conversion table between RefSeq and rfam for human

### **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

#### 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
```

Conversion table between RefSeq and rfam\_gene\_name for human

# 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 Mi-RaGE 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/

```
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

Conversion table between RefSeq and smart for human

### **Description**

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

```
data(HS refseq to smart)
```

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

HS\_refseq\_to\_ucsc 41

#### 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

Conversion table between RefSeq and ucsc for human

# **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/

```
data(HS_refseq_to_ucsc)
```

HS\_refseq\_to\_unigene Conversion table between RefSeq and unigene for human

### **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

```
data(HS_refseq_to_uniprot_genename)
```

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

44 id\_conv

#### 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/

```
data(MM\_refseq\_to\_wikigene\_name)
```

MM\_conv\_id 45

 $MM_{conv_id}$ 

miRNA conservation table of mouse

## **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/

# **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

```
data(MM refseq to affy mg u74a)
```

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 Mi-RaGE 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

## **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

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#### References

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

# **Examples**

$$data(MM\_refseq\_to\_affy\_mg\_u74av2)$$

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

# **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 Mi-RaGE 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/

```
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

## **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

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 Mi-RaGE 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

## **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

#### 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 Mi-RaGE 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/

```
data(MM refseq to affy moe430a)
```

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

## **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 Mi-RaGE 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

```
data(MM refseq to affy moex 1 0 st v1)
```

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)
```

# **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/

```
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\_mullksuba for mouse

### **Description**

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

```
data(MM refseq to affy mullksuba)
```

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 Mi-RaGE 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 mul1ksubb
```

Conversion table between RefSeq and affy\_mullksubb 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 mul1ksubb)
```

## **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

#### 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/

```
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 Conversion table between RefSeq and ccds for mouse

### **Description**

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

```
data(MM refseq to ccds)
```

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
```

Conversion table between RefSeq and codelink for mouse

# 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

MM\_refseq\_to\_embl 59

#### References

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

# **Examples**

```
data(MM_refseq_to_codelink)
```

 $MM\_refseq\_to\_embl$ 

Conversion table between RefSeq and embl for mouse

# **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/

```
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)
```

```
\begin{tabular}{ll} MM\_refseq\_to\_ensembl\_peptide\_id\\ Conversion\ table\ between\ RefSeq\ and\ ensembl\_peptide\_id\ for\ mouse\\ \end{tabular}
```

### **Description**

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

```
data(MM refseq to ensembl peptide id)
```

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)
```

# **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/

```
data(MM refseq to entrezgene)
```

MM\_refseq\_to\_fantom

MM refseq to fantom Conversion table between RefSeq and fantom for mouse

# **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

Conversion table between RefSeq and illumina_mousewg_6_v1 for mouse
```

# Description

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

```
data(MM refseq to illumina mousewg 6 v1)
```

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/

```
data(MM refseq to interpro)
```

 ${\rm MM\_refseq\_to\_ipi}$ 

Conversion table between RefSeq and ipi for mouse

# **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 Conversion table between RefSeq and merops for mouse

# **Description**

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

```
data(MM refseq to merops)
```

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 Conversion table between RefSeq and mgi\_id for mouse

# 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

#### 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 Mi-RaGE 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/

```
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)
```

 $MM\_refseq\_to\_pdb$ 

Conversion table between RefSeq and pdb for mouse

# Description

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

```
data(MM refseq to pdb)
```

70 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 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 Conversion table between RefSeq and pfam for mouse

# 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

#### 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/

```
{\rm data}({\rm 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)
```

```
{\rm 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

```
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 ref-seq\_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 ref-seq\_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.

74 MM\_refseq\_to\_rfam

#### References

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

# **Examples**

```
data(MM_refseq_to_refseq_peptide)
```

# **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
```

Conversion table between RefSeq and rfam\_gene\_name for mouse

# **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)
```

76 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 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 Conversion table between RefSeq and smart for mouse
```

### **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

Conversion table between RefSeq and ucsc for mouse

### **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
```

Conversion table between RefSeq and unigene for mouse

# **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 81

TBL2

Target gene table miRNA

# **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)
```

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#### **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.

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# 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

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