Package 'miRNATarget'

November 28, 2024

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

Version 1.44.0

Author Y-h. Taguchi <`tag@granular.com`>

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

Maintainer Y-h. Taguchi <`tag@granular.com`>

Depends R (>= 2.10), Biobase

License GPL

biocViews ExperimentData, Homo_sapiens_Data

git_url https://git.bioconductor.org/packages/miRNATarget

git_branch RELEASE_3_20

git_last_commit ad8709a

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2024-11-28

Contents

`conv_id` *miRNA conservation table of mouse/human, based upon TargetScan-Mouse/Human 6.1*

Description

This miRNA conservation table is for MiRaGE package. Actual name of data files is HS_conv_id for human and MM_conv_id for mouse, but name of loaded data frame is "conv_id".

Usage

```
data(MM_conv_id)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_conv_id)
```

`HS_conv_id` *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/

Examples

```
data(HS_conv_id)
```

`HS_refseq_to_affy_hc_g110` *Conversion table between RefSeq and affy_hc_g110 for human*

Description

This gene id conversion table between RefSeq and affy_hc_g110 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hc_g110)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hc_g110. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hc_g110" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hc_g110)
```

`HS_refseq_to_affy_hg_focus` *Conversion table between RefSeq and affy_hg_focus for human*

Description

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

Usage

```
data(HS_refseq_to_affy_hg_focus)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_focus. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_focus" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_focus)
```

`HS_refseq_to_affy_hg_u133a`

Conversion table between RefSeq and affy_hg_u133a for human

Description

This gene id conversion table between RefSeq and affy_hg_u133a is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hg_u133a)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_u133a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_u133a" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u133a)
```

`HS_refseq_to_affy_hg_u133a_2` *Conversion table between RefSeq and affy_hg_u133a_2 for human*

Description

This gene id conversion table between RefSeq and affy_hg_u133a_2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hg_u133a_2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_u133a_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_u133a_2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u133a_2)
```

`HS_refseq_to_affy_hg_u133b` *Conversion table between RefSeq and affy_hg_u133b for human*

Description

This gene id conversion table between RefSeq and affy_hg_u133b is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hg_u133b)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_u133b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_u133b" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u133b)
```

`HS_refseq_to_affy_hg_u133_plus_2` *Conversion table between RefSeq and affy_hg_u133_plus_2 for human*

Description

This gene id conversion table between RefSeq and affy_hg_u133_plus_2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hg_u133_plus_2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_u133_plus_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_u133_plus_2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u133_plus_2)
```

`HS_refseq_to_affy_hg_u95a` *Conversion table between RefSeq and affy_hg_u95a for human*

Description

This gene id conversion table between RefSeq and affy_hg_u95a is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hg_u95a)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_u95a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_u95a" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u95a)
```

`HS_refseq_to_affy_hg_u95av2` *Conversion table between RefSeq and affy_hg_u95av2 for human*

Description

This gene id conversion table between RefSeq and affy_hg_u95av2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hg_u95av2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_u95av2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_u95av2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u95av2)
```

`HS_refseq_to_affy_hg_u95b` *Conversion table between RefSeq and affy_hg_u95b for human*

Description

This gene id conversion table between RefSeq and affy_hg_u95b is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hg_u95b)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_u95b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_u95b" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u95b)
```

`HS_refseq_to_affy_hg_u95c` *Conversion table between RefSeq and affy_hg_u95c for human*

Description

This gene id conversion table between RefSeq and affy_hg_u95c is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hg_u95c)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_u95c. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_u95c" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u95c)
```

`HS_refseq_to_affy_hg_u95d`

Conversion table between RefSeq and affy_hg_u95d for human

Description

This gene id conversion table between RefSeq and affy_hg_u95d is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hg_u95d)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_u95d. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_u95d" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u95d)
```

`HS_refseq_to_affy_hg_u95e` *Conversion table between RefSeq and affy_hg_u95e for human*

Description

This gene id conversion table between RefSeq and affy_hg_u95e is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_hg_u95e)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hg_u95e. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hg_u95e" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u95e)
```

`HS_refseq_to_affy_huex_1_0_st_v2` *Conversion table between RefSeq and affy_huex_1_0_st_v2 for human*

Description

This gene id conversion table between RefSeq and affy_huex_1_0_st_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_huex_1_0_st_v2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_huex_1_0_st_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_huex_1_0_st_v2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_huex_1_0_st_v2)
```

`HS_refseq_to_affy_hugenefl` *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 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_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

Usage

```
data(HS_refseq_to_affy_hugene_1_0_st_v1)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_hugene_1_0_st_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_hugene_1_0_st_v1" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hugene_1_0_st_v1)
```

`HS_refseq_to_affy_u133_x3p` *Conversion table between RefSeq and affy_u133_x3p for human*

Description

This gene id conversion table between RefSeq and affy_u133_x3p is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_affy_u133_x3p)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_u133_x3p. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_affy_u133_x3p" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_u133_x3p)
```

`HS_refseq_to_agilent_cgh_44b` *Conversion table between RefSeq and agilent_cgh_44b for human*

Description

This gene id conversion table between RefSeq and agilent_cgh_44b is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_agilent_cgh_44b)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding agilent_cgh_44b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_agilent_cgh_44b" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_agilent_cgh_44b)
```

`HS_refseq_to_agilent_wholegenome` *Conversion table between RefSeq and agilent_wholegenome for human*

Description

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

Usage

```
data(HS_refseq_to_agilent_wholegenome)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding agilent_wholegenome. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_agilent_wholegenome" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_agilent_wholegenome)
```

`HS_refseq_to_canonical_transcript_stable_id`

Conversion table between RefSeq and canonical_transcript_stable_id for human

Description

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

Usage

```
data(HS_refseq_to_canonical_transcript_stable_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding canonical_transcript_stable_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_canonical_transcript_stable_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_canonical_transcript_stable_id)
```

`HS_refseq_to_ccds` *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/

Examples

```
data(HS_refseq_to_codelink)
```

`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

Usage

```
data(HS_refseq_to_ensembl_gene_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding ensembl_gene_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_ensembl_gene_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_ensembl_gene_id)
```

`HS_refseq_to_ensembl_peptide_id` *Conversion table between RefSeq and ensembl_peptide_id for human*

Description

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

Usage

```
data(HS_refseq_to_ensembl_peptide_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding ensembl_peptide_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_ensembl_peptide_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_ensembl_peptide_id)
```

`HS_refseq_to_ensembl_transcript_id` *Conversion table between RefSeq and ensembl_transcript_id for human*

Description

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

Usage

```
data(HS_refseq_to_ensembl_transcript_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding ensembl_transcript_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_ensembl_transcript_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_ensembl_transcript_id)
```

`HS_refseq_to_entrezgene`

Conversion table between RefSeq and entrezgene for human

Description

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

Usage

```
data(HS_refseq_to_entrezgene)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_entrezgene)
```

`HS_refseq_to_hgnc_id` *Conversion table between RefSeq and hgnc_id for human*

Description

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

Usage

```
data(HS_refseq_to_hgnc_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding hgnc_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_hgnc_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_hgnc_id)
```

`HS_refseq_to_hgnc_symbol` *Conversion table between RefSeq and hgnc_symbol for human*

Description

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

Usage

```
data(HS_refseq_to_hgnc_symbol)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding hgnc_symbol. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_hgnc_symbol" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_hgnc_symbol)
```

`HS_refseq_to_hgnc_transcript_name` *Conversion table between RefSeq and hgnc_transcript_name for human*

Description

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

Usage

```
data(HS_refseq_to_hgnc_transcript_name)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding hgnc_transcript_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_hgnc_transcript_name" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_hgnc_transcript_name)
```

`HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k` *Conversion table between RefSeq and HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k for human*

Description

This gene id conversion table between RefSeq and HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding HS_refseq_to_efg_agilent_surep It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

`HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1` *Conversion table between RefSeq and HS_refseq_to_efg_agilent_wholegenome_4x44k_v1 for human*

Description

This gene id conversion table between RefSeq and HS_refseq_to_efg_agilent_wholegenome_4x44k_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding HS_refseq_to_efg_agilent_whol
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

`HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2` *Conversion table between RefSeq and HS_refseq_to_efg_agilent_wholegenome_4x44k_v2 for human*

Description

This gene id conversion table between RefSeq and HS_refseq_to_efg_agilent_wholegenome_4x44k_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding HS_refseq_to_efg_agilent_whol
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

`HS_refseq_to_HS_refseq_to_ensembl_exon_id` *Conversion table between RefSeq and HS_refseq_to_ensembl_exon_id for human*

Description

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

Usage

```
data(HS_refseq_to_HS_refseq_to_ensembl_exon_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding HS_refseq_to_ensembl_exon_ic
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_HS_refseq_to_ensembl_exon_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_ensembl_exon_id)
```

`HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name` *Conversion table between RefSeq and HS_refseq_to_uniprot_genename_transcript_name for human*

Description

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

Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding HS_refseq_to_uniprot_genenam
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name)
```

`HS_refseq_to_HS_refseq_to_uniprot_sptrembl` *Conversion table between RefSeq and HS_refseq_to_uniprot_sptrembl for human*

Description

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

Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_sptrembl)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding HS_refseq_to_uniprot_sptrembl It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_HS_refseq_to_uniprot_sptrembl" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_uniprot_sptrembl)
```

`HS_refseq_to_HS_refseq_to_uniprot_swissprot` *Conversion table between RefSeq and HS_refseq_to_uniprot_swissprot for human*

Description

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

Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding HS_refseq_to_uniprot_swisspro It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_HS_refseq_to_uniprot_swissprot" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot)
```

`HS_refseq_to_HS_refseq_to_uniprot_swissprot_accession` *Conversion table between RefSeq and HS_refseq_to_uniprot_swissprot_accession for human*

Description

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

Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot_accession)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding HS_refseq_to_uniprot_swisspro
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_HS_refseq_to_uniprot_swissprot_accession" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot_accession)
```

`HS_refseq_to_HS_refseq_to_wikigene_id`

Conversion table between RefSeq and HS_refseq_to_wikigene_id for human

Description

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

Usage

```
data(HS_refseq_to_HS_refseq_to_wikigene_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding HS_refseq_to_wikigene_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_HS_refseq_to_wikigene_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_wikigene_id)
```

HS_refseq_to_illumina_humanht_12

Conversion table between RefSeq and illumina_humanht_12 for human

Description

This gene id conversion table between RefSeq and illumina_humanht_12 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_illumina_humanht_12)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding illumina_humanht_12. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_illumina_humanht_12" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_illumina_humanht_12)
```

`HS_refseq_to_illumina_humanwg_6_v1` *Conversion table between RefSeq and illumina_humanwg_6_v1 for human*

Description

This gene id conversion table between RefSeq and illumina_humanwg_6_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_illumina_humanwg_6_v1)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding illumina_humanwg_6_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_illumina_humanwg_6_v1" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_illumina_humanwg_6_v1)
```

`HS_refseq_to_illumina_humanwg_6_v2` *Conversion table between RefSeq and illumina_humanwg_6_v2 for human*

Description

This gene id conversion table between RefSeq and illumina_humanwg_6_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_illumina_humanwg_6_v2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding illumina_humanwg_6_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_illumina_humanwg_6_v2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_illumina_humanwg_6_v2)
```

`HS_refseq_to_illumina_humanwg_6_v3` *Conversion table between RefSeq and illumina_humanwg_6_v3 for human*

Description

This gene id conversion table between RefSeq and illumina_humanwg_6_v3 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(HS_refseq_to_illumina_humanwg_6_v3)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding illumina_humanwg_6_v3. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_illumina_humanwg_6_v3" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_illumina_humanwg_6_v3)
```

`HS_refseq_to_interpro` *Conversion table between RefSeq and interpro for human*

Description

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

Usage

```
data(HS_refseq_to_interpro)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_interpro)
```

`HS_refseq_to_ipi` *Conversion table between RefSeq and ipi for human*

Description

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

Usage

```
data(HS_refseq_to_ipi)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_ipi)
```

`HS_refseq_to_merops` *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

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

References

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

Examples

```
data(HS_refseq_to_merops)
```

`HS_refseq_to_pdb` *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/

Examples

```
data(HS_refseq_to_pdb)
```

`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

Usage

```
data(HS_refseq_to_phalanx_onearray)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding phalanx_onearray. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_phalanx_onearray" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_phalanx_onearray)
```

`HS_refseq_to_protein_id`

Conversion table between RefSeq and protein_id for human

Description

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

Usage

```
data(HS_refseq_to_protein_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding protein_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_protein_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_protein_id)
```

`HS_refseq_to_refseq_dna` *Conversion table between RefSeq and refseq_dna for human*

Description

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

Usage

```
data(HS_refseq_to_refseq_dna)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding refseq_dna. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_refseq_dna" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_refseq_dna)
```

`HS_refseq_to_refseq_genomic` *Conversion table between RefSeq and refseq_genomic for human*

Description

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

Usage

```
data(HS_refseq_to_refseq_genomic)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding refseq_genomic. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_refseq_genomic" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_refseq_genomic)
```

`HS_refseq_to_refseq_peptide` *Conversion table between RefSeq and refseq_peptide for human*

Description

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

Usage

```
data(HS_refseq_to_refseq_peptide)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding refseq_peptide. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_refseq_peptide" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_refseq_peptide)
```

`HS_refseq_to_rfam` *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

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

References

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

Examples

```
data(HS_refseq_to_rfam)
```

`HS_refseq_to_rfam_gene_name` *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 MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_rfam_gene_name)
```

`HS_refseq_to_rfam_transcript_name` *Conversion table between RefSeq and rfam_transcript_name for human*

Description

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

Usage

```
data(HS_refseq_to_rfam_transcript_name)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding rfam_transcript_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_rfam_transcript_name" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_rfam_transcript_name)
```

`HS_refseq_to_smart` *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

Usage

```
data(HS_refseq_to_smart)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_smart)
```

`HS_refseq_to_tigrfam` *Conversion table between RefSeq and tigrfam for human*

Description

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

Usage

```
data(HS_refseq_to_tigrfam)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_tigrfam)
```

`HS_refseq_to_ucsc` *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/

Examples

```
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

Usage

```
data(HS_refseq_to_uniprot_genename)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding uniprot_genename. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_uniprot_genename" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_uniprot_genename)
```

`HS_refseq_to_wikigene_name`
Conversion table between RefSeq and wikigene_name for human

Description

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

Usage

```
data(HS_refseq_to_wikigene_name)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding wikigene_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_wikigene_name" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_wikigene_name)
```

`id_conv` *Conversion table between refseq and various gene id/probe id*

Description

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

Usage

```
data(MM_refseq_to_wikigene_name)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_wikigene_name)
```

`MM_conv_id` *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

Usage

```
data(MM_refseq_to_affy_mg_u74a)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mg_u74a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mg_u74a" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mg_u74a)
```

`MM_refseq_to_affy_mg_u74av2` *Conversion table between RefSeq and affy_mg_u74av2 for mouse*

Description

This gene id conversion table between RefSeq and affy_mg_u74av2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_mg_u74av2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mg_u74av2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mg_u74av2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mg_u74av2)
```

`MM_refseq_to_affy_mg_u74b` *Conversion table between RefSeq and affy_mg_u74b for mouse*

Description

This gene id conversion table between RefSeq and affy_mg_u74b is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_mg_u74b)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mg_u74b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mg_u74b" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mg_u74b)
```

`MM_refseq_to_affy_mg_u74bv2` *Conversion table between RefSeq and affy_mg_u74bv2 for mouse*

Description

This gene id conversion table between RefSeq and affy_mg_u74bv2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_mg_u74bv2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mg_u74bv2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mg_u74bv2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mg_u74bv2)
```

`MM_refseq_to_affy_mg_u74c` *Conversion table between RefSeq and affy_mg_u74c for mouse*

Description

This gene id conversion table between RefSeq and affy_mg_u74c is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_mg_u74c)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mg_u74c. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mg_u74c" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mg_u74c)
```

`MM_refseq_to_affy_mg_u74cv2` *Conversion table between RefSeq and affy_mg_u74cv2 for mouse*

Description

This gene id conversion table between RefSeq and affy_mg_u74cv2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_mg_u74cv2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mg_u74cv2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mg_u74cv2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mg_u74cv2)
```

MM_refseq_to_affy_moe430a

Conversion table between RefSeq and affy_moe430a for mouse

Description

This gene id conversion table between RefSeq and affy_moe430a is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_moe430a)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_moe430a. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_moe430a" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_moe430a)
```

`MM_refseq_to_affy_moe430b` *Conversion table between RefSeq and affy_moe430b for mouse*

Description

This gene id conversion table between RefSeq and affy_moe430b is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_moe430b)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_moe430b. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_moe430b" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_moe430b)
```

`MM_refseq_to_affy_moex_1_0_st_v1` *Conversion table between RefSeq and affy_moex_1_0_st_v1 for mouse*

Description

This gene id conversion table between RefSeq and affy_moex_1_0_st_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_moex_1_0_st_v1)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_moex_1_0_st_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_moex_1_0_st_v1" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_moex_1_0_st_v1)
```

`MM_refseq_to_affy_mogene_1_0_st_v1` *Conversion table between RefSeq and affy_mogene_1_0_st_v1 for mouse*

Description

This gene id conversion table between RefSeq and affy_mogene_1_0_st_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_mogene_1_0_st_v1)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mogene_1_0_st_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mogene_1_0_st_v1" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mogene_1_0_st_v1)
```

`MM_refseq_to_affy_mouse430a_2`

Conversion table between RefSeq and affy_mouse430a_2 for mouse

Description

This gene id conversion table between RefSeq and affy_mouse430a_2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_mouse430a_2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mouse430a_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mouse430a_2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mouse430a_2)
```

MM_refseq_to_affy_mouse430_2

Conversion table between RefSeq and affy_mouse430_2 for mouse

---

Description

This gene id conversion table between RefSeq and affy_mouse430_2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_mouse430_2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mouse430_2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mouse430_2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mouse430_2)
```

`MM_refseq_to_affy_mu11ksuba`

Conversion table between RefSeq and affy_mu11ksuba for mouse

Description

This gene id conversion table between RefSeq and affy_mu11ksuba is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_mu11ksuba)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mu11ksuba. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mu11ksuba" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mu11ksuba)
```

`MM_refseq_to_affy_mu11ksubb`

Conversion table between RefSeq and affy_mu11ksubb for mouse

Description

This gene id conversion table between RefSeq and affy_mu11ksubb is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_affy_mu11ksubb)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding affy_mu11ksubb. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_affy_mu11ksubb" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mu11ksubb)
```

`MM_refseq_to_agilent_wholegenome` *Conversion table between RefSeq and agilent_wholegenome for mouse*

Description

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

Usage

```
data(MM_refseq_to_agilent_wholegenome)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding agilent_wholegenome. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_agilent_wholegenome" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_agilent_wholegenome)
```

`MM_refseq_to_canonical_transcript_stable_id` *Conversion table between RefSeq and canonical_transcript_stable_id for mouse*

Description

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

Usage

```
data(MM_refseq_to_canonical_transcript_stable_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding canonical_transcript_stable_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_canonical_transcript_stable_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_canonical_transcript_stable_id)
```

`MM_refseq_to_ccds` *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

Usage

```
data(MM_refseq_to_ccds)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_ccds)
```

`MM_refseq_to_codelink` *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

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

References

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

Examples

```
data(MM_refseq_to_codelink)
```

`MM_refseq_to_embl` *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/

Examples

```
data(MM_refseq_to_embl)
```

`MM_refseq_to_ensembl_gene_id`

Conversion table between RefSeq and ensembl_gene_id for mouse

---

Description

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

Usage

```
data(MM_refseq_to_ensembl_gene_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding ensembl_gene_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_ensembl_gene_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_ensembl_gene_id)
```

`MM_refseq_to_ensembl_peptide_id` *Conversion table between RefSeq and ensembl_peptide_id for mouse*

Description

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

Usage

```
data(MM_refseq_to_ensembl_peptide_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding ensembl_peptide_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_ensembl_peptide_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_ensembl_peptide_id)
```

`MM_refseq_to_ensembl_transcript_id` *Conversion table between RefSeq and ensembl_transcript_id for mouse*

Description

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

Usage

```
data(MM_refseq_to_ensembl_transcript_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding ensembl_transcript_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_ensembl_transcript_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_ensembl_transcript_id)
```

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

Description

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

Usage

```
data(MM_refseq_to_entrezgene)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_entrezgene)
```

`MM_refseq_to_fantom` *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

Usage

```
data(MM_refseq_to_illumina_mousewg_6_v1)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding illumina_mousewg_6_v1. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_illumina_mousewg_6_v1" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_illumina_mousewg_6_v1)
```

`MM_refseq_to_illumina_mousewg_6_v2` *Conversion table between RefSeq and illumina_mousewg_6_v2 for mouse*

Description

This gene id conversion table between RefSeq and illumina_mousewg_6_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_illumina_mousewg_6_v2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding illumina_mousewg_6_v2. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_illumina_mousewg_6_v2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_illumina_mousewg_6_v2)
```

`MM_refseq_to_interpro` *Conversion table between RefSeq and interpro for mouse*

Description

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

Usage

```
data(MM_refseq_to_interpro)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_interpro)
```

`MM_refseq_to_ipi` *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

Usage

```
data(MM_refseq_to_merops)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_merops)
```

`MM_refseq_to_mgi_id` *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

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

References

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

Examples

```
data(MM_refseq_to_mgi_id)
```

`MM_refseq_to_mgi_symbol` *Conversion table between RefSeq and mgi_symbol for mouse*

Description

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

Usage

```
data(MM_refseq_to_mgi_symbol)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding mgi_symbol. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_mgi_symbol" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_mgi_symbol)
```

`MM_refseq_to_mgi_transcript_name`

Conversion table between RefSeq and mgi_transcript_name for mouse

---

Description

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

Usage

```
data(MM_refseq_to_mgi_transcript_name)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding mgi_transcript_name. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_mgi_transcript_name" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_mgi_transcript_name)
```

`MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k`

Conversion table between RefSeq and MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k for mouse

---

Description

This gene id conversion table between RefSeq and MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding MM_refseq_to_efg_agilent_sure
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge_8x60k)
```

`MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1`

Conversion table between RefSeq and MM_refseq_to_efg_agilent_wholegenome_4x44k_v1 for mouse

---

Description

This gene id conversion table between RefSeq and MM_refseq_to_efg_agilent_wholegenome_4x44k_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding MM_refseq_to_efg_agilent_wh
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1)
```

`MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2` *Conversion table between RefSeq and MM_refseq_to_efg_agilent_wholegenome_4x44k_v2 for mouse*

Description

This gene id conversion table between RefSeq and MM_refseq_to_efg_agilent_wholegenome_4x44k_v2 is for MiRaGE package, based upon BioMart Gene ID Converter

Usage

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding MM_refseq_to_efg_agilent_wh
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

`MM_refseq_to_MM_refseq_to_ensembl_exon_id` *Conversion table between RefSeq and MM_refseq_to_ensembl_exon_id for mouse*

Description

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

Usage

```
data(MM_refseq_to_MM_refseq_to_ensembl_exon_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding MM_refseq_to_ensembl_exon_ It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_MM_refseq_to_ensembl_exon_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_MM_refseq_to_ensembl_exon_id)
```

`MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name` *Conversion table between RefSeq and MM_refseq_to_uniprot_genename_transcript_name for mouse*

Description

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

Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding MM_refseq_to_uniprot_genena
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name)
```

`MM_refseq_to_MM_refseq_to_uniprot_sptrembl` *Conversion table between RefSeq and MM_refseq_to_uniprot_sptrembl for mouse*

Description

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

Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_sptrembl)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding MM_refseq_to_uniprot_sptremb
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_MM_refseq_to_uniprot_sptrembl" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_MM_refseq_to_uniprot_sptrembl)
```

`MM_refseq_to_MM_refseq_to_uniprot_swissprot` *Conversion table between RefSeq and MM_refseq_to_uniprot_swissprot for mouse*

Description

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

Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding MM_refseq_to_uniprot_swisspr
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_MM_refseq_to_uniprot_swissprot" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot)
```

`MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession` *Conversion table between RefSeq and MM_refseq_to_uniprot_swissprot_accession for mouse*

Description

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

Usage

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding MM_refseq_to_uniprot_swisspr
It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession)
```

`MM_refseq_to_MM_refseq_to_wikigene_id` *Conversion table between RefSeq and MM_refseq_to_wikigene_id for mouse*

Description

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

Usage

```
data(MM_refseq_to_MM_refseq_to_wikigene_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding MM_refseq_to_wikigene_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_MM_refseq_to_wikigene_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_MM_refseq_to_wikigene_id)
```

`MM_refseq_to_pdb` *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

Usage

```
data(MM_refseq_to_pdb)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_pdb)
```

`MM_refseq_to_pfam` *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

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

References

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

Examples

```
data(MM_refseq_to_pfam)
```

MM_refseq_to_phalanx_onearray

Conversion table between RefSeq and phalanx_onearray for mouse

Description

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

Usage

```
data(MM_refseq_to_phalanx_onearray)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding phalanx_onearray. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_phalanx_onearray" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_phalanx_onearray)
```

MM_refseq_to_protein_id

Conversion table between RefSeq and protein_id for mouse

Description

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

Usage

```
data(MM_refseq_to_protein_id)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding protein_id. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_protein_id" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_protein_id)
```

MM_refseq_to_refseq_dna

Conversion table between RefSeq and refseq_dna for mouse

Description

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

Usage

```
data(MM_refseq_to_refseq_dna)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding refseq_dna. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_refseq_dna" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_refseq_dna)
```

`MM_refseq_to_refseq_peptide`

Conversion table between RefSeq and refseq_peptide for mouse

Description

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

Usage

```
data(MM_refseq_to_refseq_peptide)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding refseq_peptide. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_refseq_peptide" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_refseq_peptide)
```

`MM_refseq_to_rfam` *Conversion table between RefSeq and rfam for mouse*

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)
```

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` *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)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(TBL2_HS)
```

`TBL2_MM` *Target gene table miRNA of mouse*

Description

This target gene table miRNA of mouse is for MiRaGE package

Usage

```
data(TBL2_MM)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(TBL2_MM)
```

Index