Package 'miRNATarget'

April 13, 2017

1 /	
Title gene target tabale of miRNA for human/mouse used for MiRaGE package	
Version 1.12.0	
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Description gene target tabale of miRNA for human/mouse used for MiRaGE package	ge
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Depends R (>= 2.10), Biobase	
License GPL	
biocViews ExperimentData, Homo_sapiens_Data	
NeedsCompilation no	

R topics documented:

conv_id
HS_conv_id
HS_refseq_to_affy_hc_g110
HS_refseq_to_affy_hg_focus
HS_refseq_to_affy_hg_u133a
HS_refseq_to_affy_hg_u133a_2
HS_refseq_to_affy_hg_u133b
HS_refseq_to_affy_hg_u133_plus_2
HS_refseq_to_affy_hg_u95a
HS_refseq_to_affy_hg_u95av2
HS_refseq_to_affy_hg_u95b
HS_refseq_to_affy_hg_u95c
HS_refseq_to_affy_hg_u95d
HS_refseq_to_affy_hg_u95e
$HS_refseq_to_affy_huex_1_0_st_v2 \dots \dots$
HS_refseq_to_affy_hugenefl
$HS_refseq_to_affy_hugene_1_0_st_v1 \dots \dots$
$HS_refseq_to_affy_u133_x3p \dots \qquad 16$
HS_refseq_to_agilent_cgh_44b
HS_refseq_to_agilent_wholegenome
HS_refseq_to_canonical_transcript_stable_id
HS_refseq_to_ccds
HS_refseq_to_codelink
HS_refseq_to_embl

2 R topics documented:

HS_refseq_to_ensembl_gene_id	
HS_refseq_to_ensembl_peptide_id	
HS_refseq_to_ensembl_transcript_id	
HS_refseq_to_entrezgene	24
HS_refseq_to_hgnc_id	25
HS_refseq_to_hgnc_symbol	25
HS_refseq_to_hgnc_transcript_name	26
HS_refseq_to_HS_refseq_to_efg_agilent_sureprint_g3_ge_8x60k	27
HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v1	28
HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2	28
HS_refseq_to_HS_refseq_to_ensembl_exon_id	29
HS_refseq_to_HS_refseq_to_uniprot_genename_transcript_name	
HS_refseq_to_HS_refseq_to_uniprot_sptrembl	
HS_refseq_to_HS_refseq_to_uniprot_swissprot	
HS_refseq_to_HS_refseq_to_uniprot_swissprot_accession	
HS_refseq_to_HS_refseq_to_wikigene_id	
HS_refseq_to_illumina_humanht_12	
HS_refseq_to_illumina_humanwg_6_v1	
HS_refseq_to_illumina_humanwg_6_v2	
HS_refseq_to_illumina_humanwg_6_v3	
HS_refseq_to_interpro	
HS_refseq_to_ipi	
HS_refseq_to_merops	
HS_refseq_to_pdb	
HS_refseq_to_pfam	
HS_refseq_to_phalanx_onearray	
HS_refseq_to_protein_id	
HS_refseq_to_refseq_dna	
HS_refseq_to_refseq_genomic	
HS_refseq_to_refseq_peptide	
HS_refseq_to_rfam	
HS_refseq_to_rfam_gene_name	
HS_refseq_to_rfam_transcript_name	
HS_refseq_to_smart	
HS_refseq_to_tigrfam	
HS_refseq_to_ucsc	
HS_refseq_to_unigene	
HS_refseq_to_uniprot_genename	49
HS_refseq_to_wikigene_name	50
id_conv	51
MM_conv_id	52
MM_refseq_to_affy_mg_u74a	52
MM_refseq_to_affy_mg_u74av2	53
MM_refseq_to_affy_mg_u74b	54
MM_refseq_to_affy_mg_u74bv2	55
MM_refseq_to_affy_mg_u74c	55
MM_refseq_to_affy_mg_u74cv2	56
MM_refseq_to_affy_moe430a	57
MM_refseq_to_affy_moe430b	58
MM_refseq_to_affy_moex_1_0_st_v1	58
MM_refseq_to_affy_mogene_1_0_st_v1	59
MM_refseq_to_affy_mouse430a_2	60

MM_refseq_to_affy_mouse430_2	 	 61
MM_refseq_to_affy_mu11ksuba	 	 61
MM_refseq_to_affy_mu11ksubb	 	 62
MM_refseq_to_agilent_wholegenome	 	 63
MM_refseq_to_canonical_transcript_stable_id	 	 64
MM_refseq_to_ccds	 	 64
MM_refseq_to_codelink		65
MM_refseq_to_embl		66
MM_refseq_to_ensembl_gene_id		67
MM_refseq_to_ensembl_peptide_id		67
MM_refseq_to_ensembl_transcript_id		68
MM_refseq_to_entrezgene		69
MM_refseq_to_fantom		
MM_refseq_to_illumina_mousewg_6_v1		
MM_refseq_to_illumina_mousewg_6_v2		71
MM_refseq_to_interpro		72
MM_refseq_to_ipi		73
MM_refseq_to_merops		73
MM_refseq_to_mgi_id		74
MM_refseq_to_mgi_symbol		75
MM_refseq_to_mgi_transcript_name		
MM_refseq_to_mgr_transeript_name		76
MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v1		77
MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x44k_v2		78
MM_refseq_to_MM_refseq_to_ensembl_exon_id		79
MM_refseq_to_MM_refseq_to_uniprot_genename_transcript_name		79
MM_refseq_to_uniprot_sptrembl		80
MM_refseq_to_uniprot_swissprot		81
MM_refseq_to_uniprot_swissprot_accession		82
MM_refseq_to_wikigene_id		82
MM_refseq_to_pdb		83
MM_refseq_to_pfam		84
MM_refseq_to_phalanx_onearray		
MM_refseq_to_protein_id		
MM_refseq_to_refseq_dna		
MM_refseq_to_refseq_peptide		
MM_refseq_to_rfam		88
MM_refseq_to_rfam_gene_name		88
MM_refseq_to_rfam_transcript_name		89
MM refseq to smart		90
MM_refseq_to_tigrfam		90
- I - C		91
MM_refseq_to_ucsc		91
MM_refseq_to_unigene		
MM_refseq_to_uniprot_genename		93
MM_refseq_to_wikigene_name		94
TBL2		94
TBL2_HS		95
TBL2_MM	 	 96

Index

4 HS_conv_id

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

```
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 Mi-RaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_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 Mi-RaGE package.

Note

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

References

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

```
data(HS_refseq_to_affy_hg_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 Mi-RaGE package.

Note

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

References

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

Examples

```
\tt 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

```
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 Mi-RaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_u133a_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 Mi-RaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_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/

```
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 Mi-RaGE package.

Note

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

References

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

Examples

```
{\tt 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

```
data(HS_refseq_to_affy_hg_u95av2)
```

11

Format

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

Details

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

Note

For more details on how to generate this table, please see functions 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 Mi-RaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_affy_hg_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 Mi-RaGE package.

Note

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

References

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

```
data(HS_refseq_to_affy_hg_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 Mi-RaGE package.

Note

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

References

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

Examples

```
{\tt 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

```
data(HS_refseq_to_affy_hg_u95e)
```

Format

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

Details

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

Note

For more details on how to generate this table, please see functions 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.

15

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 Mi-RaGE package.

Note

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

References

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

```
data(HS_refseq_to_affy_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

```
data(HS_refseq_to_affy_u133_x3p)
```

Format

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

Details

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

Note

For more details on how to generate this table, please see functions 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/

```
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

```
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.

HS_refseq_to_embl 21

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/

```
{\tt 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

```
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/

```
data(HS_refseq_to_entrezgene)
```

HS_refseq_to_hgnc_id

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

```
data(HS_refseq_to_hgnc_symbol)
```

Format

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

Details

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

Note

For more details on how to generate this table, please see functions 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)
```

```
\label{eq:hs_refseq_to_efg_agilent_sureprint_g3_ge_8x60k} 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_sure. 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/

```
\label{local_data} data(HS\_refseq\_to\_HS\_refseq\_to\_efg\_agilent\_sureprint\_g3\_ge\_8x60k)
```

 $\label{eq:hs_refseq_to_efg_agilent_wholegenome_4x44k_v1} Konversion table between RefSeq and HS_refseq_to_efg_agilent_wholegenome_4x44k_v1 for human$

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_who 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)
```

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_who It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4x44k_v2)
```

```
HS_refseq_to_HS_refseq_to_ensembl_exon_id

Conversion table between RefSeq and HS_refseq_to_ensembl_exon_id

for human
```

Description

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

Usage

```
data(HS_refseq_to_HS_refseq_to_ensembl_exon_id)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_ensembl_exon_id)
```

```
\begin{tabular}{lll} HS\_refseq\_to\_HS\_refseq\_to\_uniprot\_genename\_transcript\_name \\ & Conversion & table & between & RefSeq & and \\ & HS\_refseq\_to\_uniprot\_genename\_transcript\_name & for human \\ \end{tabular}
```

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/

```
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)
```

Description

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

Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot)
```

Description

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

Usage

```
data(HS_refseq_to_HS_refseq_to_uniprot_swissprot_accession)
```

Format

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

Details

The first column includes RefSeq gene id and the second column includes corresponding HS_refseq_to_uniprot_swissprot 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

```
{\tt data}({\tt 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/

```
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/

```
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

```
data(HS_refseq_to_ipi)
```

The data set is a data frame. The number of rows is the 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

HS_refseq_to_pdb 39

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/

```
{\sf data}({\sf 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

```
data(HS_refseq_to_phalanx_onearray)
```

The data set is a data frame. The number of rows is the 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

References

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

Examples

```
data(HS_refseq_to_protein_id)
```

HS_refseq_to_refseq_dna

Conversion table between RefSeq and refseq_dna for human

Description

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

Usage

```
data(HS_refseq_to_refseq_dna)
```

Format

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

Details

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

Note

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

References

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

```
data(HS_refseq_to_refseq_dna)
```

HS_refseq_to_refseq_genomic

Conversion table between RefSeq and refseq_genomic for human

Description

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

Usage

```
data(HS_refseq_to_refseq_genomic)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_refseq_genomic)
```

```
HS_refseq_to_refseq_peptide
```

Conversion table between RefSeq and refseq_peptide for human

Description

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

```
data(HS_refseq_to_refseq_peptide)
```

44 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 ref-seq_peptide. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "HS_refseq_to_refseq_peptide" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(HS_refseq_to_refseq_peptide)
```

HS_refseq_to_rfam

Conversion table between RefSeq and rfam for human

Description

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

Usage

```
data(HS_refseq_to_rfam)
```

Format

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

Details

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

Note

References

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

Examples

```
data(HS_refseq_to_rfam)
```

HS_refseq_to_rfam_gene_name

Conversion table between RefSeq and rfam_gene_name for human

Description

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

Usage

```
data(HS_refseq_to_rfam_gene_name)
```

Format

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

Details

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

Note

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

References

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

```
data(HS_refseq_to_rfam_gene_name)
```

46 HS_refseq_to_smart

```
HS_refseq_to_rfam_transcript_name
```

Conversion table between RefSeq and rfam_transcript_name for human

Description

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

Usage

```
data(HS_refseq_to_rfam_transcript_name)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_rfam_transcript_name)
```

HS_refseq_to_smart

Conversion table between RefSeq and smart for human

Description

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

```
data(HS_refseq_to_smart)
```

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.

47

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)
```

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

48 HS_refseq_to_ucsc

References

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

Examples

```
data(HS_refseq_to_tigrfam)
```

HS_refseq_to_ucsc

Conversion table between RefSeq and ucsc for human

Description

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

Usage

```
data(HS_refseq_to_ucsc)
```

Format

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

Details

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

Note

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

References

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

```
data(HS_refseq_to_ucsc)
```

Description

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

Usage

```
data(HS_refseq_to_unigene)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_unigene)
```

```
HS_refseq_to_uniprot_genename
```

Conversion table between RefSeq and uniprot_genename for human

Description

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

```
data(HS_refseq_to_uniprot_genename)
```

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

Details

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

Note

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

References

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

Examples

```
data(HS_refseq_to_uniprot_genename)
```

HS_refseq_to_wikigene_name

Conversion table between RefSeq and wikigene_name for human

Description

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

Usage

```
data(HS_refseq_to_wikigene_name)
```

Format

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

Details

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

Note

id_conv 51

References

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

Examples

```
data(HS_refseq_to_wikigene_name)
```

id_conv

Conversion table between refseq and various gene id/probe id

Description

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

Usage

```
data(MM_refseq_to_wikigene_name)
```

Format

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

Details

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

Note

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

References

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

```
data(MM_refseq_to_wikigene_name)
```

MM_conv_id

miRNA conservation table of mouse

Description

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

Usage

```
data(MM_conv_id)
```

Format

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

Details

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

Note

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

References

For more details about TargetScanMouse, access to http://www.targetscan.org/mmu_61/

Examples

```
data(MM_conv_id)
```

```
MM_refseq_to_affy_mg_u74a
```

Conversion table between RefSeq and affy_mg_u74a for mouse

Description

This gene id conversion table between RefSeq and affy_mg_u74a is for MiRaGE package, based upon BioMart Gene ID Converter

```
data(MM_refseq_to_affy_mg_u74a)
```

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mg_u74a)
```

MM_refseq_to_affy_mg_u74av2

Conversion table between RefSeq and affy_mg_u74av2 for mouse

Description

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

Usage

```
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

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 Mi-RaGE package.

Note

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

References

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

```
data(MM\_refseq\_to\_affy\_mg\_u74b)
```

MM_refseq_to_affy_mg_u74bv2

Conversion table between RefSeq and affy_mg_u74bv2 for mouse

Description

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

Usage

```
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

```
data(MM_refseq_to_affy_mg_u74c)
```

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mg_u74c)
```

MM_refseq_to_affy_mg_u74cv2

Conversion table between RefSeq and affy_mg_u74cv2 for mouse

Description

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

Usage

```
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

References

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

Examples

```
data(MM_refseq_to_affy_mg_u74cv2)
```

MM_refseq_to_affy_moe430a

Conversion table between RefSeq and affy_moe430a for mouse

Description

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

Usage

```
data(MM_refseq_to_affy_moe430a)
```

Format

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

Details

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

Note

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

References

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

```
data(MM_refseq_to_affy_moe430a)
```

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 Mi-RaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_moe430b)
```

```
MM_refseq_to_affy_moex_1_0_st_v1
```

Conversion table between RefSeq and affy_moex_1_0_st_v1 for mouse

Description

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

```
data(MM_refseq_to_affy_moex_1_0_st_v1)
```

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_moex_1_0_st_v1)
```

```
\label{lem:model} 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/

```
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

```
data(MM_refseq_to_affy_mu11ksuba)
```

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_affy_mu11ksuba)
```

MM_refseq_to_affy_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

References

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

Examples

```
data(MM_refseq_to_affy_mu11ksubb)
```

MM_refseq_to_agilent_wholegenome

Conversion table between RefSeq and agilent_wholegenome for mouse

Description

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

Usage

```
data(MM_refseq_to_agilent_wholegenome)
```

Format

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

Details

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

Note

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

References

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

```
data(MM_refseq_to_agilent_wholegenome)
```

64 MM_refseq_to_ccds

```
MM_refseq_to_canonical_transcript_stable_id
```

Conversion table between RefSeq and canonical_transcript_stable_id for mouse

Description

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

Usage

```
data(MM_refseq_to_canonical_transcript_stable_id)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_canonical_transcript_stable_id)
```

MM_refseq_to_ccds

Conversion table between RefSeq and ccds for mouse

Description

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

```
data(MM_refseq_to_ccds)
```

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_ccds)
```

MM_refseq_to_codelink Conversion table between RefSeq and codelink for mouse

Description

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

Usage

```
data(MM_refseq_to_codelink)
```

Format

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

Details

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

Note

66 MM_refseq_to_embl

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/

```
{\tt 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

```
data(MM_refseq_to_ensembl_peptide_id)
```

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_ensembl_peptide_id)
```

```
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/

```
data(MM_refseq_to_entrezgene)
```

Description

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

Usage

```
data(MM_refseq_to_fantom)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_fantom)
```

```
MM_refseq_to_illumina_mousewg_6_v1
```

Conversion table between RefSeq and illumina_mousewg_6_v1 for mouse

Description

This gene id conversion table between RefSeq and illumina_mousewg_6_v1 is for MiRaGE package, based upon BioMart Gene ID Converter

```
data(MM_refseq_to_illumina_mousewg_6_v1)
```

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_illumina_mousewg_6_v1)
```

```
MM_refseq_to_illumina_mousewg_6_v2
```

Conversion table between RefSeq and illumina_mousewg_6_v2 for mouse

Description

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

Usage

```
data(MM_refseq_to_illumina_mousewg_6_v2)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_illumina_mousewg_6_v2)
```

MM_refseq_to_interpro Conversion table between RefSeq and interpro for mouse

Description

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

Usage

```
data(MM_refseq_to_interpro)
```

Format

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

Details

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

Note

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

References

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

```
data(MM_refseq_to_interpro)
```

MM_refseq_to_ipi 73

MM_refseq_to_ipi

Conversion table between RefSeq and ipi for mouse

Description

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

Usage

```
data(MM_refseq_to_ipi)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_ipi)
```

MM_refseq_to_merops

Conversion table between RefSeq and merops for mouse

Description

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

```
data(MM_refseq_to_merops)
```

Format

The data set is a data frame. The number of rows is the 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)
```

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 Mi-RaGE package.

Note

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

References

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

```
data(MM_refseq_to_mgi_symbol)
```

MM_refseq_to_mgi_transcript_name

Conversion table between RefSeq and mgi_transcript_name for mouse

Description

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

Usage

```
data(MM_refseq_to_mgi_transcript_name)
```

Format

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

Details

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

Note

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

References

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

Examples

```
data(MM_refseq_to_mgi_transcript_name)
```

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

```
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_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)
```

```
\label{lem: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 \\ \end{cases}
```

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_who It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "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)
```

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_who It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "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/

```
\label{lem:main_data} data(\texttt{MM\_refseq\_to\_MM\_refseq\_to\_efg\_agilent\_wholegenome\_4x44k\_v2})
```

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)
```

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)
```

```
\begin{tabular}{lll} MM\_refseq\_to\_mM\_refseq\_to\_uniprot\_sptrembl \\ & Conversion & table & between & RefSeq & and \\ & MM\_refseq\_to\_uniprot\_sptrembl for mouse \\ \end{tabular}
```

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_sptreml 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)
```

```
\begin{tabular}{lll} MM\_refseq\_to\_uniprot\_swissprot \\ & Conversion & table & between & RefSeq & and \\ & MM\_refseq\_to\_uniprot\_swissprot for mouse \\ \end{tabular}
```

Description

This gene id conversion table between RefSeq and MM_refseq_to_uniprot_swissprot is for Mi-RaGE 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/

```
{\tt data}({\tt MM\_refseq\_to\_MM\_refseq\_to\_uniprot\_swissprot})
```

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

MM_refseq_to_pdb 83

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.

84 MM_refseq_to_pfam

Note

For more details on how to generate this table, please see functions 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/

```
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

```
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 ref-seq_dna. It can be made out of getBM function in biomaRt package. Please note that the name of object loaded is not "MM_refseq_to_refseq_dna" but "id_conv", because of the requirements by MiRaGE package.

Note

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

References

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

Examples

```
data(MM_refseq_to_refseq_dna)
```

MM_refseq_to_refseq_peptide

Conversion table between RefSeq and refseq_peptide for mouse

Description

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

Usage

```
data(MM_refseq_to_refseq_peptide)
```

Format

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

Details

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

Note

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

References

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

```
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

```
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.

90 MM_refseq_to_smart

Note

For more details on how to generate this table, please see functions 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/

```
data(MM_refseq_to_smart)
```

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

```
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)
```

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/

```
data(MM_refseq_to_uniprot_genename)
```

94 TBL2

```
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"

```
data(TBL2_MM)
```

TBL2_HS 95

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.

96 TBL2_MM

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

```
*Topic data
   conv_id, 4
                                                   HS_refseq_to_HS_refseq_to_efg_agilent_wholegenome_4
   HS_conv_id, 4
   HS_refseq_to_affy_hc_g110, 5
                                                   HS_refseq_to_HS_refseq_to_ensembl_exon_id,
   HS_refseq_to_affy_hg_focus, 6
   HS_refseq_to_affy_hg_u133_plus_2,
                                                   HS_refseq_to_HS_refseq_to_uniprot_genename_transcri
   HS_refseq_to_affy_hg_u133a,7
                                                   HS_refseq_to_HS_refseq_to_uniprot_sptrembl,
   HS_refseq_to_affy_hg_u133a_2,7
                                                   HS_refseq_to_HS_refseq_to_uniprot_swissprot,
   HS_refseq_to_affy_hg_u133b, 8
   HS_refseq_to_affy_hg_u95a, 10
   HS_refseq_to_affy_hg_u95av2, 10
                                                   HS_refseq_to_HS_refseq_to_uniprot_swissprot_access:
   HS_refseq_to_affy_hg_u95b, 11
                                                   HS_refseq_to_HS_refseq_to_wikigene_id,
   HS_refseq_to_affy_hg_u95c, 12
   HS_refseq_to_affy_hg_u95d, 13
                                                   HS_refseq_to_illumina_humanht_12,
   HS_refseq_to_affy_hg_u95e, 13
   HS_refseq_to_affy_huex_1_0_st_v2,
                                                   HS_refseq_to_illumina_humanwg_6_v1,
   HS_refseq_to_affy_hugene_1_0_st_v1,
                                                   HS_refseq_to_illumina_humanwg_6_v2,
   HS_refseq_to_affy_hugenefl, 15
                                                   HS_refseq_to_illumina_humanwg_6_v3,
   HS_refseq_to_affy_u133_x3p, 16
   HS_refseq_to_agilent_cgh_44b, 17
                                                   HS_refseq_to_interpro, 37
   HS_refseq_to_agilent_wholegenome,
                                                   HS_refseq_to_ipi, 37
   {\tt HS\_refseq\_to\_canonical\_transcript\_stable\_id, \ HS\_refseq\_to\_merops, 38}
                                                   HS_refseq_to_pdb, 39
        19
                                                   HS_refseq_to_pfam, 40
   HS_refseq_to_ccds, 19
                                                   HS_refseq_to_phalanx_onearray, 40
   HS_refseq_to_codelink, 20
                                                   HS_refseq_to_protein_id, 41
   HS_refseq_to_embl, 21
                                                   HS_refseq_to_refseq_dna, 42
   HS_refseq_to_ensembl_gene_id, 22
                                                   HS_refseq_to_refseq_genomic, 43
   HS_refseq_to_ensembl_peptide_id,
                                                   HS_refseq_to_refseq_peptide, 43
                                                   HS_refseq_to_rfam, 44
   HS_refseq_to_ensembl_transcript_id,
                                                   HS_refseq_to_rfam_gene_name, 45
   HS_refseq_to_entrezgene, 24
                                                   HS_refseq_to_rfam_transcript_name,
                                                       46
   HS_refseq_to_hgnc_id, 25
                                                   HS_refseq_to_smart, 46
   HS_refseq_to_hgnc_symbol, 25
                                                   HS_refseq_to_tigrfam, 47
   HS_refseq_to_hgnc_transcript_name,
                                                   HS_refseq_to_ucsc, 48
   HS_refseq_to_HS_refseq_to_efg_agilent_surepriHS_gefseq_8k6@kmigene, 49
                                                   HS_refseq_to_uniprot_genename, 49
   HS_refseq_to_HS_refseq_to_efg_agilent_wholegeHSmeeffsedkto1wikigene_name, 50
```

98 INDEX

```
id_conv, 51
                                                   79
MM_conv_id, 52
                                               MM_refseq_to_MM_refseq_to_uniprot_sptrembl,
MM_refseq_to_affy_mg_u74a, 52
                                               MM_refseq_to_MM_refseq_to_uniprot_swissprot,
MM_refseq_to_affy_mg_u74av2, 53
MM_refseq_to_affy_mg_u74b, 54
                                               MM_refseq_to_MM_refseq_to_uniprot_swissprot_access:
MM_refseq_to_affy_mg_u74bv2, 55
MM_refseq_to_affy_mg_u74c, 55
                                               MM_refseq_to_MM_refseq_to_wikigene_id,
MM_refseq_to_affy_mg_u74cv2, 56
MM_refseq_to_affy_moe430a, 57
                                               {\tt MM\_refseq\_to\_pdb}, \textcolor{red}{83}
MM_refseq_to_affy_moe430b, 58
                                               MM_refseq_to_pfam, 84
MM_refseq_to_affy_moex_1_0_st_v1,
                                               MM_refseq_to_phalanx_onearray, 85
                                               MM_refseq_to_protein_id, 85
MM_refseq_to_affy_mogene_1_0_st_v1,
                                               MM_refseq_to_refseq_dna, 86
    59
                                               MM_refseq_to_refseq_peptide, 87
MM_refseq_to_affy_mouse430_2, 61
                                               MM_refseq_to_rfam, 88
MM_refseq_to_affy_mouse430a_2, 60
                                               MM_refseq_to_rfam_gene_name, 88
MM_refseq_to_affy_mu11ksuba, 61
                                               MM_refseq_to_rfam_transcript_name,
MM_refseq_to_affy_mu11ksubb, 62
                                                   89
MM_refseq_to_agilent_wholegenome,
                                               MM_refseq_to_smart, 90
                                               MM_refseq_to_tigrfam, 91
MM_refseq_to_canonical_transcript_stable_id,
                                               MM_refseq_to_ucsc, 91
                                               MM_refseq_to_unigene, 92
MM_refseq_to_ccds, 64
                                               MM_refseq_to_uniprot_genename, 93
MM_refseq_to_codelink, 65
                                               MM_refseq_to_wikigene_name, 94
MM_refseq_to_embl, 66
                                               TBL2, 94
MM_refseq_to_ensembl_gene_id, 67
                                               TBL2_HS, 95
MM_refseq_to_ensembl_peptide_id,
                                               TBL2_MM, 96
MM_refseq_to_ensembl_transcript_id,
                                           conv_id, 4
MM_refseq_to_entrezgene, 69
                                           HS_conv_id, 4
MM_refseq_to_fantom, 70
                                           HS_refseq_to_affy_hc_g110,5
MM_refseq_to_illumina_mousewg_6_v1,
                                           HS_refseq_to_affy_hg_focus, 6
                                           HS_refseq_to_affy_hg_u133_plus_2,9
MM_refseq_to_illumina_mousewg_6_v2,
                                           HS_refseq_to_affy_hg_u133a, 7
    71
                                           HS_refseq_to_affy_hg_u133a_2, 7
MM_refseq_to_interpro, 72
                                           HS_refseq_to_affy_hg_u133b, 8
MM_refseq_to_ipi, 73
                                           HS_refseq_to_affy_hg_u95a, 10
MM_refseq_to_merops, 73
                                           HS_refseq_to_affy_hg_u95av2, 10
MM_refseq_to_mgi_id, 74
                                           HS_refseq_to_affy_hg_u95b, 11
MM_refseq_to_mgi_symbol, 75
                                           HS_refseq_to_affy_hg_u95c, 12
MM_refseq_to_mgi_transcript_name,
                                           HS_refseq_to_affy_hg_u95d, 13
                                           HS_refseq_to_affy_hg_u95e, 13
MM_refseq_to_MM_refseq_to_efg_agilent_sur@priefts@d_ge_&&f0khuex_1_0_st_v2, 14
                                           HS_refseq_to_affy_hugene_1_0_st_v1, 16
MM_refseq_to_MM_refseq_to_efg_agilent_wholl@geen6smeq4te44tfff.hugenefl, 15
                                           HS_refseq_to_affy_u133_x3p, 16
MM_refseq_to_MM_refseq_to_efg_agilent_wholl@gea6seq4te44tgivlent_cgh_44b, 17
                                           HS_refseq_to_agilent_wholegenome, 18
MM_refseq_to_MM_refseq_to_ensembl_exon_idHS_refseq_to_canonical_transcript_stable_id,
MM_refseq_to_MM_refseq_to_uniprot_genenames_trefiseq_ipt_oadle, 19
```

INDEX 99

HS_refseq_to_codelink, 20	MM_conv_id, 52
HS_refseq_to_emb1, 21	MM_refseq_to_affy_mg_u74a, 52
HS_refseq_to_ensembl_gene_id, 22	MM_refseq_to_affy_mg_u74av2, 53
HS_refseq_to_ensembl_peptide_id, 22	MM_refseq_to_affy_mg_u74b, 54
HS_refseq_to_ensembl_transcript_id, 23	MM_refseq_to_affy_mg_u74bv2, 55
HS_refseq_to_entrezgene, 24	MM_refseq_to_affy_mg_u74c, 55
HS_refseq_to_hgnc_id, 25	MM_refseq_to_affy_mg_u74cv2, 56
HS_refseq_to_hgnc_symbol, 25	MM_refseq_to_affy_moe430a, 57
HS_refseq_to_hgnc_transcript_name, 26	MM_refseq_to_affy_moe430b, 58
$HS_refseq_to_HS_refseq_to_efg_agilent_surepr$	
27	MM_refseq_to_affy_mogene_1_0_st_v1, 59
HS_refseq_to_HS_refseq_to_efg_agilent_wholeg	
28	MM_refseq_to_affy_mouse430a_2,60
HS_refseq_to_HS_refseq_to_efg_agilent_wholeg	
28	MM_refseq_to_affy_mu11ksubb, 62
HS_refseq_to_HS_refseq_to_ensembl_exon_id,	MM_refseq_to_agilent_wholegenome, 63
29	MM_refseq_to_canonical_transcript_stable_id,
HS_refseq_to_HS_refseq_to_uniprot_genename_t	
30	MM_refseq_to_ccds, 64
HS_refseq_to_HS_refseq_to_uniprot_sptrembl,	MM_refseq_to_codelink, 65
31	MM_refseq_to_embl, 66
HS_refseq_to_HS_refseq_to_uniprot_swissprot,	
31	MM_refseq_to_ensembl_peptide_id, 67
HS_refseq_to_HS_refseq_to_uniprot_swissprot_	
32	MM_refseq_to_entrezgene, 69
HS_refseq_to_HS_refseq_to_wikigene_id,	MM_refseq_to_fantom, 70
33	MM_refseq_to_illumina_mousewg_6_v1,70
HS_refseq_to_illumina_humanht_12, 34	MM_refseq_to_illumina_mousewg_6_v2,71
HS_refseq_to_illumina_humanwg_6_v1, 34	MM_refseq_to_interpro,72
HS_refseq_to_illumina_humanwg_6_v2, 35	MM_refseq_to_ipi, 73
HS_refseq_to_illumina_humanwg_6_v3, 36	MM_refseq_to_merops, 73
HS_refseq_to_interpro, 37	MM_refseq_to_mgi_id,74
HS_refseq_to_ipi, 37	MM_refseq_to_mgi_symbol, 75
HS_refseq_to_merops, 38	MM_refseq_to_mgi_transcript_name, 76
HS_refseq_to_pdb, 39	${\tt MM_refseq_to_MM_refseq_to_efg_agilent_sureprint_g3_ge}.$
HS_refseq_to_pfam, 40	76
HS_refseq_to_phalanx_onearray, 40	${\tt MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x4-refseq_to_megenomeg$
HS_refseq_to_protein_id, 41	77
HS_refseq_to_refseq_dna, 42	MM_refseq_to_MM_refseq_to_efg_agilent_wholegenome_4x4
HS_refseq_to_refseq_genomic, 43	78
HS_refseq_to_refseq_peptide, 43	MM_refseq_to_MM_refseq_to_ensembl_exon_id,
HS_refseq_to_rfam, 44	79
HS_refseq_to_rfam_gene_name, 45	MM_refseq_to_MM_refseq_to_uniprot_genename_transcript
HS_refseq_to_rfam_transcript_name, 46	79
HS_refseq_to_smart, 46	MM_refseq_to_MM_refseq_to_uniprot_sptrembl,
HS_refseq_to_tigrfam, 47	80
HS_refseq_to_ucsc, 48	MM_refseq_to_MM_refseq_to_uniprot_swissprot,
HS_refseq_to_unigene, 49	81
HS_refseq_to_uniprot_genename, 49	${\tt MM_refseq_to_MM_refseq_to_uniprot_swissprot_accession},$
HS_refseq_to_wikigene_name, 50	82
	MM_refseq_to_MM_refseq_to_wikigene_id,
id_conv, 51	82

100 INDEX

```
MM_refseq_to_pdb, 83
MM_refseq_to_pfam, 84
{\tt MM\_refseq\_to\_phalanx\_onearray},\, 85
MM_refseq_to_protein_id, 85
MM_refseq_to_refseq_dna, 86
MM_refseq_to_refseq_peptide, 87
\texttt{MM\_refseq\_to\_rfam}, \textcolor{red}{88}
MM_refseq_to_rfam_gene_name, 88
MM_refseq_to_rfam_transcript_name, 89
{\tt MM\_refseq\_to\_smart}, \textcolor{red}{90}
MM_refseq_to_tigrfam, 91
MM_refseq_to_ucsc, 91
MM_refseq_to_unigene, 92
MM_refseq_to_uniprot_genename, 93
{\tt MM\_refseq\_to\_wikigene\_name}, 94
TBL2, 94
TBL2_HS, 95
TBL2_MM, 96
```