

Package ‘chipenrich.data’

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Title Companion package to chipenrich

Version 2.34.0

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Description Supporting data for the chipenrich package. Includes pre-defined gene sets, gene locus definitions, and mappability estimates.

biocViews ChIPSeq, Epigenetics, FunctionalGenomics, GeneSetEnrichment, HistoneModification, Regression

Depends R (>= 3.4.0)

Imports AnnotationDbi, BiocGenerics, methods, GenomicRanges, GenomeInfoDb, IRanges, readr, rtracklayer, S4Vectors, utils

License GPL-3

Encoding UTF-8

LazyData true

Suggests BiocStyle, devtools, knitr, rmarkdown, roxygen2, testthat, GO.db, org.Dm.eg.db, org.Dr.eg.db, org.Hs.eg.db, org.Mm.eg.db, org.Rn.eg.db, TxDb.Dmelanogaster.UCSC.dm3.ensGene, TxDb.Dmelanogaster.UCSC.dm6.ensGene, TxDb.Drorio.UCSC.danRer10.refGene, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Hsapiens.UCSC.hg38.knownGene, TxDb.Mmusculus.UCSC.mm9.knownGene, TxDb.Mmusculus.UCSC.mm10.knownGene, TxDb.Rnorvegicus.UCSC.rn4.ensGene, TxDb.Rnorvegicus.UCSC.rn5.refGene, TxDb.Rnorvegicus.UCSC.rn6.refGene

VignetteBuilder knitr

RoxygenNote 6.1.1

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Contents

chipenrich.data	7
enhancer.dnase_thurman.0	7
gene.enh.desc	8
GeneSet-class	8
geneset.biocarta_pathway.hsa	9
geneset.biocarta_pathway.mmu	10
geneset.biocarta_pathway.rno	10
geneset.ctd.hsa	11
geneset.ctd.mmu	11
geneset.cytoband.hsa	12
geneset.drug_bank.hsa	13
geneset.drug_bank.mmu	13
geneset.drug_bank.rno	14
geneset.GOBP.dme	14
geneset.GOBP.dre	15
geneset.GOBP.hsa	15
geneset.GOBP.mmu	16
geneset.GOBP.rno	17
geneset.GOCC.dme	17
geneset.GOCC.dre	18
geneset.GOCC.hsa	19
geneset.GOCC.mmu	19
geneset.GOCC.rno	20
geneset.GOMF.dme	21
geneset.GOMF.dre	21
geneset.GOMF.hsa	22
geneset.GOMF.mmu	23
geneset.GOMF.rno	23
geneset.hallmark.hsa	24
geneset.immunologic.hsa	25
geneset.kegg_pathway.hsa	25
geneset.kegg_pathway.mmu	26
geneset.kegg_pathway.rno	27
geneset.mesh.hsa	27
geneset.mesh.mmu	28
geneset.mesh.rno	28
geneset.metabolite.hsa	29
geneset.metabolite.mmu	29
geneset.metabolite.rno	30
geneset.microrna.hsa	30
geneset.oncogenic.hsa	31
geneset.panther_pathway.hsa	31
geneset.panther_pathway.mmu	32

geneset.panther_pathway.rno	32
geneset.pfam.hsa	33
geneset.pfam.mmu	33
geneset.pfam.rno	34
geneset.protein_interaction_biogrid.hsa	34
geneset.reactome.dme	35
geneset.reactome.dre	35
geneset.reactome.hsa	36
geneset.reactome.mmu	37
geneset.reactome.rno	37
geneset.transcription_factors.hsa	38
geneset.transcription_factors.mmu	39
geneset.transcription_factors.rno	39
locusdef.danRer10.10kb	40
locusdef.danRer10.10kb_outside	40
locusdef.danRer10.10kb_outside_upstream	41
locusdef.danRer10.1kb	42
locusdef.danRer10.1kb_outside	42
locusdef.danRer10.1kb_outside_upstream	43
locusdef.danRer10.5kb	44
locusdef.danRer10.5kb_outside	44
locusdef.danRer10.5kb_outside_upstream	45
locusdef.danRer10.exon	46
locusdef.danRer10.intron	46
locusdef.danRer10.nearest_gene	47
locusdef.danRer10.nearest_tss	48
locusdef.dm3.10kb	48
locusdef.dm3.10kb_outside	49
locusdef.dm3.10kb_outside_upstream	50
locusdef.dm3.1kb	51
locusdef.dm3.1kb_outside	51
locusdef.dm3.1kb_outside_upstream	52
locusdef.dm3.5kb	53
locusdef.dm3.5kb_outside	53
locusdef.dm3.5kb_outside_upstream	54
locusdef.dm3.exon	55
locusdef.dm3.intron	55
locusdef.dm3.nearest_gene	56
locusdef.dm3.nearest_tss	57
locusdef.dm6.10kb	58
locusdef.dm6.10kb_outside	58
locusdef.dm6.10kb_outside_upstream	59
locusdef.dm6.1kb	60
locusdef.dm6.1kb_outside	60
locusdef.dm6.1kb_outside_upstream	61
locusdef.dm6.5kb	62
locusdef.dm6.5kb_outside	62
locusdef.dm6.5kb_outside_upstream	63
locusdef.dm6.exon	64
locusdef.dm6.intron	64
locusdef.dm6.nearest_gene	65
locusdef.dm6.nearest_tss	66

locusdef.hg19.10kb	67
locusdef.hg19.10kb_outside	67
locusdef.hg19.10kb_outside_upstream	68
locusdef.hg19.1kb	69
locusdef.hg19.1kb_outside	70
locusdef.hg19.1kb_outside_upstream	70
locusdef.hg19.5kb	71
locusdef.hg19.5kb_outside	72
locusdef.hg19.5kb_outside_upstream	72
locusdef.hg19.exon	73
locusdef.hg19.intron	74
locusdef.hg19.nearest_gene	74
locusdef.hg19.nearest_tss	75
locusdef.hg38.10kb	76
locusdef.hg38.10kb_outside	77
locusdef.hg38.10kb_outside_upstream	77
locusdef.hg38.1kb	78
locusdef.hg38.1kb_outside	79
locusdef.hg38.1kb_outside_upstream	79
locusdef.hg38.5kb	80
locusdef.hg38.5kb_outside	81
locusdef.hg38.5kb_outside_upstream	81
locusdef.hg38.exon	82
locusdef.hg38.intron	83
locusdef.hg38.nearest_gene	83
locusdef.hg38.nearest_tss	84
locusdef.mm10.10kb	85
locusdef.mm10.10kb_outside	86
locusdef.mm10.10kb_outside_upstream	86
locusdef.mm10.1kb	87
locusdef.mm10.1kb_outside	88
locusdef.mm10.1kb_outside_upstream	88
locusdef.mm10.5kb	89
locusdef.mm10.5kb_outside	90
locusdef.mm10.5kb_outside_upstream	90
locusdef.mm10.exon	91
locusdef.mm10.intron	92
locusdef.mm10.nearest_gene	92
locusdef.mm10.nearest_tss	93
locusdef.mm9.10kb	94
locusdef.mm9.10kb_outside	95
locusdef.mm9.10kb_outside_upstream	95
locusdef.mm9.1kb	96
locusdef.mm9.1kb_outside	97
locusdef.mm9.1kb_outside_upstream	97
locusdef.mm9.5kb	98
locusdef.mm9.5kb_outside	99
locusdef.mm9.5kb_outside_upstream	99
locusdef.mm9.exon	100
locusdef.mm9.intron	101
locusdef.mm9.nearest_gene	101
locusdef.mm9.nearest_tss	102

locusdef.rn4.10kb	103
locusdef.rn4.10kb_outside	104
locusdef.rn4.10kb_outside_upstream	104
locusdef.rn4.1kb	105
locusdef.rn4.1kb_outside	106
locusdef.rn4.1kb_outside_upstream	106
locusdef.rn4.5kb	107
locusdef.rn4.5kb_outside	108
locusdef.rn4.5kb_outside_upstream	108
locusdef.rn4.exon	109
locusdef.rn4.intron	110
locusdef.rn4.nearest_gene	110
locusdef.rn4.nearest_tss	111
locusdef.rn5.10kb	112
locusdef.rn5.10kb_outside	112
locusdef.rn5.10kb_outside_upstream	113
locusdef.rn5.1kb	114
locusdef.rn5.1kb_outside	114
locusdef.rn5.1kb_outside_upstream	115
locusdef.rn5.5kb	116
locusdef.rn5.5kb_outside	116
locusdef.rn5.5kb_outside_upstream	117
locusdef.rn5.exon	118
locusdef.rn5.intron	118
locusdef.rn5.nearest_gene	119
locusdef.rn5.nearest_tss	120
locusdef.rn6.10kb	120
locusdef.rn6.10kb_outside	121
locusdef.rn6.10kb_outside_upstream	122
locusdef.rn6.1kb	122
locusdef.rn6.1kb_outside	123
locusdef.rn6.1kb_outside_upstream	124
locusdef.rn6.5kb	124
locusdef.rn6.5kb_outside	125
locusdef.rn6.5kb_outside_upstream	126
locusdef.rn6.exon	126
locusdef.rn6.intron	127
locusdef.rn6.nearest_gene	128
locusdef.rn6.nearest_tss	128
LocusDefinition-class	129
mappa.hg19.10kb.100mer	130
mappa.hg19.10kb.24mer	131
mappa.hg19.10kb.36mer	131
mappa.hg19.10kb.40mer	132
mappa.hg19.10kb.50mer	133
mappa.hg19.10kb.75mer	133
mappa.hg19.1kb.100mer	134
mappa.hg19.1kb.24mer	135
mappa.hg19.1kb.36mer	135
mappa.hg19.1kb.40mer	136
mappa.hg19.1kb.50mer	137
mappa.hg19.1kb.75mer	137

mappa.hg19.5kb.100mer	138
mappa.hg19.5kb.24mer	139
mappa.hg19.5kb.36mer	139
mappa.hg19.5kb.40mer	140
mappa.hg19.5kb.50mer	141
mappa.hg19.5kb.75mer	141
mappa.hg19.exon.100mer	142
mappa.hg19.exon.24mer	143
mappa.hg19.exon.36mer	143
mappa.hg19.exon.40mer	144
mappa.hg19.exon.50mer	145
mappa.hg19.exon.75mer	145
mappa.hg19.intron.100mer	146
mappa.hg19.intron.24mer	147
mappa.hg19.intron.36mer	147
mappa.hg19.intron.40mer	148
mappa.hg19.intron.50mer	149
mappa.hg19.intron.75mer	149
mappa.hg19.nearest_gene.100mer	150
mappa.hg19.nearest_gene.24mer	151
mappa.hg19.nearest_gene.36mer	151
mappa.hg19.nearest_gene.40mer	152
mappa.hg19.nearest_gene.50mer	153
mappa.hg19.nearest_gene.75mer	153
mappa.hg19.nearest_tss.100mer	154
mappa.hg19.nearest_tss.24mer	155
mappa.hg19.nearest_tss.36mer	155
mappa.hg19.nearest_tss.40mer	156
mappa.hg19.nearest_tss.50mer	157
mappa.hg19.nearest_tss.75mer	157
mappa.mm9.10kb.100mer	158
mappa.mm9.10kb.36mer	159
mappa.mm9.10kb.40mer	159
mappa.mm9.10kb.50mer	160
mappa.mm9.10kb.75mer	161
mappa.mm9.1kb.100mer	161
mappa.mm9.1kb.36mer	162
mappa.mm9.1kb.40mer	163
mappa.mm9.1kb.50mer	163
mappa.mm9.1kb.75mer	164
mappa.mm9.5kb.100mer	165
mappa.mm9.5kb.36mer	165
mappa.mm9.5kb.40mer	166
mappa.mm9.5kb.50mer	167
mappa.mm9.5kb.75mer	167
mappa.mm9.exon.100mer	168
mappa.mm9.exon.36mer	169
mappa.mm9.exon.40mer	169
mappa.mm9.exon.50mer	170
mappa.mm9.exon.75mer	171
mappa.mm9.intron.100mer	171
mappa.mm9.intron.36mer	172

mappa.mm9.intron.40mer	173
mappa.mm9.intron.50mer	173
mappa.mm9.intron.75mer	174
mappa.mm9.nearest_gene.100mer	175
mappa.mm9.nearest_gene.36mer	175
mappa.mm9.nearest_gene.40mer	176
mappa.mm9.nearest_gene.50mer	177
mappa.mm9.nearest_gene.75mer	177
mappa.mm9.nearest_tss.100mer	178
mappa.mm9.nearest_tss.36mer	179
mappa.mm9.nearest_tss.40mer	179
mappa.mm9.nearest_tss.50mer	180
mappa.mm9.nearest_tss.75mer	181
peaks_E2F4	181
peaks_H3K4me3_GM12878	182
spline.log_dtss.90ENCODE	183
tss.danRer10	183
tss.dm3	184
tss.dm6	184
tss.hg19	185
tss.hg38	185
tss.mm10	186
tss.mm9	186
tss.rn4	187
tss.rn5	187
tss.rn6	188

Index**189**

chipenrich.data*chipenrich.data: Data for chipenrich: gene set enrichment analysis for ChIP-seq data*

Description

Supporting data for the chipenrich package. Includes pre-defined gene sets, gene locus definitions, and mappability estimates.

enhancer.dnase_thurman.0*Enhancer locations*

Description

A GRanges with all the enhancer locations for hg19. The locations were found using a combination of DNase data and from Thurman et al (PMID: 22955617)

Usage**enhancer.dnase_thurman.0**

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

gene.enh.desc	<i>Gene-Enhancer descriptives</i>
---------------	-----------------------------------

Description

A data frame with gene-level descriptions of enhancer properties using `enhancers.dnase_thurman.0`. Used in the adjustment of proximity test to enhancers.

- gene_id** The Entrez ID for the a gene
- avg_denh_emp** The empirical average distance to an enhancer from 90 ENCODE ChIP-seq datasets. This is used as the adjustment.
- num_enh** The number of enhancers assigned to the gene, defined by closest gene TSS
- avgdenh** The theoretical average distance to an enhancer assuming every base pair on the genome is equally likely to have a peak binding.

Usage

`gene.enh.desc`

Format

An object of class `data.frame` with 21600 rows and 4 columns.

GeneSet-class	<i>Class "GeneSet"</i>
---------------	------------------------

Description

Class for storing sets of genes and their corresponding metadata.

Objects from the Class

Objects can be created by calls of the form `new("GeneSet")`.

These objects are used internally by the `chipenrich` package and users will not likely need to create these.

Slots

- set.gene:** Object of class "environment". Maps from geneset IDs to lists of Entrez gene IDs.
- type:** Object of class "character". The formal name for this collection of genesets.
- set.name:** Object of class "environment". Maps from geneset IDs to their descriptions/names.
- all.genes:** Object of class "character". A set of all genes present across every geneset.
- organism:** Object of class "character". Organism code for gene IDs.
- dburl:** Object of class "character". Web URL for this collection of genesets.

Note

Not typically accessed by the user - this is used internally by the chipenrich package.

Author(s)

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Examples

```
# Show information about class.
showClass("GeneSet")

# What is stored inside a geneset object?
data("geneset.metabolite.hsa");
str(geneset.metabolite.hsa);

# How are the mappings from geneset IDs to gene IDs stored?
ls.str(geneset.metabolite.hsa@set.gene);
```

geneset.biocarta_pathway.hsa

geneset.biocarta_pathway.hsa genesets for BioCarta

Description

BioCarta (biocarta_pathway) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:04 2017.

Usage

geneset.biocarta_pathway.hsa

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

https://cgap.nci.nih.gov/Pathways/BioCarta_Pathways

```
geneset.biocarta_pathway.mmu
geneset.biocarta_pathway.mmu
```

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.biocarta_pathway.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

```
geneset.biocarta_pathway.rno
geneset.biocarta_pathway.rno
```

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.biocarta_pathway.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.ctd.hsa

geneset.ctd.hsa genesets for Comparative Toxicogenomics Database

Description

Comparative Toxicogenomics Database (ctd) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:11 2017.

Usage

`geneset.ctd.hsa`

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://ctdbase.org>

geneset.ctd.mmu

geneset.ctd.mmu genesets for Comparative Toxicogenomics Database

Description

Comparative Toxicogenomics Database (ctd) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Sat Nov 10 15:56:37 2018.

Usage

`geneset.ctd.mmu`

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://ctdbase.org>

geneset.cytoband.hsa *geneset.cytoband.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.cytoband.hsa)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.drug_bank.hsa *geneset.drug_bank.hsa genesets for DrugBank*

Description

DrugBank (drug_bank) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:13 2017.

Usage

`geneset.drug_bank.hsa`

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.
dburl A character of the URL of the database underlying the genesets.
organism A character of the organism, e.g. Homo sapiens.
set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<https://www.drugbank.ca>

geneset.drug_bank.mmu *geneset.drug_bank.mmu*

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the chipenrich package.

Usage

`data(geneset.drug_bank.mmu)`

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.drug_bank.rno *geneset.drug_bank.rno*

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.drug_bank.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.GOBP.dme *geneset.GOBP.dme genesets for Drosophila melanogaster*

Description

Gene Ontology Biological Process (GOBP) genesets for *Drosophila melanogaster*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:38 2017.

Usage

```
geneset.GOBP.dme
```

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. *Homo sapiens*.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Dm.eg.db_3.4.2` and `GO.db_3.4.2`

`geneset.GOBP.dre`

geneset.GOBP.dre genesets for Danio rerio

Description

Gene Ontology Biological Process (GOBP) genesets for *Danio rerio*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:25:08 2017.

Usage

```
geneset.GOBP.dre
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. *Homo sapiens*.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Dr.eg.db_3.4.2` and `GO.db_3.4.2`

`geneset.GOBP.hsa`

geneset.GOBP.hsa genesets for Homo sapiens

Description

Gene Ontology Biological Process (GOBP) genesets for *Homo sapiens*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:22:22 2017.

Usage

```
geneset.GOBP.hsa
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Hs.eg.db_3.4.2 and GO.db_3.4.2

geneset.GOBP.mmu

geneset.GOBP.mmu genesets for Mus musculus

Description

Gene Ontology Biological Process (GOBP) genesets for *Mus musculus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:23:23 2017.

Usage

geneset.GOBP.mmu

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Mm.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOBP.rno`

geneset.GOBP.rno genesets for Rattus norvegicus

Description

Gene Ontology Biological Process (GOBP) genesets for *Rattus norvegicus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:10 2017.

Usage

```
geneset.GOBP.rno
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. *Homo sapiens*.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Rn.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOCC.dme`

geneset.GOCC.dme genesets for Drosophila melanogaster

Description

Gene Ontology Cellular Component (GOCC) genesets for *Drosophila melanogaster*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:38 2017.

Usage

```
geneset.GOCC.dme
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dm.eg.db_3.4.2 and GO.db_3.4.2

geneset.GOCC.dre

geneset.GOCC.dre genesets for Danio rerio

Description

Gene Ontology Cellular Component (GOCC) genesets for *Danio rerio*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:25:08 2017.

Usage

geneset.GOCC.dre

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dr.eg.db_3.4.2 and GO.db_3.4.2

geneset.GOCC.hsa

geneset.GOCC.hsa genesets for Homo sapiens

Description

Gene Ontology Cellular Component (GOCC) genesets for *Homo sapiens*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:22:22 2017.

Usage

`geneset.GOCC.hsa`

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. *Homo sapiens*.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Hs.eg.db_3.4.2` and `GO.db_3.4.2`

geneset.GOCC.mmu

*geneset.GOCC.mmu genesets for *Mus musculus**

Description

Gene Ontology Cellular Component (GOCC) genesets for *Mus musculus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:23:23 2017.

Usage

`geneset.GOCC.mmu`

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Mm.eg.db_3.4.2 and GO.db_3.4.2

geneset.GOCC.rno

geneset.GOCC.rno genesets for Rattus norvegicus

Description

Gene Ontology Cellular Component (GOCC) genesets for *Rattus norvegicus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:10 2017.

Usage

geneset.GOCC.rno

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Rn.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOMF.dme`

geneset.GOMF.dme genesets for Drosophila melanogaster

Description

Gene Ontology Molecular Function (GOMF) genesets for *Drosophila melanogaster*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:38 2017.

Usage

```
geneset.GOMF.dme
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. *Homo sapiens*.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Dm.eg.db_3.4.2` and `GO.db_3.4.2`

`geneset.GOMF.dre`

geneset.GOMF.dre genesets for Danio rerio

Description

Gene Ontology Molecular Function (GOMF) genesets for *Danio rerio*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:25:08 2017.

Usage

```
geneset.GOMF.dre
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dr.eg.db_3.4.2 and GO.db_3.4.2

geneset.GOMF.hsa

geneset.GOMF.hsa genesets for Homo sapiens

Description

Gene Ontology Molecular Function (GOMF) genesets for Homo sapiens. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:22:22 2017.

Usage

geneset.GOMF.hsa

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Hs.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOMF.mmu`*geneset.GOMF.mmu genesets for Mus musculus*

Description

Gene Ontology Molecular Function (GOMF) genesets for *Mus musculus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:23:23 2017.

Usage

```
geneset.GOMF.mmu
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. *Homo sapiens*.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Mm.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOMF.rno`*geneset.GOMF.rno genesets for Rattus norvegicus*

Description

Gene Ontology Molecular Function (GOMF) genesets for *Rattus norvegicus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:10 2017.

Usage

```
geneset.GOMF.rno
```

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Rn.eg.db_3.4.2 and GO.db_3.4.2

geneset.hallmark.hsa *geneset.hallmark.hsa genesets for Hallmark (MSigDB)*

Description

Hallmark (MSigDB) (hallmark) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:15 2017.

Usage

geneset.hallmark.hsa

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://software.broadinstitute.org/gsea/msigdb/collections.jsp#H>

geneset.immunologic.hsa

geneset.immunologic.hsa genesets for Immunologic Signatures (MSigDB)

Description

Immunologic Signatures (MSigDB) (immunologic) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:45 2017.

Usage

```
geneset.immunologic.hsa
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C7>

geneset.kegg_pathway.hsa

geneset.kegg_pathway.hsa genesets for KEGG Pathways

Description

KEGG Pathways (kegg_pathway) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:53 2017.

Usage

```
geneset.kegg_pathway.hsa
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://kegg.jp>

geneset.kegg_pathway.mmu

geneset.kegg_pathway.mmu

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.kegg_pathway.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.kegg_pathway.rno

geneset.kegg_pathway.rno

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.kegg_pathway.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.mesh.hsa

geneset.mesh.hsa

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.mesh.hsa)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.mesh.mmu` *geneset.mesh.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.mesh.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.mesh.rno` *geneset.mesh.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.mesh.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.metabolite.hsa
geneset.metabolite.hsa

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.metabolite.hsa)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.metabolite.mmu
geneset.metabolite.mmu

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.metabolite.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.metabolite.rno
geneset.metabolite.rno

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.metabolite.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.microrna.hsa *geneset.microrna.hsa genesets for MicroRNA Targets (MSigDB)*

Description

MicroRNA Targets (MSigDB) (microrna) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:56 2017.

Usage

```
geneset.microrna.hsa
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C3>

geneset.oncogenic.hsa *geneset.oncogenic.hsa genesets for Oncogenic Signatures (MSigDB)*

Description

Oncogenic Signatures (MSigDB) (oncogenic) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:47:23 2017.

Usage

```
geneset.oncogenic.hsa
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C6>

geneset.panther_pathway.hsa

geneset.panther_pathway.hsa

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.panther_pathway.hsa)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.panther_pathway.mmu
geneset.panther_pathway.mmu

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.panther_pathway.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.panther_pathway.rno
geneset.panther_pathway.rno

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.panther_pathway.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.pfam.hsa`*geneset.pfam.hsa genesets for Pfam*

Description

Pfam (pfam) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:47:28 2017.

Usage

`geneset.pfam.hsa`

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://pfam.xfam.org>

`geneset.pfam.mmu`*geneset.pfam.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

`data(geneset.pfam.mmu)`

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: `chipenrich.data`

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.pfam.rno	<i>geneset.pfam.rno</i>
------------------	-------------------------

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.pfam.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.protein_interaction_biogrid.hsa	<i>geneset.protein_interaction_biogrid.hsa genesets for BioGRID Protein Interactions</i>
---	--

Description

BioGRID Protein Interactions (protein_interaction_biogrid) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Tue Oct 24 16:05:53 2017.

Usage

```
geneset.protein_interaction_biogrid.hsa
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<https://thebiogrid.org>

geneset.reactome.dme *geneset.reactome.dme genesets for Drosophila melanogaster*

Description

Reactome genesets for *Drosophila melanogaster*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Mar 20 15:14:03 2017.

Usage

geneset.reactome.dme

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. Reactome.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. *Homo sapiens*.

set.gene An environment containing a list whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

geneset.reactome.dre *geneset.reactome.dre genesets for Danio rerio*

Description

Reactome genesets for *Danio rerio*. All genesets are required to have ≥ 10 Entrez IDs. Built on Tue Mar 28 13:03:21 2017.

Usage

geneset.reactome.dre

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. Reactome.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

geneset.reactome.hsa *geneset.reactome.hsa genesets for Homo sapiens*

Description

Reactome genesets for Homo sapiens. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Mar 20 15:13:45 2017.

Usage

`geneset.reactome.hsa`

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. Reactome.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

geneset.reactome.mmu *genesets for Mus musculus*

Description

Reactome genesets for *Mus musculus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Mar 20 15:13:55 2017.

Usage

`geneset.reactome.mmu`

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. Reactome.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. *Homo sapiens*.

set.gene An environment containing a list whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

geneset.reactome.rno *genesets for Rattus norvegicus*

Description

Reactome genesets for *Rattus norvegicus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Mar 20 15:13:59 2017.

Usage

`geneset.reactome.rno`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. Reactome.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

geneset.transcription_factors.hsa

geneset.transcription_factors.hsa genesets for Transcription Factor Targets (MSigDB)

Description

Transcription Factor Targets (MSigDB) (transcription_factors) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:47:33 2017.

Usage

`geneset.transcription_factors.hsa`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C3>

```
geneset.transcription_factors.mmu
geneset.transcription_factors.mmu
```

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.transcription_factors.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

```
geneset.transcription_factors.rno
geneset.transcription_factors.rno
```

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.transcription_factors.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

```
locusdef.danRer10.10kb
```

locusdef.danRer10.10kb locus definition

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.danRer10.10kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, danRer10.

organism A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: TxDb.DrERIO.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

```
locusdef.danRer10.10kb_outside
```

locusdef.danRer10.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.danRer10.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

```
locusdef.danRer10.10kb_outside_upstream
```

locusdef.danRer10.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.danRer10.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

```
locusdef.danRer10.1kb  locusdef.danRer10.1kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.danRer10.1kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:25 2018.

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

```
locusdef.danRer10.1kb_outside
locusdef.danRer10.1kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.danRer10.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:26 2018.

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

```
locusdef.danRer10.1kb_outside_upstream
```

locusdef.danRer10.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.danRer10.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:25 2018.

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

locusdef.danRer10.5kb *locusdef.danRer10.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.danRer10.5kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:26 2018.

Source

R packages: `TxDb.DrERIO.UCSC.danRer10.refGene_3.4.2` and `org.DR.eg.db_3.5.0`.

locusdef.danRer10.5kb_outside
locusdef.danRer10.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.danRer10.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

```
locusdef.danRer10.5kb_outside_upstream
```

locusdef.danRer10.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.danRer10.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:26 2018.

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

```
locusdef.danRer10.exon
```

locusdef.danRer10.exon locus definition

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.danRer10.exon
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:24 2018.

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

```
locusdef.danRer10.intron
```

locusdef.danRer10.intron locus definition

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.danRer10.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:25 2018.

Source

R packages: `TxDb.DrERIO.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

```
locusdef.danRer10.nearest_gene
```

locusdef.danRer10.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.danRer10.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:23 2018.

Source

R packages: `TxDb.DrERIO.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

```
locusdef.danRer10.nearest_tss
locusdef.danRer10.nearest_tss locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.danRer10.nearest_tss
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:22 2018.

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

```
locusdef.dm3.10kb      locusdef.dm3.10kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.dm3.10kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm3` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2` and `org.Dm.eg.db_3.5.0`.

`locusdef.dm3.10kb_outside`

locusdef.dm3.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef.dm3.10kb_outside`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm3` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:06 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

```
locusdef .dm3 .10kb_outside_upstream
```

locusdef.dm3.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef .dm3 .10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.1kb *locusdef.dm3.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.dm3.1kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, *Drosophila melanogaster*.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2` and `org.Dm.eg.db_3.5.0`.

locusdef.dm3.1kb_outside *locusdef.dm3.1kb_outside locus definition*

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm3.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.1kb_outside_upstream

locusdef.dm3.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.dm3.1kb_outside_upstream

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef . dm3 . 5kb *locusdef.dm3.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef . dm3 . 5kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef . dm3 . 5kb_outside *locusdef.dm3.5kb_outside locus definition*

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef . dm3 . 5kb_outside

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.5kb_outside_upstream

locusdef.dm3.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.dm3.5kb_outside_upstream

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.exon *locusdef.dm3.exon locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.dm3.exon
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:04 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.intron *locusdef.dm3.intron locus definition*

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.dm3.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:04 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.nearest_gene

locusdef.dm3.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

locusdef.dm3.nearest_gene

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:03 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.nearest_tss

locusdef.dm3.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

locusdef.dm3.nearest_tss

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm3` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:03 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

```
locusdef.dm6.10kb      locusdef.dm6.10kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.dm6.10kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, *Drosophila melanogaster*.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1` and `org.Dm.eg.db_3.5.0`.

```
locusdef.dm6.10kb_outside      locusdef.dm6.10kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm6.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

locusdef.dm6.10kb_outside_upstream

locusdef.dm6.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.dm6.10kb_outside_upstream

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

<code>locusdef .dm6 .1kb</code>	<i>locusdef.dm6.1kb locus definition</i>
---------------------------------	--

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

`locusdef .dm6 .1kb`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm6`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm6` genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:34 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

<code>locusdef .dm6 .1kb_outside</code>	<i>locusdef.dm6.1kb_outside locus definition</i>
---	--

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef .dm6 .1kb_outside`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

```
locusdef.dm6.1kb_outside_upstream
```

locusdef.dm6.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.dm6.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:34 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

locusdef . dm6 . 5kb

locusdef.dm6.5kb locus definition

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

`locusdef . dm6 . 5kb`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, *Drosophila melanogaster*.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

locusdef . dm6 . 5kb_outside

locusdef.dm6.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef . dm6 . 5kb_outside`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

```
locusdef.dm6.5kb_outside_upstream
```

locusdef.dm6.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.dm6.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

locusdef.dm6.exon	<i>locusdef.dm6.exon</i> <i>locus definition</i>
-------------------	--

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.dm6.exon
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:33 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

locusdef.dm6.intron	<i>locusdef.dm6.intron</i> <i>locus definition</i>
---------------------	--

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.dm6.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:34 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

```
locusdef.dm6.nearest_gene
```

locusdef.dm6.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.dm6.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:33 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

locusdef.dm6.nearest_tss

locusdef.dm6.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

locusdef.dm6.nearest_tss

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:33 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

```
locusdef.hg19.10kb      locusdef.hg19.10kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.hg19.10kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:58 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE

resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene

```
locusdef.hg19.10kb_outside
locusdef.hg19.10kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg19.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, *Homo sapiens*.

Details

Built on Fri Apr 13 09:45:59 2018.

Source

R packages: `TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2` and `org.Hs.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.Entrez`

locusdef.hg19.10kb_outside_upstream

locusdef.hg19.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.hg19.10kb_outside_upstream`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, *Homo sapiens*.

Details

Built on Fri Apr 13 09:45:58 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.Entrez

locusdef.hg19.1kb *locusdef.hg19.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

locusdef.hg19.1kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:55 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.Entrez

```
locusdef.hg19.1kb_outside
```

locusdef.hg19.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg19.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:56 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation.gtf and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezID.gtf

```
locusdef.hg19.1kb_outside_upstream
```

locusdef.hg19.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg19.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:56 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE

resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.Ent

locusdef.hg19.5kb *locusdef.hg19.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef.hg19.5kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:57 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE

resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.Ent

```
locusdef.hg19.5kb_outside
```

locusdef.hg19.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg19.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:58 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation.gtf and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezID.gtf

```
locusdef.hg19.5kb_outside_upstream
```

locusdef.hg19.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg19.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:57 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation.gtf and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntreZGeneID.txt

locusdef.hg19.exon *locusdef.hg19.exon locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.hg19.exon

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:53 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation.gtf and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntreZGeneID.txt

```
locusdef.hg19.intron  locusdef.hg19.intron locus definition
```

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.hg19.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:55 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation.gtf and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene.gff3

```
locusdef.hg19.nearest_gene
locusdef.hg19.nearest_gene locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.hg19.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `hg19`.

organism A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:45:51 2018.

Source

R packages: `TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2` and `org.Hs.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.Entrez`

`locusdef.hg19.nearest_tss`

locusdef.hg19.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

`locusdef.hg19.nearest_tss`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `hg19`.

organism A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:45:51 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene.gz

locusdef.hg38.10kb *locusdef.hg38.10kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

locusdef.hg38.10kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, *Homo sapiens*.

Details

Built on Fri Apr 13 09:49:42 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.10kb_outside
```

locusdef.hg38.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg38.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:43 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.10kb_outside_upstream
```

locusdef.hg38.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg38.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:43 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.hg38.1kb *locusdef.hg38.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

locusdef.hg38.1kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:39 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.1kb_outside
```

locusdef.hg38.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg38.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:40 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.1kb_outside_upstream
```

locusdef.hg38.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg38.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:39 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.hg38.5kb *locusdef.hg38.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef.hg38.5kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:41 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.5kb_outside
```

locusdef.hg38.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg38.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:42 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.5kb_outside_upstream
```

locusdef.hg38.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg38.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:41 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.hg38.exon *locusdef.hg38.exon locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.hg38.exon

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:37 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.intron  locusdef.hg38.intron locus definition
```

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.hg38.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:38 2018.

Source

R packages: `TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0` and `org.Hs.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.nearest_gene
locusdef.hg38.nearest_gene locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.hg38.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:49:34 2018.

Source

R packages: `TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0` and `org.Hs.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz`

`locusdef.hg38.nearest_tss`

locusdef.hg38.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

`locusdef.hg38.nearest_tss`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:49:34 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.mm10.10kb *locusdef.mm10.10kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

locusdef.mm10.10kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:51:40 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

```
locusdef.mm10.10kb_outside
```

locusdef.mm10.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm10.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:41 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

```
locusdef.mm10.10kb_outside_upstream
```

locusdef.mm10.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm10.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:40 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.1kb *locusdef.mm10.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

locusdef.mm10.1kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:37 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.1kb_outside

locusdef.mm10.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef.mm10.1kb_outside

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:38 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.1kb_outside_upstream

locusdef.mm10.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.mm10.1kb_outside_upstream

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:37 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.5kb *locusdef.mm10.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef.mm10.5kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:38 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.5kb_outside

locusdef.mm10.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef.mm10.5kb_outside

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:39 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.5kb_outside_upstream

locusdef.mm10.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.mm10.5kb_outside_upstream

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:39 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.exon *locusdef.mm10.exon locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.mm10.exon

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:35 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

```
locusdef.mm10.intron  locusdef.mm10.intron locus definition
```

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.mm10.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:51:36 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

```
locusdef.mm10.nearest_gene
locusdef.mm10.nearest_gene locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.mm10.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm10`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:51:33 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz`

`locusdef.mm10.nearest_tss`

locusdef.mm10.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

`locusdef.mm10.nearest_tss`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm10`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:51:33 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm9.10kb *locusdef.mm9.10kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

locusdef.mm9.10kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:44 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

```
locusdef.mm9.10kb_outside
  locusdef.mm9.10kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm9.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:44 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

```
locusdef.mm9.10kb_outside_upstream
  locusdef.mm9.10kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm9.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:44 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.1kb *locusdef.mm9.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

locusdef.mm9.1kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:41 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

```
locusdef.mm9.1kb_outside
```

locusdef.mm9.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm9.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:42 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

```
locusdef.mm9.1kb_outside_upstream
```

locusdef.mm9.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm9.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:41 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.5kb *locusdef.mm9.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef.mm9.5kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:42 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

```
locusdef.mm9.5kb_outside
```

locusdef.mm9.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm9.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:43 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

```
locusdef.mm9.5kb_outside_upstream
```

locusdef.mm9.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm9.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:43 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.exon *locusdef.mm9.exon* locus definition

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.mm9.exon

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:39 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

```
locusdef.mm9.intron      locusdef.mm9.intron locus definition
```

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.mm9.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:41 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

```
locusdef.mm9.nearest_gene
      locusdef.mm9.nearest_gene locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.mm9.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:37 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz`

`locusdef.mm9.nearest_tss`

locusdef.mm9.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

`locusdef.mm9.nearest_tss`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:37 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

`locusdef.rn4.10kb` *locusdef.rn4.10kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

`locusdef.rn4.10kb`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, rn4.

organism A character indicating the organism name. In this case, *Rattus norvegicus*.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn4.10kb_outside
```

locusdef.rn4.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn4.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:03 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn4.10kb_outside_upstream
```

locusdef.rn4.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn4.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

`locusdef.rn4.1kb` *locusdef.rn4.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

`locusdef.rn4.1kb`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn4.1kb_outside
```

locusdef.rn4.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn4.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn4.1kb_outside_upstream
```

locusdef.rn4.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn4.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

`locusdef.rn4.5kb` *locusdef.rn4.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

`locusdef.rn4.5kb`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn4.5kb_outside
```

locusdef.rn4.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn4.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn4.5kb_outside_upstream
```

locusdef.rn4.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn4.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn4.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

locusdef.rn4.exon *locusdef.rn4.exon* locus definition

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.rn4.exon

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn4.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:59 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn4.intron      locusdef.rn4.intron locus definition
```

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.rn4.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn4.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:00 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn4.nearest_gene
      locusdef.rn4.nearest_gene locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.rn4.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn4.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn4.nearest_tss
```

locusdef.rn4.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.rn4.nearest_tss
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn4.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

locusdef.rn5.10kb *locusdef.rn5.10kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

locusdef.rn5.10kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

locusdef.rn5.10kb_outside *locusdef.rn5.10kb_outside locus definition*

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef.rn5.10kb_outside

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:21 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn5.10kb_outside_upstream
```

locusdef.rn5.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn5.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:21 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn5.1kb      locusdef.rn5.1kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.rn5.1kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn5.1kb_outside      locusdef.rn5.1kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn5.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn5.1kb_outside_upstream
```

locusdef.rn5.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn5.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn5.5kb      locusdef.rn5.5kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.rn5.5kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn5.5kb_outside      locusdef.rn5.5kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn5.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn5.5kb_outside_upstream
```

locusdef.rn5.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn5.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

locusdef.rn5.exon *locusdef.rn5.exon locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.rn5.exon
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:17 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

locusdef.rn5.intron *locusdef.rn5.intron locus definition*

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.rn5.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn5.nearest_gene
```

locusdef.rn5.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.rn5.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:16 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn5.nearest_tss
```

locusdef.rn5.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.rn5.nearest_tss
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:16 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn6.10kb
```

locusdef.rn6.10kb locus definition

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.rn6.10kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn6`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

locusdef.rn6.10kb_outside

locusdef.rn6.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef.rn6.10kb_outside`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn6`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:40 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn6.10kb_outside_upstream
locusdef.rn6.10kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn6.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn6`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn6.1kb
locusdef.rn6.1kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.rn6.1kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

locusdef.rn6.1kb_outside

locusdef.rn6.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef.rn6.1kb_outside

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

```
locusdef.rn6.1kb_outside_upstream
  locusdef.rn6.1kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn6.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn6`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn6.5kb      locusdef.rn6.5kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.rn6.5kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

```
locusdef.rn6.5kb_outside
```

locusdef.rn6.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn6.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

```
locusdef.rn6.5kb_outside_upstream
  locusdef.rn6.5kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn6.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

```
locusdef.rn6.exon      locusdef.rn6.exon locus definition
```

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.rn6.exon
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn6`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:36 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

`locusdef.rn6.intron` *locusdef.rn6.intron locus definition*

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

`locusdef.rn6.intron`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn6`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:37 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn6.nearest_gene
```

locusdef.rn6.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.rn6.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:35 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

```
locusdef.rn6.nearest_tss
```

locusdef.rn6.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.rn6.nearest_tss
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:34 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

LocusDefinition-class *Class "LocusDefinition"*

Description

A storage class representing gene locus definitions and their corresponding metadata.

Objects from the Class

Objects can be created by calls of the form new("LocusDefinition"). These objects are used internally by the chipenrich package and users will not likely need to create these.

Slots

dframe: Object of class "data.frame". Each row represents a locus for a particular geneid.

granges: Object of class "GenomicRanges". Locus definitions stored as a GenomicRanges object.

genome.build: Object of class "character". Genome build these definitions were generated from.

organism: Object of class "character". Organism code.

Note

Not typically accessed by the user - this is used internally by the chipenrich package.

Author(s)

Ryan Welch <welchr@umich.edu>

Examples

```
# Show info about the class.
showClass("LocusDefinition");

# Example of what a locus definition object looks like.
data(locusdef.mm9.nearest_tss)
lapply(attributes(locusdef.mm9.nearest_tss), head)
```

mappa.hg19.10kb.100mer

mappa.hg19.10kb.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.100mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.10kb.24mer` *mappa.hg19.10kb.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.24mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.10kb.36mer` *mappa.hg19.10kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.10kb.40mer` *mappa.hg19.10kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.hg19.10kb.40mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.10kb.50mer` *mappa.hg19.10kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.50mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.10kb.75mer` *mappa.hg19.10kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.100mer` *mappa.hg19.1kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.24mer` *mappa.hg19.1kb.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.24mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.36mer` *mappa.hg19.1kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.40mer` *mappa.hg19.1kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.50mer` *mappa.hg19.1kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.50mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.75mer` *mappa.hg19.1kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.100mer` *mappa.hg19.5kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.hg19.5kb.100mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.24mer` *mappa.hg19.5kb.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.24mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.36mer` *mappa.hg19.5kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.40mer` *mappa.hg19.5kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.50mer` *mappa.hg19.5kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.50mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.75mer` *mappa.hg19.5kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.exon.100mer`

mappa.hg19.exon.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.exon.24mer` *mappa.hg19.exon.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.24mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.exon.36mer` *mappa.hg19.exon.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.exon.40mer` *mappa.hg19.exon.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.exon.50mer` *mappa.hg19.exon.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.50mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.exon.75mer` *mappa.hg19.exon.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.intron.100mer`
mappa.hg19.intron.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.intron.24mer`
mappa.hg19.intron.24mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.intron.36mer`
mappa.hg19.intron.36mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.intron.40mer`

mappa.hg19.intron.40mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.intron.50mer`
mappa.hg19.intron.50mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.intron.75mer`
mappa.hg19.intron.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_gene.100mer`

mappa.hg19.nearest_gene.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_gene.24mer`
mappa.hg19.nearest_gene.24mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_gene.36mer`
mappa.hg19.nearest_gene.36mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_gene.40mer`
mappa.hg19.nearest_gene.40mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_gene.50mer`
mappa.hg19.nearest_gene.50mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_gene.75mer`
mappa.hg19.nearest_gene.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_tss.100mer`

mappa.hg19.nearest_tss.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_tss.24mer`
mappa.hg19.nearest_tss.24mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_tss.36mer`
mappa.hg19.nearest_tss.36mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_tss.40mer`

mappa.hg19.nearest_tss.40mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.nearest_tss.50mer
mappa.hg19.nearest_tss.50mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.nearest_tss.75mer
mappa.hg19.nearest_tss.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.10kb.100mer` *mappa.mm9.10kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.mm9.10kb.100mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.10kb.36mer` *mappa.mm9.10kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.36mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.10kb.40mer` *mappa.mm9.10kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.40mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.10kb.50mer *mappa.mm9.10kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.50mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.10kb.75mer` *mappa.mm9.10kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.75mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.1kb.100mer` *mappa.mm9.1kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.1kb.36mer` *mappa.mm9.1kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.mm9.1kb.36mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.1kb.40mer` *mappa.mm9.1kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.40mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.1kb.50mer` *mappa.mm9.1kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.1kb.75mer` *mappa.mm9.1kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

`data(mappa.mm9.1kb.75mer)`

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.5kb.100mer` *mappa.mm9.5kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.100mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.5kb.36mer` *mappa.mm9.5kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.5kb.40mer` *mappa.mm9.5kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.5kb.50mer` *mappa.mm9.5kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.50mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.5kb.75mer` *mappa.mm9.5kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs
mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.exon.100mer mappa.mm9.exon.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.100mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs
mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.exon.36mer` *mappa.mm9.exon.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.36mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.exon.40mer` *mappa.mm9.exon.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.40mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs
mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.exon.50mer *mappa.mm9.exon.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs
mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.exon.75mer` *mappa.mm9.exon.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.intron.100mer` *mappa.mm9.intron.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.intron.36mer`

mappa.mm9.intron.36mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.intron.40mer
mappa.mm9.intron.40mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.intron.50mer
mappa.mm9.intron.50mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.intron.75mer`

mappa.mm9.intron.75mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.nearest_gene.100mer
mappa.mm9.nearest_gene.100mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.nearest_gene.36mer
mappa.mm9.nearest_gene.36mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_gene.40mer`

mappa.mm9.nearest_gene.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.nearest_gene.50mer
mappa.mm9.nearest_gene.50mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.nearest_gene.75mer
mappa.mm9.nearest_gene.75mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_tss.100mer`
mappa.mm9.nearest_tss.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.nearest_tss.36mer
mappa.mm9.nearest_tss.36mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.36mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.nearest_tss.40mer
mappa.mm9.nearest_tss.40mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_tss.50mer`

mappa.mm9.nearest_tss.50mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.nearest_tss.75mer
mappa.mm9.nearest_tss.75mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.75mer)
```

Format

A data frame containing:

```
geneid  Entrez Gene IDs
mappa  Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
peaks_E2F4
```

ChIP-seq Peaks for the E2F4 Transcription Factor

Description

A dataset containing the binding locations (peaks) of the transcription factor E2F4 called from a ChIP-seq experiment

Usage

```
peaks_E2F4
```

Format

A data frame containing 16,245 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

Source

The data and information regarding the experiment can be found in the following publication:

Lee, B. K., A. A. Bhinge, et al. (2011). "Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis." *Nucleic Acids Res* 39(9): 3558-3573.

Examples

```
# Load E2F4 peak data.  
data(peaks_E2F4)  
  
# Print the first 10 peaks in the dataset.  
print(head(peaks_E2F4))
```

peaks_H3K4me3_GM12878 *ChIP-seq Peaks for the Histone Modification H3K4me3 in GM12878*

Description

A dataset containing the binding locations (peaks) of the histone modification H3K4me3 called from a ChIP-seq experiment in the GM12878 cell line

Usage

```
peaks_H3K4me3_GM12878
```

Format

A data frame containing 57,476 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

Source

The data and information regarding the experiment can be found at the following ENCODE URL:

<http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeBroadHistone/wgEncodeBroadHistoneGm12878>

Examples

```
# Load H3K4me3 in GM12878 peak data.  
data(peaks_H3K4me3_GM12878)  
  
# Print the first 10 peaks in the dataset.  
print(head(peaks_H3K4me3_GM12878))
```

spline.log_dtss.90ENCODE
DTSS Spline adjustment

Description

A mgcv::gam object on a combined data of 90 ENCODE ChIP-seq datasets that modeled the relationship between a gene's locus length the distance from a peak to the gene's transcription start site, using a cubic spline. This is used to adjust for the proximity to TSSes test.

Usage

```
spline.log_dtss.90ENCODE
```

Format

An object of class `gam` (inherits from `glm`, `lm`) of length 46.

tss.danRer10 *tss.danRer10 TSS locations*

Description

A GRanges with all the TSSs for danRer10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.danRer10
```

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

<code>tss.dm3</code>	<i>tss.dm3 TSS locations</i>
----------------------	------------------------------

Description

A GRanges with all the TSSs for dm3. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.dm3`

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2` and `org.Dm.eg.db_3.5.0`.

<code>tss.dm6</code>	<i>tss.dm6 TSS locations</i>
----------------------	------------------------------

Description

A GRanges with all the TSSs for dm6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.dm6`

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1` and `org.Dm.eg.db_3.5.0`.

tss.hg19	<i>tss.hg19 TSS locations</i>
----------	-------------------------------

Description

A GRanges with all the TSSs for hg19. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.hg19
```

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene.gz

tss.hg38	<i>tss.hg38 TSS locations</i>
----------	-------------------------------

Description

A GRanges with all the TSSs for hg38. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.hg38
```

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

tss.mm10	<i>tss.mm10 TSS locations</i>
----------	-------------------------------

Description

A GRanges with all the TSSs for mm10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.mm10`

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

tss.mm9	<i>tss.mm9 TSS locations</i>
---------	------------------------------

Description

A GRanges with all the TSSs for mm9. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.mm9`

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

tss.rn4*tss.rn4 TSS locations*

Description

A GRanges with all the TSSs for rn4. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.rn4
```

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

tss.rn5*tss.rn5 TSS locations*

Description

A GRanges with all the TSSs for rn5. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.rn5
```

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

tss.rn6*tss.rn6 TSS locations*

Description

A GRanges with all the TSSs for rn6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.rn6
```

Format

A GRanges object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

Index

- * **classes**
 - GeneSet-class, 8
 - LocusDefinition-class, 129
- * **datasets**
 - enhancer.dnase_thurman.0, 7
 - gene.enh.desc, 8
 - geneset.biocarta_pathway.hsa, 9
 - geneset.biocarta_pathway.mmu, 10
 - geneset.biocarta_pathway.rno, 10
 - geneset.ctd.hsa, 11
 - geneset.ctd.mmu, 11
 - geneset.cytoband.hsa, 12
 - geneset.drug_bank.hsa, 13
 - geneset.drug_bank.mmu, 13
 - geneset.drug_bank.rno, 14
 - geneset.GOBP.dme, 14
 - geneset.GOBP.dre, 15
 - geneset.GOBP.hsa, 15
 - geneset.GOBP.mmu, 16
 - geneset.GOBP.rno, 17
 - geneset.GOCC.dme, 17
 - geneset.GOCC.dre, 18
 - geneset.GOCC.hsa, 19
 - geneset.GOCC.mmu, 19
 - geneset.GOCC.rno, 20
 - geneset.GOMF.dme, 21
 - geneset.GOMF.dre, 21
 - geneset.GOMF.hsa, 22
 - geneset.GOMF.mmu, 23
 - geneset.GOMF.rno, 23
 - geneset.hallmark.hsa, 24
 - geneset.immunologic.hsa, 25
 - geneset.kegg_pathway.hsa, 25
 - geneset.kegg_pathway.mmu, 26
 - geneset.kegg_pathway.rno, 27
 - geneset.mesh.hsa, 27
 - geneset.mesh.mmu, 28
 - geneset.mesh.rno, 28
 - geneset.metabolite.hsa, 29
 - geneset.metabolite.mmu, 29
 - geneset.metabolite.rno, 30
 - geneset.microrna.hsa, 30
 - geneset.oncogenic.hsa, 31
 - geneset.panther_pathway.hsa, 31
 - geneset.panther_pathway.mmu, 32
 - geneset.panther_pathway.rno, 32
 - geneset.pfam.hsa, 33
 - geneset.pfam.mmu, 33
 - geneset.pfam.rno, 34
 - geneset.protein_interaction_biogrid.hsa, 34
 - geneset.reactome.dme, 35
 - geneset.reactome.dre, 35
 - geneset.reactome.hsa, 36
 - geneset.reactome.mmu, 37
 - geneset.reactome.rno, 37
 - geneset.transcription_factors.hsa, 38
 - geneset.transcription_factors.mmu, 39
 - geneset.transcription_factors.rno, 39
 - locusdef.danRer10.10kb, 40
 - locusdef.danRer10.10kb_outside, 40
 - locusdef.danRer10.10kb_outside_upstream, 41
 - locusdef.danRer10.1kb, 42
 - locusdef.danRer10.1kb_outside, 42
 - locusdef.danRer10.1kb_outside_upstream, 43
 - locusdef.danRer10.5kb, 44
 - locusdef.danRer10.5kb_outside, 44
 - locusdef.danRer10.5kb_outside_upstream, 45
 - locusdef.danRer10.exon, 46
 - locusdef.danRer10.intron, 46
 - locusdef.danRer10.nearest_gene, 47
 - locusdef.danRer10.nearest_tss, 48
 - locusdef.dm3.10kb, 48
 - locusdef.dm3.10kb_outside, 49
 - locusdef.dm3.10kb_outside_upstream, 50
 - locusdef.dm3.1kb, 51
 - locusdef.dm3.1kb_outside, 51
 - locusdef.dm3.1kb_outside_upstream, 52

- locusdef.dm3.5kb, 53
- locusdef.dm3.5kb_outside, 53
- locusdef.dm3.5kb_outside_upstream, 54
- locusdef.dm3.exon, 55
- locusdef.dm3.intron, 55
- locusdef.dm3.nearest_gene, 56
- locusdef.dm3.nearest_tss, 57
- locusdef.dm6.10kb, 58
- locusdef.dm6.10kb_outside, 58
- locusdef.dm6.10kb_outside_upstream, 59
- locusdef.dm6.1kb, 60
- locusdef.dm6.1kb_outside, 60
- locusdef.dm6.1kb_outside_upstream, 61
- locusdef.dm6.5kb, 62
- locusdef.dm6.5kb_outside, 62
- locusdef.dm6.5kb_outside_upstream, 63
- locusdef.dm6.exon, 64
- locusdef.dm6.intron, 64
- locusdef.dm6.nearest_gene, 65
- locusdef.dm6.nearest_tss, 66
- locusdef.hg19.10kb, 67
- locusdef.hg19.10kb_outside, 67
- locusdef.hg19.10kb_outside_upstream, 68
- locusdef.hg19.1kb, 69
- locusdef.hg19.1kb_outside, 70
- locusdef.hg19.1kb_outside_upstream, 70
- locusdef.hg19.5kb, 71
- locusdef.hg19.5kb_outside, 72
- locusdef.hg19.5kb_outside_upstream, 72
- locusdef.hg19.exon, 73
- locusdef.hg19.intron, 74
- locusdef.hg19.nearest_gene, 74
- locusdef.hg19.nearest_tss, 75
- locusdef.hg38.10kb, 76
- locusdef.hg38.10kb_outside, 77
- locusdef.hg38.10kb_outside_upstream, 77
- locusdef.hg38.1kb, 78
- locusdef.hg38.1kb_outside, 79
- locusdef.hg38.1kb_outside_upstream, 79
- locusdef.hg38.5kb, 80
- locusdef.hg38.5kb_outside, 81
- locusdef.hg38.5kb_outside_upstream, 81
- locusdef.hg38.exon, 82
- locusdef.hg38.intron, 83
- locusdef.hg38.nearest_gene, 83
- locusdef.hg38.nearest_tss, 84
- locusdef.mm10.10kb, 85
- locusdef.mm10.10kb_outside, 86
- locusdef.mm10.10kb_outside_upstream, 86
- locusdef.mm10.1kb, 87
- locusdef.mm10.1kb_outside, 88
- locusdef.mm10.1kb_outside_upstream, 88
- locusdef.mm10.5kb, 89
- locusdef.mm10.5kb_outside, 90
- locusdef.mm10.5kb_outside_upstream, 90
- locusdef.mm10.exon, 91
- locusdef.mm10.intron, 92
- locusdef.mm10.nearest_gene, 92
- locusdef.mm10.nearest_tss, 93
- locusdef.mm9.10kb, 94
- locusdef.mm9.10kb_outside, 95
- locusdef.mm9.10kb_outside_upstream, 95
- locusdef.mm9.1kb, 96
- locusdef.mm9.1kb_outside, 97
- locusdef.mm9.1kb_outside_upstream, 97
- locusdef.mm9.5kb, 98
- locusdef.mm9.5kb_outside, 99
- locusdef.mm9.5kb_outside_upstream, 99
- locusdef.mm9.exon, 100
- locusdef.mm9.intron, 101
- locusdef.mm9.nearest_gene, 101
- locusdef.mm9.nearest_tss, 102
- locusdef.rn4.10kb, 103
- locusdef.rn4.10kb_outside, 104
- locusdef.rn4.10kb_outside_upstream, 104
- locusdef.rn4.1kb, 105
- locusdef.rn4.1kb_outside, 106
- locusdef.rn4.1kb_outside_upstream, 106
- locusdef.rn4.5kb, 107
- locusdef.rn4.5kb_outside, 108
- locusdef.rn4.5kb_outside_upstream, 108
- locusdef.rn4.exon, 109
- locusdef.rn4.intron, 110
- locusdef.rn4.nearest_gene, 110
- locusdef.rn4.nearest_tss, 111

locusdef.rn5.10kb, 112
locusdef.rn5.10kb_outside, 112
locusdef.rn5.10kb_outside_upstream,
113
locusdef.rn5.1kb, 114
locusdef.rn5.1kb_outside, 114
locusdef.rn5.1kb_outside_upstream,
115
locusdef.rn5.5kb, 116
locusdef.rn5.5kb_outside, 116
locusdef.rn5.5kb_outside_upstream,
117
locusdef.rn5.exon, 118
locusdef.rn5.intron, 118
locusdef.rn5.nearest_gene, 119
locusdef.rn5.nearest_tss, 120
locusdef.rn6.10kb, 120
locusdef.rn6.10kb_outside, 121
locusdef.rn6.10kb_outside_upstream,
122
locusdef.rn6.1kb, 122
locusdef.rn6.1kb_outside, 123
locusdef.rn6.1kb_outside_upstream,
124
locusdef.rn6.5kb, 124
locusdef.rn6.5kb_outside, 125
locusdef.rn6.5kb_outside_upstream,
126
locusdef.rn6.exon, 126
locusdef.rn6.intron, 127
locusdef.rn6.nearest_gene, 128
locusdef.rn6.nearest_tss, 128
mappa.hg19.10kb.100mer, 130
mappa.hg19.10kb.24mer, 131
mappa.hg19.10kb.36mer, 131
mappa.hg19.10kb.40mer, 132
mappa.hg19.10kb.50mer, 133
mappa.hg19.10kb.75mer, 133
mappa.hg19.1kb.100mer, 134
mappa.hg19.1kb.24mer, 135
mappa.hg19.1kb.36mer, 135
mappa.hg19.1kb.40mer, 136
mappa.hg19.1kb.50mer, 137
mappa.hg19.1kb.75mer, 137
mappa.hg19.5kb.100mer, 138
mappa.hg19.5kb.24mer, 139
mappa.hg19.5kb.36mer, 139
mappa.hg19.5kb.40mer, 140
mappa.hg19.5kb.50mer, 141
mappa.hg19.5kb.75mer, 141
mappa.hg19.exon.100mer, 142
mappa.hg19.exon.24mer, 143
mappa.hg19.exon.36mer, 143
mappa.hg19.exon.40mer, 144
mappa.hg19.exon.50mer, 145
mappa.hg19.exon.75mer, 145
mappa.hg19.intron.100mer, 146
mappa.hg19.intron.24mer, 147
mappa.hg19.intron.36mer, 147
mappa.hg19.intron.40mer, 148
mappa.hg19.intron.50mer, 149
mappa.hg19.intron.75mer, 149
mappa.hg19.nearest_gene.100mer,
150
mappa.hg19.nearest_gene.24mer, 151
mappa.hg19.nearest_gene.36mer, 151
mappa.hg19.nearest_gene.40mer, 152
mappa.hg19.nearest_gene.50mer, 153
mappa.hg19.nearest_gene.75mer, 153
mappa.hg19.nearest_tss.100mer, 154
mappa.hg19.nearest_tss.24mer, 155
mappa.hg19.nearest_tss.36mer, 155
mappa.hg19.nearest_tss.40mer, 156
mappa.hg19.nearest_tss.50mer, 157
mappa.hg19.nearest_tss.75mer, 157
mappa.mm9.10kb.100mer, 158
mappa.mm9.10kb.36mer, 159
mappa.mm9.10kb.40mer, 159
mappa.mm9.10kb.50mer, 160
mappa.mm9.10kb.75mer, 161
mappa.mm9.1kb.100mer, 161
mappa.mm9.1kb.36mer, 162
mappa.mm9.1kb.40mer, 163
mappa.mm9.1kb.50mer, 163
mappa.mm9.1kb.75mer, 164
mappa.mm9.5kb.100mer, 165
mappa.mm9.5kb.36mer, 165
mappa.mm9.5kb.40mer, 166
mappa.mm9.5kb.50mer, 167
mappa.mm9.5kb.75mer, 167
mappa.mm9.exon.100mer, 168
mappa.mm9.exon.36mer, 169
mappa.mm9.exon.40mer, 169
mappa.mm9.exon.50mer, 170
mappa.mm9.exon.75mer, 171
mappa.mm9.intron.100mer, 171
mappa.mm9.intron.36mer, 172
mappa.mm9.intron.40mer, 173
mappa.mm9.intron.50mer, 173
mappa.mm9.intron.75mer, 174
mappa.mm9.nearest_gene.100mer, 175
mappa.mm9.nearest_gene.36mer, 175
mappa.mm9.nearest_gene.40mer, 176
mappa.mm9.nearest_gene.50mer, 177

mappa.mm9.nearest_gene.75mer, 177
 mappa.mm9.nearest_tss.100mer, 178
 mappa.mm9.nearest_tss.36mer, 179
 mappa.mm9.nearest_tss.40mer, 179
 mappa.mm9.nearest_tss.50mer, 180
 mappa.mm9.nearest_tss.75mer, 181
 peaks_E2F4, 181
 peaks_H3K4me3_GM12878, 182
 spline.log_dtss.90ENCODE, 183
 tss.danRer10, 183
 tss.dm3, 184
 tss.dm6, 184
 tss.hg19, 185
 tss.hg38, 185
 tss.mm10, 186
 tss.mm9, 186
 tss.rn4, 187
 tss.rn5, 187
 tss.rn6, 188

chipenrich.data, 7, 10, 12–14, 26–34, 39, 130–181
 chipenrich.data-package
 (chipenrich.data), 7

enhancer.dnase_thurman.0, 7

gene.enh.desc, 8
 GeneSet-class, 8
 geneset.biocarta_pathway.hsa, 9
 geneset.biocarta_pathway.mmu, 10
 geneset.biocarta_pathway.rno, 10
 geneset.ctd.hsa, 11
 geneset.ctd.mmu, 11
 geneset.cytoband.hsa, 12
 geneset.drug_bank.hsa, 13
 geneset.drug_bank.mmu, 13
 geneset.drug_bank.rno, 14
 geneset.GOBP.dme, 14
 geneset.GOBP.dre, 15
 geneset.GOBP.hsa, 15
 geneset.GOBP.mmu, 16
 geneset.GOBP.rno, 17
 geneset.GOCC.dme, 17
 geneset.GOCC.dre, 18
 geneset.GOCC.hsa, 19
 geneset.GOCC.mmu, 19
 geneset.GOCC.rno, 20
 geneset.GOMF.dme, 21
 geneset.GOMF.dre, 21
 geneset.GOMF.hsa, 22
 geneset.GOMF.mmu, 23
 geneset.GOMF.rno, 23

geneset.hallmark.hsa, 24
 geneset.immunologic.hsa, 25
 geneset.kegg_pathway.hsa, 25
 geneset.kegg_pathway.mmu, 26
 geneset.kegg_pathway.rno, 27
 geneset.mesh.hsa, 27
 geneset.mesh.mmu, 28
 geneset.mesh.rno, 28
 geneset.metabolite.hsa, 29
 geneset.metabolite.mmu, 29
 geneset.metabolite.rno, 30
 geneset.microrna.hsa, 30
 geneset.oncogenic.hsa, 31
 geneset.panther_pathway.hsa, 31
 geneset.panther_pathway.mmu, 32
 geneset.panther_pathway.rno, 32
 geneset.pfam.hsa, 33
 geneset.pfam.mmu, 33
 geneset.pfam.rno, 34
 geneset.protein_interaction_biogrid.hsa, 34
 geneset.reactome.dme, 35
 geneset.reactome.dre, 35
 geneset.reactome.hsa, 36
 geneset.reactome.mmu, 37
 geneset.reactome.rno, 37
 geneset.transcription_factors.hsa, 38
 geneset.transcription_factors.mmu, 39
 geneset.transcription_factors.rno, 39

locusdef.danRer10.10kb, 40
 locusdef.danRer10.10kb_outside, 40
 locusdef.danRer10.10kb_outside_upstream, 41
 locusdef.danRer10.1kb, 42
 locusdef.danRer10.1kb_outside, 42
 locusdef.danRer10.1kb_outside_upstream, 43
 locusdef.danRer10.5kb, 44
 locusdef.danRer10.5kb_outside, 44
 locusdef.danRer10.5kb_outside_upstream, 45
 locusdef.danRer10.exon, 46
 locusdef.danRer10.intron, 46
 locusdef.danRer10.nearest_gene, 47
 locusdef.danRer10.nearest_tss, 48
 locusdef.dm3.10kb, 48
 locusdef.dm3.10kb_outside, 49
 locusdef.dm3.10kb_outside_upstream, 50
 locusdef.dm3.1kb, 51
 locusdef.dm3.1kb_outside, 51
 locusdef.dm3.1kb_outside_upstream, 52
 locusdef.dm3.5kb, 53

locusdef.dm3.5kb_outside, 53
locusdef.dm3.5kb_outside_upstream, 54
locusdef.dm3.exon, 55
locusdef.dm3.intron, 55
locusdef.dm3.nearest_gene, 56
locusdef.dm3.nearest_tss, 57
locusdef.dm6.10kb, 58
locusdef.dm6.10kb_outside, 58
locusdef.dm6.10kb_outside_upstream, 59
locusdef.dm6.1kb, 60
locusdef.dm6.1kb_outside, 60
locusdef.dm6.1kb_outside_upstream, 61
locusdef.dm6.5kb, 62
locusdef.dm6.5kb_outside, 62
locusdef.dm6.5kb_outside_upstream, 63
locusdef.dm6.exon, 64
locusdef.dm6.intron, 64
locusdef.dm6.nearest_gene, 65
locusdef.dm6.nearest_tss, 66
locusdef.hg19.10kb, 67
locusdef.hg19.10kb_outside, 67
locusdef.hg19.10kb_outside_upstream,
 68
locusdef.hg19.1kb, 69
locusdef.hg19.1kb_outside, 70
locusdef.hg19.1kb_outside_upstream, 70
locusdef.hg19.5kb, 71
locusdef.hg19.5kb_outside, 72
locusdef.hg19.5kb_outside_upstream, 72
locusdef.hg19.exon, 73
locusdef.hg19.intron, 74
locusdef.hg19.nearest_gene, 74
locusdef.hg19.nearest_tss, 75
locusdef.hg38.10kb, 76
locusdef.hg38.10kb_outside, 77
locusdef.hg38.10kb_outside_upstream,
 77
locusdef.hg38.1kb, 78
locusdef.hg38.1kb_outside, 79
locusdef.hg38.1kb_outside_upstream, 79
locusdef.hg38.5kb, 80
locusdef.hg38.5kb_outside, 81
locusdef.hg38.5kb_outside_upstream, 81
locusdef.hg38.exon, 82
locusdef.hg38.intron, 83
locusdef.hg38.nearest_gene, 83
locusdef.hg38.nearest_tss, 84
locusdef.mm10.10kb, 85
locusdef.mm10.10kb_outside, 86
locusdef.mm10.10kb_outside_upstream,
 86
locusdef.mm10.1kb, 87
locusdef.mm10.1kb_outside, 88
locusdef.mm10.1kb_outside_upstream, 88
locusdef.mm10.5kb, 89
locusdef.mm10.5kb_outside, 90
locusdef.mm10.5kb_outside_upstream, 90
locusdef.mm10.exon, 91
locusdef.mm10.intron, 92
locusdef.mm10.nearest_gene, 92
locusdef.mm10.nearest_tss, 93
locusdef.mm9.10kb, 94
locusdef.mm9.10kb_outside, 95
locusdef.mm9.10kb_outside_upstream, 95
locusdef.mm9.1kb, 96
locusdef.mm9.1kb_outside, 97
locusdef.mm9.1kb_outside_upstream, 97
locusdef.mm9.5kb, 98
locusdef.mm9.5kb_outside, 99
locusdef.mm9.5kb_outside_upstream, 99
locusdef.mm9.exon, 100
locusdef.mm9.intron, 101
locusdef.mm9.nearest_gene, 101
locusdef.mm9.nearest_tss, 102
locusdef.rn4.10kb, 103
locusdef.rn4.10kb_outside, 104
locusdef.rn4.10kb_outside_upstream,
 104
locusdef.rn4.1kb, 105
locusdef.rn4.1kb_outside, 106
locusdef.rn4.1kb_outside_upstream, 106
locusdef.rn4.5kb, 107
locusdef.rn4.5kb_outside, 108
locusdef.rn4.5kb_outside_upstream, 108
locusdef.rn4.exon, 109
locusdef.rn4.intron, 110
locusdef.rn4.nearest_gene, 110
locusdef.rn4.nearest_tss, 111
locusdef.rn5.10kb, 112
locusdef.rn5.10kb_outside, 112
locusdef.rn5.10kb_outside_upstream,
 113
locusdef.rn5.1kb, 114
locusdef.rn5.1kb_outside, 114
locusdef.rn5.1kb_outside_upstream, 115
locusdef.rn5.5kb, 116
locusdef.rn5.5kb_outside, 116
locusdef.rn5.5kb_outside_upstream, 117
locusdef.rn5.exon, 118
locusdef.rn5.intron, 118
locusdef.rn5.nearest_gene, 119
locusdef.rn5.nearest_tss, 120
locusdef.rn6.10kb, 120
locusdef.rn6.10kb_outside, 121

locusdef.rn6.10kb_outside_upstream, 122
 locusdef.rn6.1kb, 122
 locusdef.rn6.1kb_outside, 123
 locusdef.rn6.1kb_outside_upstream, 124
 locusdef.rn6.5kb, 124
 locusdef.rn6.5kb_outside, 125
 locusdef.rn6.5kb_outside_upstream, 126
 locusdef.rn6.exon, 126
 locusdef.rn6.intron, 127
 locusdef.rn6.nearest_gene, 128
 locusdef.rn6.nearest_tss, 128
 LocusDefinition-class, 129

mappa.hg19.10kb.100mer, 130
 mappa.hg19.10kb.24mer, 131
 mappa.hg19.10kb.36mer, 131
 mappa.hg19.10kb.40mer, 132
 mappa.hg19.10kb.50mer, 133
 mappa.hg19.10kb.75mer, 133
 mappa.hg19.1kb.100mer, 134
 mappa.hg19.1kb.24mer, 135
 mappa.hg19.1kb.36mer, 135
 mappa.hg19.1kb.40mer, 136
 mappa.hg19.1kb.50mer, 137
 mappa.hg19.1kb.75mer, 137
 mappa.hg19.5kb.100mer, 138
 mappa.hg19.5kb.24mer, 139
 mappa.hg19.5kb.36mer, 139
 mappa.hg19.5kb.40mer, 140
 mappa.hg19.5kb.50mer, 141
 mappa.hg19.5kb.75mer, 141
 mappa.hg19.exon.100mer, 142
 mappa.hg19.exon.24mer, 143
 mappa.hg19.exon.36mer, 143
 mappa.hg19.exon.40mer, 144
 mappa.hg19.exon.50mer, 145
 mappa.hg19.exon.75mer, 145
 mappa.hg19.intron.100mer, 146
 mappa.hg19.intron.24mer, 147
 mappa.hg19.intron.36mer, 147
 mappa.hg19.intron.40mer, 148
 mappa.hg19.intron.50mer, 149
 mappa.hg19.intron.75mer, 149
 mappa.hg19.nearest_gene.100mer, 150
 mappa.hg19.nearest_gene.24mer, 151
 mappa.hg19.nearest_gene.36mer, 151
 mappa.hg19.nearest_gene.40mer, 152
 mappa.hg19.nearest_gene.50mer, 153
 mappa.hg19.nearest_gene.75mer, 153
 mappa.hg19.nearest_tss.100mer, 154
 mappa.hg19.nearest_tss.24mer, 155
 mappa.hg19.nearest_tss.36mer, 155

mappa.hg19.nearest_tss.40mer, 156
 mappa.hg19.nearest_tss.50mer, 157
 mappa.hg19.nearest_tss.75mer, 157
 mappa.mm9.10kb.100mer, 158
 mappa.mm9.10kb.36mer, 159
 mappa.mm9.10kb.40mer, 159
 mappa.mm9.10kb.50mer, 160
 mappa.mm9.10kb.75mer, 161
 mappa.mm9.1kb.100mer, 161
 mappa.mm9.1kb.36mer, 162
 mappa.mm9.1kb.40mer, 163
 mappa.mm9.1kb.50mer, 163
 mappa.mm9.1kb.75mer, 164
 mappa.mm9.5kb.100mer, 165
 mappa.mm9.5kb.36mer, 165
 mappa.mm9.5kb.40mer, 166
 mappa.mm9.5kb.50mer, 167
 mappa.mm9.5kb.75mer, 167
 mappa.mm9.exon.100mer, 168
 mappa.mm9.exon.36mer, 169
 mappa.mm9.exon.40mer, 169
 mappa.mm9.exon.50mer, 170
 mappa.mm9.exon.75mer, 171
 mappa.mm9.intron.100mer, 171
 mappa.mm9.intron.36mer, 172
 mappa.mm9.intron.40mer, 173
 mappa.mm9.intron.50mer, 173
 mappa.mm9.intron.75mer, 174
 mappa.mm9.nearest_gene.100mer, 175
 mappa.mm9.nearest_gene.36mer, 175
 mappa.mm9.nearest_gene.40mer, 176
 mappa.mm9.nearest_gene.50mer, 177
 mappa.mm9.nearest_gene.75mer, 177
 mappa.mm9.nearest_tss.100mer, 178
 mappa.mm9.nearest_tss.36mer, 179
 mappa.mm9.nearest_tss.40mer, 179
 mappa.mm9.nearest_tss.50mer, 180
 mappa.mm9.nearest_tss.75mer, 181

peaks_E2F4, 181
 peaks_H3K4me3_GM12878, 182

spline.log_dtss.90ENCODE, 183

tss.danRer10, 183
 tss.dm3, 184
 tss.dm6, 184
 tss.hg19, 185
 tss.hg38, 185
 tss.mm10, 186
 tss.mm9, 186
 tss.rn4, 187
 tss.rn5, 187
 tss.rn6, 188