

Package ‘mgi.report.reader’

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Title Read Mouse Genome Informatics Reports

Version 0.0.1

Description Provides readers for easy and consistent importing of Mouse Genome Informatics (MGI) report files:
<<https://www.informatics.jax.org/downloads/reports/index.html>>. These data are provided by Baldarelli RM, Smith CL, Ringwald M, Richardson JE, Bult CJ, Mouse Genome Informatics Group. (2024) <[doi:10.1093/genetics/iyae031](https://doi.org/10.1093/genetics/iyae031)>.

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Encoding UTF-8

RoxygenNote 7.3.1

Depends R (>= 2.10)

LazyData true

Imports data.table, dplyr, rlang, stringr, tibble, vroom

URL <https://www.pattern.institute/mgi.report.reader/>,
<https://github.com/patterninstitute/mgi.report.reader/>

BugReports <https://github.com/patterninstitute/mgi.report.reader/issues>

Config/Needs/website rmarkdown

NeedsCompilation no

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chromosomes	<i>Mouse chromosomes</i>
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Description

`chromosomes()` returns mouse chromosome names.

Usage

```
chromosomes(autosomal = TRUE, sexual = TRUE, mitochondrial = TRUE)
```

Arguments

<code>autosomal</code>	Whether to include the autosomal chromosomes (1 thru 19).
<code>sexual</code>	Whether to include the sexual chromosomes (X and Y).
<code>mitochondrial</code>	Whether to include the mitochondrial chromosome (MT).

Value

A character vector of mouse chromosome names, or a subset thereof, or an empty character vector.

Examples

```
# All chromosomes.
chromosomes()

# Autosomal chromosomes.
chromosomes(autosomal = TRUE, sexual = FALSE, mitochondrial = FALSE)
```

feature_types	<i>Genome Feature Type Definitions</i>
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Description

A dataset containing different types of gene and genome features along with their Sequence Ontology (SO) identifiers and definitions.

Usage

```
feature_types
```

Format

A [tibble](#) with 71 rows and 3 variables:

feature_type Character. The type of gene or genome feature.

so_id Character. The Sequence Ontology identifier associated with the feature type.

definition Character. The definition of the feature type.

Source

The table in https://www.informatics.jax.org/userhelp/GENE_feature_types_help.shtml and a few other terms found in MGI reports.

Examples

```
print(feature_types, n = Inf)
```

read_report	<i>Read an MGI report</i>
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Description

`read_report()` reads in an MGI report.

Usage

```
read_report(  
  report_file,  
  report_type = c("MRK_List1", "MRK_List2", "MGI_MRK_Coord", "MGI_Gene_Model_Coord",  
    "MGI_GTGUP", "MRK_Sequence", "MRK_SwissProt_TrEMBL", "MRK_SwissProt", "MRK_GeneTrap",  
    "MRK_ENSEMBL", "MGI_BioTypeConflict", "PRB_PrimerSeq", "MGI_InterProDomains"),  
  n_max = Inf  
)
```

Arguments

report_file	A path or URL to an MGI report file.
report_type	Report type, one of: <ul style="list-style-type: none"> • "MRK_List1": Mouse Genetic Markers (including withdrawn marker symbols). • "MRK_List2": Mouse Genetic Markers (excluding withdrawn marker symbols). • "MGI_MRK_Coord": MGI Marker Coordinates. • "MGI_GTGUP": MGI Sequence Coordinates. • "MRK_Sequence": MGI Marker associations to Sequence (GenBank, RefSeq, Ensembl) information. • "MRK_SwissProt_TrEMBL": MGI Marker associations to SWISS-PROT and TrEMBL protein IDs. • "MRK_SwissProt": MGI Marker associations to SWISS-PROT protein IDs. • "MRK_GeneTrap": MGI Marker associations to Gene Trap IDs. • "MRK_ENSEMBL": MGI Marker associations to Ensembl sequence information. • "MGI_BioTypeConflict": MGI Marker associations to Ensembl or NCBI gene models where a gene vs. pseudogene discrepancy exists. • "PRB_PrimerSeq": MGI Marker associations with primer pairs. • "MGI_InterProDomains": InterPro domain associations to MGI markers.
n_max	Maximum number of lines to read.

Value

A [tibble](#) with the report data in tidy format.

Examples

```
base_url <- "https://www.informatics.jax.org/downloads/reports"
url <- file.path(base_url, "MRK_List1.rpt")
# Import the Mouse Genetic Markers (including withdrawn marker symbols) Report
read_report(url, "MRK_List1", n_max = 10L)
```

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