

Package ‘gmsgff’

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Type Package

Title Utilities for loading gene annotation data

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Description Provides parse_gff_to_dataframe

License mit_license

Imports tidyverse

Suggests unittest

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gmsgff-package	<i>Utilities for loading gene annotation data</i>
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Description

Provides parse_gff_to_dataframe

Details

The DESCRIPTION file: This package was not yet installed at build time.

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~~ An overview of how to use the package, including the most important ~~ functions ~~

Author(s)

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Maintainer: Gavin Band <gavin.band@well.ox.ac.uk>

References

~~ Literature or other references for background information ~~

See Also

~~ Optional links to other man pages, e.g. ~~ <pkg> ~~

Examples

```
gmsgff::parse_gff3_to_dataframe( "##gff-version 3
#description: test data
chr1\tme\tgene\t1\t1000\t.\t+\t.\tID=gene1;other_data=stuff
chr1\tme\texon\t10\t900\t.\t+\t.\tID=gene1.1;Parent=gene1
" )
```

parse_gff3_to_dataframe

Parse a gff file to a tidyverse dataframe

Description

Parse a gff file to a tidyverse dataframe

Usage

```
parse_gff3_to_dataframe(filename)
```

Value

A dataframe with the nine GFF columns, and ID and Parent fields

Author(s)

Gavin Band

Examples

```
gencode = gmsgff::parse_gff3_to_dataframe( "##gff-version 3
#description: test data
chr1\tme\tgene\t1\t1000\t.\t+\t.\tID=gene1;other_data=stuff
chr1\tme\texon\t10\t900\t.\t+\t.\tID=gene1.1;Parent=gene1
" )
```

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