

CENTREannotation

September 23, 2026

CENTREannotDb

Class object for the CENTRE annotation data

Description

The CENTRE annotation data is accessed through objects of CENTREannotDb class. That either provides access to the ENCODE screen V3 annotation for Human <https://screen.encodeproject.org> or gives access to GENCODE basic gene annotation version 40.

Usage

```
CENTREannotDb(x)
```

```
tables(x)
```

Arguments

x sqlite file path

Details

Using `tables(x)` on a CENTREannotDb object returns the tables and columns for each table in the database.

Value

class CENTREannotDb

References

Based on CompoundDb::CompDb.

Examples

```
##load the screen V3 annotation
ah <- AnnotationHub::AnnotationHub()
screen <- ah[["AH116731"]]
tables(screen) #get all tables and columns in the data base
```

fetch_data

Fetch data from the CENTREannotDb databases

Description

Main interface to fetch data from the CENTREannotation package databases through the CENTREannotDb objects.

Usage

```
fetch_data(x, columns, entries, column_filter)
```

Arguments

x	A CENTREannotDb object.
columns	Columns to select (vector or string). Equivalent to X in SELECT X.
entries	Element ID to select (vector or sting). Equivalent to ID in SELECT X FROM TABLE WHERE ID in Z. If entries or column_filter is missing the program assumes the query is SELECT X FROM TABLE.
column_filter	Column on which to apply filter. Equivalent to Z in SELECT X FROM TABLE WHERE ID in Z. If entries or column_filter is missing the program assumes the query is SELECT X FROM TABLE.

Value

data.frame with the queried data.

References

Based on the internal query engine of CompoundDb

Examples

```
ah <- AnnotationHub::AnnotationHub()
CENTREannotenhDb <- ah[["AH116731"]]
res <- fetch_data(CENTREannotenhDb,
  columns = c("enhancer_id", "start"),
  entries = c("EH38E1519134", "EH38E1519132"),
  column_filter = "enhancer_id"
)
```

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