CENTREannotation

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`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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