

# CENTREannotation

April 1, 2026

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CENTREannotDb	<i>Class object for the CENTRE annotation data</i>
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## 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
```

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 fetch\_data

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*Fetch data from the CENTREannotDb databases*


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

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