

# Package ‘CENTREprecomputed’

January 22, 2026

**Title** Hub package for the precomputed data of CENTRE and example data

**Version** 1.0.0

**Description** Interface and documentation for the Experiment Hub records needed by the CENTRE Bioconductor software package. The Experiment Hub records contains the precomputed fisher combined p-values, CRUP correlations. Additionally, the records hold ChIP-seq and RNA-seq data used for the example of the software package.

**License** Artistic-2.0

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

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**biocViews** ExperimentData, PackageTypeData, ExperimentHub, RNASeqData, ChIPSeqData, ChipOnChipData

**Depends** R (>= 4.5.0)

**Imports** ExperimentHub, RSQLite, DBI, BiocGenerics, methods

**Suggests** knitr, rmarkdown, testthat, BiocStyle

**VignetteBuilder** knitr

**URL** <https://github.com/slrvv/CENTREprecomputed>

**BugReports** <https://github.com/slrvv/CENTREprecomputed/issues>

**git\_url** <https://git.bioconductor.org/packages/CENTREprecomputed>

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**Author** Sara Lopez Ruiz de Vargas [aut, cre] (ORCID:  
<<https://orcid.org/0000-0002-1290-4774>>)

**Maintainer** Sara Lopez Ruiz de Vargas <[lopez\\_s@molgen.mpg.de](mailto:lopez_s@molgen.mpg.de)>

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CENTREprecomputed-package*CENTREprecomputed: Experiment Data package interface for the precomputed data of CENTRE and example data*

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**Description**

This is an Experiment Data package for the CENTRE Bioconductor software package. It serves as an interface for the CENTRE PrecomputedData database which contains the precomputed fisher combined p-values, CRUP correlations and the ChIP-seq and RNA-seq data used for the example. The PrecomputedDataLight.db contains the fisher combined p-value and the correlation between CRUP-PP and -EP scores for every enhancer-target (ET) pair at 500kb. The example ChIP-seq and RNA-seq can be downloaded from the ExperimentHub.

**Format**

Database with tables:

**combinedTestData** -log transformed p-values of the Wilcoxon rank sum tests for each ET pair.

**crup\_cor** correlation between CRUP-PP and -EP scores for each ET pair.

**Details**

The combined p-value is computed from the p-values of four wilcoxon-rank sum tests for each ET. The four tests are on the CAGE-seq dataset, the DNase-hypersensitive region dataset, the DNase-seq-gene expression dataset and the CRUP-EP-gene expression dataset. For more information check the CENTRE article in references

**Author(s)**

**Maintainer:** Sara Lopez Ruiz de Vargas <lopez\_s@molgen.mpg.de> ([ORCID](#))

**Source**

[http://owwww.molgen.mpg.de/~CENTRE\\_data/CENTREexperimentData/PrecomputedDataLight.db](http://owwww.molgen.mpg.de/~CENTRE_data/CENTREexperimentData/PrecomputedDataLight.db)

**References**

Trisevgeni Rapakoulia, Sara Lopez Ruiz De Vargas, Persia Akbari Omgba, Verena Laupert, Igor Ulitsky, Martin Vingron, CENTRE: a gradient boosting algorithm for Cell-type-specific ENhancer-Target pREdiction, Bioinformatics, Volume 39, Issue 11, November 2023, btad687, <https://doi.org/10.1093/bioinformatics/btad687>

**See Also**

Useful links:

- <https://github.com/slrvv/CENTREprecomputed>
- Report bugs at <https://github.com/slrvv/CENTREprecomputed/issues>

## Examples

```
library(ExperimentHub)
hub <- ExperimentHub()
eh <- query(hub, "CENTREprecomputed")
eh[["EH9540"]] ## PrecomputedData database
```

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CENTREprecompDb

*Database for the CENTRE precomputed data*

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## Description

The CENTREprecompDb object provides access to CENTRE's Precomputed SQLite Database Pre-computedDataLight.db. Inside the database is combinedTestData, crup\_cor and metadata. For more information check the computeGenericFeatures() function from the CENTRE package.

## Usage

```
CENTREprecompDb(x)

tables(x)
```

## Arguments

x                      sqlite file path

## Details

CENTREprecompDb is the object that provides access to CENTRE's database. tables(CENTREprecompDb) shows the tables inside the database and their columns.

## Value

Object of class CENTREprecompDb

## References

Based on CompoundDb::CompDb class.

## Examples

```
#The object is accessed through the ExperimentHub record
eh <- ExperimentHub::ExperimentHub()
centrepredb <- eh[["EH9540"]]
tables(centrepredb)
```

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|                    |                                                     |
|--------------------|-----------------------------------------------------|
| fetch_data_precomp | <i>Fetch data from the CENTREprecompDb database</i> |
|--------------------|-----------------------------------------------------|

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## Description

Function to fetch data from the CENTREprecomputed package database through the CENTREprecompDb object.

## Usage

```
fetch_data_precomp(x, table, columns, entries, column_filter)
```

## Arguments

|               |                                                                                                                                                                                     |
|---------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x             | CENTREprecompDb object.                                                                                                                                                             |
| table         | Table of the database on which to search. Can be combinedTestData or cor_CRUP.                                                                                                      |
| columns       | Columns to select. Equivalent to X in SELECT X.                                                                                                                                     |
| entries       | Element ID to select. 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 data queried.

## References

Based on the package CompoundDb query engine internal functions.

## See Also

```
vignette("CENTREprecomputed")
```

## Examples

```
eh <- ExperimentHub::ExperimentHub()
centrepredb <- eh[["EH9540"]]

res <- fetch_data_precomp(centrepredb,
  table = "crup_cor",
  columns = c("pair", "cor_CRUP"),
  entries = "EH38E3440167",
  column_filter = "symbol38"
)
```

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## \* **internal**

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