EuPathDB

November 11, 2026

`EuPathDB` *EuPathDB: Access EuPathDB annotations using AnnotationHub*

Description

EuPathDB provides an R interface for retrieving annotation resources from the EuPathDB databases: AmoebaDB, CryptoDB, FungiDB, GiardiaDB, MicrosporidiaDB, PiroplasmaDB, PlasmoDB, ToxoDB, TrichDB, and TriTrypDB using the Bioconductor AnnotationHub framework.

Usage

```
EuPathDB()
```

Details

There are currently two types of Bioconductor resources which can be retrieved for 172 supported organisms from the various EuPathDB databases:

- OrgDB resources
- GRanges resources

The OrgDB resources provides gene level information including chromosome, location, name, description, orthologs, and associated GO terms.

The GRanges resources provide transcript-level information such as known exons and their corresponding locations.

Each of these resources are generated using information obtained from the EuPathDB GFF files along with queries made through the various EuPathDB web APIs.

For examples of how EuPathDB can be used to query and interact with EuPathDB.org resources, take a look at the vignette: `browseVignettes(package="EuPathDB")`

Value

Used for its side-effect of opening the package vignette. A vector of experiment identifiers.

Author(s)

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See Also

AnnotationHub

GRanges

http://eupathdb.org/eupathdb/

Examples

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availableEuPathDB
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