

Package: GenomeInfoDbData (via r-universe)

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Title Species and taxonomy ID look up tables used by GenomeInfoDb

Description Files for mapping between NCBI taxonomy ID and species.
Used by functions in the GenomeInfoDb package.

Version 1.2.13

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Depends R (>= 3.3)

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Repository <https://adafede.r-universe.dev>

RemoteUrl <https://github.com/Bioconductor/GenomeInfoDbData>

RemoteRef HEAD

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GenomeInfoDb-package *Species and taxonomy ID look up tables*

Description

This package contains one mapping object:

- `specData`: A data frame with columns ‘`tax_id`’, ‘`genus`’, and ‘`species`’. Used to retrieve taxonomy ID by species and returns list of available species.

Usage

```
data(specData)
```

Details

Scripts to generate these files are in GenomeInfoDbData/inst/scripts. All originate from the tax-dummp download at <ftp://ftp.ncbi.nih.gov/pub/taxonomy/taxdump.tar.gz>.

Author(s)

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Examples

```
data(specData)
sapply(specData, class) # tax_id genus species
# "integer" "factor" "character"

subset(specData, c(genus=="Homo" & species=="sapiens"))$tax_id # [1] 9606
```

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