

# GenomeInfoDbData

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

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## 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 taxdump download at <ftp://ftp.ncbi.nih.gov/pub/taxonomy/taxdump.tar.gz>.

## Author(s)

Bioconductor Core Team

## 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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## \* **datasets**

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