Package: hpar (via r-universe)

November 25, 2026

Type Package

Title Human Protein Atlas in R

Version 1.56.0

Description The hpar package provides a simple R interface to and data from the Human Protein Atlas project.

Depends R (>= 3.5.0)

Imports utils, ExperimentHub

Suggests org.Hs.eg.db, GO.db, AnnotationDbi, knitr, BiocStyle, testthat, rmarkdown, dplyr, DT

VignetteBuilder knitr

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Collate hpa.R hpar-package.R zzz.R

biocViews Proteomics, CellBiology, DataImport, FunctionalGenomics, SystemsBiology, ExperimentHubSoftware

RoxygenNote 7.2.2

Config/pak/sysreqs libicu-dev libpng-dev libssl-dev zlib1g-dev

Repository Bioconductor 3.24

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RemoteUrl https://github.com/bioc/hpar

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browseHPA *Browser the HPA page for a gene.*

Description

Browser the HPA page for a gene.

Usage

```
browseHPA(id)
```

Arguments

id	A 'character()' with one or multipel Ensembl gene identifiers.

Value

Returns the URL(s) for the provided gene identifiers. If interactive, opens the URL(s).

Author(s)

Laurent Gatto

Examples

```
browseHPA("ENSG00000163435")
```

getHpaDate *Obtain HPA data release information*

Description

Obtain the data and release information of the Human Protein Atlas (HPA) sets distributed by 'hpar'. See http://www.proteinatlas.org/about/releases for the HPA release history.

Usage

```
getHpaDate()
```

Value

A 'character()' with the release information.

Author(s)

Laurent Gatto

Examples

```
allHparData()

getHpaVersion()
getHpaDate()
getHpaEnsembl()
```

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