

Package: hpar (via r-universe)

July 3, 2024

Type Package

Title Human Protein Atlas in R

Version 1.47.0

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

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

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

RemoteRef HEAD

RemoteSha ef6f37ad5d709cc1b65c6113afa8df59f288d52f

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browseHPA	<i>Browser the HPA page for a gene.</i>
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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	<i>Obtain HPA data release information</i>
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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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