Package 'hpar'

November 12, 2026

Type Package

Title Human Protein Atlas in R

Version 1.54.0

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

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Contents

hpar-package 2
browseHPA 3
getHpaDate 3

Index **5**

`hpar-package` *Human Protein Atlas in R*

Description

This package provides a simple interface to the Human Protein Atlas. From the Human Protein Atlas Project page: The Swedish Human Protein Atlas project, funded by the Knut and Alice Wallenberg Foundation, has been set up to allow for a systematic exploration of the human proteome using Antibody-Based Proteomics. This is accomplished by combining high-throughput generation of affinity-purified antibodies with protein profiling in a multitude of tissues and cells assembled in tissue microarrays. Confocal microscopy analysis using human cell lines is performed for more detailed protein localization. The program hosts the Human Protein Atlas portal with expression profiles of human proteins in tissues and cells.

See the vignette for available data.

HPA data usage policy

The use of data and images from the HPA site in publications and presentations is permitted provided that the following conditions are met:

- The publication and/or presentation are solely for informational and non-commercial purposes.

- The source of the data and/or image is referred to this site (www.proteinatlas.org) and/or one or more of our publications are cited.

References

- See the Human Protein Atlas Project page <http://www.proteinatlas.org> and <http://www.proteinatlas.org/about/download> for more details and documentation.

- Uhlen et al (2015). Tissue-based map of the human proteome. Science. 347(6220):1260419.

- Uhlen et al (2010). Towards a knowledge-based Human Protein Atlas. Nat Biotechnol. 28(12):1248-50.

- Berglund et al (2008). A gene-centric Human Protein Atlas for expression profiles based on antibodies. Mol Cell Proteomics. 7(10):2019-27.

- Uhlen et al (2005). A human protein atlas for normal and cancer tissues based on antibody proteomics. Mol Cell Proteomics. 4(12):1920-1932.

- Ponten et al (2008). The Human Protein Atlas - a tool for pathology. J Pathology. 216(4):387-93.

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See Also

The package vignette can be accessed with ‘vignette("hpar")‘.

`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()
```

Index

∗ **internal**
    hpar-package, 2
_PACKAGE *(*hpar-package*)*, 2

allHparData *(*getHpaDate*)*, 3

browseHPA, 3

getHpaDate, 3
getHpaEnsembl *(*getHpaDate*)*, 3
getHpaVersion *(*getHpaDate*)*, 3

hpaCancer *(*hpar-package*)*, 2
hpaCancer16.1 *(*hpar-package*)*, 2
hpaNormalTissue *(*hpar-package*)*, 2
hpaNormalTissue16.1 *(*hpar-package*)*, 2
hpar *(*hpar-package*)*, 2
hpar-package, 2
hpaSecretome *(*hpar-package*)*, 2
hpaSubcellularLoc *(*hpar-package*)*, 2
hpaSubcellularLoc14 *(*hpar-package*)*, 2
hpaSubcellularLoc16.1 *(*hpar-package*)*, 2

rnaConsensusTissue *(*hpar-package*)*, 2
rnaFantomTissue *(*hpar-package*)*, 2
rnaGeneCellLine *(*hpar-package*)*, 2
rnaGeneCellLine16.1 *(*hpar-package*)*, 2
rnaGeneTissue21.0 *(*hpar-package*)*, 2
rnaGtexTissue *(*hpar-package*)*, 2
rnaHpaTissue *(*hpar-package*)*, 2