Package ‘hpar’

January 17, 2024

Type    Package
Title   Human Protein Atlas in R
Version 1.44.0
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
License Artistic-2.0
biocViews Proteomics, CellBiology, DataImport, FunctionalGenomics,
         SystemsBiology, ExperimentHubSoftware
RoxygenNote 7.2.2
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R topics documented:

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**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.

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**browseHPA**

**Browse the HPA page for a gene.**

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**Description**

Browser the HPA page for a gene.

**Usage**

```r
browseHPA(id)
```

**Arguments**

- **id**
  
  A `character()` with one or multiple Ensembl gene identifiers.

**Value**

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

**Author(s)**

Laurent Gatto

**Examples**

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

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**getHpaDate**

**Obtain HPA data release information**

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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](http://www.proteinatlas.org/about/releases) for the HPA release history.

**Usage**

```r
getHpaDate()
```

**Value**

A `character()` with the release information.
Author(s)
Laurent Gatto

Examples

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