

hpar: The Human Protein Atlas in R

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Abstract

The Human Protein Atlas (HPA) is a systematic study of the human proteome using antibody-based proteomics. Multiple tissues and cell lines are systematically assayed using affinity-purified antibodies and confocal microscopy. The `hpar` package is an R interface to the HPA project. It distributes three data sets, provides functionality to query these and to access detailed information pages, including confocal microscopy images available on the HPA web page.

Keywords: infrastructure, bioinformatics, proteomics, microscopy

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1 Introduction

1.1 The HPA project

From the Human Protein Atlas¹ (Uhlén et al., 2005; Uhlen et al., 2010) site:

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 localisation. The program hosts the Human Protein Atlas portal with expression profiles of human proteins in tissues and cells.

The `hpar` package provides functionality to use HPA data from the R interface. It also distributes three data sets available from the HPA site.

Normal tissue data Expression profiles for proteins in human tissues based on immunohistochemistry using tissue micro arrays. The `dataframe` includes Ensembl gene identifier ("Gene"), tissue name ("Tissue"), annotated cell type ("Cell.type"), expression value ("Level"), the type of annotation (annotated protein expression (APE), based on more than one antibody, or staining, based on one antibody only) ("Expression.type"), and the reliability or validation of the expression value ("Reliability").

Subcellular location data Subcellular localisation of proteins based on immunofluorescently stained cells. The `dataframe` includes Ensembl gene identifier ("Gene"), main subcellular location of the protein ("Main.location"), other locations ("Other.location"), the type of annotation (annotated protein expression (APE), based on more than one antibody, or staining, based on one antibody only) ("Expression.type"), and the reliability or validation of the expression value ("Reliability").

RNA data RNA levels in three different cell lines, based on RNA-seq. The `dataframe` includes Ensembl gene identifier ("Gene"), analysed cell line ("Cell.line"), number of reads per kilobase gene model and million reads ("RPKM"), and abundance class ("Abundance").

1.2 HPA data usage policy

The use of data and images from the HPA 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 the HPA site (www.proteinatlas.org) and/or one or more of our publications are cited.

1.3 Installation

`hpar` is available through the Bioconductor project. Details about the package and the installation procedure can be found on its page². To install using the dedicated Bioconductor infrastructure, run :

¹<http://www.proteinatlas.org/>

²<http://bioconductor.org/packages/devel/bioc/html/hpar.html>

```
source("http://bioconductor.org/biocLite.R")
## or, if you have already used the above before
library("BiocInstaller") ## and to install the package
biocLite("hpar")
```

After installation, hpar will have to be explicitly loaded with

```
library("hpar")

## This is hpar 1.4.0. For more information,
## please type '?hpar' or 'vignette('hpar')'.
```

so that all the package's functionality and data is available to the user.

2 The hpar package

2.1 Data sets

The three data sets, named `hpaNormalTissue`, `hpaSubcellularLoc` and `hpaRna` in the package can be loaded with the `data` function, as illustrated below for `hpaNormalTissue` below. Each data set is a `dataframe` and can be easily manipulated using standard R functionality. The code chunk below illustrates some of its properties.

```
data(hpaNormalTissue)
dim(hpaNormalTissue)

## [1] 1201018      6

names(hpaNormalTissue)

## [1] "Gene"          "Tissue"        "Cell.type"    "Level"
## [5] "Expression.type" "Reliability"

## Number of genes
length(unique(hpaNormalTissue$Gene))

## [1] 15156

## Number of cell types
length(unique(hpaNormalTissue$Cell.type))

## [1] 44

head(levels(hpaNormalTissue$Cell.type))

## [1] "adipocytes"          "bile duct cells"
## [3] "cells in endometrial stroma" "cells in glomeruli"
## [5] "cells in granular layer" "cells in molecular layer"

## Number of tissues
length(unique(hpaNormalTissue$Tissue))

## [1] 48

head(levels(hpaNormalTissue$Tissue))
```

```
## [1] "adrenal gland" "appendix"      "bone marrow"  "breast"
## [5] "bronchus"      "cerebellum"

table(hpaNormalTissue$Expression.type)

##
##      APE Staining
## 290069  910949
```

2.2 HPA interface

The package provides a interface to the HPA data. The `getHpa` allows to query the data sets described in section 2.1. It takes three arguments, `id`, `hpadata` and `type`, that control the query, what data set to interrogate and how to report results respectively. The HPA data uses Ensembl gene identifiers and `id` must be a valid identifier. `hpadata` must be one of "NormalTissue", "Rna" or "SubcellularLoc". `type` can be `data` or `details`. The former is the default and returns a `dataframe` containing the information relevant to `id`. It is also possible to obtain detailed information, (including cell images) as web pages, directly from the HPA web page, using `details`.

We will illustrate this functionality with using the E74-like factor 3 gene (ENSG00000163435) as example.

```
id <- "ENSG00000163435"
head(getHpa(id, hpadata = "NormalTissue"))

##           Gene           Tissue           Cell.type Level
## 717135 ENSG00000163435 adrenal gland glandular cells None
## 717136 ENSG00000163435      appendix glandular cells High
## 717137 ENSG00000163435      appendix lymphoid tissue None
## 717138 ENSG00000163435 bone marrow hematopoietic cells None
## 717139 ENSG00000163435      breast      adipocytes None
## 717140 ENSG00000163435      breast      glandular cells None
##           Expression.type Reliability
## 717135           APE           High
## 717136           APE           High
## 717137           APE           High
## 717138           APE           High
## 717139           APE           High
## 717140           APE           High

getHpa(id, hpadata = "SubcellularLoc")

##           Gene           Main.location Other.location
## 7419 ENSG00000163435 Nucleus but not nucleoli;Cytoplasm
##           Expression.type Reliability
## 7419           APE           High

head(getHpa(id, hpadata = "Rna"))

##           Gene  sample Value Unit Abundance
## 120253 ENSG00000163435 A-431  55.9 FPKM      High
## 120254 ENSG00000163435 A-549 209.8 FPKM      High
## 120255 ENSG00000163435 CACO-2 45.6 FPKM      High
## 120256 ENSG00000163435 HEK 293  0.8 FPKM      Low
## 120257 ENSG00000163435 HeLa  55.2 FPKM      High
## 120258 ENSG00000163435 Hep-G2  9.7 FPKM      Medium
```

If we ask for `detail`, a browser page pointing to the relevant page is open (see figure 1)

```
getHpa(id, type = "details")
```

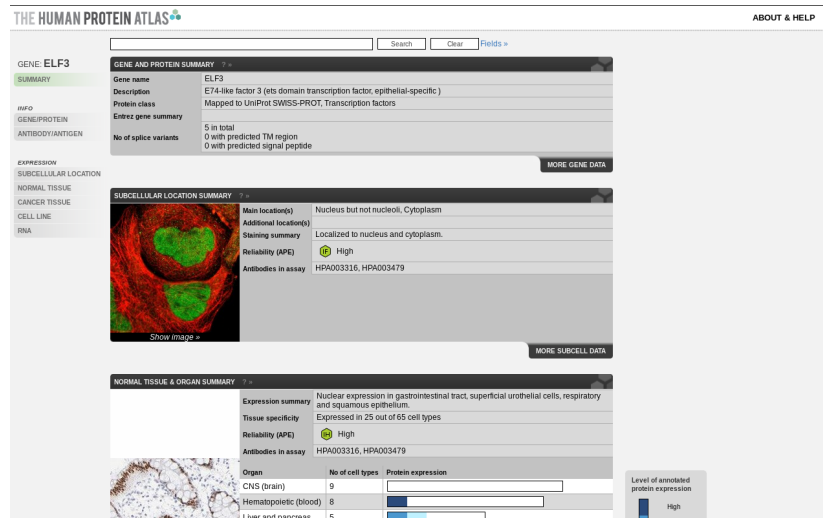


Figure 1: The HPA web page for the E74-like factor 3 gene (ENSG00000163435) gene.

If a user is interested specifically in one data set, it is possible to set `hpadata` globally and omit it in `getHpa`. This is done by setting the `hpar` options `hpadata` with the `setHparOptions` function. The current default data set can be tested with `getHparOptions`.

```
getHparOptions()

## $hpar
## $hpar$hpadata
## [1] "NormalTissue"

setHparOptions(hpadata = "SubcellularLoc")
getHparOptions()

## $hpar
## $hpar$hpadata
## [1] "SubcellularLoc"

getHpa(id)

##           Gene                               Main.location Other.location
## 7419 ENSG00000163435 Nucleus but not nucleoli;Cytoplasm
##           Expression.type Reliability
## 7419           APE           High
```

2.3 HPA release information

Information about the HPA release used to build the installed `hpar` package can be accessed with `getHpaVersion`, `getHpaDate` and `getHpaEnsembl`. Full release details can be found on the HPA release history³ page.

³<http://www.proteinatlas.org/about/releases>

```

getHpaVersion()
## [1] "Protein Atlas version 11.0"

getHpaDate()
## [1] "2013.03.11"

getHpaEnsembl()
## [1] "69.37"

```

3 A small use case

Let's compare the subcellular localisation annotation obtained from the HPA subcellular location data set and the information available in the Bioconductor annotation packages. The HPA query shown below indicates that the HECW1 (ENSG00000002746) gene main locations are nucleus (but not nucleoli) and cytoplasm.

```

id <- "ENSG00000002746"
getHpa(id, "SubcellularLoc")

##           Gene                               Main.location Other.location
## 25 ENSG00000002746 Nucleus but not nucleoli;Cytoplasm
##   Expression.type Reliability
## 25           APE           High

```

Below, we first extract all cellular component GO terms available for ENSG00000002746 from the org.Hs.eg.db human annotation and then retrieve their term definitions using the GO.db database, indicating concordant results. The IDA evidence code indicates that this information is inferred from direct assay.

```

library(org.Hs.eg.db)
library(GO.db)
ans <- select(org.Hs.eg.db, keys = id, cols = c("ENSEMBL", "GO", "ONTOLOGY"),
              keytype = "ENSEMBL")

## Warning: The 'cols' argument has been deprecated and replaced by 'columns'
## for versions of Bioc that are higher than 2.13. Please use the
## 'columns' argument anywhere that you previously used 'cols'
## Warning: 'select' resulted in 1:many mapping between keys and return rows

ans <- ans[ans$ONTOLOGY == "CC", ]
ans

##           ENSEMBL           GO EVIDENCE ONTOLOGY
## 2 ENSG00000002746 GO:0005634         IDA         CC
## 3 ENSG00000002746 GO:0005737         IDA         CC

sapply(as.list(GOTERM[ans$GO]), slot, "Term")

## GO:0005634 GO:0005737
## "nucleus" "cytoplasm"

```

Session information

- R version 3.0.2 (2013-09-25), x86_64-unknown-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, utils
- Other packages: AnnotationDbi 1.24.0, Biobase 2.22.0, BiocGenerics 0.8.0, DBI 0.2-7, GO.db 2.10.1, RSQLite 0.11.4, hpar 1.4.0, knitr 1.5, org.Hs.eg.db 2.10.1
- Loaded via a namespace (and not attached): IRanges 1.20.0, evaluate 0.5.1, formatR 0.9, highr 0.2.1, stats4 3.0.2, stringr 0.6.2, tools 3.0.2

References

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