Package ‘TPACData’

May 7, 2026

Type Package

Title Human Protein Atlas Data for Tissue-Adjusted Pathway Analysis of Cancer (TPAC)

Version 0.1.0

Description Contains summary data on gene expression in normal human tissues from the Human Protein Atlas for use with the
Tissue-Adjusted Pathway Analysis of cancer (TPAC) method.
Frost, H. Robert (2023) ``Tissue-adjusted pathway analysis of cancer (TPAC)'' <doi:10.1101/2022.03.17.484779>.

Depends R (>= 3.6.0)

Imports data.table

License GPL (>= 2)

Encoding UTF-8

LazyData true

LazyDataCompression bzip2

NeedsCompilation no

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Repository CRAN

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Contents

`hpa.data` *Gene expression data for normal human tissues from the Human Protein Atlas (HPA). This data was specially processed by the HPA group as FPKM values (file "HPA.normal.FPKM.GDCpipeline.csv") using a pipeline similar to that employed by GDC for the TCGA RNA-seq data.*

Description

A data.table with 1,088,694 rows and 4 columns (Gene, Tissue, FPKM, TissueSpecificity):

- Gene: Ensembl gene ID
- Tissue: Human tissue type
- FPKM: Mean expression of that gene in units FPKM+1
- TissueSpecificity: The fold-change in expression between mean expression in that tissue and mean in all 18 tissues.

Usage

```
hpa.data
```

Format

A data.table with 1,088,694 rows and 4 columns (Gene, Tissue, FPKM, TissueSpecificity)

Source

Human Protein Atlas

References

- Ulhen et al. (2017). A pathology atlas of the human cancer transcriptome. Science. doi: 10.1126/science.aan2507

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