

Package ‘AHPathbankDBs’

December 10, 2025

Type Package

Title Metabolites and proteins linked to PathBank pathways (for AnnotationHub)

Version 0.99.5

Encoding UTF-8

Depends R (>= 4.1.0)

Imports AnnotationHub (>= 2.23.0)

Suggests BiocStyle, magrittr, dplyr, tibble, knitr, rmarkdown

Description The package provides a comprehensive mapping table of metabolites and proteins linked to PathBank pathways. The tables include HMDB, KEGG, ChEBI, CAS, Drugbank, Uniprot IDs. The tables are provided for each of the 10 species (`"Homo sapiens"`, `"Escherichia coli"`, `"Mus musculus"`, `"Arabidopsis thaliana"`, `"Saccharomyces cerevisiae"`, `"Bos taurus"`, `"Caenorhabditis elegans"`, `"Rattus norvegicus"`, `"Drosophila melanogaster"`, and `"Pseudomonas aeruginosa"`). These table information can be used for Metabolite Set (and other) Enrichment Analysis.

VignetteBuilder knitr

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URL <https://github.com/kozo2/AHPathbankDBs>

LazyData true

RoxygenNote 7.0.2

biocViews AnnotationHub, CustomDBSchema, FunctionalAnnotation

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Author Kozo Nishida [aut, cre] (ORCID:
<<https://orcid.org/0000-0001-8501-7319>>)
Maintainer Kozo Nishida <kozo.nishida@gmail.com>

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