

# Package ‘HuntingtonDiseaseCuratedCompositeCollection’

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**Type** Package

**Title** anRichment-type collection of Huntington's Disease (HD)-related literature gene sets

**Version** 1.10

**Depends** anRichment

**Suggests** org.Hs.eg.db

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**Description** This package contains a collection of various Huntington's Disease (HD)-related gene sets collected from the literature and a simple accessor function.

**License** GPL-3

**NeedsCompilation** no

## R topics documented:

HuntingtonDiseaseCuratedCompositeCollection . . . . .	1
<b>Index</b>	<b>4</b>

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HuntingtonDiseaseCuratedCompositeCollection  
*Returns the collection of Huntington's Disease literature gene sets*

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## Description

Returns the collection of Huntington's Disease literature gene sets.

**Usage**

```
HuntingtonDiseaseCuratedCompositeCollection(
    organism = "human",
    useHomology = TRUE,
    addOldOrganismToSetNames = FALSE,
    namePattern = ".convertedFrom.%o",
    addOldOrganismToSetDescriptions = FALSE,
    descriptionPattern = " (Converted from %o.)",
    traceableOnly = FALSE)
```

**Arguments**

organism	Character string specifying the organism. Can be common name (such as "human"), scientific name ("Homo sapiens"), or scientific shorthand ("Hs"). To see all recognized organisms, use function <a href="#">organismLabels</a> . If NULL or NA, gene sets in the collection will retain their original content and organism they correspond to.
useHomology	logical: should genes in non-human organisms be matched by homology information (where available)? If this is FALSE or the homology information is not available, genes will be matched by name.
addOldOrganismToSetNames	Logical: should an indication of the old organism be appended to the set name? This may be useful to indicate that the gene sets was originally constructed for a different organism and its content may not accurately reflect the new organism.
namePattern	Character string giving the pattern that is to be added to the set name. The characters "%o" will be substituted by the actual organism name.
addOldOrganismToSetDescriptions	Logical: should an indication of the old organism be appended to the set description?
descriptionPattern	Character string giving the pattern that is to be added to the set description. The characters "%o" will be substituted by the actual organism name.
traceableOnly	Logical: should only a subset of the gene sets that are traceable to a published article or website be included?

**Details**

The gene sets in the HD literature collection are compiled from various literature sources. They represent functional categories, sets of genes from perturbation studies and others. Although the genes may have been studied in various model organisms, they are all stored as human orthologs.

This function converts all gene sets to the specified organism using `convertCollectionToOrganism`. Note that each such conversion may introduce some differences (for example, drop genes that cannot be mapped), and the gene set interpretation in the new organism may not be as accurate as in the original organism (human).

For detailed description and references for each individual gene set or gene property in the collection, the user may consider using the function `collection2dataFrames` to create a data frame that contains meta-information about gene sets (gene set names, descriptions, sources (references) etc.)

**Value**

Collection of gene lists and properties.

**Author(s)**

Gene sets were originally collected by Michael Palazzolo and Jim Wang under contract with CHDI Management/CHDI Foundation. The collection was created by Peter Langfelder.

**References**

Many of the gene sets, as well as their example use, are described in James K. T. Wang, Peter Langfelder, Steve Horvath and Michael J. Palazzolo. Exosomes and Homeostatic Synaptic Plasticity Are Linked to Each other and to Huntington's, Parkinson's, and Other Neurodegenerative Diseases by Database-Enabled Analyses of Comprehensively Curated Datasets. *Front. Neurosci.* 11 149, 2017; online 31 March 2017. <https://doi.org/10.3389/fnins.2017.00149>

**Examples**

```
## Not run:  
collection = HuntingtonDiseaseCuratedCompositeCollection(organism = "human");  
knownGroups(collection)  
  
## End(Not run)
```

# Index

## \* misc

HuntingtonDiseaseCuratedCompositeCollection,  
[1](#)

collection2dataFrames, [2](#)

HuntingtonDiseaseCuratedCompositeCollection,  
[1](#)

organismLabels, [2](#)