Description

obtain probe set IDs associated with a KO term

Usage

getKOprobes(str, useAcc=TRUE, plat="hgu95av2", na.action=na.omit)
Arguments

- **str**: string giving a KEGG orthology term
- **useAcc**: logical – use all accessible terms?
- **plat**: platform corresponding to a bioconductor annotation package, e.g., hgu95av2.db
- **na.action**: function for dealing with NA

Details

Based on keggorthology read of KEGG orthology, March 2 2010. Specifically, we run wget on ftp://ftp.genome.jp/pub/kegg/brite/ko/ko00001.keg and use parsing and modeling code given in inst/keggHTML to generate a data frame respecting the hierarchy, and then keggDF2graph to construct the graph.

Looks up the requested term and gives back the unique probe set ids on the platform.

Value

character vector, typically processed by na.omit

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```r
getKOtags("insulin")
es = acc(KOgraph, "Endocrine System")
nm = names(es[[1]])
ms
esp = lapply(nm, getKOprobes)
names(esp) = nm
sapply(esp, length)
```

```r
indRender(klike, from=nodes(klike)[1], indent=" ")
```

Description

indented textual rendering of nodes of a hierarchical graph

Usage

```r
indRender(klike, from=nodes(klike)[1], indent=" ")
```
keggDF2graph

Details

Based on keggorthology read of KEGG orthology, March 2 2010. Specifically, we run wget on ftp://ftp.genome.jp/pub/kegg/brite/ko/ko00001.keg and use parsing and modeling code given in inst/keggHTML to generate a data frame respecting the hierarchy, and then keggDF2graph to construct the graph.

Value

NULL

Author(s)

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Examples

data(KOgraph)
indRender(KOgraph, "Human Diseases")

keggDF2graph create a graph from a specific data frame format for KEGG orthology

Description

create a graph from a specific data frame format for KEGG orthology

Usage

keggDF2graph(df, root="KO.June07root")
data(KOgraph)

Arguments

df the data frame

root a name for root node

Details

the obvious directed graph structure from root to leaf nodes (pathway names) is instantiated for the orthology, nodeData attribute tag is loaded with the numerical tag for the term in KEGG, and nodeData attribute depth is loaded with depth from root

Based on keggorthology read of KEGG orthology, March 2 2010. Specifically, we run wget on ftp://ftp.genome.jp/pub/kegg/brite/ko/ko00001.keg and use parsing and modeling code given in inst/keggHTML to generate a data frame respecting the hierarchy, and then keggDF2graph to construct the graph.

Value

a graphNEL-class instance
keggDF2graph

Note

This is only a support function. The graph is serialized in the package data directory.

Author(s)

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Examples

data(keggOrthDF)
keggOrthDF[1:5,]
data(KOgraph)
nodes(KOgraph)[1:4]
nodeData(KOgraph,"tag")[1:5]
nodeData(KOgraph,"depth")[1:5]
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