

# keggorth

April 19, 2010

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getKOProbes                      *obtain probe set IDs associated with a KO term*

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## 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

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

```
getKOTags("insulin")
es = acc(KOgraph, "Endocrine System")
nm = names(es[[1]])
nm
esp = lapply(nm, getKOProbes)
names(esp) = nm
sapply(esp, length)
```

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indRender	<i>indented textual rendering of nodes of a hierarchical graph</i>
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**Description**

indented textual rendering of nodes of a hierarchical graph

**Usage**

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

**Arguments**

klike	a graph, with tree structure similar to <a href="#">KOgraph</a>
from	a node name from which the rendering should proceed to all leaves
indent	token to use for indentation – will be replicated to depth of node to be rendered to its left

**Details**

based on keggorth read of KEGG orthology, periodic, as of bioc 2.1 not folded into the annotation build system, but will be ASAP

**Value**

NULL

**Author(s)**

Vince Carey <stvjc@channing.harvard.edu>

**Examples**

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

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keggDF2graph	<i>create a graph from a specific data frame format for KEGG orthology</i>
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**Description**

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

**Usage**

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

**Arguments**

<code>df</code>	the data frame
<code>root</code>	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

**Value**

a `graphNEL-class` instance

**Note**

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

**Author(s)**

Vince Carey <stvjc@channing.harvard.edu>

**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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