

# keggorth

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getKOProbes	<i>obtain probe set IDs associated with a KO term</i>
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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

*indented textual rendering of nodes of a hierarchical graph*

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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**

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

**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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