

# Package ‘keggorthology’

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**Title** graph support for KO, KEGG Orthology

**Version** 2.54.0

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**Description** graphical representation of the Feb 2010 KEGG Orthology.  
The KEGG orthology is a set of pathway IDs that are not to be confused with the KEGG ortholog IDs.

**Depends** R (>= 2.5.0),stats,graph,hgu95av2.db

**Imports** AnnotationDbi,graph,DBI, graph, grDevices, methods, stats, tools, utils

**Suggests** RBGL,ALL

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**License** Artistic-2.0

**biocViews** Pathways, GraphAndNetwork, Visualization, KEGG

**git\_url** <https://git.bioconductor.org/packages/keggorthology>

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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**

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**

```
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="#">K0graph</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 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)**

Vince Carey <stvjc@channing.harvard.edu>

**Examples**

```
data(K0graph)
indRender(K0graph, "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="K0.June07root")
data(K0graph)
```

## 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

## 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(K0graph)
nodes(K0graph)[1:4]
nodeData(K0graph,,"tag")[1:5]
nodeData(K0graph,,"depth")[1:5]
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