

# DAVIDQuery

February 9, 2012

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DAVIDQuery-package *Retrieval from DAVID bioinformatics data resource.*

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## Description

Tools to retrieve data from DAVID, the Database for Annotation, Visualization and Integrated Discovery.

## Details

|                        |                        |
|------------------------|------------------------|
| Package:               | DAVIDQuery             |
| Type:                  | Package                |
| Version:               | 1.0                    |
| Date:                  | 2008-10-31             |
| License:               | GPL-2                  |
| LazyLoad:              | yes                    |
| Vignette and overview: | vignette("DAVIDQuery") |

## Author(s)

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## References

Home base for DAVID (in this package as DAVIDURLBase): <http://david.abcc.ncifcrf.gov>

Huang et al, DAVID gene ID conversion: <http://www.pubmedcentral.nih.gov/articlerender.fcgi?tool=pubmed&pubmedid=18841237>

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 DAVIDQuery

*DAVIDQuery*


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### Description

Launch a query against DAVID, the Database for Annotation, Visualization and Integrated Discovery. Return the results into an R object.

### Usage

```
DAVIDQuery(ids = "000161,075396", type = "UNIPROT_ACCESSION", annot, tool, URLlengthLimit = 1000, details = TRUE, verbose = FALSE, writeHTML = FALSE, testMe = FALSE, graphicMenu = FALSE)
```

### Arguments

|                             |  |
|-----------------------------|--|
| <code>ids</code>            | IDs for desired objects, as a character vector or as a single string with ids separated by ",". To be passed to the DAVID website, the format has to be the latter.  |
| <code>type</code>           | Type of input ids. If missing, a menu is constructed from the R object <code>DAVIDTypeChoices</code> . See <a href="http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html#input_list">http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html#input_list</a> for up-to-date choices.   |
| <code>annot</code>          | Type of annotation requested. If missing, a menu is constructed from the R object <code>DAVIDAnnotChoices</code> . See <a href="http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html#input_list">http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html#input_list</a> for up-to-date choices.   |
| <code>tool</code>           | Type of gene tool to use. If missing, a menu is constructed from the R object <code>DAVIDToolChoices</code> . See <a href="http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html#input_list">http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html#input_list</a> for up-to-date choices. As of this writing, the tool choices corresponding to the Functional Annotation tools cannot be handled by this package. |
| <code>URLlengthLimit</code> | Published maximum length of the constructed URL.   |
| <code>details</code>        | If TRUE (default), a list of intermediate results is returned; otherwise, just the final query result.   |
| <code>verbose</code>        | If TRUE (default is FALSE), more debugging information is printed.   |
| <code>writeHTML</code>      | If TRUE (default is FALSE), write the received intermediate HTML to files.   |
| <code>testMe</code>         | If TRUE (default is FALSE), assign default valuse and run.   |
| <code>graphicMenu</code>    | If TRUE (default is FALSE), use a GUI window for the pick menus.   |
| <code>formatIt</code>       | If TRUE (default), try to interpret the returned character table and structure the result. If false, the unadorned character table returned by DAVID.  |

### Details

The API described at [http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID\\_API.html](http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html) is used. The return is screen-scraped, a new URL is formulated and transmitted, again the return is screen-scraped to find the name of the results file, and finally that file is retrieved into a string matrix.

Obviously this approach is brittle, but it has survived the 2008 DAVID update. A real API would be better, of course.

The return value `DAVIDQueryResult` is just a character matrix. Its content structure depends on the choices of tool and annotation arguments, so there has been no attempt to manipulate it into, say, a data frame with nice column names.

### Value

If `detail==FALSE`, only `DAVIDQueryResult` is returned. This a character matrix holding the results of the tab-delimited file returned by DAVID.

If `detail==TRUE`, a list with contents useful for trouble-shooting:

```
firstURL
firstStageResult

DAVIDaction
secondURL
secondStageResult

hasSessionEnded

downloadFileName

downloadURL
DAVIDQueryResult
```

### Author(s)

Roger Day

### References

<http://david.abcc.ncifcrf.gov> [http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID\\_API.html](http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html) Article: DAVID gene ID conversion tool. Da Wei Huang, Brad T Sherman, Robert Stephens, Michael W Baseler, H Clifford Lane, and Richard A Lempicki <http://www.pubmedcentral.nih.gov/articlerender.fcgi?tool=pubmed&pubmedid=18841237>

### See Also

[DAVIDQueryLoop](#), [formatDAVIDResult](#)

### Examples

```
result = DAVIDQuery(testMe=TRUE)
print(names(result))
print(result$firstURL)
print(result$secondURL)
print(names(result$DAVIDQueryResult))
print(names(result$DAVIDQueryResult$O00161))
print(result$DAVIDQueryResult$O00161$GENE_SYMBOL) ### Uses UNIPROT ID's for input.
```

---

DAVIDQueryLoop      *Access DAVID multiple times.*

---

### Description

Make a query larger than DAVID allows in one go, by looping, respecting the limitations imposed by DAVID policies.

### Usage

```
DAVIDQueryLoop(
  idList = unlist(strsplit(strsplit("P31946 P62258 P29360 P42655 Q63631\nP01892 O1
" ")[[1]], "\n")),
  idLimit = 100,
  sleepSeconds = 10,
  hitsPerDayLimit = 200,
  verbose = FALSE,
  testMe = FALSE,
  type,
  annot,
  tool,
  graphicMenu = FALSE,
  formatEach = FALSE,
  formatAll = FALSE,
  ...)
```

### Arguments

|                 |  |
|-----------------|--|
| idList          | IDs of interest for query.   |
| idLimit         | Published limit of number of ID's to process in one call.  |
| sleepSeconds    | Published minimum time between iterations  |
| hitsPerDayLimit | Published maximum URL calls to the API per day from one address.   |
| verbose         | Print out tracking information as the queries are sent.  |
| testMe          | Runs DAVIDQueryLoop with arguments set as follows: annot=NULL, tool="geneReportFull", type="UNIPROT_ACCESSION", verbose=TRUE |
| type            | See <a href="#">DAVIDQuery</a> .   |
| annot           | See <a href="#">DAVIDQuery</a> .   |
| tool            | See <a href="#">DAVIDQuery</a> .   |
| graphicMenu     | See <a href="#">DAVIDQuery</a> .   |
| formatEach      | Passed to <a href="#">DAVIDQuery</a> as the <code>formatIt</code> argument.  |
| formatAll       | Assembled results are sent to <a href="#">formatDAVIDResult</a> .  |
| ...             | Other args to be passed to <a href="#">DAVIDQuery</a> .  |

### Value

The results of DAVIDQuery bound together with `rbind`. Not printed (returned invisibly).

**Note**

For some choice of the `tool` argument, the result returned may differ if `idLimit` is changed.

**Author(s)**

Roger Day

**See Also**

[DAVIDQuery](#)

---

DAVIDToolChoices     *Choices for the DAVID query parameters*

---

**Description**

DAVIDToolChoices, DAVIDTypeChoices, DAVIDAnnotChoices and DAVIDAffyChipChoices are data structures used to construct pick menus, when the corresponding arguments to DAVIDQuery are not provided.

**Details**

The source of these lists can be found at [http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID\\_API.html#input\\_list](http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html#input_list). The DAVIDToolChoices list is hardcoded within the package and includes an additional item representing the DAVID gene ID conversion tool. The DAVIDTypeChoices and DAVIDAnnotChoices lists are retrieved from DAVID web services at a run time so the possible future alterations and additions to these lists are likely to be handled automatically.

**Source**

[http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID\\_API.html#input\\_list](http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html#input_list)

**See Also**

[DAVIDQuery](#), [getAnnotationChoices](#), [getIdConversionChoices](#), [getAffyChipTypes](#)

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DAVIDURLBase     *Base URL for the DAVID database.*

---

**Description**

Base URL for the DAVID database.

**Source**

<http://david.abcc.ncifcrf.gov>

**See Also**

[DAVIDQuery](#) [DAVIDToolChoices](#)

affyToUniprot      *Obtain Affymetrix probeset IDs for given Uniprot IDs.*

---

**Description**

Obtain Affymetrix probeset IDs for given Uniprot IDs, using DAVIDQuery.

**Usage**

```
affyToUniprot(ids = "88736_AT", ...)
```

**Arguments**

|     |                                    |
|-----|------------------------------------|
| ids | Affymetrix probeset IDs.           |
| ... | Args to be passed to DAVIDQuery(). |

**Value**

The output of DAVIDQuery. If only the DAVIDQueryResult component is desired, include the arg details=FALSE.

**Note**

There is currently no provision for using [DAVIDQueryLoop](#).

**Author(s)**

Roger Day

**See Also**

[DAVIDQuery](#)

---

bracketedStrings      *Extract bracketed substrings.*

---

**Description**

Extract substrings that are bracketed by specified strings before and after.

**Usage**

```
bracketedStrings(s, before, after, verbose=FALSE, addNames=FALSE, drop.na=TRUE,
```

**Arguments**

|                           |  |
|---------------------------|--|
| <code>s</code>            | Vector of strings to search.   |
| <code>before</code>       | String to the left of the desired substring within <code>s</code> .  |
| <code>after</code>        | String to the right of the desired substring within <code>s</code> .   |
| <code>verbose</code>      | If TRUE, print the starting and ending index (or indices) of the desired substring(s).                                   |
| <code>addNames</code>     | If TRUE, and if <code>s</code> is a vector, set the <code>names</code> attribute of the return value to <code>s</code> . |
| <code>drop.na</code>      | If TRUE, remove empty strings from the return value.   |
| <code>warn.if.gt.1</code> | If TRUE, warn if a string has more than one pair of bracketed target strings.  |

**Value**

For a single input string `s`, the return value is the desired substring sandwiched between `before` and `after`. For a vector of inputs, list of outputs.

**Author(s)**

Roger Day

**See Also**

[DAVIDQuery](#)

**Examples**

```
bracketedStrings("quickbrownfox", "quick", "fox")
bracketedStrings(c("quickbrownfox", "quickredfox"), "quick", "fox", addNames=TRUE)
bracketedStrings("quickbrownfoxANDquickredfox", "quick", "fox")
bracketedStrings("quickbrownfoxANDquickredfox", "quick", "fox", warn.if.gt.1=FALSE)
```

---

```
catalogDAVIDResultsByTool
```

*Create a catalog of types of DAVID results.*

---

**Description**

Loops through values of `tool`, for the specified value of `annot`. Runs each DAVID query, and saves the result to create a catalog of types of DAVID results.

**Usage**

```
catalogDAVIDResultsByTool(annot = NULL, sleepSeconds = 10, details = FALSE, ...)
```

**Arguments**

|                           |  |
|---------------------------|--|
| <code>annot</code>        | See <a href="#">DAVIDQuery</a> .   |
| <code>sleepSeconds</code> | <a href="#">DAVIDQueryLoop</a> .   |
| <code>details</code>      | If TRUE, a list of intermediate results is returned for each catalog item; otherwise, just the final query result. Default is FALSE. |
| <code>...</code>          | Extra args passed to <a href="#">DAVIDQuery</a> .  |

**Details**

The purpose is to check comprehensively whether there are results that could be better formatted than the default output or the reformatting provided by `formatDAVIDResult`.

**Value**

A list of outputs from DAVIDQuery. Automatically assigned to the name `catalogOfDAVIDResultsByTool.ANNOT` where ANNOT is replaced by the `annot` argument.

**Author(s)**

Roger Day

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|                            |  |
|----------------------------|--|
| <code>convertIDList</code> | <i>Retrieves conversions from one DAVID ID type in the input ID list to a different...</i> |
|----------------------------|--|

---

**Description**

Retrieves conversions from one DAVID ID type in the input ID list to a different DAVID ID type. The mappings are returned in the form of a set of unique pairs.

**Usage**

```
convertIDList(idList, curl, fromType, toType, urlBase=DAVIDURLBase,
              testMe=FALSE, annotChoices=getIdConversionChoices(), details=FALSE,
              graphicMenu=FALSE, writeHTML=FALSE, verbose=FALSE)
```

**Arguments**

|                           |   |
|---------------------------|---|
| <code>idList</code>       | The character vector of IDs to be converted.  |
| <code>curl</code>         | RCurl handle.   |
| <code>fromType</code>     | The type of input IDs. If NULL (default), determined through the popup menu.                                  |
| <code>toType</code>       | The type to convert to. If NULL (default), determined through the popup menu.                                 |
| <code>urlBase</code>      | The DAVID main page url. Default is DAVIDURLBase.   |
| <code>testMe</code>       | If TRUE, assign default values and run. Default is FALSE.   |
| <code>annotChoices</code> | All available 'From' and 'To' ID conversion types.  |
| <code>details</code>      | If TRUE, a list of intermediate results is returned; otherwise, just the final query result. Default is TRUE. |
| <code>graphicMenu</code>  | If TRUE, use a GUI window for the pick menus. Default is FALSE.   |
| <code>writeHTML</code>    | If TRUE writes the conversion result html page into the 'conversionResult.html' file. Default is FALSE.       |
| <code>verbose</code>      | If TRUE enables diagnostic messages.  |

## Details

Due to the recent redesign of the DAVID online query system, it is no longer possible to use the DAVID API (as described in the documentation for `DAVIDQuery`) to perform gene ID conversion. For this reason, the gene ID conversion is implemented as a separate function programmatically reproducing the Gene ID Conversion tool workflow as follows. First, the list of IDs to be converted from the given ID type is submitted to the DAVID tools service using the HTTP message post. Second, the DAVID check 'at least 80 percent of samples should be mapped' turned off by accessing the hidden URL "submitAnyway.jsp" This ensures that the input ID list can contain any percentage of correct IDs and still be mapped properly. Third, the request for ID conversion is sent by posting the HTTP message to the DAVID conversion service. The resulting page is scrapped, the URL of the conversion result file is obtained and the file is retrieved. As the conversion results file is a well formatted table represented by a tab delimited .txt file, no further formatting of the `DAVIDQueryResult` is needed.

## Value

A `DAVIDQuery` result. The informative part is a data frame consisting of columns 'From', 'To', 'Species' and 'Gene.Name'. The 'From' column contains ID list submitted for conversion, the 'To' column contains the conversion results, while 'Species' and 'Gene.Name' contain species and gene description, correspondingly. The IDs for which conversion is not found (ambiguous IDs in DAVID terms) are not returned. The missing IDs can be found comparing the input ID set and the unique ID set in the 'From' column. If no conversion at all is found the function returns `NULL`.

## Author(s)

Roger Day, Alex Lisovich

## See Also

[DAVIDQuery](#), [getIdConversionChoices](#)

## Examples

```
## Not run:
idList=c("P04264", "P13645");
data<-convertIDList(idList,fromType="UNIPROT_ACCESSION",toType="AFFYMETRIX_3PRIME_IVT_ID")

## End(Not run)
```

---

`formatDAVIDResult` *Format the character table returned by DAVID.*

---

## Description

These functions attempt to format the character table `result` returned by DAVID.

**Usage**

```

formatDAVIDResult(result, verbose=FALSE)
formatAnnotationReport(result)
formatGeneReport(result)
formatGeneReportFull(result)
formatList(result)
formatGene2Gene(result)

```

**Arguments**

|         |   |
|---------|---|
| result  | Character table returned by DAVID.  |
| verbose | If TRUE, print tool. Warn if tool=="geneReportFull" that the result will be returned invisibly due to its size. |

**Details**

formatDAVIDResult switches out to one of formatGeneReport, formatGeneReportFull, formatGene2Gene, or formatList, depending on the tool argument of DAVIDQuery() used to specify what query report to do. The tool argument is passed as an attribute attached to result.

**WARNINGS:** Not all values of tool have an associated format.

These format utilities are not guaranteed to work correctly for all combinations of inputs into DAVIDQuery(), or to continue to work correctly if or when the DAVID API changes. If results appear incorrect, one can use the option DAVIDQuery(formatIt=FALSE) to see the unformatted output, and/or paste DAVIDQuery(details=TRUE) [firstURL] into a browser.

In the case of formatGene2Gene, the gene column of the details component might not always contain a single identifier.

**Value**

For tool=="geneAnnotationReport", a list, one component for each element in the ids arg. Each component has subcomponents

|               |  |
|---------------|--|
| Gene Name     | Self-explanatory.  |
| Species       | Self-explanatory.  |
| <id>          | The identifier(s) in the query. The name is whatever the id type was.  |
| <other items> | Items produced for the input, specified by the annot arg of the query. |

For tool=="geneReport" or tool=="list", a character matrix with column names scraped from DAVIDQueryResult, usually:

|             |  |
|-------------|--|
| <gene name> | Using the same ID type as the type argument of DAVIDQuery(). |
| Gene Name   | Self-explanatory.  |
| Species     | Self-explanatory.  |

In addition, for tool=="geneReport", the first line of the returned output is saved as an attribute before discarding it.

For tool=="geneReportFull", a list, one component for each element in the ids arg. Each component has subcomponents

Gene Name      Self-explanatory.  
 Species        Self-explanatory.  
 <other items>  
                  The union of items produced for the input identifiers (generically called "genes"  
                  in DAVID). (The set of attributes is not fixed.)

For `tool=="formatGene2Gene"`, a list with one component for each Functional Group. Each component has components

median         See DAVID documentation.  
 geo            See DAVID documentation.  
 diagram        An attempt to parse the fourth column of the Functional Group line of the input.  
                  See DAVID documentation and consult the DAVID team.  
 details        A data frame with columns  
                  **gene** "gene" as identified in the `ids` arg to `DAVIDQuery`  
                  **geneName** gene name  
                  **url** The URL for the Gene Report page at NIAID.

As of this writing, the tool choices corresponding to most Functional Annotation tools cannot be handled by this package.

---

`getAffyChipTypes`      *Retrieve all Affymetrix array type available from DAVID database.*

---

## Description

Retrieve all Affymetrix array type available from DAVID database.

## Usage

```
getAffyChipTypes(urlBase=DAVIDURLBase, curl=RCurl::getCurlHandle(),
  verbose=TRUE)
```

## Arguments

`urlBase`        the DAVID main page url. Default is `DAVIDURLBase`.  
`curl`            `RCurl` handle. Default is `getCurlHandle()`  
`verbose`        if `TRUE` enables diagnostic messages

## Details

When the `getAffyChipTypes` gets called the first time within the R session, it retrieves the set of annotation values from the DAVID web services, stores them within the `DAVIDAffyChipChoices` data structure and then reuses it in subsequent calls.

## Value

data frame containing (name,value) pair columns The first column is a decorated Affymetrix array name, i.e. the name which appears in the corresponding drop-down list on the DAVID web site. The second column is an actual DAVID URL address of the file containing the Affymetrix probeset IDs

**Author(s)**

Roger Day, Alex Lisovich

**See Also**

[getAnnotationChoices](#), [getIdConversionChoices](#), [getAffyProbesetList](#), [DAVIDQuery](#)

**Examples**

```
## Not run:
#retrieve the set of all possible Affymetrix array types
chipTypes<-getAffyChipTypes();
#display choice dialog
item<-menu(graphics = TRUE, title = "Select Array Type", chipTypes[, "name"]);
#retrieve array type for subsequent usage
ident<-chipTypes[item, "value"];

## End(Not run)
```

---

```
getAffyProbesetList
```

*Retrieve Affy probeset IDs from DAVID.*

---

**Description**

For a given Affymetrix microarray chip, retrieve Affy probeset IDs from DAVID. Optionally, a menu is used to pick the chip name.

**Usage**

```
getAffyProbesetList(chipname = NULL, menu = TRUE, verbose=FALSE)
```

**Arguments**

|          |   |
|----------|---|
| chipname | Full name or regular expression.                                  |
| menu     | Select chipname from a menu (default=TRUE)                        |
| verbose  | Print a bit of tracing information along the way (default=FALSE). |

**Details**

If menu==TRUE, DAVID's table of chip names is retrieved. If chipname is a regular expression, then the menu (if requested) is subsetted accordingly. When the user selects or specifies one of the names, the associated file of probeset names is retrieved, again directly from DAVID, not from Affymetrix.

**Value**

Character vector of probeset names with 'chipType' attribute containing the chip name.

**Note**

Use with caution. The returned file is not guaranteed to be correct. In the example above, with the chip "Human Genome U133 Plus 2.0", the list returned includes 40907 probeset IDs on the chip (and no others), but appears to be missing 13768 others.

**Author(s)**

Roger Day, Alex Lisovich

**Examples**

```
head(getAffyProbesetList("Human Genome U133 Plus 2.0", menu=FALSE, verbose=TRUE))
## Not run:
length(getAffyProbesetList("133|95"))

## End(Not run)
```

---

getAnnotationChoices

*Retrieve all possible annotation values used in the annotation report tool...*

---

**Description**

Retrieve all possible annotation values used in the annotation report tool

**Usage**

```
getAnnotationChoices(urlBase=DAVIDURLBase, curl=RCurl::getCurlHandle(),
  verbose=TRUE)
```

**Arguments**

|         |   |
|---------|---|
| urlBase | the DAVID main page url. Default is DAVIDURLBase. |
| curl    | RCurl handle. Default is getCurlHandle()          |
| verbose | if TRUE enables diagnostic messages               |

**Details**

When the getAnnotationChoices gets called the first time within the R session, it retrieves the set of annotation values from the DAVID web services, stores them within the DAVIDAnnotChoices data structure and then reuses it in subsequent calls.

**Value**

the list of possible annotation tags, i.e. GOTERM\_MF\_4, GOTERM\_MF\_5, BLOCKS\_ID etc. used with the annotationReport tool.

**Author(s)**

Roger Day, Alex Lisovich

**See Also**

[getIdConversionChoices](#), [getAffyChipTypes](#), [convertIDList](#), [DAVIDQuery](#)

**Examples**

```
## Not run:
#retrieve annotation values
annotChoices<-getAnnotationChoices();
#display choice dialog
item<-menu(graphics = TRUE, title = "Select Identifier",  annotChoices$from[, "name"]);
#retrieve identifier for subsequent conversion
ident<-annotChoices$from[item, "value"];

## End(Not run)
```

---

```
getIdConversionChoices
```

*Retrieve all possible values defining the type of the submitted ID list as well as...*

---

**Description**

Retrieve all possible values defining the type of the submitted ID list as well as the type of conversion when using the ID conversion tool

**Usage**

```
getIdConversionChoices(urlBase=DAVIDURLBase,
  curl=RCurl::getCurlHandle(), verbose=TRUE)
```

**Arguments**

|         |   |
|---------|---|
| urlBase | the DAVID main page url. Default is DAVIDURLBase. |
| curl    | RCurl handle. Default is getCurlHandle()          |
| verbose | if TRUE enables diagnostic messages               |

**Details**

When the `getIdConversionChoices` gets called the first time within the R session, it retrieves the set of annotation values from the DAVID web services, stores them within the `DAVIDTypeChoices` data structure and then reuses it in subsequent calls.

**Value**

the list containing two data frames, 'to' and 'from', the first representing set of possible identifiers used when submitting the ID list, and the second representing set of possible identifiers the ID list can be converted to

**Author(s)**

Roger Day, Alex Lisovich

**See Also**

[getAnnotationChoices](#), [getAffyChipTypes](#), [convertIDList](#), [DAVIDQuery](#)

**Examples**

```
## Not run:
#retrieve the ID set for conversion
idChoices<-getIdConversionChoices();
#display choice dialog
item<-menu(graphics = TRUE, title = "Select Identifier", idChoices$from[, "name"]);
#retrieve identifier for subsequent conversion
ident<-idChoices$from[item, "value"];

## End(Not run)
```

---

|               |                      |
|---------------|----------------------|
| idExampleList | <i>idExampleList</i> |
|---------------|----------------------|

---

**Description**

List of ids used in DAVID examples on page [http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID\\_API.html](http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html)

**See Also**

[testGene2Gene](#)

---

|               |                                  |
|---------------|----------------------------------|
| testGene2Gene | <i>Test DAVID gene2gene tool</i> |
|---------------|----------------------------------|

---

**Description**

This function tests and demonstrates the use of DAVIDQuery to access the gene2gene tool.

**Usage**

```
testGene2Gene(ids = "33246_AT, 32469_AT, 1786_AT, 32680_AT, 1355_G_AT, 37968_AT, 33530
```

**Arguments**

|      |   |
|------|---|
| ids  | Arg passed to <a href="#">DAVIDQuery</a> .        |
| type | Arg passed to <a href="#">DAVIDQuery</a> .        |
| ...  | Other args passed to <a href="#">DAVIDQuery</a> . |

**Details**

Input Affy IDS are taken from the example on the DAVID web site.

**Value**

The value returned by DAVIDQuery using tool=gene2gene.

**Author(s)**

Roger Day

**See Also**

[DAVIDQuery](#)

**Examples**

```
testGene2Gene(details=FALSE)
### Run example from http://david.abcc.ncifcrf.gov/gene2gene.jsp
testGene2Gene(ids=idExampleList, type="ENTREZ_GENE_ID", details=FALSE)
### Run example from http://david.abcc.ncifcrf.gov/content.jsp?file=DAVID_API.html
```

---

uniprotToAffy

*Obtain Affymetrix probeset IDs for given Uniprot IDs.*

---

**Description**

Obtain Affymetrix probeset IDs for given Uniprot IDs, using DAVIDQuery.

**Usage**

```
uniprotToAffy(uid = "000161", ...)
```

**Arguments**

|     |  |
|-----|--|
| uid | Uniprot IDs, either a string with the IDs separated by commas, or else a character vector. |
| ... | Args to be passed to DAVIDQuery().   |

**Value**

The output of [DAVIDQuery](#). If only the DAVIDQueryResult component is desired, include the arg details=FALSE. If probesets from a specific chip are desired, then you can intersect these results with the results of [getAffyProbesetList](#).

**Note**

There is currently no provision for using [DAVIDQueryLoop](#).

**Author(s)**

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**See Also**

[DAVIDQuery](#)

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