

# Package ‘**ontoProc**’

April 15, 2020

**Title** processing of ontologies of anatomy, cell lines, and so on

**Description** Support harvesting of diverse bioinformatic ontologies, making particular use of the ontologyIndex package on CRAN. We provide snapshots of key ontologies for terms about cells, cell lines, chemical compounds, and anatomy, to help analyze genome-scale experiments, particularly cell x compound screens. Another purpose is to strengthen development of compelling use cases for richer interfaces to emerging ontologies.

**Version** 1.8.1

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**Imports** Biobase, S4Vectors, methods, AnnotationDbi, stats, utils, shiny, graph, Rgraphviz, ontologyPlot, dplyr, magrittr

**Suggests** knitr, org.Hs.eg.db, org.Mm.eg.db, testthat, BiocStyle

**Depends** R (>= 3.5), ontologyIndex

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**License** Artistic-2.0

**LazyLoad** yes

**LazyData** yes

**biocViews** Infrastructure, GO

**RoxygenNote** 6.1.1

**VignetteBuilder** knitr

**Encoding** UTF-8

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

**git\_branch** RELEASE\_3\_10

**git\_last\_commit** 5447ef6

**git\_last\_commit\_date** 2020-03-08

**Date/Publication** 2020-04-14

## R topics documented:

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|            |  |
|------------|--|
| allGOterms | <i>allGOterms: data.frame with ids and terms</i> |
|------------|--|

---

**Description**

allGOterms: data.frame with ids and terms

**Usage**

allGOterms

**Format**

data.frame instance

**Source**

This is a snapshot of all the terms available from GO.db (3.4.2), August 2017, using keys(GO.db, keytype="TERM").

**Examples**

```
data(allGOterms)
head(allGOterms)
```

---

|                  |                                  |
|------------------|----------------------------------|
| c,TermSet-method | <i>combine TermSet instances</i> |
|------------------|----------------------------------|

---

**Description**

combine TermSet instances

**Usage**

```
## S4 method for signature 'TermSet'
c(x, ...)
```

**Arguments**

|     |                      |
|-----|----------------------|
| x   | TermSet instance     |
| ... | additional instances |

**Value**

TermSet instance

---

|              |   |
|--------------|---|
| cellTypeToGO | <i>utilities for approximate matching of cell type terms to GO categories and annotations</i> |
|--------------|---|

---

**Description**

utilities for approximate matching of cell type terms to GO categories and annotations

**Usage**

```
cellTypeToGO(celltypeString, gotab, ...)

cellTypeToGenes(celltypeString, gotab, orgDb, cols = c("ENSEMBL",
"SYMBOL"), ...)
```

**Arguments**

|                |  |
|----------------|--|
| celltypeString | character atom to be used to search GO terms using                                 |
| gotab          | a data.frame with columns GO (goids) and TERM (term strings) <a href="#">agrep</a> |
| ...            | additional arguments to <a href="#">agrep</a>                                      |
| orgDb          | instances of orgDb   |
| cols           | columns to be retrieved in select operation  |

**Value**

data.frame  
data.frame

**Note**

Very primitive, uses agrep to try to find relevant terms.

**Examples**

```
data(allGOterms)
library(org.Hs.eg.db)
head(cellTypeToGO("serotonergic neuron", allGOterms))
head(cellTypeToGenes("serotonergic neuron", allGOterms, org.Hs.eg.db))
```

---

|              |  |
|--------------|--|
| cleanCLNames | <i>obtain named character vector of terms from Cell Line Ontology, omitting obsolete and trailing 'cell'</i> |
|--------------|--|

---

**Description**

obtain named character vector of terms from Cell Line Ontology, omitting obsolete and trailing 'cell'

**Usage**

```
cleanCLNames()
```

**Value**

character()

**Examples**

```
cleanCLNames()[1:10]
```

---

|         |   |
|---------|---|
| CLfeats | <i>produce a data.frame of features relevant to a Cell Ontology class</i> |
|---------|---|

---

**Description**

produce a data.frame of features relevant to a Cell Ontology class

**Usage**

```
CLfeats(ont, tag = "CL:0001054")
```

**Arguments**

|     |                                    |
|-----|------------------------------------|
| ont | instance of ontologyIndex ontology |
| tag | character(1) a CL: class tag       |

**Value**

a data.frame instance

**Note**

This function will look in the intersection\_of and has\_part, lacks\_part components of the CL entry to find properties asserted of or inherited by the cell type identified in 'tag'

**Examples**

```
cl = getCellOnto()
pr = getPROnto()
go = getGeneOnto()
CLfeats(cl, tag="CL:0001054")
```

---

ctmarks

*app to review molecular properties of cell types via cell ontology*

---

**Description**

app to review molecular properties of cell types via cell ontology

**Usage**

```
ctmarks(cl)
```

**Arguments**

cl                    an import of a Cell Ontology (or extended Cell Ontology) in ontology\_index form

**Value**

a data.frame with features for selected cell types

**Note**

Prototype of harvesting of cell ontology by searching has\_part, has\_plasma\_membrane\_part, intersection\_of and allied ontology relationships. Uses shiny. Can perform better if getPROnto() and getGeneOnto() values are in .GlobalEnv as pr and go respectively.

---

|              |  |
|--------------|--|
| cyclicSigset | <i>as in Bakken et al. (2017 PMID 29322913) create gene signatures for k cell types, each of which fails to express all but one gene in a set of k genes</i> |
|--------------|--|

---

### Description

as in Bakken et al. (2017 PMID 29322913) create gene signatures for k cell types, each of which fails to express all but one gene in a set of k genes

### Usage

```
cyclicSigset(idvec, conds = c("hasExp", "lacksExp"),
  tags = paste0("CL:X", 1:length(idvec)))
```

### Arguments

|       |   |
|-------|---|
| idvec | character vector of identifiers, must have names() set to identify cells bearing genes                                |
| conds | character(2) tokens used to indicate condition to which signature element contributes                                 |
| tags  | character vector of cell-type identifiers; for Cell Ontology use CL: as prefix, one element for each element of idvec |

### Value

a long data.frame

### Examples

```
sigels = c("CL:X01"="GRIK3", "CL:X02"="NTNG1", "CL:X03"="BAGE2",
  "CL:X04"="MC4R", "CL:X05"="PAX6", "CL:X06"="TSPAN12", "CL:X07"="hSHISA8",
  "CL:X08"="SNCG", "CL:X09"="ARHGEF28", "CL:X10"="EGF")
sigdf = cyclicSigset(sigels)
head(sigdf)
```

---

|         |   |
|---------|---|
| demoApp | <i>demonstrate the use of makeSelectInput</i> |
|---------|---|

---

### Description

demonstrate the use of makeSelectInput

### Usage

```
demoApp()
```

### Value

Run only for side effect of starting a shiny app.

**Examples**

```

if (interactive()) {
  require(shiny)
  print(demoApp())
}

```

---

dropStop

*dropStop is a utility for removing certain words from text data*


---

**Description**

dropStop is a utility for removing certain words from text data

**Usage**

```
dropStop(x, drop, lower = TRUE, splitby = " ")
```

**Arguments**

|         |  |
|---------|--|
| x       | character vector of strings to be cleaned                  |
| drop    | character vector of words to scrub                         |
| lower   | logical, if TRUE, x converted with <a href="#">tolower</a> |
| splitby | character, used with strsplit to tokenize x                |

**Value**

a list with one element per input string, split by " ", with elements in drop removed

**Examples**

```

data(minicorpus)
minicorpus[1:3]
dropStop(minicorpus)[1:3]

```

---

fastGrep

*some fields of interest are lists, and grep per se should not be used – this function checks and uses grep within vapply when appropriate*


---

**Description**

some fields of interest are lists, and grep per se should not be used – this function checks and uses grep within vapply when appropriate

**Usage**

```
fastGrep(patt, onto, field, ...)
```

**Arguments**

|       |  |
|-------|--|
| patt  | a regular expression whose presence in field should be checked |
| onto  | an ontologyIndex instance                                      |
| field | the ontologyIndex component to be searched                     |
| ...   | passed to grep   |

**Value**

logical vector indicating vector or list elements where a match is found

**Examples**

```
cheb = getChebiOnto()
ind = fastGrep("17-AAG", cheb, "synonym")
cheb$name[ind]
```

---

|             |  |
|-------------|--|
| getCellOnto | <i>load ontologies that may include non-ascii strings and therefore cannot be in data folder</i> |
|-------------|--|

---

**Description**

load ontologies that may include non-ascii strings and therefore cannot be in data folder

**Usage**

```
getCellOnto(useNew = TRUE)
getCellLineOnto()
getEF0Onto()
getChebiLite()
getCellosaurusOnto()
getUBERON_NE()
getChebiOnto()
getOncotreeOnto()
getDiseaseOnto()
getGeneOnto()
getHCAOnto()
getPROnto()
getPATOnto()
```



**Arguments**

useNew                    logical(1) only for getCellOnto if TRUE cell ontology of July 2018, otherwise use legacy

**Value**

instance of ontology\_index (S3) from ontologyIndex  
instance of ontology\_index (S3) from ontologyIndex

**Note**

Provenance information is kept in the form of excerpts of top records in `'dir(system.file("obo", package="ontoProc"), full=TRUE)'`

getChebiOnto loads ontoRda/chebi\_full.rda

getOncotreeOnto loads ontoRda/oncotree.rda

getDiseaseOnto loads ontoRda/diseaseOnto.rda

getHCAOnto loads ontoRda/hcaOnto.rda produced from hcao.owl at <https://github.com/HumanCellAtlas/ontology/releases> 2/11/2019, python pronto was used to convert OWL to OBO.

getPROnto loads ontoRda/PROnto.rda, produced from <http://purl.obolibrary.org/obo/pr.obo> 'reasoned' ontology from OBO foundry, 02-08-2019. In contrast to other ontologies, this is imported via get\_OBO with 'extract\_tags='minimal''.

getPATOnto loads ontoRda/patoOnto.rda, produced from <https://raw.githubusercontent.com/pato-ontology/pato/master/pato.obo> from OBO foundry, 02-08-2019.

**Examples**

```
co = getCellOnto(useNew=TRUE)
co
clo = getCellLineOnto()
length(clo$id)
che = getChebiLite()
length(che$id)
efo = getEFOnto()
length(efo$id)
```

---

getLeavesFromTerm            *obtain childless descendents of a term (including query)*

---

**Description**

obtain childless descendents of a term (including query)

**Usage**

```
getLeavesFromTerm(x, ont)
```

**Arguments**

x                            a character(1) id element for ontology\_index instance  
ont                           an ontology\_index instance as defined in ontologyIndex package

**Value**

character vector of 'leaves' of ontology tree

**Examples**

```
ch = getChebiOnto()
alldr = getLeavesFromTerm("CHEBI:23888", ch)
head(ch$name[alldr[1:15]])
```

---

humrna

*humrna: a data.frame of SRA metadata related to RNA-seq in humans*

---

**Description**

humrna: a data.frame of SRA metadata related to RNA-seq in humans

**Usage**

```
humrna
```

**Format**

data.frame

**Note**

arbitrarily chosen from RNA-seq studies for taxon 9606

**Source**

NCBI SRA

**Examples**

```
data(humrna)
names(humrna)
head(humrna[, 1:5])
```

---

|              |   |
|--------------|---|
| improveNodes | <i>inject linefeeds for node names for graph, with textual annotation from ontology</i> |
|--------------|---|

---

**Description**

inject linefeeds for node names for graph, with textual annotation from ontology

**Usage**

```
improveNodes(g, ont)
```

**Arguments**

|     |   |
|-----|---|
| g   | graphNEL instance                       |
| ont | instance of ontology from ontologyIndex |

---

|            |  |
|------------|--|
| ldfToTerms | <i>use output of cyclicSigset to generate a series of character vectors constituting OBO terms</i> |
|------------|--|

---

**Description**

use output of cyclicSigset to generate a series of character vectors constituting OBO terms

**Usage**

```
ldfToTerms(ldf, propmap, sigels, prologMaker = function(id, ...)
  sprintf("id: %s", id))
```

**Arguments**

|             |   |
|-------------|---|
| ldf         | a 'long format' data.frame as created by cyclicSigset   |
| propmap     | a character vector with names of elements corresponding to 'abbreviated' relationship tokens and element values corresponding to full relationship-naming strings |
| sigels      | a named character vector associating cell types (names) to genes expressed in a cyclic set, one element per type  |
| prologMaker | a function with arguments (id, ...), in which id is character(1), that generates a vector of strings that will be used for each cell type-specific term.          |

**Value**

a character vector, strings can be concatenated to OBO

**Note**

ldfToTerms is not sufficiently general to produce terms for any reasonably populated long data frame/propmap combination, but it is a working example for the cyclic set context.

**Examples**

```

# a set of cell types -- names are cell type token, values are genes expressed in a
# cyclic set -- each cell type expresses exactly one gene in the set and fails to
# express all the other genes in the set. See Figs 3 and 4 of Bakken et al [PMID 29322913].
sigels = c("CL:X01"="GRIK3", "CL:X02"="NTNG1", "CL:X03"="BAGE2",
           "CL:X04"="MC4R", "CL:X05"="PAX6", "CL:X06"="TSPAN12", "CL:X07"="hSHISA8",
           "CL:X08"="SNCG", "CL:X09"="ARHGEF28", "CL:X10"="EGF")
# create the associated long data frame
ldf = cyclicSigset(sigels)
# describe the abbreviations
pmap = c("hasExp"="has_expression_of", lacksExp="lacks_expression_of")

# now define the prolog for each cell type
makeIntnProlog = function(id, ...) {
# make type-specific prologs as key-value pairs
  c(
    sprintf("id: %s", id),
    sprintf("name: %s-expressing cortical layer 1 interneuron, human", ...),
    sprintf("def: '%s-expressing cortical layer 1 interneuron, human described via RNA-seq observations' [PMID
            "is_a: CL:0000099 ! interneuron",
            "intersection_of: CL:0000099 ! interneuron")
  )
}
tms = ldfToTerms(ldf, pmap, sigels, makeIntnProlog)
cat(tms[[1]], sep="\n")

```

liberalMap

*Produce a data.frame with a set of naive terms mapped to all matching ontology ids and their formal terms*

**Description**

Produce a data.frame with a set of naive terms mapped to all matching ontology ids and their formal terms

**Usage**

```
liberalMap(terms, onto, useAgrep = FALSE, ...)
```

**Arguments**

|          |   |
|----------|---|
| terms    | character() vector, can use grep-compatible regular expressions |
| onto     | an instance of ontologyIndex::ontology_index                    |
| useAgrep | logical(1) if TRUE, agrep will be used                          |
| ...      | passed to agrep if used   |

**Value**

a data.frame

**Examples**

```
cands = c("astrocyte$", "oligodendrocyte", "oligodendrocyte precursor",
  "neoplastic", "^neuron$", "^vascular", "badterm")
co = ontoProc::getCellOnto()
liberalMap(cands, co)
```

---

|                 |  |
|-----------------|--|
| makeSelectInput | <i>generate a selectInput control for an ontologyIndex slice</i> |
|-----------------|--|

---

**Description**

generate a selectInput control for an ontologyIndex slice

**Usage**

```
makeSelectInput(onto, term, type = "siblings", inputId, label,
  multiple = TRUE, ...)
```

**Arguments**

|          |   |
|----------|---|
| onto     | ontologyIndex instance  |
| term     | character(1) term used as basis for term list option set in the control                     |
| type     | character(1) 'siblings' or 'children', relationship to 'term' that the options will satisfy |
| inputId  | character(1) for use in server  |
| label    | character(1) for labeling in ui   |
| multiple | logical(1) passed to <a href="#">selectInput</a>  |
| ...      | additional parameters passed to <a href="#">selectInput</a>                                 |

**Value**

a [selectInput](#) control

**Examples**

```
makeSelectInput
```

---

```
make_graphNEL_from_ontology_plot
```

*obtain graphNEL from ontology\_plot instance of ontologyPlot*

---

### Description

obtain graphNEL from ontology\_plot instance of ontologyPlot

### Usage

```
make_graphNEL_from_ontology_plot(x)
```

### Arguments

x                    instance of S3 class ontology\_plot

### Value

instance of S4 graphNEL class

### Examples

```
requireNamespace("Rgraphviz")
requireNamespace("graph")
c1 = getCellOnto()
c13k = c("CL:0000492", "CL:0001054", "CL:0000236", "CL:0000625",
        "CL:0000576", "CL:0000623", "CL:0000451", "CL:0000556")
p3k = ontologyPlot::onto_plot(c1, c13k)
gnel = make_graphNEL_from_ontology_plot(p3k)
gnel = improveNodes(gnel, c1)
graph::graph.par(list(nodes=list(shape="plaintext", cex=.8)))
gnel = Rgraphviz::layoutGraph(gnel)
Rgraphviz::renderGraph(gnel)
```

---

```
mapOneNaive
```

*use grep or agrep to find a match for a naive token into ontology*

---

### Description

use grep or agrep to find a match for a naive token into ontology

### Usage

```
mapOneNaive(naive, onto, useAgrep = FALSE, ...)
```

### Arguments

naive                character(1)  
 onto                an instance of ontologyIndex::ontology\_index  
 useAgrep            logical(1) if TRUE, agrep will be used  
 ...                 passed to agrep if used

**Value**

if a match is found, the result of `grep/agrep` with `value=TRUE` is returned; otherwise a named `NA_character_` is returned

named vector, names are ontology identifiers, values are matched strings

**Examples**

```
co = ontoProc::getCellOnto()
mapOneNaive("astrocyte", co)
```

---

|            |   |
|------------|---|
| minicorpus | <i>minicorpus: a vector of annotation strings found in 'study title' of SRA metadata.</i> |
|------------|---|

---

**Description**

minicorpus: a vector of annotation strings found in 'study title' of SRA metadata.

**Usage**

```
minicorpus
```

**Format**

character vector

**Note**

arbitrarily chosen from titles of RNA-seq studies for taxon 9606

**Source**

NCBI SRA

**Examples**

```
data(minicorpus)
head(minicorpus)
```

---

|              |  |
|--------------|--|
| nomenCheckup | <i>repair nomenclature mismatches (to curated term set) in a vector of terms</i> |
|--------------|--|

---

**Description**

repair nomenclature mismatches (to curated term set) in a vector of terms

**Usage**

```
nomenCheckup(cand, namedOffic, n = 1, tagcolname = "tag", ...)
```

**Arguments**

|            |   |
|------------|---|
| cand       | character vector of candidate terms   |
| namedOffic | named character vector of curated terms, the names are regarded as tags, intended to be identifiers in curated ontologies |
| n          | numeric(1) number of nearest neighbors to return  |
| tagcolname | character(1) prefix used to name columns for tags in output   |
| ...        | passed to <a href="#">adist</a>   |

**Value**

a data.frame instance with 2n+1 columns (column 1 is candidate, remaining n pairs of columns are (term, tag) for n nearest neighbors as measured by [adist](#)).

**Examples**

```

candidates = c("JHH7", "HUT102", "HS739T", "NCIH716")
# the candidates are cell line names returned in the text dump from
# https://portals.broadinstitute.org/ccle/page?gene=AHR
# note that one must travel to the third nearest neighbor
# to find the match (and tag) for Hs 739.T
# in this example, we compare to cell line names in Cell Line Ontology
nomenCheckup(candidates, cleanCLOnames(), n=3, tagcolname="clo")

```

---

|            |   |
|------------|---|
| onto_plot2 | <i>high-level use of graph/Rgraphviz for rendering ontology relations</i> |
|------------|---|

---

**Description**

high-level use of graph/Rgraphviz for rendering ontology relations

**Usage**

```
onto_plot2(ont, terms2use, cex = 0.8, ...)
```



**Arguments**

ont instance of ontology from ontologyIndex  
 terms2use character vector  
 cex numeric(1) defaults to .8, supplied to Rgraphviz::graph.par  
 ... passed to onto\_plot of ontologyPlot

**Examples**

```
c1 = getCellOnto()
c13k = c("CL:0000492", "CL:0001054", "CL:0000236", "CL:0000625",
        "CL:0000576", "CL:0000623", "CL:0000451", "CL:0000556")
onto_plot2(c1, c13k)
```

onto\_roots *list parentless nodes in ontology\_index instance*

**Description**

list parentless nodes in ontology\_index instance

**Usage**

```
onto_roots(x)
```

**Arguments**

x an ontology\_index instance

**Value**

a report (produced by cat()) of root ids and associated names

**Examples**

```
onto_roots
```

packDesc2019 *packDesc2019: overview of ontoProc resources*

**Description**

packDesc2019: overview of ontoProc resources

**Usage**

```
packDesc2019
```

**Format**

data.frame instance

**Note**

Brief survey of functions available to load serialized ontology\_index instances imported from OBO.

**Examples**

```
head(packDesc2019)
```

---

PROSYM

*PROSYM: HGNC symbol synonyms for PR (protein ontology) entries identified in Cell Ontology*

---

**Description**

PROSYM: HGNC symbol synonyms for PR (protein ontology) entries identified in Cell Ontology

**Usage**

```
PROSYM
```

**Format**

```
data.frame instance
```

**Note**

This is a snapshot of the synonyms component of an `extract_tags='everything'` import of PR. The `'EXACT.*PRO-short.*:DNx'` pattern is used to retrieve HGNC symbols. See `?getPROnto` for more provenance information.

**Source**

OBO Foundry

**Examples**

```
data(PROSYM)
head(PROSYM)
```

---

recognizedPredicates    *enumerate ontological relationships used in ontoProc utilities*

---

**Description**

enumerate ontological relationships used in ontoProc utilities

**Usage**

```
recognizedPredicates()
```

**Value**

character vector, names of elements are abbreviated tokens that may be used in code

**Examples**

```
head(recognizedPredicates())
```

---

secLevGen                    *simple generation of children of 'choices' given as terms, returned as TermSet*

---

**Description**

simple generation of children of 'choices' given as terms, returned as TermSet

**Usage**

```
secLevGen(choices, ont)
```

**Arguments**

choices                    vector of terms  
ont                         instance of ontology\_index (S3) from ontologyIndex package

**Value**

TermSet instance

**Examples**

```
efoOnto = getEF0Onto()  
secLevGen( "disease", efoOnto )
```

---

|               |   |
|---------------|---|
| selectFromMap | <i>select a set of elements from a term 'map' and return a contribution to a data.frame</i> |
|---------------|---|

---

**Description**

select a set of elements from a term 'map' and return a contribution to a data.frame

**Usage**

```
selectFromMap(namedvec, index)
```

**Arguments**

|          |  |
|----------|--|
| namedvec | named character vector, as returned from <a href="#">mapOneNaive</a> |
| index    | numeric() or integer(), typically of length one                      |

**Value**

a data.frame; if index does not inherit from numeric, a data.frame of one row with columns 'ontoid' and 'term' populated with NA\_character\_ is returned, otherwise a similarly named data.frame is returned with contents from the selected elements of namedvec

**Examples**

```
co = ontoProc::getCellOnto()
mast = mapOneNaive("astrocyte", co)
selectFromMap(mast, 1)
```

---

|           |   |
|-----------|---|
| seur3kTab | <i>tabulate the basic outcome of PBMC 3K tutorial of Seurat</i> |
|-----------|---|

---

**Description**

tabulate the basic outcome of PBMC 3K tutorial of Seurat

**Usage**

```
seur3kTab()
```

**Value**

a data.frame

**Examples**

```
seur3kTab()
```

---

|              |   |
|--------------|---|
| siblings_TAG | <i>generate a TermSet with siblings of a given term, excluding that term by default</i> |
|--------------|---|

---

### Description

generate a TermSet with siblings of a given term, excluding that term by default  
 acquire the label of an ontology subject tag  
 acquire the labels of children of an ontology subject tag

### Usage

```
siblings_TAG(Tagstring = "EFO:1001209", ontology, justSibs = TRUE)
label_TAG(Tagstring = "EFO:0000311", ontology)
children_TAG(Tagstring = "EFO:1001209", ontology)
```

### Arguments

|           |  |
|-----------|--|
| Tagstring | a character(1) that identifies a term              |
| ontology  | instance of ontology_index (S3) from ontologyIndex |
| justSibs  | character(1)                                       |

### Value

TermSet instance  
 character(1)  
 TermSet instance

### Note

for label\_TAG, Tagstring may be a vector

### Examples

```
efoOnto = getEFOnto()
siblings_TAG( "EFO:1001209", efoOnto )
efoOnto = getEFOnto()
label_TAG( "EFO:0000311", efoOnto )
efoOnto = getEFOnto()
children_TAG( ontology = efoOnto )
```

---

|           |  |
|-----------|--|
| stopWords | <i>stopWords: vector of stop words from xpo6.com</i> |
|-----------|--|

---

**Description**

stopWords: vector of stop words from xpo6.com

**Usage**

stopWords

**Format**

character vector

**Note**

"Stop words" are english words that are assumed to contribute limited semantic value in the analysis of free text.

**Source**

<http://xpo6.com/list-of-english-stop-words/>

**Examples**

```
data(stopWords)
head(stopWords)
```

---

|              |  |
|--------------|--|
| sym2CellOnto | <i>use Cell Ontology and Protein Ontology to identify cell-type defining conditions in which a given gene is named</i> |
|--------------|--|

---

**Description**

use Cell Ontology and Protein Ontology to identify cell-type defining conditions in which a given gene is named

**Usage**

```
sym2CellOnto(sym, cl, pr)
```

**Arguments**

|     |  |
|-----|--|
| sym | gene symbol, must be used in protein ontology as a PRO:DNx exact match token |
| cl  | result of getCellOnto()  |
| pr  | result of getPROnto()  |

**Value**

DataFrame if any hits are found. A field 'cond' abbreviates the identified conditions: (has/lacks)PMP (plasma membrane part) (hi/lo)PMAmt (plasma membrane amount), (has/lacks)Part.

**Note**

Currently just checks for \*plasma\_membrane\_part, \*plasma\_membrane\_amount, and \*Part conditions.

**Examples**

```
if (!exists("cl")) cl = getCellOnto()
if (!exists("pr")) pr = getPROnto()
sym2CellOnto("ITGAM", cl, pr)
sym2CellOnto("FOXP3", cl, pr)
```

---

TermSet-class

*manage ontological data with tags and a DataFrame instance*


---

**Description**

manage ontological data with tags and a DataFrame instance  
abbreviated display for TermSet instances

**Usage**

```
## S4 method for signature 'TermSet'
show(object)
```

**Arguments**

object            instance of TermSet class

**Value**

instance of TermSet

**Examples**

```
efoOnto = getEFOnto()
defsibs = siblings_TAG("EFO:1001209", efoOnto)
class(defsibs)
defsibs
```

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