

# scop.db

February 3, 2010

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scopCHILDREN

*Map SCOP identifiers to their children*

---

## Description

scopCHILDREN maps SCOP entry identifier to their children.

## Details

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

## Examples

```
# Convert to a list
xx <- as.list(scopCHILDREN)
if (length(xx) > 0) {
  xx[2:3]
}
```

---

scopCLASSIFICATION

*Map SCOP identifiers to domain classification*

---

## Description

scopCLASSIFICATION maps SCOP entry identifier to a compact representation of a SCOP domain classification.

## Details

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

**Examples**

```
# Convert to a list
xx <- as.list(scopCLASSIFICATION)
if(length(xx) > 0){
  xx[2:3]
}
```

---

scop\_dbconn

*Collect information about the package annotation DB*


---

**Description**

Some convenience functions for getting a connection object to (or collecting information about) the package annotation DB.

**Usage**

```
scop_dbconn()
scop_dbfile()
scop_dbschema(file="", show.indices=FALSE)
scop_dbInfo()
```

**Arguments**

`file` A connection, or a character string naming the file to print to (see the file argument of the `cat` function for the details).

`show.indices` The CREATE INDEX statements are not shown by default. Use `show.indices=TRUE` to get them.

**Details**

`scop_dbconn` returns a connection object to the package annotation DB. **IMPORTANT:** Don't call `dbDisconnect` on the connection object returned by `scop_dbconn` or you will break all the `AnnDbObj` objects defined in this package!

`scop_dbfile` returns the path (character string) to the package annotation DB (this is an SQLite file).

`scop_dbschema` prints the schema definition of the package annotation DB.

`scop_dbInfo` prints other information about the package annotation DB.

**Examples**

```
## Show the first three rows.
dbGetQuery(scop_dbconn(), "select * from des limit 3")

## The connection object returned by scop_dbconn() was created with:
dbConnect(SQLite(), dbname=scop_dbfile(), cache_size=64000, synchronous=0)

scop_dbschema()

scop_dbInfo()
```

---

`scop.db`*annotation data package*

---

### Description

Welcome to the scop.db annotation Package. The annotation package was built using a downloadable R package - PAnnBuilder (download and build your own). The purpose is to provide detailed information about structural classification of proteins from SCOP database: [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73) Release 1.73, November 2007

Each of these objects has their own manual page detailing where relevant data was obtained along with examples of how to use it. Many of these objects also have a reverse map available. When this is true, expect to usually find relevant information on the same manual page as the forward map.

### Examples

```
# You can learn what objects this package supports with the following command:  
ls("package:scop.db")
```

---

`scopDE`*Map SCOP identifiers to their description*

---

### Description

scopDE maps SCOP entry identifier to their description.

### Details

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

### Examples

```
# Convert to a list  
xx <- as.list(scopDE)  
if(length(xx) > 0){  
  xx[2:3]  
}
```

---

scopMAPCOUNTS	<i>Number of mapped keys for the maps in package scop.db</i>
---------------	--

---

### Description

scopMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package scop.db.

### Details

This "map count" information is precalculated and stored in the package annotation DB. This allows some quality control and is used by the `checkMAPCOUNTS` function defined in AnnotationDbi to compare and validate different methods (like `count.mappedkeys(x)` or `sum(!is.na(as.list(x)))`) for getting the "map count" of a given map.

### See Also

[mappedkeys](#), [count.mappedkeys](#), [checkMAPCOUNTS](#)

### Examples

```
scopMAPCOUNTS
mapnames <- names(scopMAPCOUNTS)
scopMAPCOUNTS[mapnames[1]]
x <- get(mapnames[1])
sum(!is.na(as.list(x)))
count.mappedkeys(x) # much faster!

## Check the "map count" of all the maps in package scop.db
checkMAPCOUNTS("scop.db")
```

---

scopNAME	<i>Map SCOP identifiers to name</i>
----------	-------------------------------------

---

### Description

scopNAME maps SCOP entry identifier to a "short name"

### Details

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

### Examples

```
# Convert to a list
xx <- as.list(scopNAME)
if (length(xx) > 0) {
  xx[2:3]
}
```

---

`scopPARENT`*Map SCOP identifiers to their parents*

---

**Description**

scopPARENT maps SCOP entry identifier to their parents.

**Details**

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

**Examples**

```
# Convert to a list
xx <- as.list(scopPARENT)
if (length(xx) > 0) {
  xx[2:3]
}
```

---

`scopPDB2CF`*Map PDB identifier to SCOP fold entry*

---

**Description**

scopPDB2CF maps a PDB identifier to a vector of SCOP fold entry. The vector name corresponds to the PDB chains.

**Details**

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

**Examples**

```
# Convert to a list
xx <- as.list(scopPDB2CF)
if (length(xx) > 0) {
  xx[2:3]
}
```

---

`scopPDB2CL`*Map PDB identifier to SCOP class identifier*

---

**Description**

scopPDB2CL maps a PDB identifier to a vector of SCOP class identifier. The vector name corresponds to the PDB chains.

**Details**

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

**Examples**

```
# Convert to a list
xx <- as.list(scopPDB2CL)
if(length(xx) > 0){
  xx[2:3]
}
```

---

`scopPDB2DM`*Map PDB identifier to SCOP protein domain identifier*

---

**Description**

scopPDB2DM maps a PDB identifier to a vector of SCOP protein domain identifier. The vector name corresponds to the PDB chains.

**Details**

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

**Examples**

```
# Convert to a list
xx <- as.list(scopPDB2DM)
if(length(xx) > 0){
  xx[2:3]
}
```

---

`scopPDB2FA`*Map PDB identifier to SCOP family identifier*

---

**Description**

scopPDB2FA maps a PDB identifier to a vector of SCOP family identifier. The vector name corresponds to the PDB chains.

**Details**

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

**Examples**

```
# Convert to a list
xx <- as.list(scopPDB2FA)
if(length(xx) > 0){
  xx[2:3]
}
```

---

`scopPDB2PX`*Map PDB identifier to SCOP domain entry identifier*

---

**Description**

scopPDB2PX maps a PDB identifier to a vector of SCP domain entry identifier. The vector name corresponds to the PDB chains.

**Details**

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

**Examples**

```
# Convert to a list
xx <- as.list(scopPDB2PX)
if(length(xx) > 0){
  xx[2:3]
}
```

---

`scopPDB2SF`*Map PDB identifier to SCOP superfamily identifier*

---

**Description**

scopPDB2SF maps a PDB identifier to a vector of SCOP superfamily identifier. The vector name corresponds to the PDB chains.

**Details**

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

**Examples**

```
# Convert to a list
xx <- as.list(scopPDB2SF)
if(length(xx) > 0){
  xx[2:3]
}
```

---

`scopPDB2SP`*Map PDB identifier to SCOP species identifier*

---

**Description**

scopPDB2SP maps a PDB identifier to a vector of SCOP species identifier. The vector name corresponds to the PDB chains.

**Details**

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

**Examples**

```
# Convert to a list
xx <- as.list(scopPDB2SP)
if(length(xx) > 0){
  xx[2:3]
}
```



---

`scopTYPE`*Map SCOP identifiers to their types*

---

**Description**

scopTYPE provides mappings between SCOP entry identifiers and their types.

**Details**

Possible entry types are: cl - class

cf - fold

sf - superfamily

fa - family

dm - protein domain

sp - species

px - domain entry

Mappings were based on data provided by: SCOP ([http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.des.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.hie.scop.txt_1.73); [http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt\\_1.73](http://scop.mrc-lmb.cam.ac.uk/scop/parse/dir.cla.scop.txt_1.73)) on Release 1.73, November 2007

**Examples**

```
# Convert to a list
xx <- as.list(scopTYPE)
if (length(xx) > 0) {
  xx[2:3]
}
```

# Index

## \*Topic **datasets**

scopMAPCOUNTS, 4

AnnDbObj, 2

checkMAPCOUNTS, 4

count.mappedkeys, 4

dbDisconnect, 2

mappedkeys, 4

scop.db, 3

scop\_dbconn, 2

scop\_dbfile (scop\_dbconn), 2

scop\_dbInfo (scop\_dbconn), 2

scop\_dbschema (scop\_dbconn), 2

scopCHILDREN, 1

scopCLASSIFICATION, 1

scopDE, 3

scopMAPCOUNTS, 4

scopNAME, 4

scopPARENT, 5

scopPDB2CF, 5

scopPDB2CL, 6

scopPDB2DM, 6

scopPDB2FA, 7

scopPDB2PX, 7

scopPDB2SF, 8

scopPDB2SP, 8

scopTYPE, 9