

# Package ‘Iyer517’

April 12, 2018

**Version** 1.20.0

**Title** exprSets for Iyer, Eisen et al 1999 Science paper

**Author** Vishy Iyer <vishy@cmgm.stanford.edu>

**Maintainer** Vince Carey <stvjc@channing.harvard.edu>

**Description** representation of public Iyer data  
from <http://genome-www.stanford.edu/serum/clusters.html>

**License** Artistic-2.0

**Depends** Biobase (>= 2.5.5)

**biocViews** ExperimentData

**NeedsCompilation** no

## R topics documented:

get.dna2 . . . . .	1
Iyer517 . . . . .	2
IyerAnnotated . . . . .	3

<b>Index</b>	<b>4</b>
--------------	----------

---

get.dna2	<i>query genbank for an EST accession id</i>
----------	----------------------------------------------

---

## Description

extends the get.dna function of E Paradis CRAN package "ape"

## Usage

```
get.dna2(access.nb)
```

## Arguments

access.nb      an EST accession id

## Details

queries ncbi

**Value**

a vector of nucleotide codes

**Note**

try `ape::get.dna` if this fails

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**See Also**

`ape::get.dna`

**Examples**

```
if (interactive())
{
  data(IyerAnnotated)
  get.dna2(IyerAnnotated$GB[1])
}
```

---

Iyer517

*exprSet* instance *Iyer517*, time series on transcriptional response of fibroblasts to serum

---

**Description**

an expression set for timed measurements of transcriptional response of fibroblasts to serum in presence or absence of cycloheximide

**Slots**

**exprs:** Object of class matrix, value: 517 x 19 expression levels (normed to 1 at time 0)  
**se.exprs:** Object of class matrix, value: absent  
**description:** Object of class MIAME, value: string  
**annotation:** Object of class character, value: ""  
**notes:** Object of class character, value: ""  
**phenoData:** Object of class phenoData, value: data frame with info on timing  
**class:** Object of class character, value: 'exprSet'

**References**

Iyer et al 1999 Science v283 83-87

**Examples**

```
data(Iyer517)
show(Iyer517)
plot(apply(exprs(Iyer517)[1:100,1:13],2,mean),main="Cluster A",
      xlab="index in time seq", ylab="ratio to time 0", log="y")
```

---

IyerAnnotated	<i>Partly annotated version of Iyer517 data</i>
---------------	-------------------------------------------------

---

**Description**

GenBank ids, LocusLink ids (where available) and GO tags (where available) for the 517 cDNAs in the dataset.

**Usage**

```
data(IyerAnnotated); data(Iyer517GO)
```

**Format**

**Iyer517GO**: An environment with keys given by the 'GB' identifiers of probes and values given by vectors of GO tags (named by evidence codes) obtained via locuslink mapping

**IyerAnnotated**: A data frame with 517 observations on the following 9 variables.

**Iclust** a factor with levels N A B ... – the cluster groups A-J of the Iyer paper, with N for those rows that were not clustered

**GB** a factor with levels AA001025 AA001722 ... accession numbers (often genbank) for probes

**seqno** a numeric vector indicating the order of the cDNA in the Iyer report on clustering. (Elements 2:101 formed cluster A, etc.)

**locusid** a numeric vector of locuslink ids, formed using AnnBuilder

**GO1** a character vector of GO tags (there were up to five based on the LL:GO mapping available March 2003 – these should be ignored in favor of the new Iyer517GO environment)

**GO2** a character vector

**GO3** a character vector

**GO4** a character vector

**GO5** a character vector

**Details**

Annotating this dataset is a good exercise for AnnBuilder. Many of the probes seem to have no annotation.

**Source**

<http://genome-www.stanford.edu/serum/data.html>

**References**

Iyer et al, Science v283: 83-87 (1999)

**Examples**

```
data(IyerAnnotated)
table(is.na(IyerAnnotated$GO1))
data(Iyer517GO)
get(ls(env=Iyer517GO)[1], env=Iyer517GO)
```

# Index

\*Topic **datasets**

IyerAnnotated, [3](#)

\*Topic **methods**

Iyer517, [2](#)

\*Topic **models**

get.dna2, [1](#)

get.dna2, [1](#)

Iyer517, [2](#)

Iyer517GO (IyerAnnotated), [3](#)

IyerAnnotated, [3](#)