

# Package ‘Iyer517’

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**Version** 1.44.0

**Title** exprSets for Iyer, Eisen et all 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

**git\_url** <https://git.bioconductor.org/packages/Iyer517>

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`get.dna2`*query genbank for an EST accession id*

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**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])
}
```

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Iyer517	<i>exprSet instance Iyer517, time series on transcriptional response of fibroblasts to serum</i>
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**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")
```

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IyerAnnotated	<i>Partly annotated version of Iyer517 data</i>
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**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)
```

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