

Package ‘Iyer517’

July 17, 2025

Version 1.51.0

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

git_url <https://git.bioconductor.org/packages/Iyer517>

git_branch devel

git_last_commit 8e546a8

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-07-17

Contents

get.dna2	1
Iyer517	2
IyerAnnotated	3

Index	5
--------------	----------

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

Partly annotated version of Iyer517 data

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$G01))
data(Iyer517G0)
get(ls(env=Iyer517G0)[1],env=Iyer517G0)
```

Index

- * **datasets**

- IyerAnnotated, [3](#)

- * **methods**

- Iyer517, [2](#)

- * **models**

- get.dna2, [1](#)

get.dna2, [1](#)

Iyer517, [2](#)

Iyer517G0 (IyerAnnotated), [3](#)

IyerAnnotated, [3](#)