

Package ‘Iyer517’

February 18, 2025

Version 1.49.0

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>

git_branch devel

git_last_commit 08a18a0

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2025-02-18

Contents

| | |
|-------------------------|----------|
| get.dna2 | 2 |
| Iyer517 | 3 |
| IyerAnnotated | 3 |
| Index | 5 |

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

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 | <i>exprSet instance Iyer517, time series on transcriptional response of fibroblasts to serum</i> |
|---------|--|

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

* **datasets**

IyerAnnotated, [3](#)

* **methods**

Iyer517, [3](#)

* **models**

get.dna2, [2](#)

get.dna2, [2](#)

Iyer517, [3](#)

Iyer517G0 (IyerAnnotated), [3](#)

IyerAnnotated, [3](#)