

Package: maskBAD (via r-universe)

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Title Masking probes with binding affinity differences

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Depends R (>= 2.10), gcrma (>= 2.27.1), affy

Suggests hgu95av2probe, hgu95av2cdf

Description Package includes functions to analyze and mask microarray expression data.

License GPL (>= 2)

biocViews Microarray

Repository <https://bioc.r-universe.dev>

RemoteUrl <https://github.com/bioc/maskBAD>

RemoteRef HEAD

RemoteSha 4ae4138a323c612755a6e2d654244444fb6f8fe4

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exmask	<i>Output object of the function mask</i>
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Description

This data is the output object of the function mask for the AffyBatch object newAffyBatch.

Usage

exmask

Format

List of 1 or 2 objects.

Source

??

References

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newAffyBatch	<i>AffyBatch with reduced genes</i>
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Description

This data is an AffyBatch object with a subset of 100 genes with human chimpanzee data (cdf hgu95av2) - 10 individuals each.

Usage

newAffyBatch

Format

AffyBatch object

Source

??

References

Khaitovich et al., Parallel Patterns of Evolution in the Genomes and Transcriptomes of Humans and Chimpanzees, Science 2005

newCdf	<i>Object of type environment</i>
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Description

The environment object is part of the masked object newAffyBatch.

Usage

```
newCdf
```

Format

Object of type environment

Source

??

References

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sequenceMask	<i>Object containing sequence information for probes.</i>
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Description

This data is a table with information about sequence difference between human and chimpanzee for all available probes.

Usage

```
sequenceMask
```

Format

```
data.frame.
```

Source

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References

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