Package 'maskBAD'

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Version 1.36.0

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

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R topics documented:

exmask *Output object of the function mask*

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

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References

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newAffyBatch *AffyBatch with reduced genes*

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

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References

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

newCdf *Object of type environment*

Description

The environment object is part of the masked object `newAffyBatch`.

Usage

```
newCdf
```

Format

Object of type environment

Source

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References

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sequenceMask *Object containing sequence information for probes.*

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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Index