Package ‘maskBAD’

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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
Description Package includes functions to analyze and mask microarray expression data.
License GPL version 2 or newer
biocViews Microarray
NeedsCompilation no

R topics documented:

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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.
**newCdf**

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

### Usage
```r
ewAffyBatch
```

### Format
AffyBatch object

### Source
??

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

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**newCdf**

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

### Usage
```r
ewCdf
```

### Format
Object of type environment

### Source
??

### References
??
**sequenceMask**

**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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