Package 'RnBeads.mm10'

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Title RnBeads.mm10

Description Automatically generated RnBeads annotation package for the assembly mm10.

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License GPL-3

Version 2.4.1

Depends R (>= 3.5.0), GenomicRanges

Suggests RnBeads

git_url https://git.bioconductor.org/packages/RnBeads.mm10

git_branch RELEASE_3_15

git_last_commit adca03d

git_last_commit_date 2022-06-22

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R topics documented:

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mm10   *Annotation tables for mm10*

Description

Scaffold of annotation tables for the mm10 assembly. This structure is automatically loaded upon
initialization of the annotation, that is, by the first valid call to any of the following functions:
rnb.get.assemblies, rnb.get.chromosomes, rnb.get.annotation, rnb.set.annotation, rnb.get.mapping,
rnb.annotation.size. Adding an annotation amounts to attaching its table(s) and mapping struc-
tures to this scaffold.

Format

> `list` of up to six elements - `"GENOME"`, `"CHROMOSOMES"`, `"regions"`, `"sites"`, `"controls"` and `"mappings"`. These elements are described below.
>
> `"GENOME"` Name of the Bioconductor package that contains the genomic sequence for this genome assembly.
>
> `"CHROMOSOMES"` Supported chromosomes for this genome assembly. The elements of this `character` vector follow the Ensembl convention (`"1"`, `"2"`, ...), and the names of this vector - the convention of the UCSC Genome Browser (`"chr1"`, `"chr2"`, ...).
>
> `"regions"` `list` of NULLs; the names of the elements correspond to the built-in region annotation tables. Once the default annotations are loaded, the attribute `"builtin"` is a `logical` vector storing, for each region annotation, whether it is the default (built-in) or custom.
>
> `"sites"` `list` of NULLs; the names of the elements correspond to the site and probe annotation tables.
>
> `"controls"` `list` of NULLs; the names of the elements correspond to the control probe annotation tables. The attribute `"sites"` is a `character` vector pointing to the site annotation that encompasses the respective control probes.
>
> `"mappings"` `list` of NULLs; the names of the elements correspond to the built-in region annotation tables.

Author(s)

RnBeads Annotation Creator

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