

# Package ‘RnBeads.mm10’

October 7, 2015

**Title** RnBeads.mm10

**Description** Annotation tables and mappings for mm10 used by RnBeads

**Date** 2013-01-27

**Version** 1.0.0

**Depends** R (>= 2.15), GenomicRanges

**Suggests** RnBeads (>= 0.99.0), BSgenome.Mmusculus.UCSC.mm10,

**License** GPL-3

**NeedsCompilation** no

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mm10	<i>MM10 - Annotation tables</i>
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## Description

Scaffold of annotation tables for MM10. 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 structures to this scaffold.

**Format**

list of four elements - "regions", "sites", "controls" and "mappings". These elements are described below.

"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 annotation tables.

"mappings" list of NULLs; the names of the elements correspond to the built-in region annotation tables.

**Author(s)**

Yassen Assenov

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