

TxDB.Osativa.MSU.RGAP7

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Annotation package for TxDb object(s)

Description

This package provides access to a TxDb object for *Oryza sativa* based on the Rice Genome Annotation Project (RGAP) Release 7 annotation (MSU7). The TxDb object provides transcript, exon, CDS and gene ranges for the IRGSP-1.0 / MSU7 genome assembly.

The TxDb object itself is not shipped with the package: it is hosted on AnnotationHub and retrieved at runtime, as shown below. The package additionally provides [msu_to_rap](#) for converting MSU locus identifiers to RAP-DB identifiers.

Note

This data resource was built from the RGAP Release 7 GFF3 annotation (MSU7, IRGSP-1.0).

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See Also

[transcripts](#), [transcriptsBy](#), [msu_to_rap](#)

Examples

```
## The TxDb object is downloaded from AnnotationHub, so this example is
## only run when AnnotationHub is installed and the resource is
## reachable.
if (requireNamespace("AnnotationHub", quietly=TRUE)) {
  txdb <- tryCatch({
    ah <- AnnotationHub::AnnotationHub()
    ah[["AH122276"]]
  }, error=function(e) NULL)

  if (!is.null(txdb)) {
    txdb
    ## retrieve all genes
    GenomicFeatures::genes(txdb)
  }
}
```

```
    }
}
```

msu_to_rap

Convert MSU (RGAP7) gene identifiers to RAP-DB identifiers

Description

Translates a vector of MSU/RGAP7 locus identifiers (e.g. LOC_0s01g01010) into RAP-DB identifiers (e.g. 0s01g0100100) using `riceidconverter::RiceIDConvert()`. The input order is preserved and identifiers that cannot be converted are dropped.

Usage

```
msu_to_rap(msu_ids, universe = NULL, dedup = TRUE)
```

Arguments

<code>msu_ids</code>	Character vector of MSU/RGAP7 gene identifiers.
<code>universe</code>	Optional character vector of allowed RAP-DB identifiers (for example <code>rownames(obj[["RNA"]])</code> of a Seurat object). When supplied, the result is restricted to identifiers present in <code>universe</code> , keeping the order of <code>msu_ids</code> .
<code>dedup</code>	Logical; if TRUE (default) duplicated RAP-DB identifiers are removed.

Value

A character vector of RAP-DB identifiers, in the order of `msu_ids`.

Note

Requires the **riceidconverter** package.

Examples

```
msu_ids <- c("LOC_0s01g01010", "LOC_0s01g01019", "LOC_0s01g01040")

if (requireNamespace("riceidconverter", quietly=TRUE)) {
  ## MSU -> RAP-DB, input order preserved
  rap_ids <- msu_to_rap(msu_ids)
  rap_ids

  ## restrict the result to identifiers present in another object,
  ## e.g. rownames(obj[["RNA"]]) of a Seurat object
  msu_to_rap(msu_ids, universe=rap_ids[1])
}
```

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