TxDb.Osativa.MSU.RGAP7

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`TxDb.Osativa.MSU.RGAP7`

Transcript annotation database for rice

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 using the AnnotationHub package. 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

```
## Retrieve the TxDb from AnnotationHub (requires network access):
## ah <- AnnotationHub::AnnotationHub()
## txdb <- ah[["AH122276"]]
## 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_Os01g01010`) into RAP-DB identifiers (e.g. `Os01g0100100`) 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

`msu_ids`	Character vector of MSU/RGAP7 gene identifiers.
`universe`	Optional character vector of allowed RAP-DB identifiers (for example `rownames(obj[["RNA"]])` of a Seurat object). When supplied, the result is restricted to identifiers present in `universe`, keeping the order of `msu_ids`.
`dedup`	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_Os01g01010", "LOC_Os01g01019", "LOC_Os01g01040")

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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