

# Package ‘ricegeneann’

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**Type** Package

**Title** Gene Annotation of Rice (Oryza Sativa L.spp.japonica)

**Version** 1.0.2

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**Description** Gene annotation of rice (Oryza Sativa L.spp.japonica).

The package is based on the annotation file from the website <[http://plants.ensembl.org/Oryza\\_sativa/Info/Index](http://plants.ensembl.org/Oryza_sativa/Info/Index)>.

Input gene's name then return some information, including the from position, the end position, the position type and the chromosome number.

**Depends** R (>= 3.5.0)

**Imports** riceidconverter

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.0.2

**NeedsCompilation** no

**Repository** CRAN

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## Contents

|                              |   |
|------------------------------|---|
| ricegeneannotation . . . . . | 2 |
| ricegeneann . . . . .        | 2 |

|              |          |
|--------------|----------|
| <b>Index</b> | <b>3</b> |
|--------------|----------|

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ricegeneannotation      *Annotation of genes of rice (Oryza Sativa)*

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**Description**

ricegeneann Annotate the gene of rice (Oryza Sativa)

**Usage**

```
ricegeneannotation(myID, type)
```

**Arguments**

|      |                       |
|------|-----------------------|
| myID | A vector of entrez id |
| type | Keytype of input id   |

**Value**

Return a vector or a datafram

**Author(s)**

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**Examples**

```
convert_id <- ricegeneannotation('0s01g0100500', 'RAP')
convert_id <- ricegeneannotation(myID = '0s01g0100500',
                                type = 'RAP')
```

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ricegeneann      *Annotation of genes of rice (Oryza Sativa)*

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**Description**

ricegeneann Annotation of genes of rice (Oryza Sativa). Input a or some gene name then return a or some information, including the from position, end position, position type and the chromosome number.

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# Index

ricegeneannotation, 2  
ricegeneann, 2