snp_gene

Description

snp_gene() performs an annotation of a given list of genes searching information in dbSNP database belonging to NCBI

Usage

```
snp_gene(dat=NULL,
type=c("info","hgnc","entrezid"),
p=F
)
```

Arguments

`dat`
> there are three options: the result obtained using dbSNP_info function or a character vector containing gene HGNC name or gene entrezid identifier

`term`
> argument indicating the type of data to be entered into the function. There are three options:
>
> - "info" the search is performed with the genes obtained by applying the function dbSNP_info()
>
> - "hgnc" the search is performed with the HGN nomenclature
>
> - "entrezid" the search is performed with the ID gene

`p`
> Parallelization. If is FALSE (default), the search is carried out without parallelisation. If TRUE, the function parallelises the searches.

Value

a dataframe containing the following values:

term
Entered term to search info

hgnc
Name provided by HGNC

entrez_id
HGNC identifier

gene_des
Gene description

gene_type
Gene type

refseq
RefSeq status

also
Also known as

info
Summary gene description

GO_id
Ontology index

GO_des
Ontology description

Examples

[Run examples](#)

```
library(SNPannot)

temp <- data.table::fread("https://ftp.ebi.ac.uk/pub/databases/spot/pg
temp$pos<-paste0(temp$"chr_name",":",temp$"chr_position")
temp<-data.frame(temp)
```