SIFT.Hsapiens.dbSNP132

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`SIFT.Hsapiens.dbSNP132`

SIFT predictions for Homo sapiens dbSNP build 132

Description

Database of SIFT predictions for Homo sapiens dbSNP build 132

Details

- Methods : See ?'SIFTDb-class' for methods.
- Creation of Database Tables : This package includes SIFT predictions for dbSNP build 132 human coding non-synonymous SNPs.
- Source Files :
  - Source : ftp://ftp.jcvi.org/pub/data/sift/dbSNP_132/
  - Software : SIFT 4.0.3
  - Databases : PSI-BLAST
  - Source Files : collated_predictions_dbSNP132.tgz SIFT predictions for all snps in dbSNP build 132 readme_collated_predictions_dbSNP132.txt description of data columns
  - Description : This package contains SIFT annotations for 437544 human SNPs included in dbSNP build 132.

Author(s)

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References

SIFT Home: http://sift.jcvi.org/

Kumar P, Henikoff S, Ng PC. Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. Nat Protoc. 2009;4(7):1073-81

Ng PC, Henikoff S. Predicting the Effects of Amino Acid Substitutions on Protein Function Annu Rev Genomics Hum Genet. 2006;7:61-80.

Ng PC, Henikoff S. SIFT: predicting amino acid changes that affect protein function. Nucleic Acids Res. 2003 Jul 1;31(13):3812-4.

See Also

SIFTDb-class

see ? SIFTDbColumns for column descriptions

Examples

```
library(SIFT.Hsapiens.dbSNP132)

## metadata
metadata(SIFT.Hsapiens.dbSNP132)

## column descriptions can be found at ?SIFTDbColumns
head(keys(SIFT.Hsapiens.dbSNP132))
cols(SIFT.Hsapiens.dbSNP132)

## subset on keys and cols
rsids <- c("rs17970171", "rs2142947", "rs3026284")
subst <- c("RSID", "METHOD", "PREDICTION", "SCORE")
select(SIFT.Hsapiens.dbSNP132, keys=rsids, cols=subst)
select(SIFT.Hsapiens.dbSNP132, keys=rsids)
```

Index

∗ **data**
SIFT.Hsapiens.dbSNP132, 1
∗ **package**
SIFT.Hsapiens.dbSNP132, 1

SIFT.Hsapiens.dbSNP132, 1
SIFT.Hsapiens.dbSNP132-package
*(*SIFT.Hsapiens.dbSNP132*)*, 1
SIFTDb-class, *2*