# SIFT.Hsapiens.dbSNP137

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`SIFT.Hsapiens.dbSNP137`

*PROVEAN/SIFT predictions for Homo sapiens dbSNP build 137*

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## Description

Database of PROVEAN/SIFT predictions for Homo sapiens dbSNP build 137

## Details

The SIFT tool is no longer actively maintained. A few of the orginal authors have started the PROVEAN (Protein Variation Effect Analyzer) project. PROVEAN is a software tool which predicts whether an amino acid substitution or indel has an impact on the biological function of a protein. PROVEAN is useful for filtering sequence variants to identify nonsynonymous or indel variants that are predicted to be functionally important.

See the web pages for a complete description of the methods.

- PROVEAN Home: `http://provean.jcvi.org/index.php/`
- SIFT Home: `http://sift.jcvi.org/`

Though SIFT is not under active development, the PROVEAN team still provids the SIFT scores in the pre-computed downloads. This package, `SIFT.Hsapiens.dbSNP137`, contains both SIFT and PROVEAN scores. One notable difference between this and the previous SIFT database package is that `keys` in `SIFT.Hsapiens.dbSNP132` are rs IDs whereas in `SIFT.Hsapiens.dbSNP137` they are NCBI dbSNP IDs.

## Methods

- Methods : See ?'PROVEANDb-class' in the VariantAnnotation package for a complete listing of available methods.
- Creation of Database Tables : This package includes PROVEAN/SIFT predictions for dbSNP build 137 human coding non-synonymous SNPs.
- Source Files :
  - Source : http://provean.jcvi.org/downloads.php
  - Software : PROVEAN 1.1, SIFT 4.0.3
  - Databases : PSI-BLAST
  - Source Files : dbsnp137.coding.variants.prediction.tsv.gz PROVEAN/SIFT predictions for coding snps in dbSNP build 137
  - Description : This package contains PROVEAN/SIFT annotations human SNPs included in dbSNP build 137.

## Column descriptions

These names are displayed when `columns` is called on the PROVEANDb object (i.e., columns(SIFT.Hsapiens.dbSNP137)

- DBSNPID : NCBI dbSNP ID
- VARIANT : comma separted values of <chromosome>,<position>,<reference allele>,<variant allele>, <comment(optional)>
- PROTEINID : Ensembl protein ID
- LENGTH : length of the protein
- STRAND :'+', '-' or NA
- CODONCHANGE : codon change including flanking codons
- POS : postion of amino acid residue affected
- RESIDUEREF : reference amino acid residue
- RESIDUEALT : variant amino acid residue
- TYPE : synonymous | nonsynonymous | frameshift | ...
- PROVEANSCORE : PROVEAN score (see http://provean.jcvi.org/about.php#about_1)
- PROVEANPRED : deleterious or neutral (cutoff=-2.5)
- PROVEANNUMSEQ : number of sequences used for prediction
- PROVEANNUMCLUST : number of clusters used for prediction
- SIFTSCORE : SIFT score (range 0 to 1)
- SIFTPRED : tolerated or damaging (cutoff=0.05)
- SIFTMEDIAN : median sequence information used to measure the diversity of the sequences used for prediction
- SIFTNUMSEQ : number of sequences used for prediction

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## References

The PROVEAN tool has replaced SIFT: http://provean.jcvi.org/about.php

Choi Y, Sims GE, Murphy S, Miller JR, Chan AP (2012) Predicting the Functional Effect of Amino Acid Substitutions and Indels. PLoS ONE 7(10): e46688.

Choi Y (2012) A Fast Computation of Pairwise Sequence Alignment Scores Between a Protein and a Set of Single-Locus Variants of Another Protein. In Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine (BCB '12). ACM, New York, NY, USA, 414-417.

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

PROVEANDb-class

## Examples

```
library(SIFT.Hsapiens.dbSNP137)

## metadata
metadata(SIFT.Hsapiens.dbSNP137)

## keys are the DBSNPID (NCBI dbSNP ID)
dbsnp <- keys(SIFT.Hsapiens.dbSNP137)
head(dbsnp)
columns(SIFT.Hsapiens.dbSNP137)

## Return all columns. Note that the key, DBSNPID,
## is always returned.
select(SIFT.Hsapiens.dbSNP137, dbsnp[10])
## subset on keys and cols
cols <- c("VARIANT", "PROVEANPRED", "SIFTPRED")
select(SIFT.Hsapiens.dbSNP137, dbsnp[20:23], cols)
```

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