

# Package ‘vulcandata’

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**Type** Package

**Title** VirtUaL ChIP-Seq data Analysis using Networks, dummy dataset

**Version** 1.20.0

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**Description** This package provides a dummy regulatory network and ChIP-Seq dataset for running examples in the vulcan package

**License** LGPL-3

**LazyData** TRUE

**biocViews** ExperimentData, Homo\_sapiens\_Data, CancerData, ChIPSeqData

**NeedsCompilation** no

**Encoding** UTF-8

**RoxygenNote** 6.0.1

**Imports** utils

**git\_url** <https://git.bioconductor.org/packages/vulcandata>

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vulcanexample

*Function to load an example VULCAN dataset into the workspace*

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**Description**

This function loads a dummy ChIP-Seq dataset used for VULCAN examples.

**Usage**

```
vulcanexample()
```

**Value**

A list of components:

**peakcounts** A matrix of raw peak counts, peaks as rows, samples as columns

**peakrpkm** A matrix of peak RPKMs, peaks as rows, samples as columns

**samples** A vector of sample names and conditions

**Examples**

```
vobj<-vulcanexample()  
names(vobj)  
vobj$peakcounts[1:5,]
```

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vulcansheet

*Function to generate an import sheet CSV file for the vulcan test set*

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**Description**

This function generates a user-specific example sheet with appropriate paths on a dummy ChIP-Seq dataset

**Usage**

```
vulcansheet(outfile = "sheetfile.csv")
```

**Arguments**

outfile            Path and file name for the CSV sheet file

**Value**

nothing

**Examples**

```
vfile<-tempfile()  
vulcansheet(vfile)  
tmp<-read.csv(vfile)  
head(tmp)  
unlink(vfile)
```

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