SUSACTRIADE version 0.1.0 (R-Package)

REFERENCE BOOK

query adapted to understand implication of a gene list in SNC field for Susac syndrome

Usage

```
sncquery(list.of.genes, gene.num.limit = 250, custom.search = NA)
```

Arguments

`quantification`   of articles found in SNC field for each input gene

Examples

```
snc<-sncquery(set$gene)
snc<-
sncquery(c("DISC1","NRG1","DRD2","DRD3","B2M","TBP","BMAL1","NPAS2","HES7",
"GRIK3","NEUROD1","ICAM1"))
```

[Package *susactriade* version 0.1.0]

Hypergeometric test performed with results of the snc query

Usage

```
snctest(snc)
```

Examples

```
sncfisher<-snctest(snc)
```

[Package *susactriade* version 0.1.0]

query adapted to understand implication of a gene list in retinal field for Susac syndrome

Usage

```
retinalquery(list.of.genes, gene.num.limit = 250, custom.search = NA)
```

Arguments

`quantification`   of articles found in retinal field for each input gene

Examples

```
retinal<-retinalquery(set$gene)
retinal<-
retinalquery(c("DISC1","NRG1","DRD2","DRD3","B2M","TBP","BMAL1","NPAS2","HE
S7","GRIK3","NEUROD1","ICAM1"))
```

[Package *susactriade* version 0.1.0]

Hypergeometric test performed with results of the retinal query

Usage

```
retinaltest(retinal)
```

Examples

```
retinalfisher<-retinaltest(retinal)
```

[Package *susactriade* version 0.1.0]

query adapted to understand implication of a gene list in cochleovestibular field for Susac syndrome

Usage

```
cochleoquery(list.of.genes, gene.num.limit = 250, custom.search = NA)
```

Arguments

`quantification`   of articles found in cochleovestibular field for each input gene

Examples

```
cochleo<-cochleoquery(set$gene)
cochleo<-
cochleoquery(c("DISC1","NRG1","DRD2","DRD3","B2M","TBP","BMAL1","NPAS2","HE
S7","GRIK3","NEUROD1","ICAM1"))
```

Hypergeometric test performed with results of the cochleo query

Usage

```
cochleotest(cochleo)
```

Examples

```
cochleofisher<-cochleotest(cochleo)
```