

Package: TCMR

Title: Traditional Chinese Medicine Network Pharmacology

Version: 1.0.0

Authors@R:

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```

Description: A visualization tool for network pharmacology data analysis.

License: GPL (>= 3)

Encoding: UTF-8

Roxygen: list(markdown = TRUE)

RoxygenNote: 7.2.3

Imports: aplot, circelize, dplyr, ggplot2, ggraph, ggtree, grDevices, igraph,
 magrittr, RColorBrewer, stats, tidyr, ComplexHeatmap, cols4all, cowplot,
 ggrepel, ggsankey, rlang, stringr, UpSetR, ggvenn, tidygraph
biocViews: ComplexHeatmap, ggtree, clusterProfiler, DOSE, org.Hs.eg.db

Remotes:

```
github::davidsjoberg/ggsankey
```

Depends: R (>= 2.10)

LazyData: true

Suggests:

```
clusterProfiler,  
DOSE,  
knitr,  
org.Hs.eg.db,  
testthat (>= 3.0.0),  
tidyverse,  
utils
```

Config/testthat/edition: 3

VignetteBuilder: knitr

NeedsCompilation: no

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