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title: "gene ontology\_R.md" author: "charvi khanna" date: "2025-09-08" output: pdf\_document: default  
html\_document: df\_print: paged

```
if (!requireNamespace("BiocManager", quietly = TRUE))  
  install.packages("BiocManager")
```

```
BiocManager::install("clusterProfiler")
```

```
## Bioconductor version 3.21 (BiocManager 1.30.26), R 4.5.1 (2025-06-13 ucrt)
```

```
## Warning: package(s) not installed when version(s) same as or greater than current; use  
## 'force = TRUE' to re-install: 'clusterProfiler'
```

```
## Installation paths not writeable, unable to update packages  
## path: C:/Program Files/R/R-4.5.1/library  
## packages:  
## boot, Matrix
```

```
## Old packages: 'DESeq2', 'magick', 'RSQLite', 'SparseArray', 'xfun'
```

```
BiocManager::install("org.Hs.eg.db")
```

```
## Bioconductor version 3.21 (BiocManager 1.30.26), R 4.5.1 (2025-06-13 ucrt)
```

```
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## boot, Matrix
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```
## Old packages: 'DESeq2', 'magick', 'RSQLite', 'SparseArray', 'xfun'
```

```
library(clusterProfiler)
```

```
##
```

```
## clusterProfiler v4.16.0 Learn more at https://yulab-smu.top/contribution-knowledge-mining/
```

```
##
```

```
## Please cite:
```

```
##
```

```
## G Yu. Thirteen years of clusterProfiler. The Innovation. 2024,
```

```
## 5(6):100722
```

```
##
```

```
## Attaching package: 'clusterProfiler'
```

```
## The following object is masked from 'package:stats':
```

```
##
```

```
## filter
```

```
library(org.Hs.eg.db)
```

```
## Loading required package: AnnotationDbi
```

```
## Loading required package: stats4
```

```
## Loading required package: BiocGenerics
```

```
## Loading required package: generics
```

```
##
```

```
## Attaching package: 'generics'
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      as.difftime, as.factor, as.ordered, intersect, is.element, setdiff,
```

```
##      setequal, union
```

```
##
```

```
## Attaching package: 'BiocGenerics'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##      IQR, mad, sd, var, xtabs
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      anyDuplicated, aperm, append, as.data.frame, basename, cbind,
```

```
##      colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
```

```
##      get, grep, grepl, is.unsorted, lapply, Map, mapply, match, mget,
```

```
##      order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
```

```
##      rbind, Reduce, rownames, sapply, saveRDS, table, tapply, unique,
```

```
##      unsplit, which.max, which.min
```

```
## Loading required package: Biobase
```

```
## Welcome to Bioconductor
```

```
##
```

```
##      Vignettes contain introductory material; view with
```

```
##      'browseVignettes()'. To cite Bioconductor, see
```

```
##      'citation("Biobase")', and for packages 'citation("pkgname")'.
```

```
## Loading required package: IRanges
```

```
## Loading required package: S4Vectors
```

```
##
```

```
## Attaching package: 'S4Vectors'
```

```
## The following object is masked from 'package:clusterProfiler':
##
##      rename

## The following object is masked from 'package:utils':
##
##      findMatches

## The following objects are masked from 'package:base':
##
##      expand.grid, I, unname

##
## Attaching package: 'IRanges'

## The following object is masked from 'package:clusterProfiler':
##
##      slice

## The following object is masked from 'package:grDevices':
##
##      windows

##
## Attaching package: 'AnnotationDbi'

## The following object is masked from 'package:clusterProfiler':
##
##      select

##
```

```
my_gene_list <- c("TP53", "KRAS", "EGFR", "MYC", "JUN", "FOS", "AKT1", "STAT3")

go_results <- enrichGO(
  gene = my_gene_list,
  OrgDb = "org.Hs.eg.db",
  ont = "BP",
  keyType = "SYMBOL"
)

dotplot(go_results)
```

