Package: genefindr (via r-universe)

June 8, 2026

Title Rapid Gene Characterization Using Public Genomic Databases

Version 1.0.0

Description A user-friendly interface for characterizing gene function by disease type and tissue site, integrating curated data from publicly available genomic and proteomic databases to support candidate gene prioritization in experimental workflows.

Depends R (>= 4.1.0)

License GPL-3

Encoding UTF-8

RoxygenNote 8.0.0

Imports httr2, gtexr

URL `https://github.com/martincyd/genefindr`

BugReports `https://github.com/martincyd/genefindr/issues`

Suggests knitr, rmarkdown, spelling

VignetteBuilder knitr

NeedsCompilation no

Author Cydnie Martin [aut, cre]

Maintainer Cydnie Martin <`martincydenise@gmail.com`>

Repository https://cran.r-universe.dev

Date/Publication 2026-06-08 18:30:02 UTC

RemoteUrl https://github.com/cran/genefindr

RemoteRef HEAD

RemoteSha fc048ad0cf38ceb99111c498373a09be1704433a

Contents

`findr` *Characterize a gene using public genomic databases*

Description

Characterize a gene using public genomic databases

Usage

```
findr(gene, disease = NULL, site = NULL)
```

Arguments

`gene`	Character. Gene symbol (e.g. "TP53")
`disease`	Character. Disease context (e.g. "alzheimer")
`site`	Character. Cancer site (e.g. "breast", "lung"). Can be a vector for multi-site comparison.

Value

Invisibly returns a data frame of results

Examples

```
findr("TP53", site = "breast")
```

`findr_multi` *Characterize multiple genes using public genomic databases*

Description

Characterize multiple genes using public genomic databases

Usage

```
findr_multi(genes, disease = NULL, site = NULL, output = "print")
```

Arguments

`genes`	Character vector. Gene symbols (e.g. c("TP53", "BRCA1"))
`disease`	Character. Disease context
`site`	Character. Cancer site
`output`	Character. "print" or "table"

Value

Invisibly returns a data frame of results

Examples

```
findr_multi(c("TP53", "BRCA1"), site = "breast")
```

Index