

Package ‘genefindr’

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

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Repository CRAN

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findr	<i>Characterize a gene using public genomic databases</i>
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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	<i>Characterize multiple genes using public genomic databases</i>
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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"

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Value

Invisibly returns a data frame of results

Examples

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

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