

# Package ‘oncoEnrichR’

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**Type** Package

**Title** Functional annotation and enrichment analysis of genesets in the context of cancer

**Version** 0.7.5

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**URL** <https://github.com/sigven/oncoEnrichR>

**BugReports** <https://github.com/sigven/oncoEnrichR/issues>

**Description** oncoEnrichR performs annotation and prioritization of genesets discovered from high-throughput experiments within cancer biology. The tool queries a number of high-quality resources, including Project Score (cellular fitness in genome-scale drop-out screens), Open Targets Platform (comprehensive target-drug and target-disease associations), TCGA (genetic aberrations and gene expression patterns in human tumor samples), STRING (protein-protein interaction networks), CORUM (curated protein complexes), COMPPI (subcellular compartments), and Gene Ontology/MSigDB/REACTOME/KEGG (functional enrichment/over-representation analysis with respect to gene function and cellular pathways). The package outputs an interactive HTML report in which the user can interrogate the the various types of annotations and analyses performed with the geneset.

**Depends** R (>= 4.0)

**biocViews**

**Imports** tidyverse (>= 1.3.0), visNetwork (>= 2.0.9), plotly (>= 4.9.1), pals (>= 1.5), org.Hs.eg.db, clusterProfiler (>= 3.16.1), igraph, reshape2 (>= 1.4.4), rlogging, gganatogram, maftools (>= 2.4.12)

**License** MIT

**Encoding** UTF-8

**Remotes** mjkallen/rlogging, jespermaag/gganatogram

**LazyData** true

**RoxygenNote** 7.1.1

**Roxygen** list(markdown = TRUE)

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onco_enrich	<i>Function that interrogates and analyzes a list of human protein-coding genes for cancer relevance</i>
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Description

Function that interrogates and analyzes a list of human protein-coding genes for cancer relevance

Usage

```
onco_enrich(  
  query,  
  query_source = "symbol",  
  ignore_unknown = FALSE,  
  project_title = "Project title",  
  project_owner = "Project owner",  
  project_description = "Project description",  
  background_enrichment = NULL,  
  background_enrichment_source = "symbol",  
  background_enrichment_description = "All protein-coding genes",  
  p_value_cutoff_enrichment = 0.05,  
  p_value_adjustment_method = "BH",  
  q_value_cutoff_enrichment = 0.2,  
  min_geneset_size = 10,  
  max_geneset_size = 500,  
  simplify_go = F,  
  ppi_add_nodes = 50,  
  ppi_score_threshold = 900,  
  show_gene_summary = F,  
  show_ppi = T,  
  show_drugs_in_ppi = F,  
  show_disease = T,  
  show_drug = T,  
  show_enrichment = T,  
  show_tcga_aberration = T,  
  show_tcga_coexpression = T,  
  show_subcell_comp = T,  
  show_crispr_lof = T,  
  show_complex = T  
)
```

Arguments

query	character vector with gene/query identifiers
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query_source	character indicating source of query (one of "uniprot_acc", "symbol", "entrez-gene", or "ensembl_gene_id")
ignore_unknown	logical indicating if analysis should continue when unknown query identifiers are encountered
project_title	project title (title of report)
project_owner	name of project owner
project_description	project background information
background_enrichment	character vector with gene identifiers, used as reference/background for enrichment/over-representation analysis
background_enrichment_source	character indicating source of background ("uniprot_acc", "symbol", "entrezgene", "ensembl_gene_id")
background_enrichment_description	character indicating type of background (e.g. "All lipid-binding proteins (n = 200)")
p_value_cutoff_enrichment	cutoff p-value for enrichment/over-representation analysis
p_value_adjustment_method	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
q_value_cutoff_enrichment	cutoff q-value for enrichment analysis
min_geneset_size	minimal size of geneset annotated by term for testing in enrichment/over-representation analysis
max_geneset_size	maximal size of geneset annotated by term for testing in enrichment/over-representation analysis
simplify_go	remove highly similar GO terms in results from GO enrichment/over-representation analysis
ppi_add_nodes	number of nodes to add to query set when computing the protein-protein interaction network (STRING)
ppi_score_threshold	minimum score (0-1000) for retrieval of protein-protein interactions (STRING)
show_gene_summary	logical indicating if report should fetch summary of gene function (from RefSeq/mygene.info, will increase processing time)
show_ppi	logical indicating if report should contain protein-protein interaction data (STRING)
show_drugs_in_ppi	logical indicating if targeted drugs (> phase 3) should be displayed in protein-protein interaction network (Open Targets Platform)
show_disease	logical indicating if report should contain disease associations (Open Targets Platform)
show_enrichment	logical indicating if report should contain functional enrichment/over-representation analysis (MSigDB, GO, KEGG, REACTOME etc.)
show_tcga_aberration	logical indicating if report should contain TCGA aberration plots (amplifications/deletions)

show_tcga_coexpression	logical indicating if report should contain TCGA co-expression data (RNAseq) of queryset with oncogenes/tumor suppressor genes
show_subcell_comp	logical indicating if report should list subcellular compartment annotations (CompPI)
show_crispr_lof	logical indicating if report should list results from CRISPR/Cas9 loss-of-fitness screens (Project Score)
show_complex	logical indicating if report should list proteins in known protein complexes (CORUM)

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write	<i>Function that writes the contents in the oncoEnrichR report object to an interactive HTML report</i>
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## Description

Function that writes the contents in the oncoEnrichR report object to an interactive HTML report

## Usage

```
write(report, project_directory, report_name, format = "html")
```

## Arguments

report	object with oncoEnrichR report data (returned by oncoEnrichR::onco_enrich)
project_directory	working directory
report_name	prefix filename for report output
format	file format of output (html/json)

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