

main

July 12, 2021

## 1 GO module enrichment

```
[1]: import functools
import numpy as np
import pandas as pd
import collections as cx
from pybiomart import Dataset
from gtfparse import read_gtf
from scipy.stats import fisher_exact
from statsmodels.stats.multitest import multipletests

# GO analysis
from goatools.base import download_go_basic_obo
from goatools.base import download_ncbi_associations
from goatools.obo_parser import GODag
from goatools.anno.genetogo_reader import Gene2GoReader
from goatools.goea.go_enrichment_ns import GOEnrichmentStudyNS
```

### 1.1 Functions

#### 1.1.1 Cached functions

```
[2]: @functools.lru_cache()
def get_gtf_genes_df():
    gtf_df = read_gtf("/ceph/genome/human/gencode25/gtf.CHR/_m/gencode.v25.
↳annotation.gtf")
    return gtf_df[gtf_df["feature"] == "gene"][['gene_id', 'gene_name']]

@functools.lru_cache()
def get_wgcna_modules():
    return pd.read_csv("../_m/modules.csv", index_col=0)

@functools.lru_cache()
def get_database():
    dataset = Dataset(name="hsapiens_gene_ensembl",
                      host="http://www.ensembl.org",
```

```

        use_cache=True)
db = dataset.query(attributes=["ensembl_gene_id",
                             "external_gene_name",
                             "entrezgene_id"],
                  use_attr_names=True).dropna(subset=['entrezgene_id'])

return db

```

### 1.1.2 Simple functions

```

[3]: def convert2entrez(mod):
    df = get_wgcna_modules()[(get_wgcna_modules().module) == mod].copy()
    df["ensemblID"] = df.index.str.replace("\\.*", "", regex=True)
    return df.merge(get_database(), left_on='ensemblID',
                   right_on='ensembl_gene_id')

def obo_annotation(alpha=0.05):
    # database annotation
    fn_obo = download_go_basic_obo()
    fn_gene2go = download_ncbi_associations() # must be gunzip to work
    obodag = GODag(fn_obo) # downloads most up-to-date
    anno_hs = Gene2GoReader(fn_gene2go, taxids=[9606])
    # get associations
    ns2assoc = anno_hs.get_ns2assc()
    for nspc, id2gos in ns2assoc.items():
        print("{NS} {N:}, annotated human genes".format(NS=nspc, N=len(id2gos)))
    goeaobj = GGOEnrichmentStudyNS(
        get_database()['entrezgene_id'], # List of human genes with entrez IDs
        ns2assoc, # geneid/GO associations
        obodag, # Ontologies
        propagate_counts = False,
        alpha = alpha, # default significance cut-off
        methods = ['fdr_bh'])
    return goeaobj

def run_goea(mod):
    df = convert2entrez(mod)
    geneids_study = {z[0]:z[1] for z in zip(df['entrezgene_id'],
    ↪df['external_gene_name'])}
    goeaobj = obo_annotation()
    goea_results_all = goeaobj.run_study(geneids_study)
    goea_results_sig = [r for r in goea_results_all if r.p_fdr_bh < 0.05]
    ctr = cx.Counter([r.NS for r in goea_results_sig])
    print('Significant results[{TOTAL}] = {BP} BP + {MF} MF + {CC} CC'.format(
        TOTAL=len(goea_results_sig),
        BP=ctr['BP'], # biological_process

```

```
MF=ctr['MF'], # molecular_function
CC=ctr['CC'])) # cellular_component
goeobj.wr_xlsx("GO_analysis_module_%s.xlsx" % mod, goea_results_sig)
goeobj.wr_txt("GO_analysis_module_%s.txt" % mod, goea_results_sig)
```

## 1.2 Gene annotation

```
[4]: gtf = get_gtf_genes_df()
      gtf.head(2)
```

```
INFO:root:Extracted GTF attributes: ['gene_id', 'gene_type', 'gene_status',
'gene_name', 'level', 'havana_gene', 'transcript_id', 'transcript_type',
'transcript_status', 'transcript_name', 'transcript_support_level', 'tag',
'havana_transcript', 'exon_number', 'exon_id', 'ont', 'protein_id', 'ccdsid']
```

```
[4]:      gene_id gene_name
0   ENSG00000223972.5   DDX11L1
12  ENSG00000227232.5   WASH7P
```

### 1.2.1 Load WGCNA module

```
[5]: wgcna_df = get_wgcna_modules().merge(gtf, left_index=True, right_on="gene_id",
      ↪how="left")
      wgcna_df.head(2)
```

```
[5]:      module      gene_id gene_name
12   grey  ENSG00000227232.5   WASH7P
139  grey  ENSG00000279457.3  F0538757.1
```

```
[6]: wgcna_df[(wgcna_df.gene_id.str.startswith("chr"))]
```

```
[6]: Empty DataFrame
      Columns: [module, gene_id, gene_name]
      Index: []
```

```
[7]: wgcna_df[(wgcna_df.gene_name == 'DRD2')]
```

```
[7]:      module      gene_id gene_name
1445279  grey  ENSG00000149295.13   DRD2
```

```
[8]: wgcna_df.to_csv("module_annotated.csv", index=False)
```

## 1.3 GO enrichment for each cluster

```
[9]: for mod in get_wgcna_modules().module.unique():
      run_goea(mod)
```

```
requests.get(http://purl.obolibrary.org/obo/go/go-basic.obo, stream=True)
      WROTE: go-basic.obo
```

```

FTP RETR ftp.ncbi.nlm.nih.gov gene/DATA gene2go.gz -> gene2go.gz
  gunzip gene2go.gz
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.049954 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 13472 IDs ... 81% 10,935 of
13,472 study items found in association
100% 13,472 of 13,472 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
  10,697 GO terms are associated with 10,935 of 13,472 study items
METHOD fdr_bh:
  632 GO terms found significant (< 0.05=alpha) (612 enriched + 20
purified): statsmodels fdr_bh
  9,202 study items associated with significant GO IDs (enriched)
  407 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 13472 IDs ... 86% 11,525 of
13,472 study items found in association
100% 13,472 of 13,472 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,713 of 29,107 population items
  1,606 GO terms are associated with 11,525 of 13,472 study items
METHOD fdr_bh:
  371 GO terms found significant (< 0.05=alpha) (363 enriched + 8
purified): statsmodels fdr_bh
  11,275 study items associated with significant GO IDs (enriched)
  716 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 13472 IDs ... 83% 11,185 of
13,472 study items found in association
100% 13,472 of 13,472 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,839 of 29,107 population items

```

3,822 GO terms are associated with 11,185 of 13,472 study items  
METHOD fdr\_bh:  
270 GO terms found significant (< 0.05=alpha) (261 enriched + 9  
purified): statsmodels fdr\_bh  
10,403 study items associated with significant GO IDs (enriched)  
246 study items associated with significant GO IDs (purified)  
Significant results[1273] = 632 BP + 270 MF + 371 CC  
1273 items Wrote: GO\_analysis\_module\_grey.xlsx  
1273 GOEA results for 11957 study items. Wrote: GO\_analysis\_module\_grey.txt  
EXISTS: go-basic.obo  
EXISTS: gene2go  
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms  
HMS:0:00:04.712296 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
gene2go  
BP 18,506 annotated human genes  
CC 19,424 annotated human genes  
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...  
70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 146 IDs ... 90% 131 of  
146 study items found in association  
100% 146 of 146 study items found in population(29107)  
Calculating 12,438 uncorrected p-values using fisher  
12,438 GO terms are associated with 17,849 of 29,107 population items  
781 GO terms are associated with 131 of 146 study items  
METHOD fdr\_bh:  
7 GO terms found significant (< 0.05=alpha) ( 7 enriched + 0  
purified): statsmodels fdr\_bh  
12 study items associated with significant GO IDs (enriched)  
0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 146 IDs ... 92% 135 of  
146 study items found in association  
100% 146 of 146 study items found in population(29107)  
Calculating 1,756 uncorrected p-values using fisher  
1,756 GO terms are associated with 18,713 of 29,107 population items  
210 GO terms are associated with 135 of 146 study items  
METHOD fdr\_bh:  
21 GO terms found significant (< 0.05=alpha) ( 21 enriched + 0  
purified): statsmodels fdr\_bh

```

    107 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 146 IDs ... 89%    130 of
146 study items found in association
100%    146 of    146 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    247 GO terms are associated with    130 of    146 study items
METHOD fdr_bh:
    5 GO terms found significant (< 0.05=alpha) ( 5 enriched + 0
purified): statsmodels fdr_bh
    102 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[33] = 7 BP + 5 MF + 21 CC
    33 items WROTE: GO_analysis_module_pink.xlsx
    33 GOEA results for    125 study items. WROTE: GO_analysis_module_pink.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.936176 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 39 IDs ... 82%    32 of
39 study items found in association
100%    39 of    39 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,849 of 29,107 population items
    261 GO terms are associated with    32 of    39 study items
METHOD fdr_bh:
    2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0
purified): statsmodels fdr_bh
    4 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 39 IDs ... 90%    35 of

```

```

39 study items found in association
100%    39 of    39 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
    98 GO terms are associated with    35 of    39 study items
METHOD fdr_bh:
    3 GO terms found significant (< 0.05=alpha) ( 3 enriched + 0
purified): statsmodels fdr_bh
    7 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 39 IDs ... 85%    33 of
39 study items found in association
100%    39 of    39 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    82 GO terms are associated with    33 of    39 study items
METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[5] = 2 BP + 0 MF + 3 CC
    5 items WROTE: GO_analysis_module_darkgreen.xlsx
    5 GOEA results for    7 study items. WROTE:
GO_analysis_module_darkgreen.txt
    EXISTS: go-basic.obo
    EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.487098 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 156 IDs ... 97%    152 of
156 study items found in association
100%    156 of    156 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher

```

```

12,438 GO terms are associated with 17,849 of 29,107 population items
1,026 GO terms are associated with 152 of 156 study items
METHOD fdr_bh:
    22 GO terms found significant (< 0.05=alpha) ( 22 enriched + 0
purified): statsmodels fdr_bh
    75 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 156 IDs ... 99% 154 of
156 study items found in association
100% 156 of 156 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
    187 GO terms are associated with 154 of 156 study items
METHOD fdr_bh:
    27 GO terms found significant (< 0.05=alpha) ( 27 enriched + 0
purified): statsmodels fdr_bh
    130 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 156 IDs ... 96% 149 of
156 study items found in association
100% 156 of 156 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    258 GO terms are associated with 149 of 156 study items
METHOD fdr_bh:
    20 GO terms found significant (< 0.05=alpha) ( 20 enriched + 0
purified): statsmodels fdr_bh
    134 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[69] = 22 BP + 20 MF + 27 CC
69 items WROTE: GO_analysis_module_black.xlsx
69 GOEA results for 149 study items. WROTE: GO_analysis_module_black.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.659221 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
74% 21,430 of 29,107 population items found in association

```



Load MF Gene Ontology Analysis ...

70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 464 IDs ... 86% 397 of 464 study items found in association

100% 464 of 464 study items found in population(29107)

Calculating 12,438 uncorrected p-values using fisher

12,438 GO terms are associated with 17,849 of 29,107 population items

1,997 GO terms are associated with 397 of 464 study items

METHOD fdr\_bh:

11 GO terms found significant ( $< 0.05=\alpha$ ) ( 11 enriched + 0 purified): statsmodels fdr\_bh

90 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 464 IDs ... 89% 412 of 464 study items found in association

100% 464 of 464 study items found in population(29107)

Calculating 1,756 uncorrected p-values using fisher

1,756 GO terms are associated with 18,713 of 29,107 population items

407 GO terms are associated with 412 of 464 study items

METHOD fdr\_bh:

42 GO terms found significant ( $< 0.05=\alpha$ ) ( 42 enriched + 0 purified): statsmodels fdr\_bh

374 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 464 IDs ... 88% 408 of 464 study items found in association

100% 464 of 464 study items found in population(29107)

Calculating 4,434 uncorrected p-values using fisher

4,434 GO terms are associated with 17,839 of 29,107 population items

614 GO terms are associated with 408 of 464 study items

METHOD fdr\_bh:

5 GO terms found significant ( $< 0.05=\alpha$ ) ( 5 enriched + 0 purified): statsmodels fdr\_bh

305 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Significant results[58] = 11 BP + 5 MF + 42 CC

58 items Wrote: GO\_analysis\_module\_turquoise.xlsx

58 GOEA results for 413 study items. Wrote:

GO\_analysis\_module\_turquoise.txt

EXISTS: go-basic.obo

EXISTS: gene2go

go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms

HMS:0:00:04.559263 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ: gene2go

BP 18,506 annotated human genes  
CC 19,424 annotated human genes  
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...  
70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 463 IDs ... 67% 311 of  
463 study items found in association

100% 463 of 463 study items found in population(29107)

Calculating 12,438 uncorrected p-values using fisher

12,438 GO terms are associated with 17,849 of 29,107 population items

1,061 GO terms are associated with 311 of 463 study items

METHOD fdr\_bh:

31 GO terms found significant ( $< 0.05=\alpha$ ) ( 30 enriched + 1  
purified): statsmodels fdr\_bh

137 study items associated with significant GO IDs (enriched)

1 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 463 IDs ... 75% 345 of  
463 study items found in association

100% 463 of 463 study items found in population(29107)

Calculating 1,756 uncorrected p-values using fisher

1,756 GO terms are associated with 18,713 of 29,107 population items

265 GO terms are associated with 345 of 463 study items

METHOD fdr\_bh:

33 GO terms found significant ( $< 0.05=\alpha$ ) ( 29 enriched + 4  
purified): statsmodels fdr\_bh

221 study items associated with significant GO IDs (enriched)

65 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 463 IDs ... 69% 321 of  
463 study items found in association

100% 463 of 463 study items found in population(29107)

Calculating 4,434 uncorrected p-values using fisher

4,434 GO terms are associated with 17,839 of 29,107 population items

345 GO terms are associated with 321 of 463 study items

METHOD fdr\_bh:

12 GO terms found significant ( $< 0.05=\alpha$ ) ( 11 enriched + 1  
purified): statsmodels fdr\_bh

71 study items associated with significant GO IDs (enriched)

3 study items associated with significant GO IDs (purified)

Significant results[76] = 31 BP + 12 MF + 33 CC  
 76 items WROTE: GO\_analysis\_module\_blue.xlsx  
 76 GOEA results for 271 study items. WROTE: GO\_analysis\_module\_blue.txt  
 EXISTS: go-basic.obo  
 EXISTS: gene2go  
 go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms  
 HMS:0:00:04.626144 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
 gene2go  
 BP 18,506 annotated human genes  
 CC 19,424 annotated human genes  
 MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...  
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 206 IDs ... 78% 161 of  
 206 study items found in association  
 100% 206 of 206 study items found in population(29107)  
 Calculating 12,438 uncorrected p-values using fisher  
 12,438 GO terms are associated with 17,849 of 29,107 population items  
 1,033 GO terms are associated with 161 of 206 study items  
 METHOD fdr\_bh:  
 0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0  
 purified): statsmodels fdr\_bh  
 0 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 206 IDs ... 83% 171 of  
 206 study items found in association  
 100% 206 of 206 study items found in population(29107)  
 Calculating 1,756 uncorrected p-values using fisher  
 1,756 GO terms are associated with 18,713 of 29,107 population items  
 242 GO terms are associated with 171 of 206 study items  
 METHOD fdr\_bh:  
 2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0  
 purified): statsmodels fdr\_bh  
 59 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 206 IDs ... 80% 165 of  
 206 study items found in association  
 100% 206 of 206 study items found in population(29107)

```

Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,839 of 29,107 population items
  300 GO terms are associated with 165 of 206 study items
METHOD fdr_bh:
  0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
  0 study items associated with significant GO IDs (enriched)
  0 study items associated with significant GO IDs (purified)
Significant results[2] = 0 BP + 0 MF + 2 CC
  2 items WROTE: GO_analysis_module_green.xlsx
  2 GOEA results for 59 study items. WROTE: GO_analysis_module_green.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.371620 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 308 IDs ... 81% 249 of
308 study items found in association
100% 308 of 308 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
  1,346 GO terms are associated with 249 of 308 study items
METHOD fdr_bh:
  0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
  0 study items associated with significant GO IDs (enriched)
  0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 308 IDs ... 87% 268 of
308 study items found in association
100% 308 of 308 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,713 of 29,107 population items
  307 GO terms are associated with 268 of 308 study items
METHOD fdr_bh:

```

```

    13 GO terms found significant (< 0.05=alpha) ( 13 enriched + 0
purified): statsmodels fdr_bh
    158 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 308 IDs ... 84%    260 of
308 study items found in association
100%    308 of    308 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    470 GO terms are associated with    260 of    308 study items
METHOD fdr_bh:
    1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0
purified): statsmodels fdr_bh
    27 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[14] = 0 BP + 1 MF + 13 CC
    14 items WROTE: GO_analysis_module_yellow.xlsx
    14 GOEA results for    166 study items. WROTE: GO_analysis_module_yellow.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.645400 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 91 IDs ... 88%    80 of
91 study items found in association
100%    91 of    91 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,849 of 29,107 population items
    544 GO terms are associated with    80 of    91 study items
METHOD fdr_bh:
    5 GO terms found significant (< 0.05=alpha) ( 5 enriched + 0
purified): statsmodels fdr_bh
    29 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

```

Run CC Gene Ontology Analysis: current study set of 91 IDs ... 95% 86 of  
91 study items found in association

100% 91 of 91 study items found in population(29107)

Calculating 1,756 uncorrected p-values using fisher

1,756 GO terms are associated with 18,713 of 29,107 population items

185 GO terms are associated with 86 of 91 study items

METHOD fdr\_bh:

22 GO terms found significant ( $< 0.05=\alpha$ ) ( 22 enriched + 0  
purified): statsmodels fdr\_bh

58 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 91 IDs ... 89% 81 of  
91 study items found in association

100% 91 of 91 study items found in population(29107)

Calculating 4,434 uncorrected p-values using fisher

4,434 GO terms are associated with 17,839 of 29,107 population items

197 GO terms are associated with 81 of 91 study items

METHOD fdr\_bh:

3 GO terms found significant ( $< 0.05=\alpha$ ) ( 3 enriched + 0  
purified): statsmodels fdr\_bh

9 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Significant results[30] = 5 BP + 3 MF + 22 CC

30 items Wrote: GO\_analysis\_module\_purple.xlsx

30 GOEA results for 62 study items. Wrote: GO\_analysis\_module\_purple.txt

EXISTS: go-basic.obo

EXISTS: gene2go

go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms

HMS:0:00:04.379890 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
gene2go

BP 18,506 annotated human genes

CC 19,424 annotated human genes

MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...

70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...

74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...

70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 29 IDs ... 83% 24 of  
29 study items found in association

100% 29 of 29 study items found in population(29107)

Calculating 12,438 uncorrected p-values using fisher  
 12,438 GO terms are associated with 17,849 of 29,107 population items  
 293 GO terms are associated with 24 of 29 study items  
 METHOD fdr\_bh:  
 0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0  
 purified): statsmodels fdr\_bh  
 0 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 29 IDs ... 83% 24 of  
 29 study items found in association  
 100% 29 of 29 study items found in population(29107)  
 Calculating 1,756 uncorrected p-values using fisher  
 1,756 GO terms are associated with 18,713 of 29,107 population items  
 88 GO terms are associated with 24 of 29 study items  
 METHOD fdr\_bh:  
 7 GO terms found significant (< 0.05=alpha) ( 7 enriched + 0  
 purified): statsmodels fdr\_bh  
 10 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 29 IDs ... 86% 25 of  
 29 study items found in association  
 100% 29 of 29 study items found in population(29107)  
 Calculating 4,434 uncorrected p-values using fisher  
 4,434 GO terms are associated with 17,839 of 29,107 population items  
 81 GO terms are associated with 25 of 29 study items  
 METHOD fdr\_bh:  
 0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0  
 purified): statsmodels fdr\_bh  
 0 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)

Significant results[7] = 0 BP + 0 MF + 7 CC  
 7 items WROTE: GO\_analysis\_module\_orange.xlsx  
 7 GOEA results for 10 study items. WROTE: GO\_analysis\_module\_orange.txt  
 EXISTS: go-basic.obo  
 EXISTS: gene2go  
 go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms  
 HMS:0:00:04.650817 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
 gene2go  
 BP 18,506 annotated human genes  
 CC 19,424 annotated human genes  
 MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...  
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...

```

74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 70 IDs ... 87%      61 of
70 study items found in association
100%      70 of      70 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
12,438 GO terms are associated with 17,849 of 29,107 population items
404 GO terms are associated with      61 of      70 study items
METHOD fdr_bh:
4 GO terms found significant (< 0.05=alpha) ( 4 enriched + 0
purified): statsmodels fdr_bh
7 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 70 IDs ... 91%      64 of
70 study items found in association
100%      70 of      70 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
1,756 GO terms are associated with 18,713 of 29,107 population items
155 GO terms are associated with      64 of      70 study items
METHOD fdr_bh:
7 GO terms found significant (< 0.05=alpha) ( 7 enriched + 0
purified): statsmodels fdr_bh
18 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 70 IDs ... 84%      59 of
70 study items found in association
100%      70 of      70 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
4,434 GO terms are associated with 17,839 of 29,107 population items
143 GO terms are associated with      59 of      70 study items
METHOD fdr_bh:
3 GO terms found significant (< 0.05=alpha) ( 3 enriched + 0
purified): statsmodels fdr_bh
8 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)
Significant results[14] = 4 BP + 3 MF + 7 CC
14 items WROTE: GO_analysis_module_greenyellow.xlsx
14 GOEA results for 19 study items. WROTE:
GO_analysis_module_greenyellow.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.644683 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:

```



```

gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 54 IDs ... 91%      49 of
54 study items found in association
100%      54 of      54 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
  407 GO terms are associated with      49 of      54 study items
  METHOD fdr_bh:
    4 GO terms found significant (< 0.05=alpha) ( 4 enriched + 0
purified): statsmodels fdr_bh
    11 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 54 IDs ... 96%      52 of
54 study items found in association
100%      54 of      54 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,713 of 29,107 population items
  172 GO terms are associated with      52 of      54 study items
  METHOD fdr_bh:
    19 GO terms found significant (< 0.05=alpha) ( 19 enriched + 0
purified): statsmodels fdr_bh
    49 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 54 IDs ... 91%      49 of
54 study items found in association
100%      54 of      54 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,839 of 29,107 population items
  157 GO terms are associated with      49 of      54 study items
  METHOD fdr_bh:
    6 GO terms found significant (< 0.05=alpha) ( 6 enriched + 0
purified): statsmodels fdr_bh
    44 study items associated with significant GO IDs (enriched)

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    0 study items associated with significant GO IDs (purified)
Significant results[29] = 4 BP + 6 MF + 19 CC
    29 items WROTE: GO_analysis_module_midnightblue.xlsx
    29 GOEA results for    52 study items. WROTE:
GO_analysis_module_midnightblue.txt
    EXISTS: go-basic.obo
    EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.313489 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 405 IDs ... 86%    349 of
405 study items found in association
100%    405 of    405 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,849 of 29,107 population items
    2,052 GO terms are associated with    349 of    405 study items
METHOD fdr_bh:
    240 GO terms found significant (< 0.05=alpha) (239 enriched +    1
purified): statsmodels fdr_bh
    291 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 405 IDs ... 93%    375 of
405 study items found in association
100%    405 of    405 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
    300 GO terms are associated with    375 of    405 study items
METHOD fdr_bh:
    69 GO terms found significant (< 0.05=alpha) ( 69 enriched +    0
purified): statsmodels fdr_bh
    354 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 405 IDs ... 90%    366 of

```

405 study items found in association  
 100% 405 of 405 study items found in population(29107)  
 Calculating 4,434 uncorrected p-values using fisher  
 4,434 GO terms are associated with 17,839 of 29,107 population items  
 557 GO terms are associated with 366 of 405 study items  
 METHOD fdr\_bh:  
 55 GO terms found significant (< 0.05=alpha) ( 55 enriched + 0  
 purified): statsmodels fdr\_bh  
 323 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)  
 Significant results[364] = 240 BP + 55 MF + 69 CC  
 364 items Wrote: GO\_analysis\_module\_brown.xlsx  
 364 GOEA results for 373 study items. Wrote: GO\_analysis\_module\_brown.txt  
 EXISTS: go-basic.obo  
 EXISTS: gene2go  
 go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms  
 HMS:0:00:04.560230 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
 gene2go  
 BP 18,506 annotated human genes  
 CC 19,424 annotated human genes  
 MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...  
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 186 IDs ... 90% 167 of  
 186 study items found in association

100% 186 of 186 study items found in population(29107)  
 Calculating 12,438 uncorrected p-values using fisher  
 12,438 GO terms are associated with 17,849 of 29,107 population items  
 1,195 GO terms are associated with 167 of 186 study items  
 METHOD fdr\_bh:  
 13 GO terms found significant (< 0.05=alpha) ( 13 enriched + 0  
 purified): statsmodels fdr\_bh

46 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 186 IDs ... 92% 171 of  
 186 study items found in association

100% 186 of 186 study items found in population(29107)  
 Calculating 1,756 uncorrected p-values using fisher  
 1,756 GO terms are associated with 18,713 of 29,107 population items

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    196 GO terms are associated with    171 of    186 study items
METHOD fdr_bh:
    16 GO terms found significant (< 0.05=alpha) ( 16 enriched + 0
purified): statsmodels fdr_bh
    138 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 186 IDs ... 89%    166 of
186 study items found in association
100%    186 of    186 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    343 GO terms are associated with    166 of    186 study items
METHOD fdr_bh:
    6 GO terms found significant (< 0.05=alpha) ( 6 enriched + 0
purified): statsmodels fdr_bh
    118 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[35] = 13 BP + 6 MF + 16 CC
    35 items WROTE: GO_analysis_module_red.xlsx
    35 GOEA results for    163 study items. WROTE: GO_analysis_module_red.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.396688 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 45 IDs ... 98%    44 of
45 study items found in association
100%    45 of    45 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,849 of 29,107 population items
    536 GO terms are associated with    44 of    45 study items
METHOD fdr_bh:
    12 GO terms found significant (< 0.05=alpha) ( 12 enriched + 0
purified): statsmodels fdr_bh

```

```

    34 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 45 IDs ... 98%      44 of
45 study items found in association
100%      45 of      45 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
    94 GO terms are associated with      44 of      45 study items
METHOD fdr_bh:
    2 GO terms found significant (< 0.05=alpha) (  2 enriched +  0
purified): statsmodels fdr_bh
    26 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 45 IDs ... 98%      44 of
45 study items found in association
100%      45 of      45 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    132 GO terms are associated with      44 of      45 study items
METHOD fdr_bh:
    4 GO terms found significant (< 0.05=alpha) (  4 enriched +  0
purified): statsmodels fdr_bh
    39 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[18] = 12 BP + 4 MF + 2 CC
    18 items Wrote: GO_analysis_module_lightyellow.xlsx
    18 GOEA results for      43 study items. Wrote:
GO_analysis_module_lightyellow.txt
    EXISTS: go-basic.obo
    EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.574669 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

```

```

Run BP Gene Ontology Analysis: current study set of 19 IDs ...100%      19 of
19 study items found in association
100%      19 of      19 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
  164 GO terms are associated with      19 of      19 study items
  METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 19 IDs ...100%      19 of
19 study items found in association
100%      19 of      19 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,713 of 29,107 population items
  61 GO terms are associated with      19 of      19 study items
  METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 19 IDs ...100%      19 of
19 study items found in association
100%      19 of      19 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,839 of 29,107 population items
  64 GO terms are associated with      19 of      19 study items
  METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
  0 items. NOT WRITING GO_analysis_module_sienna3.xlsx
  0 GOEA results. NOT WRITING GO_analysis_module_sienna3.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.632776 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...

```

```

70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 33 IDs ... 82%      27 of
33 study items found in association
100%      33 of      33 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
12,438 GO terms are associated with 17,849 of 29,107 population items
218 GO terms are associated with      27 of      33 study items
METHOD fdr_bh:
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
0 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 33 IDs ... 88%      29 of
33 study items found in association
100%      33 of      33 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
1,756 GO terms are associated with 18,713 of 29,107 population items
86 GO terms are associated with      29 of      33 study items
METHOD fdr_bh:
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
0 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 33 IDs ... 91%      30 of
33 study items found in association
100%      33 of      33 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
4,434 GO terms are associated with 17,839 of 29,107 population items
95 GO terms are associated with      30 of      33 study items
METHOD fdr_bh:
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
0 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
0 items. NOT WRITING GO_analysis_module_darkgrey.xlsx
0 GOEA results. NOT WRITING GO_analysis_module_darkgrey.txt
EXISTS: go-basic.obo
EXISTS: gene2go

```

go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms  
HMS:0:00:04.545939 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
gene2go

BP 18,506 annotated human genes

CC 19,424 annotated human genes

MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...

70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...

74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...

70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 28 IDs ...100% 28 of  
28 study items found in association

100% 28 of 28 study items found in population(29107)

Calculating 12,438 uncorrected p-values using fisher

12,438 GO terms are associated with 17,849 of 29,107 population items

202 GO terms are associated with 28 of 28 study items

METHOD fdr\_bh:

4 GO terms found significant (< 0.05=alpha) ( 4 enriched + 0  
purified): statsmodels fdr\_bh

8 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 28 IDs ...100% 28 of  
28 study items found in association

100% 28 of 28 study items found in population(29107)

Calculating 1,756 uncorrected p-values using fisher

1,756 GO terms are associated with 18,713 of 29,107 population items

77 GO terms are associated with 28 of 28 study items

METHOD fdr\_bh:

10 GO terms found significant (< 0.05=alpha) ( 10 enriched + 0  
purified): statsmodels fdr\_bh

24 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 28 IDs ...100% 28 of  
28 study items found in association

100% 28 of 28 study items found in population(29107)

Calculating 4,434 uncorrected p-values using fisher

4,434 GO terms are associated with 17,839 of 29,107 population items

111 GO terms are associated with 28 of 28 study items

METHOD fdr\_bh:

11 GO terms found significant (< 0.05=alpha) ( 11 enriched + 0



```

purified): statsmodels fdr_bh
    27 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[25] = 4 BP + 11 MF + 10 CC
    25 items Wrote: GO_analysis_module_white.xlsx
    25 GOEA results for    27 study items. Wrote: GO_analysis_module_white.txt
    EXISTS: go-basic.obo
    EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.633881 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 43 IDs ... 84%      36 of
43 study items found in association
100%    43 of    43 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,849 of 29,107 population items
    207 GO terms are associated with    36 of    43 study items
    METHOD fdr_bh:
        0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 43 IDs ... 77%      33 of
43 study items found in association
100%    43 of    43 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
    85 GO terms are associated with    33 of    43 study items
    METHOD fdr_bh:
        1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0
purified): statsmodels fdr_bh
        4 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

```

```

Run MF Gene Ontology Analysis: current study set of 43 IDs ... 74%      32 of
43 study items found in association
100%      43 of      43 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    61 GO terms are associated with      32 of      43 study items
    METHOD fdr_bh:
        2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0
purified): statsmodels fdr_bh
        4 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[3] = 0 BP + 2 MF + 1 CC
    3 items WROTE: GO_analysis_module_lightgreen.xlsx
    3 GOEA results for      4 study items. WROTE:
GO_analysis_module_lightgreen.txt
    EXISTS: go-basic.obo
    EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.572526 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 24 IDs ... 92%      22 of
24 study items found in association
100%      24 of      24 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,849 of 29,107 population items
    178 GO terms are associated with      22 of      24 study items
    METHOD fdr_bh:
        0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 24 IDs ... 92%      22 of
24 study items found in association
100%      24 of      24 study items found in population(29107)

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Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,713 of 29,107 population items
  68 GO terms are associated with      22 of      24 study items
METHOD fdr_bh:
  0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
  0 study items associated with significant GO IDs (enriched)
  0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 24 IDs ... 79%      19 of
24 study items found in association
100%      24 of      24 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,839 of 29,107 population items
  81 GO terms are associated with      19 of      24 study items
METHOD fdr_bh:
  0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
  0 study items associated with significant GO IDs (enriched)
  0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
  0 items. NOT WRITING GO_analysis_module_saddlebrown.xlsx
  0 GOEA results. NOT WRITING GO_analysis_module_saddlebrown.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.583317 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 53 IDs ... 96%      51 of
53 study items found in association
100%      53 of      53 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
  337 GO terms are associated with      51 of      53 study items
METHOD fdr_bh:

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    4 GO terms found significant (< 0.05=alpha) ( 4 enriched + 0
purified): statsmodels fdr_bh
    4 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 53 IDs ... 98%      52 of
53 study items found in association
100%      53 of      53 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
    125 GO terms are associated with      52 of      53 study items
METHOD fdr_bh:
    5 GO terms found significant (< 0.05=alpha) ( 5 enriched + 0
purified): statsmodels fdr_bh
    46 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 53 IDs ... 94%      50 of
53 study items found in association
100%      53 of      53 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    114 GO terms are associated with      50 of      53 study items
METHOD fdr_bh:
    8 GO terms found significant (< 0.05=alpha) ( 8 enriched + 0
purified): statsmodels fdr_bh
    43 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[17] = 4 BP + 8 MF + 5 CC
    17 items WROTE: GO_analysis_module_lightcyan.xlsx
    17 GOEA results for      50 study items. WROTE:
GO_analysis_module_lightcyan.txt
    EXISTS: go-basic.obo
    EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.619552 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...

```

70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 26 IDs ... 88% 23 of  
26 study items found in association  
100% 26 of 26 study items found in population(29107)  
Calculating 12,438 uncorrected p-values using fisher  
12,438 GO terms are associated with 17,849 of 29,107 population items  
154 GO terms are associated with 23 of 26 study items  
METHOD fdr\_bh:  
26 GO terms found significant (< 0.05=alpha) ( 26 enriched + 0  
purified): statsmodels fdr\_bh  
21 study items associated with significant GO IDs (enriched)  
0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 26 IDs ... 92% 24 of  
26 study items found in association  
100% 26 of 26 study items found in population(29107)  
Calculating 1,756 uncorrected p-values using fisher  
1,756 GO terms are associated with 18,713 of 29,107 population items  
34 GO terms are associated with 24 of 26 study items  
METHOD fdr\_bh:  
2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0  
purified): statsmodels fdr\_bh  
22 study items associated with significant GO IDs (enriched)  
0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 26 IDs ... 96% 25 of  
26 study items found in association  
100% 26 of 26 study items found in population(29107)  
Calculating 4,434 uncorrected p-values using fisher  
4,434 GO terms are associated with 17,839 of 29,107 population items  
45 GO terms are associated with 25 of 26 study items  
METHOD fdr\_bh:  
10 GO terms found significant (< 0.05=alpha) ( 10 enriched + 0  
purified): statsmodels fdr\_bh  
23 study items associated with significant GO IDs (enriched)  
0 study items associated with significant GO IDs (purified)

Significant results[38] = 26 BP + 10 MF + 2 CC  
38 items WROTE: GO\_analysis\_module\_steelblue.xlsx  
38 GOEA results for 25 study items. WROTE:  
GO\_analysis\_module\_steelblue.txt  
EXISTS: go-basic.obo  
EXISTS: gene2go  
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms  
HMS:0:00:04.637184 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
gene2go  
BP 18,506 annotated human genes  
CC 19,424 annotated human genes

MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...

70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...

74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...

70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 96 IDs ... 82% 79 of  
96 study items found in association

100% 96 of 96 study items found in population(29107)

Calculating 12,438 uncorrected p-values using fisher

12,438 GO terms are associated with 17,849 of 29,107 population items

408 GO terms are associated with 79 of 96 study items

METHOD fdr\_bh:

1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0  
purified): statsmodels fdr\_bh

6 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 96 IDs ... 90% 86 of  
96 study items found in association

100% 96 of 96 study items found in population(29107)

Calculating 1,756 uncorrected p-values using fisher

1,756 GO terms are associated with 18,713 of 29,107 population items

114 GO terms are associated with 86 of 96 study items

METHOD fdr\_bh:

0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0  
purified): statsmodels fdr\_bh

0 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 96 IDs ... 80% 77 of  
96 study items found in association

100% 96 of 96 study items found in population(29107)

Calculating 4,434 uncorrected p-values using fisher

4,434 GO terms are associated with 17,839 of 29,107 population items

161 GO terms are associated with 77 of 96 study items

METHOD fdr\_bh:

0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0  
purified): statsmodels fdr\_bh

0 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Significant results[1] = 1 BP + 0 MF + 0 CC

1 items WROTE: GO\_analysis\_module\_magenta.xlsx

1 GOEA results for 6 study items. WROTE:  
GO\_analysis\_module\_magenta.txt  
EXISTS: go-basic.obo  
EXISTS: gene2go  
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms  
HMS:0:00:04.325556 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
gene2go  
BP 18,506 annotated human genes  
CC 19,424 annotated human genes  
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...  
70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 70 IDs ... 84% 59 of  
70 study items found in association  
100% 70 of 70 study items found in population(29107)  
Calculating 12,438 uncorrected p-values using fisher  
12,438 GO terms are associated with 17,849 of 29,107 population items  
409 GO terms are associated with 59 of 70 study items  
METHOD fdr\_bh:  
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0  
purified): statsmodels fdr\_bh  
0 study items associated with significant GO IDs (enriched)  
0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 70 IDs ... 87% 61 of  
70 study items found in association  
100% 70 of 70 study items found in population(29107)  
Calculating 1,756 uncorrected p-values using fisher  
1,756 GO terms are associated with 18,713 of 29,107 population items  
109 GO terms are associated with 61 of 70 study items  
METHOD fdr\_bh:  
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0  
purified): statsmodels fdr\_bh  
0 study items associated with significant GO IDs (enriched)  
0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 70 IDs ... 90% 63 of  
70 study items found in association  
100% 70 of 70 study items found in population(29107)  
Calculating 4,434 uncorrected p-values using fisher

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4,434 GO terms are associated with 17,839 of 29,107 population items
139 GO terms are associated with      63 of      70 study items
METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) (  0 enriched +  0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
    0 items. NOT WRITING GO_analysis_module_tan.xlsx
    0 GOEA results. NOT WRITING GO_analysis_module_tan.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.675666 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 36 IDs ... 89%      32 of
36 study items found in association
100%      36 of      36 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
12,438 GO terms are associated with 17,849 of 29,107 population items
310 GO terms are associated with      32 of      36 study items
METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) (  0 enriched +  0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 36 IDs ... 94%      34 of
36 study items found in association
100%      36 of      36 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
1,756 GO terms are associated with 18,713 of 29,107 population items
95 GO terms are associated with      34 of      36 study items
METHOD fdr_bh:
    3 GO terms found significant (< 0.05=alpha) (  3 enriched +  0

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purified): statsmodels fdr_bh
    22 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 36 IDs ... 97%    35 of
36 study items found in association
100%    36 of    36 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    102 GO terms are associated with    35 of    36 study items
METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[3] = 0 BP + 0 MF + 3 CC
    3 items WROTE: GO_analysis_module_darkturquoise.xlsx
    3 GOEA results for    22 study items. WROTE:
GO_analysis_module_darkturquoise.txt
    EXISTS: go-basic.obo
    EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.584321 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 56 IDs ... 93%    52 of
56 study items found in association
100%    56 of    56 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,849 of 29,107 population items
    447 GO terms are associated with    52 of    56 study items
METHOD fdr_bh:
    3 GO terms found significant (< 0.05=alpha) ( 3 enriched + 0
purified): statsmodels fdr_bh
    18 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

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```

Run CC Gene Ontology Analysis: current study set of 56 IDs ... 95%      53 of
56 study items found in association
100%      56 of      56 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
    132 GO terms are associated with      53 of      56 study items
METHOD fdr_bh:
    7 GO terms found significant (< 0.05=alpha) ( 7 enriched + 0
purified): statsmodels fdr_bh
    40 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 56 IDs ... 96%      54 of
56 study items found in association
100%      56 of      56 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    164 GO terms are associated with      54 of      56 study items
METHOD fdr_bh:
    4 GO terms found significant (< 0.05=alpha) ( 4 enriched + 0
purified): statsmodels fdr_bh
    46 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[14] = 3 BP + 4 MF + 7 CC
    14 items Wrote: GO_analysis_module_cyan.xlsx
    14 GOEA results for      50 study items. Wrote: GO_analysis_module_cyan.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.724443 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 26 IDs ... 92%      24 of
26 study items found in association
100%      26 of      26 study items found in population(29107)

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Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
    142 GO terms are associated with      24 of      26 study items
  METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) (  0 enriched +  0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 26 IDs ... 96%      25 of
26 study items found in association
100%      26 of      26 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,713 of 29,107 population items
    56 GO terms are associated with      25 of      26 study items
  METHOD fdr_bh:
    2 GO terms found significant (< 0.05=alpha) (  2 enriched +  0
purified): statsmodels fdr_bh
    6 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 26 IDs ... 85%      22 of
26 study items found in association
100%      26 of      26 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,839 of 29,107 population items
    50 GO terms are associated with      22 of      26 study items
  METHOD fdr_bh:
    2 GO terms found significant (< 0.05=alpha) (  2 enriched +  0
purified): statsmodels fdr_bh
    2 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[4] = 0 BP + 2 MF + 2 CC
  4 items WROTE: GO_analysis_module_violet.xlsx
  4 GOEA results for      6 study items. WROTE: GO_analysis_module_violet.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.349747 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...

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```

74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 17 IDs ... 88%      15 of
17 study items found in association
100%      17 of      17 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
12,438 GO terms are associated with 17,849 of 29,107 population items
133 GO terms are associated with      15 of      17 study items
METHOD fdr_bh:
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
0 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 17 IDs ... 88%      15 of
17 study items found in association
100%      17 of      17 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
1,756 GO terms are associated with 18,713 of 29,107 population items
44 GO terms are associated with      15 of      17 study items
METHOD fdr_bh:
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
0 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 17 IDs ... 82%      14 of
17 study items found in association
100%      17 of      17 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
4,434 GO terms are associated with 17,839 of 29,107 population items
51 GO terms are associated with      14 of      17 study items
METHOD fdr_bh:
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
0 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
0 items. NOT WRITING GO_analysis_module_paleturquoise.xlsx
0 GOEA results. NOT WRITING GO_analysis_module_paleturquoise.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.661904 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go

```

BP 18,506 annotated human genes  
CC 19,424 annotated human genes  
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...  
70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 21 IDs ...100% 21 of  
21 study items found in association  
100% 21 of 21 study items found in population(29107)  
Calculating 12,438 uncorrected p-values using fisher  
12,438 GO terms are associated with 17,849 of 29,107 population items  
165 GO terms are associated with 21 of 21 study items  
METHOD fdr\_bh:  
13 GO terms found significant (< 0.05=alpha) ( 13 enriched + 0  
purified): statsmodels fdr\_bh  
19 study items associated with significant GO IDs (enriched)  
0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 21 IDs ...100% 21 of  
21 study items found in association  
100% 21 of 21 study items found in population(29107)  
Calculating 1,756 uncorrected p-values using fisher  
1,756 GO terms are associated with 18,713 of 29,107 population items  
51 GO terms are associated with 21 of 21 study items  
METHOD fdr\_bh:  
3 GO terms found significant (< 0.05=alpha) ( 3 enriched + 0  
purified): statsmodels fdr\_bh  
12 study items associated with significant GO IDs (enriched)  
0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 21 IDs ...100% 21 of  
21 study items found in association  
100% 21 of 21 study items found in population(29107)  
Calculating 4,434 uncorrected p-values using fisher  
4,434 GO terms are associated with 17,839 of 29,107 population items  
68 GO terms are associated with 21 of 21 study items  
METHOD fdr\_bh:  
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0  
purified): statsmodels fdr\_bh  
0 study items associated with significant GO IDs (enriched)  
0 study items associated with significant GO IDs (purified)

Significant results[16] = 13 BP + 0 MF + 3 CC  
 16 items WROTE: GO\_analysis\_module\_yellowgreen.xlsx  
 16 GOEA results for 20 study items. WROTE:  
 GO\_analysis\_module\_yellowgreen.txt  
 EXISTS: go-basic.obo  
 EXISTS: gene2go  
 go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms  
 HMS:0:00:04.364474 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
 gene2go  
 BP 18,506 annotated human genes  
 CC 19,424 annotated human genes  
 MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...  
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 23 IDs ... 91% 21 of  
 23 study items found in association  
 100% 23 of 23 study items found in population(29107)  
 Calculating 12,438 uncorrected p-values using fisher  
 12,438 GO terms are associated with 17,849 of 29,107 population items  
 411 GO terms are associated with 21 of 23 study items  
 METHOD fdr\_bh:  
 9 GO terms found significant (< 0.05=alpha) ( 9 enriched + 0  
 purified): statsmodels fdr\_bh  
 15 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 23 IDs ...100% 23 of  
 23 study items found in association  
 100% 23 of 23 study items found in population(29107)  
 Calculating 1,756 uncorrected p-values using fisher  
 1,756 GO terms are associated with 18,713 of 29,107 population items  
 46 GO terms are associated with 23 of 23 study items  
 METHOD fdr\_bh:  
 4 GO terms found significant (< 0.05=alpha) ( 4 enriched + 0  
 purified): statsmodels fdr\_bh  
 15 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 23 IDs ...100% 23 of  
 23 study items found in association

100% 23 of 23 study items found in population(29107)  
 Calculating 4,434 uncorrected p-values using fisher  
 4,434 GO terms are associated with 17,839 of 29,107 population items  
 87 GO terms are associated with 23 of 23 study items  
 METHOD fdr\_bh:  
 6 GO terms found significant (< 0.05=alpha) ( 6 enriched + 0  
 purified): statsmodels fdr\_bh  
 21 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)  
 Significant results[19] = 9 BP + 6 MF + 4 CC  
 19 items WROTE: GO\_analysis\_module\_darkolivegreen.xlsx  
 19 GOEA results for 21 study items. WROTE:  
 GO\_analysis\_module\_darkolivegreen.txt  
 EXISTS: go-basic.obo  
 EXISTS: gene2go  
 go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms  
 HMS:0:00:04.967264 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
 gene2go  
 BP 18,506 annotated human genes  
 CC 19,424 annotated human genes  
 MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...  
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 22 IDs ... 91% 20 of  
 22 study items found in association

100% 22 of 22 study items found in population(29107)  
 Calculating 12,438 uncorrected p-values using fisher  
 12,438 GO terms are associated with 17,849 of 29,107 population items  
 204 GO terms are associated with 20 of 22 study items  
 METHOD fdr\_bh:  
 0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0  
 purified): statsmodels fdr\_bh  
 0 study items associated with significant GO IDs (enriched)  
 0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 22 IDs ... 91% 20 of  
 22 study items found in association

100% 22 of 22 study items found in population(29107)  
 Calculating 1,756 uncorrected p-values using fisher  
 1,756 GO terms are associated with 18,713 of 29,107 population items

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    77 GO terms are associated with      20 of      22 study items
METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) (  0 enriched +  0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 22 IDs ... 91%      20 of
22 study items found in association
100%      22 of      22 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    82 GO terms are associated with      20 of      22 study items
METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) (  0 enriched +  0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
    0 items. NOT WRITING GO_analysis_module_darkmagenta.xlsx
    0 GOEA results. NOT WRITING GO_analysis_module_darkmagenta.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.777650 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 57 IDs ... 88%      50 of
57 study items found in association
100%      57 of      57 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,849 of 29,107 population items
    521 GO terms are associated with      50 of      57 study items
METHOD fdr_bh:
    10 GO terms found significant (< 0.05=alpha) ( 10 enriched +  0
purified): statsmodels fdr_bh

```



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    2 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 57 IDs ... 93%      53 of
57 study items found in association
100%      57 of      57 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
    105 GO terms are associated with      53 of      57 study items
METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 57 IDs ... 93%      53 of
57 study items found in association
100%      57 of      57 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    147 GO terms are associated with      53 of      57 study items
METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[10] = 10 BP + 0 MF + 0 CC
    10 items Wrote: GO_analysis_module_salmon.xlsx
    10 GOEA results for      2 study items. Wrote: GO_analysis_module_salmon.txt
EXISTS: go-basic.obo
EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.876665 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 37 IDs ... 92%      34 of

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```

37 study items found in association
100%    37 of    37 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,849 of 29,107 population items
        219 GO terms are associated with    34 of    37 study items
    METHOD fdr_bh:
        0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 37 IDs ... 97%    36 of
37 study items found in association
100%    37 of    37 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
        72 GO terms are associated with    36 of    37 study items
    METHOD fdr_bh:
        3 GO terms found significant (< 0.05=alpha) ( 3 enriched + 0
purified): statsmodels fdr_bh
        24 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 37 IDs ... 86%    32 of
37 study items found in association
100%    37 of    37 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
        90 GO terms are associated with    32 of    37 study items
    METHOD fdr_bh:
        1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0
purified): statsmodels fdr_bh
        2 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[4] = 0 BP + 1 MF + 3 CC
    4 items WROTE: GO_analysis_module_darkred.xlsx
    4 GOEA results for    24 study items. WROTE:
GO_analysis_module_darkred.txt
    EXISTS: go-basic.obo
    EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.846772 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...

```

```

70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 39 IDs ... 85%      33 of
39 study items found in association
100%      39 of      39 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
12,438 GO terms are associated with 17,849 of 29,107 population items
209 GO terms are associated with      33 of      39 study items
METHOD fdr_bh:
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
0 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 39 IDs ... 92%      36 of
39 study items found in association
100%      39 of      39 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
1,756 GO terms are associated with 18,713 of 29,107 population items
66 GO terms are associated with      36 of      39 study items
METHOD fdr_bh:
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
0 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 39 IDs ... 82%      32 of
39 study items found in association
100%      39 of      39 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
4,434 GO terms are associated with 17,839 of 29,107 population items
91 GO terms are associated with      32 of      39 study items
METHOD fdr_bh:
0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
0 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
0 items. NOT WRITING GO_analysis_module_royalblue.xlsx
0 GOEA results. NOT WRITING GO_analysis_module_royalblue.txt
EXISTS: go-basic.obo
EXISTS: gene2go

```

go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms  
HMS:0:00:04.579317 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:  
gene2go

BP 18,506 annotated human genes

CC 19,424 annotated human genes

MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...

70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...

74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...

70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 47 IDs ... 87% 41 of  
47 study items found in association

100% 47 of 47 study items found in population(29107)

Calculating 12,438 uncorrected p-values using fisher

12,438 GO terms are associated with 17,849 of 29,107 population items

262 GO terms are associated with 41 of 47 study items

METHOD fdr\_bh:

0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0  
purified): statsmodels fdr\_bh

0 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 47 IDs ... 89% 42 of  
47 study items found in association

100% 47 of 47 study items found in population(29107)

Calculating 1,756 uncorrected p-values using fisher

1,756 GO terms are associated with 18,713 of 29,107 population items

101 GO terms are associated with 42 of 47 study items

METHOD fdr\_bh:

1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0  
purified): statsmodels fdr\_bh

20 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 47 IDs ... 89% 42 of  
47 study items found in association

100% 47 of 47 study items found in population(29107)

Calculating 4,434 uncorrected p-values using fisher

4,434 GO terms are associated with 17,839 of 29,107 population items

101 GO terms are associated with 42 of 47 study items

METHOD fdr\_bh:

0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0

```

purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[1] = 0 BP + 0 MF + 1 CC
    1 items WROTE: GO_analysis_module_grey60.xlsx
    1 GOEA results for    20 study items. WROTE: GO_analysis_module_grey60.txt
    EXISTS: go-basic.obo
    EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.567898 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 32 IDs ...100%      32 of
32 study items found in association
100%      32 of      32 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,849 of 29,107 population items
    259 GO terms are associated with      32 of      32 study items
METHOD fdr_bh:
    7 GO terms found significant (< 0.05=alpha) ( 7 enriched + 0
purified): statsmodels fdr_bh
    4 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 32 IDs ... 97%      31 of
32 study items found in association
100%      32 of      32 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
    39 GO terms are associated with      31 of      32 study items
METHOD fdr_bh:
    1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0
purified): statsmodels fdr_bh
    18 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

```

```

Run MF Gene Ontology Analysis: current study set of 32 IDs ...100%      32 of
32 study items found in association
100%      32 of      32 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,839 of 29,107 population items
    86 GO terms are associated with      32 of      32 study items
  METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[8] = 7 BP + 0 MF + 1 CC
  8 items WROTE: GO_analysis_module_darkorange.xlsx
  8 GOEA results for      18 study items. WROTE:
GO_analysis_module_darkorange.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.461756 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 21 IDs ... 71%      15 of
21 study items found in association
100%      21 of      21 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
    124 GO terms are associated with      15 of      21 study items
  METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 21 IDs ... 95%      20 of
21 study items found in association
100%      21 of      21 study items found in population(29107)

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```

Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,713 of 29,107 population items
  48 GO terms are associated with      20 of      21 study items
METHOD fdr_bh:
  0 GO terms found significant (< 0.05=alpha) (  0 enriched +  0
purified): statsmodels fdr_bh
  0 study items associated with significant GO IDs (enriched)
  0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 21 IDs ... 95%      20 of
21 study items found in association
100%      21 of      21 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,839 of 29,107 population items
  49 GO terms are associated with      20 of      21 study items
METHOD fdr_bh:
  1 GO terms found significant (< 0.05=alpha) (  1 enriched +  0
purified): statsmodels fdr_bh
  19 study items associated with significant GO IDs (enriched)
  0 study items associated with significant GO IDs (purified)
Significant results[1] = 0 BP + 1 MF + 0 CC
  1 items WROTE: GO_analysis_module_skyblue3.xlsx
  1 GOEA results for      19 study items. WROTE:
GO_analysis_module_skyblue3.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.287452 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,506 annotated human genes
CC 19,424 annotated human genes
MF 18,191 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 21 IDs ... 71%      15 of
21 study items found in association
100%      21 of      21 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
  108 GO terms are associated with      15 of      21 study items

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METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 21 IDs ... 81%      17 of
21 study items found in association
100%      21 of      21 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
    46 GO terms are associated with      17 of      21 study items
METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 21 IDs ... 81%      17 of
21 study items found in association
100%      21 of      21 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    40 GO terms are associated with      17 of      21 study items
METHOD fdr_bh:
    0 GO terms found significant (< 0.05=alpha) ( 0 enriched + 0
purified): statsmodels fdr_bh
    0 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
    0 items. NOT WRITING GO_analysis_module_skyblue.xlsx
    0 GOEA results. NOT WRITING GO_analysis_module_skyblue.txt

```

[ ]: