

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  purple  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:0:00:04.481962 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 8079 IDs ... 75% 6,032 of
8,079 study items found in association
100% 8,079 of 8,079 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
  8,465 GO terms are associated with 6,032 of 8,079 study items
METHOD fdr_bh:
  34 GO terms found significant (< 0.05=alpha) ( 30 enriched + 4
purified): statsmodels fdr_bh
  1,853 study items associated with significant GO IDs (enriched)
  205 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 8079 IDs ... 79% 6,407 of
8,079 study items found in association
100% 8,079 of 8,079 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
  1,300 GO terms are associated with 6,407 of 8,079 study items
METHOD fdr_bh:
  46 GO terms found significant (< 0.05=alpha) ( 43 enriched + 3
purified): statsmodels fdr_bh
  5,860 study items associated with significant GO IDs (enriched)
  34 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 8079 IDs ... 77% 6,193 of
8,079 study items found in association
100% 8,079 of 8,079 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

```

2,967 GO terms are associated with 6,193 of 8,079 study items
METHOD fdr_bh:
32 GO terms found significant (< 0.05=alpha) (28 enriched + 4
purified): statsmodels fdr_bh
5,327 study items associated with significant GO IDs (enriched)
119 study items associated with significant GO IDs (purified)
Significant results[112] = 34 BP + 32 MF + 46 CC
112 items Wrote: GO_analysis_module_grey.xlsx
112 GOEA results for 6488 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:0:00:05.118964 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 1092 IDs ... 78% 850 of
1,092 study items found in association
100% 1,092 of 1,092 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
3,124 GO terms are associated with 850 of 1,092 study items
METHOD fdr_bh:
64 GO terms found significant (< 0.05=alpha) (61 enriched + 3
purified): statsmodels fdr_bh
377 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 1092 IDs ... 84% 912 of
1,092 study items found in association
100% 1,092 of 1,092 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
550 GO terms are associated with 912 of 1,092 study items
METHOD fdr_bh:
67 GO terms found significant (< 0.05=alpha) (65 enriched + 2
purified): statsmodels fdr_bh

```

726 study items associated with significant GO IDs (enriched)
50 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 1092 IDs ... 80%      873 of
1,092 study items found in association
100% 1,092 of 1,092 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
856 GO terms are associated with 873 of 1,092 study items
METHOD fdr_bh:
30 GO terms found significant (< 0.05=alpha) ( 27 enriched + 3
purified): statsmodels fdr_bh
726 study items associated with significant GO IDs (enriched)
20 study items associated with significant GO IDs (purified)
Significant results[161] = 64 BP + 30 MF + 67 CC
161 items WROTE: GO_analysis_module_blue.xlsx
161 GOEA results for 892 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:0:00:04.659532 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 223 IDs ... 96%      213 of
223 study items found in association
100% 223 of 223 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
1,042 GO terms are associated with 213 of 223 study items
METHOD fdr_bh:
5 GO terms found significant (< 0.05=alpha) ( 5 enriched + 0
purified): statsmodels fdr_bh
37 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 223 IDs ... 98%      219 of

```

```

223 study items found in association
100% 223 of 223 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
347 GO terms are associated with 219 of 223 study items
METHOD fdr_bh:
47 GO terms found significant (< 0.05=alpha) ( 47 enriched + 0
purified): statsmodels fdr_bh
212 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 223 IDs ... 96% 215 of
223 study items found in association
100% 223 of 223 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
407 GO terms are associated with 215 of 223 study items
METHOD fdr_bh:
8 GO terms found significant (< 0.05=alpha) ( 8 enriched + 0
purified): statsmodels fdr_bh
191 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)
Significant results[60] = 5 BP + 8 MF + 47 CC
60 items WROTE: GO_analysis_module_cyan.xlsx
60 GOEA results for 221 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:0:00:04.782061 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 ... 91% 51 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

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```

    339 GO terms are associated with      51 of      56 study items
METHOD fdr_bh:
    35 GO terms found significant (< 0.05=alpha) ( 35 enriched + 0
purified): statsmodels fdr_bh
    39 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 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
    89 GO terms are associated with      53 of      56 study items
METHOD fdr_bh:
    5 GO terms found significant (< 0.05=alpha) ( 5 enriched + 0
purified): statsmodels fdr_bh
    42 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
    113 GO terms are associated with      54 of      56 study items
METHOD fdr_bh:
    12 GO terms found significant (< 0.05=alpha) ( 12 enriched + 0
purified): statsmodels fdr_bh
    51 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[52] = 35 BP + 12 MF + 5 CC
    52 items WROTE: GO_analysis_module_violet.xlsx
    52 GOEA results for      52 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:0:00:04.629960 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 225 IDs ... 89% 201 of
225 study items found in association

100% 225 of 225 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

900 GO terms are associated with 201 of 225 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 CC Gene Ontology Analysis: current study set of 225 IDs ... 92% 208 of
225 study items found in association

100% 225 of 225 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

283 GO terms are associated with 208 of 225 study items

METHOD fdr_bh:

6 GO terms found significant ($< 0.05=\alpha$) (6 enriched + 0
purified): statsmodels fdr_bh

169 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 225 IDs ... 95% 214 of
225 study items found in association

100% 225 of 225 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

328 GO terms are associated with 214 of 225 study items

METHOD fdr_bh:

2 GO terms found significant ($< 0.05=\alpha$) (2 enriched + 0
purified): statsmodels fdr_bh

187 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Significant results[9] = 1 BP + 2 MF + 6 CC

9 items Wrote: GO_analysis_module_tan.xlsx

9 GOEA results for 207 study items. Wrote: 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:0:00:05.232856 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go

MF 18,191 annotated human genes

CC 19,424 annotated human genes

BP 18,506 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 112 IDs ... 86% 96 of
112 study items found in association

100% 112 of 112 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

489 GO terms are associated with 96 of 112 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 112 IDs ... 89% 100 of
112 study items found in association

100% 112 of 112 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

168 GO terms are associated with 100 of 112 study items

METHOD fdr_bh:

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

17 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 112 IDs ... 96% 107 of
112 study items found in association

100% 112 of 112 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

193 GO terms are associated with 107 of 112 study items

METHOD fdr_bh:

2 GO terms found significant ($< 0.05=\alpha$) (2 enriched + 0
purified): statsmodels fdr_bh

90 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_darkred.xlsx

```

3 GOEA results for 93 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:0:00:05.274700 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 101 IDs ... 86%      87 of
101 study items found in association
100%    101 of    101 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
  508 GO terms are associated with    87 of    101 study items
  METHOD fdr_bh:
    2 GO terms found significant (< 0.05=alpha) ( 2 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 101 IDs ... 90%      91 of
101 study items found in association
100%    101 of    101 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
  186 GO terms are associated with    91 of    101 study items
  METHOD fdr_bh:
    3 GO terms found significant (< 0.05=alpha) ( 3 enriched + 0
purified): statsmodels fdr_bh
    45 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 101 IDs ... 95%      96 of
101 study items found in association
100%    101 of    101 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
 198 GO terms are associated with 96 of 101 study items
 METHOD fdr_bh:
 4 GO terms found significant ($< 0.05=\alpha$) (4 enriched + 0
 purified): statsmodels fdr_bh
 83 study items associated with significant GO IDs (enriched)
 0 study items associated with significant GO IDs (purified)
 Significant results[9] = 2 BP + 4 MF + 3 CC
 9 items WROTE: GO_analysis_module_darkgreen.xlsx
 9 GOEA results for 87 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:0:00:04.786410 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
 gene2go
 MF 18,191 annotated human genes
 CC 19,424 annotated human genes
 BP 18,506 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 1681 IDs ... 88% 1,486 of
 1,681 study items found in association
 100% 1,681 of 1,681 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
 4,526 GO terms are associated with 1,486 of 1,681 study items
 METHOD fdr_bh:
 66 GO terms found significant ($< 0.05=\alpha$) (63 enriched + 3
 purified): statsmodels fdr_bh
 747 study items associated with significant GO IDs (enriched)
 14 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 1681 IDs ... 93% 1,556 of
 1,681 study items found in association
 100% 1,681 of 1,681 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
 837 GO terms are associated with 1,556 of 1,681 study items
 METHOD fdr_bh:

```

    95 GO terms found significant (< 0.05=alpha) ( 95 enriched + 0
purified): statsmodels fdr_bh
    1,501 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 1681 IDs ... 91% 1,532 of
1,681 study items found in association
100% 1,681 of 1,681 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
    1,423 GO terms are associated with 1,532 of 1,681 study items
METHOD fdr_bh:
    42 GO terms found significant (< 0.05=alpha) ( 39 enriched + 3
purified): statsmodels fdr_bh
    1,384 study items associated with significant GO IDs (enriched)
    9 study items associated with significant GO IDs (purified)
Significant results[203] = 66 BP + 42 MF + 95 CC
    203 items WROTE: GO_analysis_module_turquoise.xlsx
    203 GOEA results for 1578 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:0:00:04.451831 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 222 IDs ... 88% 195 of
222 study items found in association
100% 222 of 222 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
    1,128 GO terms are associated with 195 of 222 study items
METHOD fdr_bh:
    15 GO terms found significant (< 0.05=alpha) ( 15 enriched + 0
purified): statsmodels fdr_bh
    37 study items associated with significant GO IDs (enriched)

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    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 222 IDs ... 90%    200 of
222 study items found in association
100%    222 of    222 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
    309 GO terms are associated with    200 of    222 study items
METHOD fdr_bh:
    26 GO terms found significant (< 0.05=alpha) ( 26 enriched + 0
purified): statsmodels fdr_bh
    151 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 222 IDs ... 87%    194 of
222 study items found in association
100%    222 of    222 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
    365 GO terms are associated with    194 of    222 study items
METHOD fdr_bh:
    9 GO terms found significant (< 0.05=alpha) ( 9 enriched + 0
purified): statsmodels fdr_bh
    152 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[50] = 15 BP + 9 MF + 26 CC
    50 items Wrote: GO_analysis_module_purple.xlsx
    50 GOEA results for 187 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:0:00:04.591606 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 352 IDs ... 83%    292 of
352 study items found in association

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100%    352 of    352 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
    1,360 GO terms are associated with    292 of    352 study items
METHOD fdr_bh:
    7 GO terms found significant (< 0.05=alpha) ( 7 enriched + 0
purified): statsmodels fdr_bh
    38 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 352 IDs ... 89%    315 of
352 study items found in association
100%    352 of    352 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
    357 GO terms are associated with    315 of    352 study items
METHOD fdr_bh:
    26 GO terms found significant (< 0.05=alpha) ( 25 enriched + 1
purified): statsmodels fdr_bh
    252 study items associated with significant GO IDs (enriched)
    6 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 352 IDs ... 85%    299 of
352 study items found in association
100%    352 of    352 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
    436 GO terms are associated with    299 of    352 study items
METHOD fdr_bh:
    4 GO terms found significant (< 0.05=alpha) ( 4 enriched + 0
purified): statsmodels fdr_bh
    234 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[37] = 7 BP + 4 MF + 26 CC
    37 items Wrote: GO_analysis_module_green.xlsx
    37 GOEA results for 295 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:0:00:04.719302 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

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

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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 81 IDs ... 88%      71 of
81 study items found in association
100%      81 of      81 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
  499 GO terms are associated with      71 of      81 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 81 IDs ... 93%      75 of
81 study items found in association
100%      81 of      81 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
  119 GO terms are associated with      75 of      81 study items
  METHOD fdr_bh:
    4 GO terms found significant (< 0.05=alpha) (  4 enriched +  0
purified): statsmodels fdr_bh
    57 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 81 IDs ... 88%      71 of
81 study items found in association
100%      81 of      81 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
  178 GO terms are associated with      71 of      81 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[4] = 0 BP + 0 MF + 4 CC
  4 items WROTE: GO_analysis_module_white.xlsx
  4 GOEA results for      57 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:0:00:05.388450 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:

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gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 416 IDs ... 89%    370 of
416 study items found in association
100%    416 of    416 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
  1,968 GO terms are associated with    370 of    416 study items
  METHOD fdr_bh:
    7 GO terms found significant (< 0.05=alpha) ( 7 enriched + 0
purified): statsmodels fdr_bh
    63 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 416 IDs ... 94%    390 of
416 study items found in association
100%    416 of    416 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
  347 GO terms are associated with    390 of    416 study items
  METHOD fdr_bh:
    32 GO terms found significant (< 0.05=alpha) ( 32 enriched + 0
purified): statsmodels fdr_bh
    359 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 416 IDs ... 90%    376 of
416 study items found in association
100%    416 of    416 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
  666 GO terms are associated with    376 of    416 study items
  METHOD fdr_bh:
    10 GO terms found significant (< 0.05=alpha) ( 10 enriched + 0
purified): statsmodels fdr_bh
    307 study items associated with significant GO IDs (enriched)

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    0 study items associated with significant GO IDs (purified)
Significant results[49] = 7 BP + 10 MF + 32 CC
    49 items WROTE: GO_analysis_module_yellow.xlsx
    49 GOEA results for 383 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:0:00:05.041970 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 330 IDs ... 91%    300 of
330 study items found in association
100%    330 of    330 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
    1,539 GO terms are associated with    300 of    330 study items
    METHOD fdr_bh:
        2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0
purified): statsmodels fdr_bh
        28 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 330 IDs ... 93%    307 of
330 study items found in association
100%    330 of    330 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
    329 GO terms are associated with    307 of    330 study items
    METHOD fdr_bh:
        26 GO terms found significant (< 0.05=alpha) ( 26 enriched + 0
purified): statsmodels fdr_bh
        208 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 330 IDs ... 91%    299 of
330 study items found in association

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100% 330 of 330 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
 500 GO terms are associated with 299 of 330 study items
 METHOD fdr_bh:
 2 GO terms found significant (< 0.05=alpha) (2 enriched + 0
 purified): statsmodels fdr_bh
 214 study items associated with significant GO IDs (enriched)
 0 study items associated with significant GO IDs (purified)
 Significant results[30] = 2 BP + 2 MF + 26 CC
 30 items Wrote: GO_analysis_module_red.xlsx
 30 GOEA results for 289 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:0:00:04.558729 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
 gene2go
 MF 18,191 annotated human genes
 CC 19,424 annotated human genes
 BP 18,506 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 73 IDs ... 97% 71 of
 73 study items found in association

100% 73 of 73 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
 213 GO terms are associated with 71 of 73 study items
 METHOD fdr_bh:
 14 GO terms found significant (< 0.05=alpha) (14 enriched + 0
 purified): statsmodels fdr_bh
 54 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 73 IDs ... 97% 71 of
 73 study items found in association

100% 73 of 73 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
 96 GO terms are associated with 71 of 73 study items

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METHOD fdr_bh:
    22 GO terms found significant (< 0.05=alpha) ( 22 enriched + 0
purified): statsmodels fdr_bh
    68 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 73 IDs ... 96%      70 of
73 study items found in association
100%      73 of      73 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
    77 GO terms are associated with      70 of      73 study items
METHOD fdr_bh:
    10 GO terms found significant (< 0.05=alpha) ( 10 enriched + 0
purified): statsmodels fdr_bh
    68 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[46] = 14 BP + 10 MF + 22 CC
    46 items WROTE: GO_analysis_module_skyblue.xlsx
    46 GOEA results for      71 study items. WROTE:
GO_analysis_module_skyblue.txt
    EXISTS: go-basic.obo
    EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.925874 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 52 IDs ... 94%      49 of
52 study items found in association
100%      52 of      52 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
    306 GO terms are associated with      49 of      52 study items
METHOD fdr_bh:
    3 GO terms found significant (< 0.05=alpha) ( 3 enriched + 0
purified): statsmodels fdr_bh

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      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 52 IDs ... 98%      51 of
52 study items found in association
100%      52 of      52 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
      146 GO terms are associated with      51 of      52 study items
METHOD fdr_bh:
      16 GO terms found significant (< 0.05=alpha) ( 16 enriched + 0
purified): statsmodels fdr_bh
      48 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 52 IDs ... 98%      51 of
52 study items found in association
100%      52 of      52 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
      125 GO terms are associated with      51 of      52 study items
METHOD fdr_bh:
      4 GO terms found significant (< 0.05=alpha) ( 4 enriched + 0
purified): statsmodels fdr_bh
      47 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)
Significant results[23] = 3 BP + 4 MF + 16 CC
      23 items Wrote: GO_analysis_module_darkmagenta.xlsx
      23 GOEA results for      51 study items. Wrote:
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:0:00:04.505284 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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

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Run BP Gene Ontology Analysis: current study set of 72 IDs ... 86%      62 of
72 study items found in association
100%      72 of      72 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
    459 GO terms are associated with      62 of      72 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 72 IDs ... 89%      64 of
72 study items found in association
100%      72 of      72 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
    120 GO terms are associated with      64 of      72 study items
  METHOD fdr_bh:
    3 GO terms found significant (< 0.05=alpha) ( 3 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 MF Gene Ontology Analysis: current study set of 72 IDs ... 82%      59 of
72 study items found in association
100%      72 of      72 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
    178 GO terms are associated with      59 of      72 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_saddlebrown.xlsx
  3 GOEA results for 29 study items. WROTE:
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:0:00:04.707804 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 100 IDs ... 94% 94 of
100 study items found in association
100% 100 of 100 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
978 GO terms are associated with 94 of 100 study items
METHOD fdr_bh:
47 GO terms found significant (< 0.05=alpha) (47 enriched + 0
purified): statsmodels fdr_bh
68 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 100 IDs ... 95% 95 of
100 study items found in association
100% 100 of 100 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
180 GO terms are associated with 95 of 100 study items
METHOD fdr_bh:
18 GO terms found significant (< 0.05=alpha) (18 enriched + 0
purified): statsmodels fdr_bh
77 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 100 IDs ... 95% 95 of
100 study items found in association
100% 100 of 100 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
296 GO terms are associated with 95 of 100 study items
METHOD fdr_bh:
5 GO terms found significant (< 0.05=alpha) (5 enriched + 0
purified): statsmodels fdr_bh
78 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)

Significant results[70] = 47 BP + 5 MF + 18 CC
70 items WROTE: GO_analysis_module_darkturquoise.xlsx
70 GOEA results for 95 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:0:00:05.362310 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 164 IDs ... 92%    151 of
164 study items found in association
100%    164 of    164 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
1,232 GO terms are associated with    151 of    164 study items
METHOD fdr_bh:
182 GO terms found significant (< 0.05=alpha) (182 enriched +    0
purified): statsmodels fdr_bh
136 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 164 IDs ... 98%    160 of
164 study items found in association
100%    164 of    164 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
200 GO terms are associated with    160 of    164 study items
METHOD fdr_bh:
41 GO terms found significant (< 0.05=alpha) ( 41 enriched +    0
purified): statsmodels fdr_bh
151 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 164 IDs ... 93%    153 of
164 study items found in association
100%    164 of    164 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
304 GO terms are associated with    153 of    164 study items

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METHOD fdr_bh:
    21 GO terms found significant (< 0.05=alpha) ( 21 enriched + 0
purified): statsmodels fdr_bh
    137 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[244] = 182 BP + 21 MF + 41 CC
    244 items Wrote: GO_analysis_module_grey60.xlsx
    244 GOEA results for 160 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:0:00:04.592357 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 898 IDs ... 83%    744 of
898 study items found in association
100%    898 of    898 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
    2,858 GO terms are associated with    744 of    898 study items
METHOD fdr_bh:
    57 GO terms found significant (< 0.05=alpha) ( 55 enriched + 2
purified): statsmodels fdr_bh
    302 study items associated with significant GO IDs (enriched)
    3 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 898 IDs ... 88%    792 of
898 study items found in association
100%    898 of    898 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
    552 GO terms are associated with    792 of    898 study items
METHOD fdr_bh:
    71 GO terms found significant (< 0.05=alpha) ( 71 enriched + 0
purified): statsmodels fdr_bh
    730 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 898 IDs ... 85%    766 of
898 study items found in association
100%    898 of    898 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
    858 GO terms are associated with    766 of    898 study items
METHOD fdr_bh:
    31 GO terms found significant (< 0.05=alpha) ( 30 enriched + 1
purified): statsmodels fdr_bh
    602 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[159] = 57 BP + 31 MF + 71 CC
    159 items WROTE: GO_analysis_module_brown.xlsx
    159 GOEA results for 799 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:0:00:05.085673 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 48 IDs ... 90%    43 of
48 study items found in association
100%    48 of    48 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
    371 GO terms are associated with    43 of    48 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 48 IDs ... 94%    45 of
48 study items found in association

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100%      48 of      48 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
    136 GO terms are associated with      45 of      48 study items
METHOD fdr_bh:
    12 GO terms found significant (< 0.05=alpha) ( 12 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 MF Gene Ontology Analysis: current study set of 48 IDs ... 94%      45 of
48 study items found in association
100%      48 of      48 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
    112 GO terms are associated with      45 of      48 study items
METHOD fdr_bh:
    1 GO terms found significant (< 0.05=alpha) (  1 enriched +  0
purified): statsmodels fdr_bh
    36 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[13] = 0 BP + 1 MF + 12 CC
    13 items Wrote: GO_analysis_module_sienna3.xlsx
    13 GOEA results for      43 study items. Wrote:
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:0:00:04.711722 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 196 IDs ... 92%      180 of
196 study items found in association
100%     196 of     196 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

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    1,462 GO terms are associated with      180 of      196 study items
METHOD fdr_bh:
    38 GO terms found significant (< 0.05=alpha) ( 38 enriched +    0
purified): statsmodels fdr_bh
    81 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 196 IDs ... 93%      182 of
196 study items found in association
100%      196 of      196 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      182 of      196 study items
METHOD fdr_bh:
    12 GO terms found significant (< 0.05=alpha) ( 12 enriched +    0
purified): statsmodels fdr_bh
    147 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 196 IDs ... 91%      179 of
196 study items found in association
100%      196 of      196 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
    359 GO terms are associated with      179 of      196 study items
METHOD fdr_bh:
    11 GO terms found significant (< 0.05=alpha) ( 11 enriched +    0
purified): statsmodels fdr_bh
    143 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[61] = 38 BP + 11 MF + 12 CC
    61 items WROTE: GO_analysis_module_lightcyan.xlsx
    61 GOEA results for      170 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:0:00:05.085548 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 154 IDs ... 91% 140 of
154 study items found in association

100% 154 of 154 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

924 GO terms are associated with 140 of 154 study items

METHOD fdr_bh:

30 GO terms found significant ($< 0.05=\alpha$) (30 enriched + 0
purified): statsmodels fdr_bh

57 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 154 IDs ... 95% 146 of
154 study items found in association

100% 154 of 154 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

246 GO terms are associated with 146 of 154 study items

METHOD fdr_bh:

27 GO terms found significant ($< 0.05=\alpha$) (27 enriched + 0
purified): statsmodels fdr_bh

137 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 154 IDs ... 96% 148 of
154 study items found in association

100% 154 of 154 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

309 GO terms are associated with 148 of 154 study items

METHOD fdr_bh:

21 GO terms found significant ($< 0.05=\alpha$) (21 enriched + 0
purified): statsmodels fdr_bh

136 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Significant results[78] = 30 BP + 21 MF + 27 CC

78 items WROTE: GO_analysis_module_lightgreen.xlsx

78 GOEA results for 149 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:0:00:05.010068 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go

MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 138 IDs ... 94% 130 of
138 study items found in association

100% 138 of 138 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

855 GO terms are associated with 130 of 138 study items

METHOD fdr_bh:

7 GO terms found significant (< 0.05=alpha) (7 enriched + 0
purified): statsmodels fdr_bh

33 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 138 IDs ... 96% 133 of
138 study items found in association

100% 138 of 138 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

263 GO terms are associated with 133 of 138 study items

METHOD fdr_bh:

19 GO terms found significant (< 0.05=alpha) (19 enriched + 0
purified): statsmodels fdr_bh

124 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 138 IDs ... 94% 130 of
138 study items found in association

100% 138 of 138 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

290 GO terms are associated with 130 of 138 study items

METHOD fdr_bh:

5 GO terms found significant (< 0.05=alpha) (5 enriched + 0
purified): statsmodels fdr_bh

122 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Significant results[31] = 7 BP + 5 MF + 19 CC
 31 items WROTE: GO_analysis_module_royalblue.xlsx
 31 GOEA results for 133 study items. WROTE:
 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:0:00:05.314044 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
 gene2go
 MF 18,191 annotated human genes
 CC 19,424 annotated human genes
 BP 18,506 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 219 IDs ... 89% 196 of
 219 study items found in association
 100% 219 of 219 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
 948 GO terms are associated with 196 of 219 study items
 METHOD fdr_bh:
 4 GO terms found significant (< 0.05=alpha) (4 enriched + 0
 purified): statsmodels fdr_bh
 35 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 219 IDs ... 94% 206 of
 219 study items found in association
 100% 219 of 219 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
 319 GO terms are associated with 206 of 219 study items
 METHOD fdr_bh:
 21 GO terms found significant (< 0.05=alpha) (20 enriched + 1
 purified): statsmodels fdr_bh
 182 study items associated with significant GO IDs (enriched)
 2 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 219 IDs ... 91% 199 of
 219 study items found in association

100% 219 of 219 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
 351 GO terms are associated with 199 of 219 study items
 METHOD fdr_bh:
 5 GO terms found significant (< 0.05=alpha) (5 enriched + 0
 purified): statsmodels fdr_bh
 178 study items associated with significant GO IDs (enriched)
 0 study items associated with significant GO IDs (purified)
 Significant results[30] = 4 BP + 5 MF + 21 CC
 30 items Wrote: GO_analysis_module_salmon.xlsx
 30 GOEA results for 201 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:0:00:06.446500 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
 gene2go
 MF 18,191 annotated human genes
 CC 19,424 annotated human genes
 BP 18,506 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 306 IDs ... 93% 286 of
 306 study items found in association
 100% 306 of 306 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
 1,249 GO terms are associated with 286 of 306 study items
 METHOD fdr_bh:
 7 GO terms found significant (< 0.05=alpha) (7 enriched + 0
 purified): statsmodels fdr_bh
 104 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 306 IDs ... 97% 298 of
 306 study items found in association
 100% 306 of 306 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
 352 GO terms are associated with 298 of 306 study items


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METHOD fdr_bh:
    16 GO terms found significant (< 0.05=alpha) ( 15 enriched + 1
purified): statsmodels fdr_bh
    256 study items associated with significant GO IDs (enriched)
    1 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 306 IDs ... 93%    285 of
306 study items found in association
100%    306 of    306 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
    365 GO terms are associated with    285 of    306 study items
METHOD fdr_bh:
    17 GO terms found significant (< 0.05=alpha) ( 17 enriched + 0
purified): statsmodels fdr_bh
    262 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[40] = 7 BP + 17 MF + 16 CC
    40 items WROTE: GO_analysis_module_pink.xlsx
    40 GOEA results for    285 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:0:00:07.310902 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 154 IDs ... 93%    143 of
154 study items found in association
100%    154 of    154 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
    1,383 GO terms are associated with    143 of    154 study items
METHOD fdr_bh:
    63 GO terms found significant (< 0.05=alpha) ( 63 enriched + 0
purified): statsmodels fdr_bh
    103 study items associated with significant GO IDs (enriched)

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    0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 154 IDs ... 95%    146 of
154 study items found in association
100%    154 of    154 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
    209 GO terms are associated with    146 of    154 study items
METHOD fdr_bh:
    16 GO terms found significant (< 0.05=alpha) ( 16 enriched + 0
purified): statsmodels fdr_bh
    135 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 154 IDs ... 93%    143 of
154 study items found in association
100%    154 of    154 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
    288 GO terms are associated with    143 of    154 study items
METHOD fdr_bh:
    5 GO terms found significant (< 0.05=alpha) ( 5 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[84] = 63 BP + 5 MF + 16 CC
    84 items Wrote: GO_analysis_module_lightyellow.xlsx
    84 GOEA results for 141 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:0:00:06.333858 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 261 IDs ... 89%    232 of

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261 study items found in association
100%    261 of    261 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
    1,402 GO terms are associated with    232 of    261 study items
METHOD fdr_bh:
    3 GO terms found significant (< 0.05=alpha) ( 3 enriched + 0
purified): statsmodels fdr_bh
    23 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 261 IDs ... 95%    248 of
261 study items found in association
100%    261 of    261 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
    382 GO terms are associated with    248 of    261 study items
METHOD fdr_bh:
    24 GO terms found significant (< 0.05=alpha) ( 24 enriched + 0
purified): statsmodels fdr_bh
    225 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 261 IDs ... 95%    249 of
261 study items found in association
100%    261 of    261 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
    419 GO terms are associated with    249 of    261 study items
METHOD fdr_bh:
    5 GO terms found significant (< 0.05=alpha) ( 5 enriched + 0
purified): statsmodels fdr_bh
    219 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[32] = 3 BP + 5 MF + 24 CC
    32 items WROTE: GO_analysis_module_magenta.xlsx
    32 GOEA results for    243 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:0:00:06.677788 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis ...

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```

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 93 IDs ... 97%      90 of
93 study items found in association
100%      93 of      93 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
471 GO terms are associated with      90 of      93 study items
METHOD fdr_bh:
1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0
purified): statsmodels fdr_bh
3 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 93 IDs ... 95%      88 of
93 study items found in association
100%      93 of      93 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
176 GO terms are associated with      88 of      93 study items
METHOD fdr_bh:
2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0
purified): statsmodels fdr_bh
47 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 93 IDs ... 90%      84 of
93 study items found in association
100%      93 of      93 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
191 GO terms are associated with      84 of      93 study items
METHOD fdr_bh:
1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0
purified): statsmodels fdr_bh
65 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)
Significant results[4] = 1 BP + 1 MF + 2 CC
4 items WROTE: GO_analysis_module_orange.xlsx
4 GOEA results for      74 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:0:00:04.500018 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go

MF 18,191 annotated human genes

CC 19,424 annotated human genes

BP 18,506 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 310 IDs ... 94% 292 of
310 study items found in association

100% 310 of 310 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

1,177 GO terms are associated with 292 of 310 study items

METHOD fdr_bh:

17 GO terms found significant ($< 0.05=\alpha$) (17 enriched + 0
purified): statsmodels fdr_bh

152 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 310 IDs ... 96% 298 of
310 study items found in association

100% 310 of 310 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

362 GO terms are associated with 298 of 310 study items

METHOD fdr_bh:

33 GO terms found significant ($< 0.05=\alpha$) (31 enriched + 2
purified): statsmodels fdr_bh

279 study items associated with significant GO IDs (enriched)

8 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 310 IDs ... 96% 297 of
310 study items found in association

100% 310 of 310 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

370 GO terms are associated with 297 of 310 study items

METHOD fdr_bh:

17 GO terms found significant ($< 0.05=\alpha$) (17 enriched + 0

```

purified): statsmodels fdr_bh
    267 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[67] = 17 BP + 17 MF + 33 CC
    67 items Wrote: GO_analysis_module_black.xlsx
    67 GOEA results for 299 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:0:00:04.705588 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 61 IDs ... 92%      56 of
61 study items found in association
100%      61 of      61 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
    405 GO terms are associated with      56 of      61 study items
    METHOD fdr_bh:
        1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0
purified): statsmodels fdr_bh
        5 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 61 IDs ... 92%      56 of
61 study items found in association
100%      61 of      61 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
    75 GO terms are associated with      56 of      61 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 61 IDs ... 97%      59 of
61 study items found in association
100%      61 of      61 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
  149 GO terms are associated with      59 of      61 study items
  METHOD fdr_bh:
    2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0
purified): statsmodels fdr_bh
    44 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[3] = 1 BP + 2 MF + 0 CC
  3 items WROTE: GO_analysis_module_paleturquoise.xlsx
  3 GOEA results for      44 study items. WROTE:
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:0:00:05.302565 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 52 IDs ... 94%      49 of
52 study items found in association
100%      52 of      52 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
  511 GO terms are associated with      49 of      52 study items
  METHOD fdr_bh:
    12 GO terms found significant (< 0.05=alpha) ( 12 enriched + 0
purified): statsmodels fdr_bh
    25 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 52 IDs ... 96%      50 of
52 study items found in association
100%      52 of      52 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
    86 GO terms are associated with      50 of      52 study items
METHOD fdr_bh:
  3 GO terms found significant (< 0.05=alpha) ( 3 enriched + 0
purified): statsmodels fdr_bh
  27 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 52 IDs ... 98%      51 of
52 study items found in association
100%      52 of      52 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
    121 GO terms are associated with      51 of      52 study items
METHOD fdr_bh:
  9 GO terms found significant (< 0.05=alpha) ( 9 enriched + 0
purified): statsmodels fdr_bh
  47 study items associated with significant GO IDs (enriched)
  0 study items associated with significant GO IDs (purified)
Significant results[24] = 12 BP + 9 MF + 3 CC
  24 items WROTE: GO_analysis_module_darkolivegreen.xlsx
  24 GOEA results for      48 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:0:00:05.173565 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 230 IDs ... 87%      200 of
230 study items found in association
100%      230 of      230 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
    964 GO terms are associated with      200 of      230 study items

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METHOD fdr_bh:
    1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0
purified): statsmodels fdr_bh
    16 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 230 IDs ... 93%    214 of
230 study items found in association
100%    230 of    230 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
    241 GO terms are associated with    214 of    230 study items
METHOD fdr_bh:
    5 GO terms found significant (< 0.05=alpha) ( 5 enriched + 0
purified): statsmodels fdr_bh
    188 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 230 IDs ... 91%    209 of
230 study items found in association
100%    230 of    230 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
    359 GO terms are associated with    209 of    230 study items
METHOD fdr_bh:
    9 GO terms found significant (< 0.05=alpha) ( 9 enriched + 0
purified): statsmodels fdr_bh
    185 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[15] = 1 BP + 9 MF + 5 CC
    15 items WROTE: GO_analysis_module_greenyellow.xlsx
    15 GOEA results for    212 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:0:00:04.732825 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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

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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 87 IDs ... 94% 82 of
87 study items found in association

100% 87 of 87 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

579 GO terms are associated with 82 of 87 study items

METHOD fdr_bh:

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

17 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 87 IDs ... 95% 83 of
87 study items found in association

100% 87 of 87 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

141 GO terms are associated with 83 of 87 study items

METHOD fdr_bh:

16 GO terms found significant ($< 0.05=\alpha$) (16 enriched + 0
purified): statsmodels fdr_bh

61 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 87 IDs ... 92% 80 of
87 study items found in association

100% 87 of 87 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

219 GO terms are associated with 80 of 87 study items

METHOD fdr_bh:

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

17 study items associated with significant GO IDs (enriched)

0 study items associated with significant GO IDs (purified)

Significant results[26] = 5 BP + 5 MF + 16 CC

26 items Wrote: GO_analysis_module_darkorange.xlsx

26 GOEA results for 64 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:0:00:04.809330 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go

MF 18,191 annotated human genes

CC 19,424 annotated human genes
BP 18,506 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 209 IDs ... 89% 185 of
209 study items found in association
100% 209 of 209 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
987 GO terms are associated with 185 of 209 study items
METHOD fdr_bh:
7 GO terms found significant (< 0.05=alpha) (7 enriched + 0
purified): statsmodels fdr_bh
36 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 209 IDs ... 95% 198 of
209 study items found in association
100% 209 of 209 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
261 GO terms are associated with 198 of 209 study items
METHOD fdr_bh:
17 GO terms found significant (< 0.05=alpha) (17 enriched + 0
purified): statsmodels fdr_bh
178 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 209 IDs ... 93% 194 of
209 study items found in association
100% 209 of 209 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
327 GO terms are associated with 194 of 209 study items
METHOD fdr_bh:
8 GO terms found significant (< 0.05=alpha) (8 enriched + 0
purified): statsmodels fdr_bh
160 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)
Significant results[32] = 7 BP + 8 MF + 17 CC

32 items WROTE: GO_analysis_module_midnightblue.xlsx
 32 GOEA results for 196 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:0:00:06.279096 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
 gene2go
 MF 18,191 annotated human genes
 CC 19,424 annotated human genes
 BP 18,506 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 66 IDs ... 88% 58 of
 66 study items found in association
 100% 66 of 66 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
 341 GO terms are associated with 58 of 66 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 66 IDs ... 91% 60 of
 66 study items found in association
 100% 66 of 66 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
 96 GO terms are associated with 60 of 66 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 66 IDs ... 89% 59 of
 66 study items found in association
 100% 66 of 66 study items found in population(29107)

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Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,839 of 29,107 population items
  129 GO terms are associated with      59 of      66 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_steelblue.xlsx
  0 GOEA results. NOT WRITING 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:0:00:05.367815 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 84 IDs ... 81%      68 of
84 study items found in association
100%      84 of      84 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
  487 GO terms are associated with      68 of      84 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 84 IDs ... 89%      75 of
84 study items found in association
100%      84 of      84 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
  129 GO terms are associated with      75 of      84 study items
METHOD fdr_bh:

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    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 84 IDs ... 82%      69 of
84 study items found in association
100%      84 of      84 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
    163 GO terms are associated with      69 of      84 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:0:00:05.323938 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 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 ...100%      26 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
    198 GO terms are associated with      26 of      26 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)

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Run CC Gene Ontology Analysis: current study set of 26 IDs ...100%      26 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
    77 GO terms are associated with      26 of      26 study items
METHOD fdr_bh:
    4 GO terms found significant (< 0.05=alpha) (  4 enriched +  0
purified): statsmodels fdr_bh
    17 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 ...100%      26 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
    79 GO terms are associated with      26 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)
Significant results[7] = 3 BP + 0 MF + 4 CC
    7 items WROTE: GO_analysis_module_yellowgreen.xlsx
    7 GOEA results for    17 study items. WROTE:
GO_analysis_module_yellowgreen.txt

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[]: