

# Choosing Resources

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RITAN indexes multiple resources and choosing which of them are most relevant for your study can be a challenge. To help with this process, we provide below a set of examples from different types of studies and the thinking behind which resources were used.

## Resources Indexed by default

```
library(RITANdata)
library(RITAN)
library(knitr)
kable( attr(network_list, 'network_data_sources') )
kable( sapply(geneset_list, length), col.names = c('# Genesets') )
```

While many resources contain information about protein complexes (obligate interactions) and protein-protein interactions (often transient), some use experimental techniques that are specific for physical interactions. Determining which resources indicate physical, through-metabolite, and through-DNA (i.e. transcription factors) interactions, we recommend: 1) each resource's primary publication 2) the pathguide website 3) the following guidelines

## Example: Protein Complexes & Protein-Protein Interaction (PPI)

```
genes <- geneset_list$MSigDB_C5$APICAL_JUNCTION_COMPLEX
e <- network_overlap( genes, resources = c('HPRD', 'CCSB', 'Biogrid', 'STRING'), minStringScore = 700 )
## We also strongly encourage use of the BioPlex database, which we do not distribute with RITAN in comp
```

## Example: Metabolic Network Interaction

```
genes2 <- geneset_list$MSigDB_C5$AMINE_METABOLIC_PROCESS
e2 <- network_overlap( genes, resources = c('PID', 'HumanNet', 'Biogrid') )
```

## Example: Expression Signalling

```
genes2 <- geneset_list$MSigDB_C5$AMINE_METABOLIC_PROCESS
e2 <- network_overlap( genes, resources = c('ChEA', 'HumanNet') )
```