

Biological Databases ICA

B242415

Script Overview

Figure 1: Flowchart of data collection script

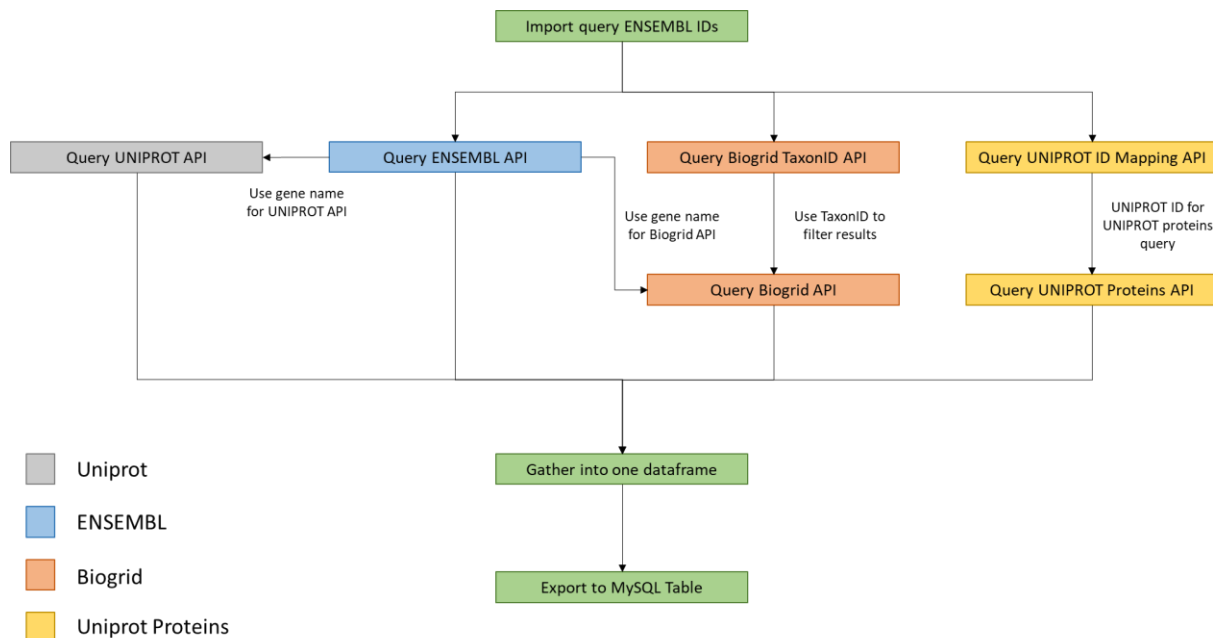


Figure 1 Legend: Flowchart of program showcasing the databases queried, different API access points, and how information flows between different processes. The color of the boxes (except green) indicates the database being queried. Script takes query Ensembl IDs and queries it against the Ensembl API. It also queries the Biogrid taxonID API to get the taxonID to query against the Biogrid API along with the gene name from the Ensembl API so it selects only organism specific information. The gene name from the Ensembl API is also used to query against the UNIPROT API to extract data. The Ensembl ID is also used to query against the UNIPROT ID mapping API to get a uniprot ID to query against the UNIPROT Proteins API. All relevant data is extracted and put into a data frame where it is exported to a MySQL database.

Figure 2: Final MySQL table columns and their descriptions

Column Name	Description
EnsemblID	Ensemble ID (From: Imported query genes)
UniprotID	Uniprot ID (From: Uniprot ID mapping API)
GeneName	Gene common name (From: Ensembl API)
GeneProduct	Product from gene (From: Ensembl API)
ProteinName	Protein Name (From: Uniprot Proteins)
UniparcID	Uniparc ID (From: Uniprot API)
RefseqID	Refseq ID (From: Uniprot API)
pdbID	Protein Data Base ID (From: Uniprot API)
BiogridID	Biogrid ID (From: Uniprot API)
StringID	String ID (From: Uniprot API)

goID	Gene ontology ID (From: Uniprot API)
goDescription	Gene ontologies with their descriptions
EnsemblObjectType	Ensembl ID Object (From: Ensembl API)
GeneDescription	Description of gene (From: Ensembl API)
Species	Origin species of query gene (From: Ensembl API)
TaxonID	Taxonomy ID of query origin species (From: Biogrid TaxonID API)
DNASeq	DNA Sequence (bases) (From: Ensembl API)
ChromosomeLoci	Chromosome gene is located in (From: Ensembl API)
Strand	Strand (From: Ensembl API)
StartPos	Start position of gene (From: Ensembl API)
EndPos	End position of gene (From: Ensembl API)
Keywords	Keywords associated with protein (From: Uniprot Proteins)
ProteinFamily	Protein family (From: Uniprot API)
ProteinSeq	Protein Sequence (From: Uniprot Proteins)
ProteinLength	Protein length (residues) (From: Uniprot API)
ProteinMass	Protein mass (Da) (From: Uniprot API)
ProteinFunction	Protein function description (From: Uniprot API)
ProteinFeatures	Protein features description (From: Uniprot API)
ProteinSubunits	Protein subunit information (From: Uniprot API)
ProteinDevStage	Developmental stage protein is associated with (From: Uniprot API)
ProteinTissueLoci	Tissue specificity of protein (From: Uniprot API)
ProteinSubCellLoci	Sub cellular location of protein (From: Uniprot API)
ProteinResidueMod	Protein residue modifications (From: Uniprot API)
ProteinPTM	Post translational modification of protein (From: Uniprot API)
Interactions	Proteins which interact with query (From: Biogrid API)

Important Design Features

1. Queries 4 databases, using 7 API access points to gather data.
 - a. Databases used: Ensembl (Martin et al., 2023), Biogrid (Oughtred et al., 2021), Uniprot (The UniProt Consortium, 2023), Uniprot Proteins (Containing Uniprot sequences, + other services imported from Large Scale Data Sources (LSS) including: 1000Genomes, ExAC, PeptideAtlas etc.) (Nightingale et al., 2017).
 - b. API Access Points used: Ensembl Lookup REST API, Ensembl Sequence REST API, Uniprot website REST API, Uniprot Proteins REST API, Biogrid organisms REST API, Biogrid REST API.
2. Packages used: http (Wickham, 2023), jsonlite (Ooms, 2014), RCurl (Lang, 2023), curl (Ooms, 2023), RMySQL (Ooms et al., 2023), queryup (Voisinne, 2019)
3. Gene queries can be set by the user, with either modifying the querygenes variable or by importing a .csv file with all the Ensembl IDs for the queries. Query genes can be set by the user with different query genes and different number of query genes (Number of query genes can be scalable from a small amount to a very large amount of Ensembl IDs, only limited by API limits). No information about the queries are hard coded, meaning all the information is automatically extracted from the Ensembl IDs only.
4. Not all genes are protein coding, and since the information extracted focuses on proteins, it is able to still process genes that are not protein coding. (eg. snoRNAs, pseudogenes etc.). Also able to process returns from APIs that are different eg. For empty or variable biogrid returns (eg. Different number of interacting proteins between queries), failed ID mapping, different uniprot protein returns etc.

5. Showcases 2 different ways of connecting to an API: url generation and packages such as queryup.
6. Showcases GET and POST requests for APIs.
7. Progress is printed onto terminal to show user the progress of the script.
8. Extracts information from Uniprot only on the main protein, and discards information about various isoforms relating to a gene name.
9. Sys.sleep() to avoid rate limitation from APIs. Time is set via sleeptime variable and is default to 0.1
 - a. Ensembl: 55000 requests per hr (Yates et al., 2015) therefore minimum sleeptime is Sys.sleep(0.0655)
 - b. Assumed other APIs followed similar rate limits therefore set default to 0.1s

Hypothetical Use Case

Biological question:

A differential expression RNA seq experiment has identified several genes, along with their ensembl IDs, that are differentially expressed after a change in condition (eg. Disease, treatment, time etc.). These genes may produce proteins which help the organism to survive better, and researchers want to know more about how the gene helps the organism survive. They may also want to use the gene products as drug targets or target genes for synthetic biology. Researchers want to find out more about the identified genes to find:

1. Gene and product names, information and descriptions
 - a. GeneName, GeneProduct, ProteinName, EnsemblObjectType, GeneDescription, Species, ChromosomeLoci
2. Gene and gene product IDs to signpost further information in other databases
 - a. EnsemblID, UniprotID, UniparcID, RefseqID, pdbID, BiogridID, StringID, TaxonID
3. Gene ontology to find what processes the gene is associated with
 - a. goID, goDescription, Keywords
4. DNA sequences and information for further downstream experiments (eg. For designing primers for subcloning or gene knockdown experiments)
 - a. DNaseq, Strand, StartPos, EndPos
5. Protein sequences and information for further downstream experiments (eg. structure prediction if protein 3D structure is not elucidated via protein structure prediction methods such as AlphaFold, then for in silico drug discovery methods eg. Ligand binding etc.)
 - a. ProteinSeq, ProteinFamily, ProteinLength, ProteinMass, ProteinResidueMod, ProteinPTM
6. Protein information to further guide researchers on choosing genes for downstream applications (eg. Deciding which proteins would be potential drug targets etc).
 - a. ProteinFunction, ProteinFeatures, ProteinSubunits, ProteinDevStage, ProteinTissueLoci, ProteinSubCellLoci
7. Finding interactions which may suggest processes it is associated with, alongside any regulatory pathways that could be manipulated
 - a. Interactions

References

References

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APPENDIX

- Contains script file, schema file and data file. Recommended to search for file names to get to beginning of each section. Recommended to also convert to word document for copy/pasting to avoid including the headers and page numbers in the copied sections.

Script File:

```
#!/usr/bin/Rscript
```

```
#import libraries
```

```
library(httr)
```

```
library(jsonlite)
```

```
#install.packages("RCurl")
```

```
library(RCurl)
```

```
library(curl)
```

```
library(RMySQL)
```

```
# install.packages("queryup")
```

```
library(queryup)
```

```
#Set Sys.sleep() time
```

```
sleeptime <- 0.1
```

```
##### FUNCTIONS #####
```

```
#capitalize first letter (for species renaming for biogrid)
```

```
capitalize <- function(x){
```

```
  paste(toupper(substring(x, 1, 1)),
```

```
    tolower(substring(x, 2, nchar(x))),
```

```
    sep = "")
```

```
}
```

```
##### Import Query Genes #####
```

```
#original genes
```

```
querygenes <-  
c("ENSMUSG00000015002","ENSMUSG00000017548","ENSMUSG00000032333","ENSMUSG000000  
36202","ENSMUSG00000041272","ENSMUSG00000050953","ENSMUSG00000058589","ENSMUSG0  
0000064722","ENSMUSG00000074830","ENSMUSG00000078592")  
  
#read query from csv file and convert to list (UNCOMMENT TO USE THIS FUNCTION)  
# querygenes <-read.csv("./Genelidentifiers.csv", header=FALSE)  
# querygenes <-as.character(querygenes)  
  
##### Creating Dataframe Columns #####  
#creating intial vectors to create dataframe later  
##ensembl lookup  
commonname <- c()  
genedescription <- c()  
species <- c()  
strand <- c()  
biotype <- c()  
objecttype <- c()  
chromosome <- c()  
startpos <- c()  
endpos <- c()  
##ensembl seq  
seq <- c()  
##uniprot id mapping  
uniprotid <- rep(NA ,length(querygenes))  
##uniprot proteins  
proteinname <- rep(NA, length(querygenes))  
proteinseq <- rep(NA, length(querygenes))  
keywords <- rep(NA, length(querygenes))  
##biogrid tax id  
taxonid <- rep(NA, length(querygenes))
```

```
##biogrid interactions
```

```
interactswith <- rep(NA, length(querygenes))
```

```
##uniprot data
```

```
proteinlength<- rep(NA ,length(querygenes))
```

```
proteinmass<- rep(NA ,length(querygenes))
```

```
proteinfunction <- rep(NA ,length(querygenes))
```

```
proteinfeatures <- rep(NA ,length(querygenes))
```

```
proteinUniParc <- rep(NA ,length(querygenes))
```

```
proteinsubunit <- rep(NA ,length(querygenes))
```

```
proteindevstage <- rep(NA ,length(querygenes))
```

```
proteintissuespec <- rep(NA ,length(querygenes))
```

```
proteingo <- rep(NA ,length(querygenes))
```

```
proteingoid <- rep(NA ,length(querygenes))
```

```
proteinsubcellloci <- rep(NA ,length(querygenes))
```

```
proteinmodres <- rep(NA ,length(querygenes))
```

```
proteinptm <- rep(NA ,length(querygenes))
```

```
proteinfam <- rep(NA ,length(querygenes))
```

```
proteinrefseq <- rep(NA ,length(querygenes))
```

```
proteinpdb <- rep(NA ,length(querygenes))
```

```
proteinbiogrid <- rep(NA ,length(querygenes))
```

```
proteinstring <- rep(NA ,length(querygenes))
```

```
##### Querying ENSEMBL API #####
```

```
#connect to ensembl api for lookup for each gene in query
```

```
ensemblapibase <- "https://rest.ensembl.org/lookup/id/"
```

```
ensemblapicontent <- "?content-type=application/json"
```

```
ensemblapiseqbase <- "https://rest.ensembl.org/sequence/id/"
```

```
ensemblapiseqcontent <- "?content-type=text/plain"
```

```
#for loop for querying every gene in query to ensembl api and appending desired results to initial list
```



```
for (query in querygenes){  
  #query ensembl-lookup  
  cat("Gathering Ensembl lookup data for: ", query, "\n")  
  ensemblquery <- paste(ensemblapibase, query, ensemblapicontent, sep="")  
  ensembllookup <- GET(ensemblquery)  
  ensembljson <- fromJSON(toJSON(content(ensembllookup)))  
  ensembljson <- as.data.frame(t(ensembljson))  
  
  #sleep for 0.1s to avoid being rate limited  
  Sys.sleep(sleeptime)  
  
  #extracting desired data  
  commonname <- c(commonname, as.character(ensembljson$display_name))  
  genedescription <- c(genedescription, as.character(ensembljson$description))  
  species <- c(species, as.character(ensembljson$species))  
  strand <- c(strand, as.character(ensembljson$strand))  
  biotype <- c(biotype, as.character(ensembljson$biotype))  
  objecttype <- c(objecttype, as.character(ensembljson$object_type))  
  chromosome <- c(chromosome, as.character(ensembljson$seq_region_name))  
  startpos <- c(startpos, as.character(ensembljson$start))  
  endpos <- c(endpos, as.character(ensembljson$end))  
  
  #query ensembl-sequence  
  cat("Gathering Ensembl sequence data for: ", query, "\n")  
  ensemblquery1 <- paste(ensemblapiseqbase, query, ensemblapiseqcontent, sep="")  
  ensembllookup1 <- GET(ensemblquery1)  
  ensemblseq <- as.character(ensembllookup1)  
  seq <- c(seq, ensemblseq)  
  
  #sleep for 0.1s to avoid being rate limited  
  Sys.sleep(sleeptime)
```

```
}
```

```
##### Querying UNIPROT ID Mapping API #####

#get uniprot ID for query genes via id mapping api
count <- 1
for (query in querygenes){
  #query uniprot ID mapping to get jobID
  cat("Submitting ID mapping job to Uniprot for: ", query, "\n")
  idmappost <- postForm(
    "https://rest.uniprot.org/idmapping/run",
    from="Ensembl",
    to="UniProtKB",
    ids=query
  )

  #sleep to wait for job completion
  Sys.sleep(1)

  #take id mapping jobID to get results
  cat("Getting Uniprot ID from jobs for : ", query, "\n")
  idmapjobid <- as.character(fromJSON(idmappost))
  idmapapi <- paste("https://rest.uniprot.org/idmapping/results/", idmapjobid, sep="")
  h <- basicTextGatherer()
  curlPerform(url=idmapapi, writefunction=h$update)
  idmapped <- h$value()
  idmappedjson <- fromJSON(idmapped)

  if(is.null(idmappedjson$failedIds) == TRUE){
    idmappedjson <- as.data.frame(idmappedjson)
    uniprotid[count] <- idmappedjson[1,2]
  }
}
```

```
} else {  
  print("No protein mapped to gene")  
}  
  
#sleep to avoid rate limit  
Sys.sleep(sleeptime)  
count <- count + 1  
}  
  
##### Querying UNIPROT PROTEINS API #####  
#query uniprot proteins API using uniprot ids and gather info  
uniprotapibase <- "www.ebi.ac.uk/prot eins/api/prot eins/"  
  
count=1  
for (query in querygenes){  
  #check if protein coding  
  if(is.na(uniprotid[count]) == FALSE){  
    #call api and import data  
    cat("Getting Uniprot Proteins API data from", query, ":\t", uniprotid[count], "\n")  
    uniprotapicall <- paste(uniprotapibase, uniprotid[count], sep="")  
    uniprotget <- GET(uniprotapicall)  
    uniprotget1 <- fromJSON(toJSON(content(uniprotget)))  
  
    if (is.null(uniprotget1$protein$submittedName$fullName$value) == FALSE){  
      proteinname[count] <- as.character(uniprotget1$protein$submittedName$fullName$value)  
    } else {  
      proteinname[count] <- as.character(uniprotget1$protein$recommendedName$fullName$value)  
    }  
  
    #protein sequence
```

```
proteinseq[count] <- uniprotget1$sequence$sequence

#keywords
keywordconcat <- c()
for (keywordin in uniprotget1$keywords$value) {
  keywordconcat <- paste(keywordconcat, keywordin, sep=",")
}

keywords[count] <- keywordconcat

} else {
  cat("No protein data for ", query, ": \t", uniprotid[count], "\n")
}

#sleep to avoid rate limit
Sys.sleep(sleeptime)
count = count + 1
}

##### Querying BIOGRID TaxonID API #####
#biogrid api to get taxID
print("Gathering TaxonID from BiogridAPI")
biogridtaxibase <- "https://webservice.thebiogrid.org/organisms/?accesskey="
biogridtaxidtoken <- "34e9134bdaaefe8eeb2012f1099ed599"
biogridtaxidparams <- "" #&format=json
biogridtaxidapi <- paste(biogridtaxibase, biogridtaxidtoken, biogridtaxidparams, sep="")
biogridtaxidget <- GET(biogridtaxidapi)
biogridtaxidgetcontent <- content(biogridtaxidget)
biogridtaxidjson <- read.table(text=biogridtaxidgetcontent, sep="\t")
```

```
#biogrid format speciesname of species list
```

```
count = 1
```

```
for(entry in species){
```

```
  species[count] <- gsub("_", " ", capitalize(species[count]))
```

```
  count = count + 1
```

```
}
```

```
#get taxonid for each
```

```
count=1
```

```
for (queryspecies in species){
```

```
  taxcount = 1
```

```
  cat("Gathering TaxonID for: ", queryspecies, "\n")
```

```
  for (taxid in biogridtaxidjson[,2]){
```

```
    if(taxid == queryspecies){
```

```
      print(taxid)
```

```
      taxonid[count] <- biogridtaxidjson[taxcount, 1]
```

```
    }
```

```
    taxcount = taxcount + 1
```

```
  }
```

```
  count = count + 1
```

```
}
```

```
##### Querying BIOGRID API #####
```

```
#biogrid access token and base api
```

```
biogridtoken <- "&accesskey=34e9134bdaaefe8eeb2012f1099ed599"
```

```
biogridbaseapi <- "https://webservice.thebiogrid.org/interactions/"
```

```
biogridapiparams <-  
"?additionalIdentifierTypes=OFFICIAL_SYMBOL&includeInteractors=true&format=jsonExtended&geneList="
```

biogridapiparamstaxid <- "&taxId="

#query biogrid api to extract information

count=1

for (query in commonname){

 biogridapiquery <- paste(biogridbaseapi, biogridapiparams, query, biogridapiparamstaxid,
 taxonid[count], biogridtoken, sep = "")

 biogridget <- GET(biogridapiquery)

 biogridjson <- fromJSON(toJSON(content(biogridget)))

 cat("Biogrid query for: ", query, "\n")

 biogridinteracts <- c()

 for(i in 1:length(biogridjson)){

 if (length(biogridjson) == 0){

 biogridinteracts <- NA

 }else {

 biogridinteracts <- c(biogridinteracts, as.character(biogridjson[[i]][8]))

 }

 }

 interactswith[count] <- paste(unlist(unique(biogridinteracts)), collapse = ",")

 count = count + 1

 Sys.sleep(sleeptime)

}

```
##### Querying UNIPROT API #####
```

```
#query Uniprot api
```

```
count=1
```

```
for (query in commonname){
```

```
  if(is.na(uniprotid[count]) == FALSE ){
```

```
    uniprotquery1 <- query_uniprot(
```

```
      query=list("gene_exact"=c(query), "organism_id"=c(taxonid[count])),
```

```
      base_url="https://rest.uniprot.org/uniprotkb/",
```

```
      columns=c("accession", "gene_primary", "protein_name",
```

```
        "length", "mass", "cc_activity_regulation", "ft_binding", "cc_catalytic_activity",
```

```
        "ft_dna_bind", "ec", "cc_function", "feature_count", "keywordid", "protein_existence",
```

```
        "uniparc_id", "cc_subunit", "cc_developmental_stage", "cc_tissue_specificity",
```

```
        "go_p", "go_c", "go", "go_f", "go_id", "cc_subcellular_location", "ft_chain",
```

```
        "ft_mod_res", "cc_ptm", "protein_families", "xref_refseq", "xref_pdb", "xref_biogrid",
"xref_string"),
```

```
      max_keys=200,
```

```
      updateProgress = NULL,
```

```
      show_progress=TRUE
```

```
    )
```

```
    cat("Uniprot query for: ", query, "\n")
```

```
    proteinlength[count] <- uniprotquery1$Length[1]
```

```
    proteinmass[count] <- uniprotquery1$Mass[1]
```

```
    proteinfeatures[count] <- uniprotquery1$Features[1]
```

```
    proteinUniParc[count] <- uniprotquery1$UniParc[1]
```

```
    proteinsubunit[count] <- uniprotquery1$`Subunit structure`[1]
```

```
    proteindevstage[count] <- uniprotquery1$`Developmental stage`[1]
```

```
    proteintissuespec[count] <- uniprotquery1$`Tissue specificity`[1]
```

```
    proteingo[count] <- uniprotquery1$`Gene Ontology (GO)`[1]
```

```
    proteingoid[count] <- uniprotquery1$`Gene Ontology IDs`[1]
```

```
proteinsubcellloci[count] <- uniprotquery1$`Subcellular location [CC]`[1]
proteinmodres[count] <- uniprotquery1$`Modified residue`[1]
proteinptm[count] <- uniprotquery1$`Post-translational modification`[1]
proteinfam[count] <- uniprotquery1$`Protein families`[1]
proteinrefseq[count] <- uniprotquery1$RefSeq[1]
proteinpdb[count] <- uniprotquery1$PDB[1]
proteinbiogrid[count] <- uniprotquery1$BioGRID[1]
proteinstring[count] <- uniprotquery1$STRING[1]
proteinfunction[count] <- uniprotquery1$`Function [CC]`[1]
} else {
  cat("No uniprot entry for ", query, "\n")
}

count = count + 1
Sys.sleep(sleeptime)
}

##### Final Dataframe Generation #####
#Renaming cols
EnsemblID <- querygenes
UniprotID <- uniprotid
GeneName <- commonname
ProteinName <- proteinname
UniparcID <- proteinUniParc
RefseqID <- proteinrefseq
pdbID <- proteinpdb
BiogridID <- proteinbiogrid
StringID <- proteinstring
goID <- proteingoid
goDescription <- proteingo
EnsemblObjectType <- objecttype
```



```
GeneDescription <- genedescription
Species <- species
TaxonID <- taxonid
GeneProduct <- biotype
DNaseq <- seq
ChromosomeLoci <- chromosome
Strand <- strand
StartPos <- startpos
EndPos <- endpos
Keywords <- keywords
ProteinSeq <- proteinseq
ProteinFamily <- proteinfam
ProteinLength <- proteinlength
ProteinMass <- proteinmass
ProteinFunction <- proteinfunction
ProteinFeatures <- proteinfeatures
ProteinSubunits <- proteinsubunit
ProteinDevStage <- proteindevstage
ProteinTissueLoci <- proteintissuespec
ProteinSubCellLoci <- proteinsubcellloci
Interactions <- interactswith
ProteinResidueMod <- proteinmodres
ProteinPTM <- proteiptm

#final df
finaldf <- data.frame(EnsemblID,
  UniprotID,
  GeneName,
  GeneProduct,
  ProteinName,
  UniparcID,
```

RefseqID,
pdbID,
BiogridID,
StringID,
goID,
goDescription,
EnsemblObjectType,
GeneDescription,
Species,
TaxonID,
DNASeq,
ChromosomeLoci,
Strand,
StartPos,
EndPos,
Keywords,
ProteinFamily,
ProteinSeq,
ProteinLength,
ProteinMass,
ProteinFunction,
ProteinFeatures,
ProteinSubunits,
ProteinDevStage,
ProteinTissueLoci,
ProteinSubCellLoci,
ProteinResidueMod,
ProteinPTM,
Interactions
)

```
##### Exporting to MySql #####  
#Section contains Biological Databases class code (Tomlinson, 2023)  
#exporting finaldf to sql  
  
db <-dbConnect(MySQL(),  
               user='s2600569',  
               password='KlsIXlQX',  
               dbname='s2600569')  
  
dbWriteTable(db,name='Summary',value=finaldf, overwrite = TRUE)  
dbClearResult(dbListResults(db)[[1]])  
  
ac <- dbListConnections(MySQL())  
for(con in ac){  
  dbDisconnect(con)  
}  
dbListConnections(MySQL())
```

MySQL Dump:**1. Schema File**

```
-- MySQL dump 10.13 Distrib 8.0.35, for Linux (x86_64)
--
-- Host: localhost Database: B242415
--
-- Server version 8.0.35-0ubuntu0.22.04.1

/*!40101 SET @OLD_CHARACTER_SET_CLIENT=@@CHARACTER_SET_CLIENT */;
/*!40101 SET @OLD_CHARACTER_SET_RESULTS=@@CHARACTER_SET_RESULTS */;
/*!40101 SET @OLD_COLLATION_CONNECTION=@@COLLATION_CONNECTION */;
/*!50503 SET NAMES utf8mb4 */;
/*!40103 SET @OLD_TIME_ZONE=@@TIME_ZONE */;
/*!40103 SET TIME_ZONE='+00:00' */;
/*!40014 SET @OLD_UNIQUE_CHECKS=@@UNIQUE_CHECKS, UNIQUE_CHECKS=0 */;
/*!40014 SET @OLD_FOREIGN_KEY_CHECKS=@@FOREIGN_KEY_CHECKS, FOREIGN_KEY_CHECKS=0 */;
/*!40101 SET @OLD_SQL_MODE=@@SQL_MODE, SQL_MODE='NO_AUTO_VALUE_ON_ZERO' */;
/*!40111 SET @OLD_SQL_NOTES=@@SQL_NOTES, SQL_NOTES=0 */;

--
-- Table structure for table `Summary`
--

DROP TABLE IF EXISTS `Summary`;
/*!40101 SET @saved_cs_client = @@character_set_client */;
/*!50503 SET character_set_client = utf8mb4 */;
CREATE TABLE `Summary` (
  `row_names` text,
  `EnsemblID` text,
  `UniprotID` text,
```

`GeneName` text,
`GeneProduct` text,
`ProteinName` text,
`UniparcID` text,
`RefseqID` text,
`pdbID` text,
`BiogridID` text,
`StringID` text,
`goID` text,
`goDescription` text,
`EnsemblObjectType` text,
`GeneDescription` text,
`Species` text,
`TaxonID` bigint DEFAULT NULL,
`DNASeq` text,
`ChromosomeLoci` text,
`Strand` text,
`StartPos` text,
`EndPos` text,
`Keywords` text,
`ProteinFamily` text,
`ProteinSeq` text,
`ProteinLength` text,
`ProteinMass` text,
`ProteinFunction` text,
`ProteinFeatures` text,
`ProteinSubunits` text,
`ProteinDevStage` text,
`ProteinTissueLoci` text,
`ProteinSubCellLoci` text,
`ProteinResidueMod` text,

```
`ProteinPTM` text,  
`Interactions` text  
) ENGINE=InnoDB DEFAULT CHARSET=utf8mb4 COLLATE=utf8mb4_0900_ai_ci;  
/*!40101 SET character_set_client = @saved_cs_client */;  
/*!40103 SET TIME_ZONE=@OLD_TIME_ZONE */;  
  
/*!40101 SET SQL_MODE=@OLD_SQL_MODE */;  
/*!40014 SET FOREIGN_KEY_CHECKS=@OLD_FOREIGN_KEY_CHECKS */;  
/*!40014 SET UNIQUE_CHECKS=@OLD_UNIQUE_CHECKS */;  
/*!40101 SET CHARACTER_SET_CLIENT=@OLD_CHARACTER_SET_CLIENT */;  
/*!40101 SET CHARACTER_SET_RESULTS=@OLD_CHARACTER_SET_RESULTS */;  
/*!40101 SET COLLATION_CONNECTION=@OLD_COLLATION_CONNECTION */;  
/*!40111 SET SQL_NOTES=@OLD_SQL_NOTES */;  
  
-- Dump completed on 2023-11-06 20:50:55
```

2. Data File

```
-- MySQL dump 10.13 Distrib 8.0.35, for Linux (x86_64)  
--  
-- Host: localhost Database: B242415  
--  
-- Server version 8.0.35-0ubuntu0.22.04.1  
  
/*!40101 SET @OLD_CHARACTER_SET_CLIENT=@@CHARACTER_SET_CLIENT */;  
/*!40101 SET @OLD_CHARACTER_SET_RESULTS=@@CHARACTER_SET_RESULTS */;  
/*!40101 SET @OLD_COLLATION_CONNECTION=@@COLLATION_CONNECTION */;  
/*!50503 SET NAMES utf8mb4 */;  
/*!40103 SET @OLD_TIME_ZONE=@@TIME_ZONE */;  
/*!40103 SET TIME_ZONE='+00:00' */;  
/*!40014 SET @OLD_UNIQUE_CHECKS=@@UNIQUE_CHECKS, UNIQUE_CHECKS=0 */;
```

```

/*!40014 SET @OLD_FOREIGN_KEY_CHECKS=@@FOREIGN_KEY_CHECKS, FOREIGN_KEY_CHECKS=0
*/;

/*!40101 SET @OLD_SQL_MODE=@@SQL_MODE, SQL_MODE='NO_AUTO_VALUE_ON_ZERO' */;

/*!40111 SET @OLD_SQL_NOTES=@@SQL_NOTES, SQL_NOTES=0 */;

```

```
--
```

```
-- Dumping data for table `Summary`
```

```
--
```

```
LOCK TABLES `Summary` WRITE;
```

```
/*!40000 ALTER TABLE `Summary` DISABLE KEYS */;
```

INSERT	INTO	`Summary`	VALUES
('1', 'ENSMUSG00000015002', 'Q8BG67', 'Efr3a', 'protein_coding', 'Protein		EFR3	homolog
A', 'UPI00000EBA50', 'NP_598527.2			[Q8BG67-
1];', '218290;', '10090.ENSMUSP00000015146;', 'GO:0001533;		GO:0005829;	GO:0005886;
GO:0042803; GO:0072659; GO:0098609;', 'cornified envelope [GO:0001533]; cytosol [GO:0005829];			
plasma membrane [GO:0005886]; protein homodimerization activity [GO:0042803]; cell-cell adhesion			
[GO:0098609]; protein localization to plasma membrane [GO:0072659]', 'Gene', 'EFR3 homolog A			
[Source:MGI		Symbol;Acc:MGI:1923990]', 'Mus	
musculus', '10090', 'GGTCGGCCACCGCGTCGTCGACGGGGCGCGGATCACGGCCGGTGGTCGCTGTACCCGG			
TCGGCGTCCGCTCTCTCGGCAATTCGTCCTCCGCCCGACGAGGCGTCCGTGGCCGGGCTTCCGCAGTCATGCT			
GCGGTGCGGCGGCTCGCGCTTCCCCTCTGAGTCCCGGGACGGCGGCGAGCGCGGCGAACTCGGGTCGCCAT			
GCCTACCCGTGAGTGTCGGGCCAGGCCGGGCGGGCGGGCAGCGCCTCCAGGAAGCGCCGGTCCGCCCTGAGT			
TAGTTTCGCTTAGACTTCAGCGTCCCGTGGGCGGGGAGCGCGGGATCTCTGTGCACCCTCGGGGAACTGAGG			
CGGGAGCGTTACGGGAACTGACGGCGGGCCCGCGGTGACGGCGCGGTAACGGAGACCACTGCGACCCGGGAA			
GCCCCGGGCTGGTCCACTCGCCGCGCGGGCCCACTCGACTGTGGCCCCAAGGTCGAGGCCTGTGCTGCCTTAGT			
TTGAGGGACTTAGGTCCGAGGGACAGGCTGCAGCCCTCCCTGCGGCCAGAGGCCGGGCTGCCCCGAAGTGTG			
TCAGTCTGACTACTTCTTGGCTGACTTGACGCGGTTTTGGCTTGCCCGCCTGCGGTGGGACCCGGGCTCCACT			
CATAGCAAGCATCCCGCTGTCCCAGAGGGACGATAGGTTTCGAGATGACCCCGGTAGTCGAGGCTTTGAGAG			
AGAGACACTGTACTACAAGTACTACACAGTTGCTAAGAGTGACCCAGATACTACGCTGAGGCTTTAAATCATG			
TGGCTCACATTGATTACGTGCTAACTGGGTGGCTGATGCTGGTTATGGGTTTTTGAGGGTCTTTGCAAGTAGTGC			
TCTTGTAAGTGTGCTTGCCATAGAATCTTTAAAGACTTGTAATGTTTTCTCGGAATTCCTAACTAGCCCTGCAT			
GGTTTCTGTAGACATAAGTACGGGATTTCTAGGCAGCTTCAAATGCACAATTTCTTCTAGTGTTGGGTAAAGATTT			
CTTTCTGAATACTAGAATGGTTTGCCTCATAGCTGTGTCAAACCTTTATCATAATGTAAAGGTCACTTTGACCCCT			
CAAATACCAAGTGTGTTTTATTTGTTTGACGTTATTCTGTGTTTCTTACTTTACATTTCTGCTTGATTCTCCAGC			
CTGGAGGTATATTCTCTGCCTATCTTGTTTCATGATCATATTGCCAGTTTTATTATTCCTTACACTCATGTTCTATTATT			
TGACTATTTGGAATTAGCACCGTGCCAATCTTCTGGGAAACGAAAGGGGAGAAAGATAAAGGACATCAAAAGA			
TGAGACTGCATATGGACTGTCTTGGTAAATTTCCATTAAATTTCTGCAAAATCATCGAGCTTTTAGTTATGTGCTA			
GCATTTAGTTTCTAGAGAGGATGCTGATAGTTACATTTTAGGATGTTTGATTTATTACTGTGTCCAGTGAGTTT			
TGGATGAACCTTCGGTGTGAGATTGCTCACCGTGAGTAGGAGGTCAAGAGAAATGATCATGACTTATCTGTCAATT			
TGTTGCTGTGCATCACCTGGAATCAAAGGGAGATACTGATGTGGACAGAAGTTCAGCTCTGAAATGGTAGCTCT			
TGCTTTTTTTCTCCTGATGGTCAGAGCCCTCAAGGTGTCCGAGATTCTTCAAGTGGGAGGAGTGCTTCTTAGATG			

CCCCGTGTCTAAAGTAGACTAAATGTATAAGCAGAGACTGTGACACAGTCAGTCACTGTAGTATGGTATTATGGGT
GCTTTTAGGAAAAAGAAATTAATTTTTTATAAAAAAATCGTTATTTAGATGCTCAGCCAGTTAACCGTTAAGTGTTT
TAGCTAATGAAATGCAGTGCTTTTCTACAAAAGTGAAGGGTTAAAGAGGATCGCTTTAATCTCTAGGTTCTAGAA
CTCTGCAAGCAGCTCACAGATAAATCATTCTATTGTTGTTTTTGTGTTCACTTGGAATTGAAATGACACTGATAG
CAGAAGCCACCTTCACATGCTGGAGCCACGCTGGCCAAGCAAGTGTGTGCCTAAGGAGTATTGTTAGTTGGAG
TTGTTTAGTGAGCCAAGAAGCTCTTGAGGAAGCAACTAGAAGGATGTCTGCAAGAAAGGTCCAGCACAGAACA
GCTCCTGTCCTTGTCATTCTGTGTTTAGTCTGTAGTTGGCTGGCTGACATCAGGGCTCTCATTAGATGATTTTTTTT
CAAACCTAGACTATTGTTAACTTTTAATTTCAAAGGCTTTGAGTTGGAAGGAAAGTTGAGGTTTCTTAATCCA
ATCTTTTATTTTTGAAGATCAGGAGGCAGAGGCACAGATTTTTTTTTTAAATCACAAATTCATTTTGTTTTAG
ACAGTGGCTCATTATATAGAGCAGGCTATCCTAGAGCTTCTGATCCTTATGCCACTGCTAAAGGGCTGTGGATGTG
TAACACCATGTATAGGTTTTAGTAAGTTTTGATGGCTTCTTGAGGTCATAAATAGAGAAGAACCAGTACTTGGAC
ACATATTTGGCCCTTTACCCAATATCTTCATTGAGCATGGATAATGTTTATTTGTCTTTAGCCAAAGTTGAATAAAA
TTTTTGTTTCTTTATAAGCTATACTGACAAAAATGTAAGCTATGCCAAATCTATGAATTTTTTGTAACTTAGAG
AGACATTTGCTTATAAAAAAGTTGATCATTGCCCCAGACTTCAGTCCTGCCACAGGAATCTGGGAAGAAGGCGG
GAGTCTGCAGGTGTGCTAAGCGATACTCCATTATAAAGGCATGAATTTAAAGTCTAACAACTGCTTTTATGGAA
GGGGCTTCTTAATTCATCCACATTGCGTGTTTAAAAACAGGCCCAATAAGATGTGCTCTTATGTATGAGAAATTAT
AGATATTAGCTGGGAGAATTCAGTGAAGTGTGTTGTTGTTTATTAACTGTTTTCAGTGTGTGGCTGATGCTTT
CTTTTGACACTTAGATATCATTGCTATTAGGTTAGGTCTGTTAGACGGTGGTAATGTGGGCGTCCCCCTATACTTGA
ATAAGGCTAATTATTTAACTGTTATCGCTGTCTTACAGACGAAGTGCAGAATGAAGGATGGGTGATAATTGGAG
TTTTTGAAACAATACATGTTGTGTTAGCTTTATATCACTGAGACAAACCTGCAAAAAGACATCTTGAGAGAAGATT
GAACTTGACGCATGGCTTCAGAGGTGCCAGTCCAGAGTCCACTGAATCCATTGCTGTTAGACCTGTGGAAGTAT
AGAAACATGGCCAGAAAGGATGGTAGAGGAAGGCTCTCACAAGAAAGCTGTTACCTTTAACAGCCAGAAAA
GAGACATAGAGGAGGCTCCAGAGGCCCGGCCACCCACAGTTATTTCTTTACTTTAGTGCACGAGTGTTCCATT
TGCTACGTTAAAGCTCACTAGCTAGCAACCAAGCCTGTGCTCTTCTTTAGTTTACCAATTTGACAGAATCTGGAA
TCAACTGGAGGACAGGTCCCCGAGCATACTCATGAGGAATTACCCTGATTGGGCTAAATGAGAGGGAACGACC
AGTCCACTGTGGGTGTCATCTCTTTGCAGGAATCCTGGCTTGTTAAATTAAGGAAGATTGCTGAACTCCAG
CATGCATTCATCAGCTCTGCTTTCTCATCATGCATACGATATATCCACCGCTTCAGACTTCTGCTGCTTTGTGTTTT
CTGTCTATAAAGGACTATACTCTTGAGCTCTTGAGCCAGAATAAACCTTTCTTCTTGAAGTATTGTGAGACTAT
TTTATCACAGCAACAAGAAAAGAACTTAAAGCCTCTAGCAAATGAGGTCAGTGGGCATTTAACATTGAGACCC
ATCGGACATTGAGTTTATGCATTCATGTTATTTGGTTTGGAGTCTTGATGTTTCATTATTTATATTATCGTTTGTG
CATGTTTCTCCCCCTGTGTTCTCCACATTTCTCCTTTATCTCTCCAGCCTTCTCCTTCACCCAGAGCTGTAAGT
AAGTTTTGTATTTGTTTTCTTCTCACAGGATGACTTTTGCCTTGATACTGCTTTGATTGCTATCTGGGAGACCTGT
TTTTCTTTTCTTTTCTTTTAAAAATAGGGTCTCTCTGATTGTTGGCCGGCCTGGAATGTAAGTTGTAGACTTGGG
TGGATTCAACTCAGAGATCTGCCCACCTCTACCTTCTAAGTGTGCTGGGATTAAGACATGCATCCCCACAGCATG
AACCATAAGCCTCAATAAATTCATTGAGTAAAGCAGACCTGTCTTAAAGATTATGCAAATGTTGAGATAAG
GCTGGAGGAGGTGGGAGCCAGAAATGGAATAGTTTCTTTGCCCTTGTAAGTGCAGAGGAATGGGATAGTTTCA
TGTGCCATTGTAGTGCAGAGAAGCAATTAAGGACTGAGAATATGTTACAGCCACAGTGGCTATTTGTAGGCATA
CTAGCACTTTCCAATTACTGTTTGTGTTTGTGTTTTAATAAAGATAATCAGATTTTTTACCAGACTTTCCGGG
ATGTTTTTTGAGGTGGAAGACAGTGCAGATGTCTGCACTTCACTATAAATGAGAATTTTACGCCTTTGTACCAT
TGGTCCCTTGACCAGCTATTTTGGTGGTGGTGGTGGCTAAAGGAGGAAGTAGTAGCAGGAGCCTATGCTTTAT
AGAATACTAGCAACATCTTTGGCTTTTATCTACAAAGGCCACTAGCAGTACCTGCCTCCACCAAAGACCCCCAC
AGTTGGAAGAACCAAACTGTTTACAGACATTACGGTATATCCCCTGGAGGACAGAATTTAACTTCA
AAGAACTGCTCTAGTTCTAAATATTAAATATTACAAATCAAGCTGTGTCCACAGCCTGTCTGCTTTCAGACCATT
AGGATGTTTCAGCCAGCCTGTGACCTGAAATGACTCCTTAACCCAGAGGCTTAGATAGCTTCTAGGCCTGTTCTGG
TCAGCAGTGATCTACTTGAAGTTGGCCCTAGAATTGACTCTAATCAGGTTACTTCAGGGACTGGGAATGTATAGC
ACCTCCCTTGCAGTATATCACTTTTTTACCAGGATTTAAGGAATGTTTTATGTATCTCAGTAAACGGTCTGAATAA
TTGGGCAGATGAGAGGAAGAAGCTAGTTTTCTGGGGGAAGTCAGTAAAAGCAAGGCCAGTGGAAGCCAAGTT
CCTCTGGTTTTCTAGGGTAATAAAAAACAACAATAATAACAGCAATAATAAAGCTATTATTATTGCTGTTGTT

ATTATTGCTAGTTGTCCCTTACCCTTTCACATACATAAAAGGAAAAAAAAGGTCCTTTGTGGTCTAGTAGGCAGAG
CTAGGAGCTGTGTGTGTGAAATGAAATATCATGGTTGAACTCTGGCATTGGATGATCTAGTCATTTAGTATTCTTCT
AGTAGTGTGATGGGCTATAGTTGGCAAACCTCATTCTCTACAGGATAGCATATTTCTCTTTAGTGACTCTTTCTCTT
TATATTCTAGATAGTGCAATTCTGGATTTTAGTAAAGATGGTACCATTACTCCTGTAGTTTTAGAGCATCTCCGTTAC
ACCCTGAGTATTCTTATCTGAATAGCTTTTTGAATAGAGGCTCCACGATATGTGTTTGTGTGTGTGTGGGGGGGGT
TTGGGTGTGGGTGTGTTTAATTATCTTTTTTTACATACTCCATTTTGTATGACATTAAAGTTGCCTTTTCTGACT
TTAGGCAGGAAATGGTCAACCTGTTATTCTATGGAAGTAGGAAAATTTTTGTGGATATTATTATTATTGAAATATT
ATGTATTATAATATATAGTAGAAGACATGAAAAGGCCAGTTGGCCACCAACTATTTAGGAAAGATGGCCAAGA
GGATAGGATATCAACATTTTATCCAGGTTAAACATATTATATATTTTGCTAAATGAACCCTATTGAGAATCTAATGGA
TGTTCTGATGATTCTCCTCAGAAAAATGAAAAATGTTACCCCAAATTTCTAAATAGTTTGAAATGACTTACAGAC
ACAGCAGAATTTGTTAGAAAAATCAAACAGATCACCACAATGGAGTGAAGTCCATTGTTACTCAGCAGAAACAT
AAGTACTCTGCTTTGGCTTTTTCTCTGCTGAGTTTTACATATTTTCCCAAATATTTTAATTATGTGGCTGAATCTTC
AGCATATTTTGTAAAAATAATGTGTCAAGAATTATACTCAAGAATCACTTAAGACAGTAGTTGAGCCATGAGGA
TATTTAGTCCAGTTGGCAAAGGGGCAGCTGAAATCAGGAAGACTTGTGTACCATTCTGATCATGCTTTGCC
TCTAGAACCCAGGCTGTCTGAATCGTGAGAGTGCCTCACTACGTACATCCCATTCTCCATGACAGAAAGAGTT
GAGAAGTTTAGTAGAATCATGGCTAACTCAGGAGCTAAGATAATTTATTAAGTTAAAACTGACAGTTTATTTAT
ACAAATCTGAAAGTAAAAATACTACCAGCCTTATGTAGTTAAGAGTACACACTTATATTTACTATCCATTTTATTAATA
AAGAATTGCAGATTAAGAGCTGCTGGGGATTGGTTCTAGAGCTTTGATTTAATTCTGAATCTTTGTGTCCAAACA
GTGAAGGTCCTTGACCCCTATTGCTTTTTGATCGATCAATAAGATGCCAGTGGCTATTGGCGAGGCAAAGGGA
GATGGAATGGGACCTTAGATTGTGCAGGCTAGGAAGTGGGAAAAACAGACAGAATTGCCATGACTCAGGG
GAGAGAGATGGATCAGATTTAGAGCTGCAGAGGGAAGACCATCTGAAACGTAGGAGGGTAGGGAACTGGCC
CCAGAAGGGCTGCCAGAAACAGAGACCAGTGAGCCTCACAGAAGGTAACAGGGCAGCAAAGTTAAAGGTAG
ATTTTAGGAAGTGTTGAGCTAGGAGTACAGGAAGGAAAGTATGCTAGCCGTGGGAGGATTAGAACTGCCAG
TCTTTGAGTTTTATTGGAGGATCCAAAGAGTTTCTGGGTGAGTGGCTGAAAGTGCTTGACCTACTGGGAGCCA
AAGTGGAGTAGCTAACTCACTGCTACAAAAAGCCAAACCATTTTTGGTTTGATAGGTTGTCAGAACATAATAT
ATGGAGGCAGTGAGGTTCAATACAAATGCTAGAAGTGCAGGTTGGTTCAAATTTCTTTGGAAAGCAGATTAAAA
ATGTATTATCAACTGGTCTAGGGTTTCTATCCATTGGCCCAGTGACTTTACTTCTAGGAATCTCTTCTTAAATGAATT
TTTTAAATTATTTATTTATTTATTAATCACTTTATTTGTTTACATTTCAAATGTTATCCCTCTGCCGGGTCTCCTTCCA
TGAACCCCCACCCCCACCCTCACCTCATCCCCATCCCTTTTGCCTCCCCTGCCCACTACCCACTCCTGCCTCATCC
CTCTAGCATTTCCCTTCTCTGAGGCATCAAACCTCCACAGGACCAAGTGTCTCCCTTCTCAATGATGCCAGATGAG
GCAGTCCTCTCTTACATATGTAGCAGGAGCCGTGGACTGGCCATCGTTTACTCTTTGTTGGTAGTTTAGTCCCTGG
AAGCTCTGCGGTATTGGGTAAATTGATATTGTTGTTCTTCTACAGGGTTGCAATCCCCTCCAGCTTCAGTGCTCT
CTCTAACTCTCCATTGGGGTTCCTGGGATCGGTCCAAAGGTTGGCTGTGAGTGTCTGCGGCTGTCTTAGACAG
GTGCTGGCAGGGCCTCAGCATAGTCATACCAGGCTTCTGTCTGTAAGCAGGTCTTACCAAAGAACATTGAGATAT
TTTTGCATCAAATGTCTGTGAAAACCTAGAACTTGTTTCCAGTAACAGGGAGTTGATACATGTTAATAATAGAA
CATCCTTTGAAGCCACACAGTGGTGGCCACGCCTTAATCCAGCACTTGAGAGGCAGAGGCAGGCAGGATTTT
TGAGTTTGAGGCCAGCCTGTTCTACAGAGTGAGTTCCAGGACAGCCAGGGCTACACAGAGAAACCTGTCTCC
AAAAAACCAAAACCAAAACAAAAACCAAAAAACAAAAAACAAAAAACAAATATTATGCATTAATTA
AAAGAATACTCATGAAGCCACGCAATAGTAATCCAGCCCTTAGGACACTAACTAGGATTTGAGGCAACCTTAG
GCCACATAGTGAGATCCTGTCTCTAATCAACAAATTAGACTAAAATAACACCAAGCAGACATATACAGTGTTTTA
CCCCATAACACAGGCTGAGCTGAACTAGCATTCCCACTGCCTCAGCTTCCCAATTGCTGGGGATTATAATTGTGT
ACTAGTATGCCTGGGGAATTTGTTTTCTTAATTTGATTTCCAAATTTTCTACAGTTAACTCTATAATTAGAAAA
AAATAGAGCTTAAGGTTACAGCCTTAATGCAACTTTTCCAAACCAAAACAAGACATTGGAACCTACTGAACAGTT
TCTTCTGTAGCCTGCAGACTAGGAGGAAAAAAAACAAACCAACCAATGGTGTTAGCTACATAGGAAAGCGGT
GCCTGGCATCTGATTGCTGTGAGATGCTCAGAGATGTGAGCTTCAGTGAGTGCTTTGCCGAGGTCTGGCAGTGT
GTTGGTGAACAGGAAGCACAGGAGGGGCAATCTATCACTTGTCTCTTCTGATTGAAGTGTTTTATGCTTTATTA
AGTAGTGGTTTTAGTCTTGAAATCCTGAACGGGTGAGATGAGTCACTGTGGGGGAGTTCAAGTGATGGGAGTTG
ATAGTTTTTTGTATCTTCTTTGGAATGAATGTCTATTGTGGAGTGAATACAGTTTTAAGCAAGTGGGATCACAAAG

TGAATGTTGGCAGTTCCTGCTATGATTAATGTCAGACCTGTCAAAATTCTGCCAGGCTCATTAGTTCTTGAAATG
AGCCAGTTCTTGAGGATGTTCTGAAGGAAATAGAAGCTAAATAGTATTTTTATTCTTTCCATGGAAGGCATCCCAT
TCCTCCTTGGCACCTTTGTCTCTGCTCTAACTCTGGATGTTATTGTTGGCATAATTCTATATTTATTAAGAAAG
GAACACTTTCCCATGTACCTCTAACTAAATTTATCTCTTCTAAATTTAGCCATTAAACCATTGTTCATAGCCTT
CAGGAGGAGTTCTAACTGCCATCATGTCCCCTCTTACTTGATGAGTTATTTAGCCACACCTTTTCTCTTTACCACCT
GCACTCCAGTAGTTTTCTGGATAATGGTAAATATTCTTCACATGTGACTCCCTAATGGGCATTTTAAAGCAGCTGTC
TTGATAATCACTACCTTATTTTTGGTGCTCCAGTTGCAAGTTAACTTTAAGTGGCTCTCATACCTGCTGAGTAGAC
TGAAGTACAAGGTACCACATTTGCTGTTATGATTCCTGGGATCTCGTGAACATGCAAAACACGCTTGATTTGCAC
AGATCCTGAGAAATGAGAGGAGTGCCCCCTTTGTGACATCTAACTTAAATTGTTGGTTTTAGGAACTTAGTTAAA
AGGTTTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTCTAGATAATTGACTCAATAACTGGGAAAAGATAATATCTCTTAAA
AATTTGTAGATGCAACATTATATTTATGTGATTGGTTTTAGAGGTAGAAATACTTGTTAATGTATTAGGACAAGCAT
GTTGGCAGAAAAGGATAGTTAACTCAGGACTTAGGCTGACATTCAGAAGTTCATTGTCTTCAATTTGCTGAAGC
AGATGGGTAACCTGTCCACTCCACCCTAGCATTTGATTGGCTTTAGAAAGGTGAAATATACTTGGCACAATGGA
CAGTCTTAGCCTTGTAACACAGCACTTCATAAAATGGAACCTCTTAGATCCCAGAAAGAGATGACAGATAGATGG
GTCAGTTCTTTTCATAGTGACTTTATTTACGAAACTCCATTCCCTCGTGTGGCACAGGATGTTTGCTGCTTTTAAAC
CTCATCGGCAGGGAGAGGAAGGGAAGCCTGAGGTGCCTCTGAAACATGAGCTTTCAAAATGCCCCCTTCCATG
CCAGGTGCGGTAATGTGAAGAAGGTGCCAAAGACATTGAGCAGGTGGCCCACCCAGTGTTGGCTAGAGTAGCT
TTGCTTTTTGTTTTGTTTTGTTTTGTTTTAATCTCTTATATGTGATGTTCTACATTCAATTTCTGTAGGAAAGTGACA
TTGACTGCTTTTAAAAAGTAGATAGAAAATACAAGATGTTTACAGTCAAAAGCTCATGAACTCTGAGGCAAAACC
CAAAGCAATTCAGCTGATGGTGTCTCACCTTTTTGGACTACCAGTCTCCAGGACTGAATATATTATAGCTCCTCTAT
GTAGTTATTTCTGTTACAGATGATGCAAGTGTGCTAGTAGATCCAGGGATGTTCTCTTTCAATTTTGCTTTTCTGGT
GGATATGTTAGGGACATACTTAGTATTTTGATGCCTACATTTGCATGGCATAGATAAGATAGAGAATGCAGGGTTG
GATAAAGAAGTCCCTAGCTCCAAAAAGTTATACCATTATTTATGCACATGCAACATAAAGGAGATTTAAAAAAA
AAGCCTTGAGAAATGGGGCTGTGGTAGTTTCAAGGAGAGAGAGATATCCATGACACTAACAGAAAGATGAATAGA
CAGTACTTTCAAAAAGCAGAGTGCCTTAAATGATATGACAGAAATAGTGAGCGTACCAGAAAGGCTAGCGTAGG
GGAAATACTCAAAAGTAAATCCTAAGAGTGGGAAAATGACCGTGACACACGCACGCGCGCACACACACACA
CACACACACACACATGGGTGCGGGGGGGCGGATTATTAACCTTTTTGTCCAGTGTGAGATAGATACTGTTAT
AGCTGTTGTCTTTGCTAGTGGAGCACAGTCTAATGGGGGAGCACAGTCTATTGGGGAAGAAAGCTGTGTTTAGC
AAATTGATCCTAACCAGAGAGTTAGATGACGGTTTGTAATTGTTTTCTTTTTTGTGTTTTGTGAGACAGGGT
TTCTCTGTGTAGCCCTGGCTGTCTGGAACCTACTCTGTAGACCAGGCTGGCCTCGAACTCAGAAATCCACCTGC
CTCTGCCTGCCAAGTGCTGGGATTAAAGGCATGCGCCACCCTGCCCCTGAGTTTCTATGCTAGTCAGGCTATC
TGTTTATGGTAGCTTTTGAAGTAGTTCAAAGTAGCAAGAAATAGTAGTAGTGACATTCTTTACAGTCTGACCTGAT
ATTATGACAATCGAGAAAAAATTTATGTAGCATCAAGGAAGGTGTTTTAAATTTTGAACCTCAAAGTAGTTGTC
ATATTTAGGCCCAACACATGTAACCTATACTTCTGTTCTTAACTGTCTTGCCACTGCTTCTGTCCGGGAGAAG
AGACTGTCAAATTATATTAAGTGATGCAAACTGGTAGTTGGGAAGTTTGCAATAGAAGTTAGGGCACCTCAGT
ATGTGTAATCTAAAGTGAAGTGATAGAACCAGACTACTAGTAGCTTATTCTATTGCTGCTGTGTTCAAGCTTCATT
GGATTATGATTTGTGAAAGAATTGAGTGGTTTTAGGCAGCAAATGGCTGTCTGTATGTAATAAAGTTCTTGAG
GAAAGGCTTGTTTCAAAGACAGAATTGAAGAGTGTGTTAGAGACGTGTTGTCTGTCACTAAGAGCATCAGTTTGC
TTCATTGAGACCTTTCTCCTCTTACACTAATACTGCTCTCTCTCCCTTCCCTGTGAGCTCTTCAGGGTGGTGTGATG
TGGTGATCGGGGTCTGTTTGCTCTTACACTATGTAGATTACTGCTCTTTCTGTTGGGTCTTCCCTGATAGGTATAG
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[illegible]

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[illegible]

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 LTIRPPSPSGTLTVTSGHTQYQSVPVYEMKFPDLCVY','819','92613','FUNCTION: Component of a complex
 required to localize phosphatidylinositol 4-kinase (PI4K) to the plasma membrane. The complex acts
 as a regulator of phosphatidylinositol 4-phosphate (PtdIns(4)P) synthesis. In the complex, EFR3A
 probably acts as the membrane-anchoring component. Also involved in responsiveness to G-protein-
 coupled receptors; it is however unclear whether this role is direct or indirect.
 {ECO:0000250|UniProtKB:Q14156}.'','Alternative sequence (1); Chain (1); Modified residue (4);
 Sequence conflict (4)','SUBUNIT: Component of a phosphatidylinositol 4-kinase (PI4K) complex,
 composed of PI4KA, EFR3 (EFR3A or EFR3B), TTC7 (TTC7A or TTC7B) and HYCC (HYCC1 or HYCC2).
 {ECO:0000250|UniProtKB:Q14156}.'','TISSUE SPECIFICITY: Widely expressed (PubMed:25380825).
 Expressed in neurons of the superior olivary complex of the auditory brainstem. Also expressed at
 lower levels in the cochlear nucleus, the lateral lemniscal nuclei and the inferior colliculus
 (PubMed:15363888). {ECO:0000269|PubMed:15363888,
 ECO:0000269|PubMed:25380825}.'','SUBCELLULAR LOCATION: Cell membrane

{ECO:0000269|PubMed:15363888}; Lipid-anchor {ECO:0000250|UniProtKB:Q14156}. Cytoplasm, cytosol {ECO:0000250|UniProtKB:Q14156}. Note=Palmitoylation anchors the protein to the plasma membrane. A small amount is observed in the cytosol. {ECO:0000250|UniProtKB:Q14156}.';MOD_RES 360; /note="Phosphoserine"; /evidence="ECO:0007744|PubMed:21183079"; MOD_RES 363; /note="Phosphoserine"; /evidence="ECO:0007744|PubMed:21183079"; MOD_RES 420; /note="Phosphoserine"; /evidence="ECO:0000250|UniProtKB:Q14156"; MOD_RES 692; /note="Phosphoserine"; /evidence="ECO:0007744|PubMed:19144319"; PTM: Palmitoylated at its N-terminus, anchoring the protein to the plasma membrane. {ECO:0000250|UniProtKB:Q14156}.';Atg16l1'),('2','ENSMUSG00000017548','Q80U70','Suz12','protein_coding','Polycomb protein

Suz12','UPI00001B2F55','NP_001156490.1;NP_954666.1;','','206694;','10090.ENSMUSP0000001769 2;','GO:0000122; GO:0000978; GO:0001222; GO:0001739; GO:0003682; GO:0003723; GO:0005634; GO:0005654; GO:0005677; GO:0005730; GO:0006325; GO:0008047; GO:0008283; GO:0008284; GO:0009048; GO:0016586; GO:0016604; GO:0021510; GO:0031490; GO:0032526; GO:0032682; GO:0032993; GO:0035064; GO:0035098; GO:0042054; GO:0042532; GO:0043565; GO:0045596; GO:0046872; GO:0048709; GO:0050680; GO:0098532; GO:0106222; GO:0140718; GO:1990841; GO:1990904','chromatin silencing complex [GO:0005677]; ESC/E(Z) complex [GO:0035098]; nuclear body [GO:0016604]; nucleolus [GO:0005730]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; protein-DNA complex [GO:0032993]; ribonucleoprotein complex [GO:1990904]; RSC-type complex [GO:0016586]; sex chromatin [GO:0001739]; chromatin binding [GO:0003682]; chromatin DNA binding [GO:0031490]; enzyme activator activity [GO:0008047]; histone methyltransferase activity [GO:0042054]; lncRNA binding [GO:0106222]; metal ion binding [GO:0046872]; methylated histone binding [GO:0035064]; promoter-specific chromatin binding [GO:1990841]; RNA binding [GO:0003723]; RNA polymerase II cis-regulatory region sequence-specific DNA binding [GO:0000978]; sequence-specific DNA binding [GO:0043565]; transcription corepressor binding [GO:0001222]; cell population proliferation [GO:0008283]; chromatin organization [GO:0006325]; dosage compensation by inactivation of X chromosome [GO:0009048]; facultative heterochromatin formation [GO:0140718]; histone H3-K27 trimethylation [GO:0098532]; negative regulation of cell differentiation [GO:0045596]; negative regulation of chemokine production [GO:0032682]; negative regulation of epithelial cell proliferation [GO:0050680]; negative regulation of transcription by RNA polymerase II [GO:0000122]; negative regulation of tyrosine phosphorylation of STAT protein [GO:0042532]; oligodendrocyte differentiation [GO:0048709]; positive regulation of cell population proliferation [GO:0008284]; response to retinoic acid [GO:0032526]; spinal cord development [GO:0021510]','Gene','SUZ12 polycomb repressive complex 2 subunit [Source:MGI Symbol;Acc:MGI:1261758]','Mus musculus',10090,'CCGAAGCGGAGCGGGGCTCGGAGGAGACACTTTTTTTTTTCTCCCTCCTTCCCTCCTCTCTCCTCCCTTCCCTTCCCCCTCTCCTCCCCTCTCCTCCTTCCCCCTCGGTCCGCTGGAGCCTGCTGGGGCGAG CGGTTGGTGTAGCAGGCGCGCTCACTCTCCGGGGCCGCCCGCGGGTAGCTGGCGGGGGGAGGAGGCAGGA ACCGCGATGGCGCCTCAGAAGCACGGCGGTGGGGGAGGGGGCGGCTCGGGGCCAGCGCGGGGTCCGGGG GAGGCGGCTTCGGGGGTTGCGCGGCGGCGGTGGCGGCGGCGGCTTCGGGCGGCAAATCCGCGGCGGGGG CTGTGGAGGCGGCGGCAGTTACTCGGCCTCCTCCTCCTCGGCGGCGGCCGCGGCGGCGGCGGGGGCCGC GGTGTTGCCGTGAAGAAGCCGAAAATGGAGCACGTCCAGGCTGACCACGAGCTTTTCTCCAGGCCTTTGAG AGTGAGTGTGAGCGGCTTCGAGGGCAGGGGTGCCCTCTCCGGCGTTTCGGGGCACGGGGCACTCCGCCGGGT TCTCGGAGAGTCCACTTGCTTTGGGAGTGAGGGAGGACTCGCTGGGGAACGCCGGGGTCCCGAGCAGGTCC TGACTCCCGGAAGGGTCGCCCCGGGGCCCCAGGTTTCAGAGCAGCCTTGAGAGTGGGGACGTGACGGTTGA ACTGAGCGCATATAGATCCCAGACGAGTTGGTGTTCGTTTGTGTCTTCCTTACTCCACAAGTACAGGGATTAT AGTTGTAGGTTTCGGGGGGACGAGACACAGCCTGTCCGAGATGAGTGTGTAAAGCCGAGGAAATTGTCATG GGTCTGAAATGCGTTCGTACCACTCTGGCTGCGTGTGAGTGAACACGCAGCATTTGAAACCTTTTAAGCTTTTC AAACCTTTCCGCCCATTTTATGGGTGCGTAGACTGAGAGAGACAGAATGGGGCAAGCGTCCTCTCCGTGGACAA

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53

(VRN2-EMF2-FIS2-SU(Z)12)

family', 'MAPQKHGGGGGGSGPSAGSGGGGFGGSAAVAAAASGGKSGGGGCGGGGSYSASSSSAAAAA
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 LREMQQKLEKGESATPSNEEIAEEQNGTANGFSETNSKEKALETGVSQVQKQSKQKL', '741', '83026', 'FUNCTION:
 Polycomb group (PcG) protein. Component of the PRC2/EED-EZH2 complex, which methylates
 'Lys-9' (H3K9me) and 'Lys-27' (H3K27me) of histone H3, leading to transcriptional repression of the
 affected target gene. The PRC2/EED-EZH2 complex may also serve as a recruiting platform for DNA
 methyltransferases, thereby linking two epigenetic repression systems (By similarity). Genes repressed
 by the PRC2/EED-EZH2 complex include HOXA7, HOXB6 and HOXC8.
 {ECO:0000250|UniProtKB:Q15022, ECO:0000269|PubMed:15385962,
 ECO:0000269|PubMed:15516932, ECO:0000269|PubMed:17339329}.', 'Chain (1); Compositional bias
 (1); Cross-link (6); Modified residue (4); Region (5); Zinc finger (1)', 'SUBUNIT: Component of the PRC2
 complex, which consists of the core subunits EED, EZH1 or EZH2, SUZ12, and RBBP4, and various
 combinations of accessory subunits including AEBP2, JARID2, PHF19, MTF2 and EPOP
 (PubMed:19026780, PubMed:20144788). Within the complex, interacts (via C2H2 zinc finger domain)
 with JARID2 and EPOP; JARID2 and EPOP compete for SUZ12 binding (By similarity). Also interacts with
 AEBP2 and PHF19 (By similarity). Forms a monomeric PRC2.2 (class 2) complex consisting of at least
 SUZ12, RBBP4, AEBP2 and JARID2 (By similarity). Forms a dimeric PRC2.1 (class 1, PRC-PCL) complex
 consisting of at least SUZ12, RBBP4, and PHF19 or MTF2; PHF19 and MTF2 stabilize the dimeric
 structure which enhances PRC2 interaction with chromatin (By similarity). The minimum components
 required for methyltransferase activity of the PRC2/EZH2 complex are EED, EZH2 and SUZ12 (By
 similarity). The PRC2 complex may also interact with DNMT1, DNMT3A, DNMT3B and PHF1 via the
 EZH2 subunit and with SIRT1 via the SUZ12 subunit. Interacts with WDR77 (PubMed:16712789).
 Interacts with histone H1. Interacts with CDYL (By similarity). Interacts with BMAL1
 (PubMed:23970558). Interacts with EZHIP (via C-terminal region) (By similarity). Interacts with
 ARMC12 (By similarity). {ECO:0000250|UniProtKB:Q15022, ECO:0000269|PubMed:16712789,
 ECO:0000269|PubMed:19026780, ECO:0000269|PubMed:20144788,
 ECO:0000269|PubMed:23970558}.', 'DEVELOPMENTAL STAGE: Expression increases in prostate during
 prostate tumor development. {ECO:0000269|PubMed:15684044}.', 'TISSUE SPECIFICITY: Expressed in
 embryonic stem cells. {ECO:0000269|PubMed:22226355}.', 'SUBCELLULAR LOCATION: Nucleus
 {ECO:0000269|PubMed:16415857}. Chromosome {ECO:0000269|PubMed:16415857}.
 Note=Localizes to the inactive X chromosome in trophoblast stem cells.', 'MOD_RES 20;
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 /note="Phosphoserine"; /evidence="ECO:0007744|PubMed:21183079"; MOD_RES 585;
 /note="Phosphoserine"; /evidence="ECO:0007744|PubMed:21183079"; PTM: Sumoylated,
 probably by PIAS2.
 {ECO:0000250|UniProtKB:Q15022}.', 'Ezh2, Eed, Jarid2, Suz12, Kdm5a, Ezh1, Mtf2, Htt, Phf19, Foxp3, E130
 012A19Rik, Asxl2, Brca1, Elf5, Ehmt2, A430105I19Rik, Gdap1, Pcnt, AU022751'), ('3', 'ENSMUSG000000323
 33', 'A0A0B4J1F1', 'Stoml1', 'protein_coding', 'Stomatin-like
 1', 'UPI00000E8CB9', 'NP_081218.3;', '213233;', '10090.ENSUSMUSP00000034883;', 'GO:0005886;

GO:0006869; GO:0008200; GO:0031410; GO:0031902; GO:0045121; GO:0060395; GO:1901586; GO:1990830', 'cytoplasmic vesicle [GO:0031410]; late endosome membrane [GO:0031902]; membrane raft [GO:0045121]; plasma membrane [GO:0005886]; ion channel inhibitor activity [GO:0008200]; cellular response to leukemia inhibitory factor [GO:1990830]; lipid transport [GO:0006869]; negative regulation of acid-sensing ion channel activity [GO:1901586]; SMAD protein signal transduction [GO:0060395]', 'Gene', 'stomatin-like 1 [Source:MGI Symbol;Acc:MGI:1916356]', 'Mus musculus', 10090, 'GGAGTAAAGCCGGAAGCAGTGGGAACGAGGAGGGGCGGAGCTGCCACAGGCTGGGCA GGGCAGTCTCCCAGCAGAGGATCGGGGCGTGTCCCGGTTAGAAGTCATGCTTGAAGGTCTGGCTACCGGGCA CTGCCCTTAGGGGATTTTATCGTTTCCAGCAGTCGAGCTTCGGCTTTCTGGGTTCGCAGAAGGGCTGCTTGTC CCCAGAGCCGGGCGAGCGTGGGGCCGGGGCCGGTGAGTGCTACCCAGCACCGCGGACAGAGGGGCACCCC AAGACCTGTACTCTCTGCCTCTAGGAGGAAGGAGAGTGAAGGGGATAGGATATGAAGTGGGTGCCAGACAAG GTGTGGGGATGCTACCACCGATTTGTTCTCCCTACGGCACCGAGCTGTAGCTTTGGAAGCCGCGCAGCCCCATCTT CCCTAATCTTAGCCCATCCCGTTACTATTTCCAGGATAGCCCATCATGCATAGAAAAGAAAACAGAGCCCTAGGCGAG GGGAGCCATAACCCACAAGGCATTTGTAGAGAAATGAAAAAGAGTCGCCCTAGGGTAGCAGCGCAGGGAG CAGGAGTCTCCTGTGTCTGGTGAAGATGCACAGAACAGAAAGCTGGGCCTGCAAGCTGCCTGGCTTGTTGC TTTGGCTTCTCTCTCAAAGCCTGACTGTCCTTGGAGTATTCTGGTCTCTGTGGTTCTCTGTATTGACGGTGC ATTGAAAGCTTTGGCAATGCTGAACGAATCCTCCATTTCTGCCCGTTCTTTTTTGTGTTGTTGTTGTTTGTGTTGT TTGTGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGACAGGGTTTCTCTGTATAGCCCTGGCTCTCCTGGA ACTCACTTTGTAGACCAGGCTGGCCTTGAAGTCAAGAAATCTGCCTGCCTCTGCCTCCCAAGTGCTGCGATTAAAA GCGTGCACCACCACGCCCCGGCTCTTCTGCCCGGTTCTTAGGATTCTCCTTCCCTGAAGAGGTGAGGAATTAGTT TATGACTTAGACTGTCCTGCAGGCAGGGGCTTCTTGAAGGATAGAACAGACGTCTCTTGTACCTTCTGTCTAG GGCTGGGGAGGAGAGAACAGATAGCAAGCTCATCCCCAGATTCTGGGCCTGTTTGTCAACACCCATTGAGGAT TCTTAGTTCTTCTGCCAAAAGGCTTGAATTGAAGTACACTATAGATATAGATAGATAGATAGATAGATAGATATA GATATAGATATAGTTCTTTAGGGCATTAAAGTGGGAATAAACTAACTAGCACTTTAGTCCCACTGTGACTGTT ACTTGTGAGCATTAGTTTTATCCTTAGTAGCTGAAGCCTTCTCTGTAATGACCCCTTGAAGCATACTTGTGGT GTGGCCAGTAGAATGTGTTAACACCAGCAGTGTCCACTCCACCCAGCATGAGTGCTCTTATTCCAGGTTTGGGT GGGCGGTACTCATTAGGCAAGGGCTTGTGGTCCATGCTATGTCCAGCAATGAGAAATCGAATGGATCATGTTCT CAGATTCTGTGGCTCTCACCTGGGAGAGAAAAGTCTCCTGTAGGGTGTGTACCGGTTAGTTATGGTGGAGGTC CCTAACTCGCTATGGGGAGCTTTTGGGGCAGAACACAGGCCAAAACATACACATGGCCCACTGTACTCTGGGACA CGGTGCCTGAAATTGTCTGCCAGGCCAGCTGGTGTCTGTGGTTGCTTCTGCTCTTTTGGCCCCAGACGCGCC GGAGAGCTGGCCCTCCTGTCTCTGCCATGGCCTCGTCAGTGTCTGGGGTTCTTGCTGCTGCTGCTCACCTTCCC CATTTCCGGCTGTTTGTCTGAAGGTAGGGCTGGCTGGATGCTGTGGGGGAGTGGGGAGGCACAACGAAGG TGTTGATGAGTGGATTCCCCGATTTTGGCCTCTAACTGCTATCACACCTCTAGGAAATAGGTAAGGCAAGGGTTG TTCATTTTATAATGGCTCATCCTGGTTGTCAACTTGACATGCCTGTGAAGAGGGAACTTCAACTAAGGGATTGCTC AGTCTGTGGCCACGTCTTTGGGGGCATTTTGATTGCTTGATTAGTGTAGGAGGGCCTACCCCTACCCCTGTGG TGCAGAGAGTTGGGCCTGAGCTAGCTGAGCAAATGCACAGATGGTGCAGGTGAGGTGGGGGGGGGGGGGAT GGGGGAGGTGGGGGGTGGTGGCAATCATCCTTCTGTGGTCTCTGCTTCACTTCTGCCCCAGTTTCTGTCT TGAGTTTCTGCTTTAGTTTCTCCCTCAGTGATAGTCTGTAACCTAGATGCCAATAAACTCTTTTCTCCCCAGGTT TCTTTTGATCATGATGTTTCTCCAGTAACATGAGAACTAGGGCAGTTCCCATCCTTCAATGGATAAACTGAAG CCCAGACTGAACCAACGGCATCTCGGGAGCCAGGAAGGAGCAGAAATTGTTTTCTAGGTCCTGGAATCTGGAC ATATATATTCCTTTGCAAATCATCCTCCCTTTGGCTCAGATCCAATCAAAGAAAAGCACCCAGCATACCCAGCA AGCATGGAATAATGAACTCAGGTCTTGCTTTGCATAACGGTTGCTTAATAGGTAAGGGTGAAAGATACAGATGT AGTTGAACAACACATCTGACTGCTTCAGGGTAGGTGAAGCCCAAGCAGGCTTTCCCTTTGCATAGCCCTAGGC AGTGAAGTCCCTAGAAAGCCTCTGTGTTTGTGAGTCTAGAAAGGAGCGCTGAGGTGAAGCCAGGTCTACCTC TACAGTGCCACTGAAGCAAATGTCCTGTAACCAGGGATGTGAGACCTGGCCCTCTTATCAAAGCGATCCAGGG ATCTGATAGTAGTGAACCTCAGGGCATTCTTAGAGCAGCCTAGCCTTTTCTCAGCCAATCCAAGAGCAAACA GTTCTGTTGAATGAGTCATGTGTAGCTTCAGGCCCCAGAGGTGAAGTTTCCCTGATCAAGTCAGTACTTGTGGG

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[illegible]

Modified residue (1); Motif (1); Sequence conflict (3); Topological domain (1); Transmembrane (1)'; SUBUNIT: Interacts with STOM; may redistribute STOM from the plasma membrane to late endosomes. {ECO:0000250|UniProtKB:Q9UBI4}.'; TISSUE SPECIFICITY: Expressed in dorsal root ganglion neurons. {ECO:0000269|PubMed:24247984}.'; SUBCELLULAR LOCATION: Membrane {ECO:0000305}; Single-pass type III membrane protein {ECO:0000305}. Cytoplasmic vesicle {ECO:0000269|PubMed:24247984}. Cell membrane {ECO:0000269|PubMed:24247984}; Single-pass type III membrane protein {ECO:0000305}. Late endosome membrane {ECO:0000250|UniProtKB:Q9UBI4}. Membrane raft {ECO:0000250|UniProtKB:Q9UBI4}.'; MOD_RES 28; /note="\Phosphoserine\"; /evidence="\ECO:0000250|UniProtKB:Q9UBI4\";\", 'Asic1,Asic3\";\", '4\";\", 'ENSMUSG00000036202\";\", 'Q6PR54\";\", 'Rif1\";\", 'protein_coding\";\", 'Telomere-associated protein RIF1\";\", 'UPI000053E885\";\", 'NP_780447.4 [Q6PR54-3]; XP_006498240.1; XP_011237438.1 [Q6PR54-2];\", '206234\";\", '10090.ENSMUSP00000108313\";\", 'GO:0000122; GO:0000723; GO:0000781; GO:0000785; GO:0000793; GO:0001939; GO:0001940; GO:0005634; GO:0005654; GO:0005737; GO:0005886; GO:0006281; GO:0006974; GO:0007049; GO:0031509; GO:0031965; GO:0035019; GO:0035861; GO:0043247; GO:0045814; GO:0045830; GO:0051233; GO:0051574; GO:0140445; GO:1990830; GO:2000042; GO:2001034\";\", 'chromatin [GO:0000785]; chromosome, telomeric region [GO:0000781]; chromosome, telomeric repeat region [GO:0140445]; condensed chromosome [GO:0000793]; cytoplasm [GO:0005737]; female pronucleus [GO:0001939]; male pronucleus [GO:0001940]; nuclear membrane [GO:0031965]; nucleoplasm [GO:0005654]; nucleus [GO:0005634]; plasma membrane [GO:0005886]; site of double-strand break [GO:0035861]; spindle midzone [GO:0051233]; cell cycle [GO:0007049]; cellular response to leukemia inhibitory factor [GO:1990830]; DNA damage response [GO:0006974]; DNA repair [GO:0006281]; negative regulation of double-strand break repair via homologous recombination [GO:2000042]; negative regulation of gene expression, epigenetic [GO:0045814]; negative regulation of transcription by RNA polymerase II [GO:0000122]; positive regulation of double-strand break repair via nonhomologous end joining [GO:2001034]; positive regulation of histone H3-K9 methylation [GO:0051574]; positive regulation of isotype switching [GO:0045830]; somatic stem cell population maintenance [GO:0035019]; subtelomeric heterochromatin formation [GO:0031509]; telomere maintenance [GO:0000723]; telomere maintenance in response to DNA damage [GO:0043247]\";\", 'Gene\";\", 'replication timing regulatory factor 1 [Source:MGI Symbol;Acc:MGI:1098622]\";\", 'Mus musculus\";\", '10090\";\", 'CCGCCATCTTGGTCGTGGAGGAGCGGGCTGCACGCGTGAGTAAATAAGCGCGAGCCGGGAGCGGACGGCGGGCCCCGGGGCGGCGAGCTGCGGAGCGGACTTCCCGCGTGGGGGGTGAGGAGCGGGAGGCTCGGCTCGGCCCGGCCGGCGCCGCTCTGCCCCCTCGCGGCCGTGCTGCCTGGGAAGCGGCGGCGGGAGCCGGGCAGGCGGGAGGCCGGCCTGCGAGCGCGGCCCGGCGTGCAGGTGAGGGCGCCGCGCGGGCCGTGCCACCGTTACTGGGTGTCTTCCGGCCTCGCTGCAGGGTGGCGGCCGACATGACGGCCCCAGGTCGCAGCCCCCTGGAGCCGCTTCTGGAGACTTGGGAAGACCCCTCGGTGCCTCCGGGAGAGCAGACGGACGCCTACCTAACTCTGACCAGGTGAGGCGGGCCGGGGGACGAGCCCGGGGCGGGAGCCGGGGCAGCCGTGGGGACCCGGCGGACGCGGGTAGTTCGGGGTGACCGGGGCCATTGCCTGCCGAGTGACGTTGCGGGGCGCAGCGGCGGCGTCCGAGGGCTTCTCGGGGACGAGCGGTTCTGTATTTTTTGTCTGGCCCGCAGACGGGAAAGCCTTTAAAGAAAAGTTTGGAGTCGAGAGGCGTTTGGAGAGCAGGGCTTTGCCCTGCGAACCTCGGACGCCGTGGGAAAGTTGGCGATCCGGAGTTAGTGGGTTTAGTTAGGGTCTTTGGCTCAGGCTCGCTCCAGTGCTCATCCCCGACCCGGCCTCGAAC TTGTGGTTCTGCCGGAGTGTTGAGATTACAGGTGCGCGAGTCAGCAAACCGGCCCCAGAATTGGCTTAAAAA AAAAAAAAAAAAAAGCAGAGCCAGGAACCCGTTTTGACTTATTTGAAAGGCTTTAGAAAAATTTCTGAATTTT GTTAAACTTTCTGATTTTCTGAGTTAGAAAACATGATTAGGGAAAGGGATTCCCACTTTCTTTTCTCATGTAAAAA TTACAAAAAAGAAAAAGAAAAATACGTTTTTCGAGGCCAAAAAGCTTTGAGGCAAGTTACCGCTTATATGTGGT CTAACCTAAACATTTTTTCTCTATACCTTTAAACTTTTTAAAGAAAGAGGTTAATTCCAAGGGCTTGAAAGTCGT CTTTAAAACTTAAACAAAAAGCCAGTTACGAGTTAGAGTGCCTGCGGCTCCAGGTGTTGGATGGCTCTGGAA

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[illegible]

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LALQLDSEDLYSYTGSQLFEMHEKLGTMANSIIRNLQSRWRSPA HENS','2419','266228','FUNCTION: Key
regulator of TP53BP1 that plays a key role in the repair of double-strand DNA breaks (DSBs) in response
to DNA damage: acts by promoting non-homologous end joining (NHEJ)-mediated repair of DSBs
(PubMed:23333305, PubMed:23306437, PubMed:23306439). In response to DNA damage, interacts

with ATM-phosphorylated TP53BP1 (PubMed:23333305, PubMed:23306437, PubMed:23306439). Interaction with TP53BP1 leads to dissociate the interaction between NUDT16L1/TIRR and TP53BP1, thereby unmasking the tandem Tudor-like domain of TP53BP1 and allowing recruitment to DNA DSBs (By similarity). Once recruited to DSBs, RIF1 and TP53BP1 act by promoting NHEJ-mediated repair of DSBs (PubMed:23333305, PubMed:23306437). In the same time, RIF1 and TP53BP1 specifically counteract the function of BRCA1 by blocking DSBs resection via homologous recombination (HR) during G1 phase (PubMed:23333305, PubMed:23306437). Also required for immunoglobulin class-switch recombination (CSR) during antibody genesis, a process that involves the generation of DNA DSBs (PubMed:23333305, PubMed:23333306, PubMed:23306439). Promotes NHEJ of dysfunctional telomeres (PubMed:23333305). {ECO:0000250|UniProtKB:Q5UIP0, ECO:0000269|PubMed:23306437, ECO:0000269|PubMed:23306439, ECO:0000269|PubMed:23333305, ECO:0000269|PubMed:23333306}.'Alternative sequence (2); Chain (1); Compositional bias (9); Modified residue (38); Region (10); Sequence conflict (26)'.SUBUNIT: Interacts with TP53BP1 (when phosphorylated by ATM) (PubMed:23333305, PubMed:23306437, PubMed:23306439). May interact with TRF2 (PubMed:15042697). Interacts with SHLD2 (By similarity). Interacts with ERCC6 (via WHD region) (By similarity). {ECO:0000250|UniProtKB:Q5UIP0, ECO:0000269|PubMed:23306437, ECO:0000269|PubMed:23306439, ECO:0000269|PubMed:23333305, ECO:0000305|PubMed:15042697}.'DEVELOPMENTAL STAGE: Found in the nucleus of germinal-vesicle (GV) stage oocytes prior to fertilization. Accumulates in the male and female pronucleus after fertilization. Expressed in the nuclei of all blastomeres from the two cell stage to the compacted morula stage, although absent from the polar body and inner cell mass (ICM). Found in the nuclei of polar and mural trophectoderm cells from 3.5 dpc, and at high levels in the epiblast from 5.5 dpc to 7.5 dpc. Expressed by primitive germ cells (PGCs) in both male and female from 9.5 dpc to 13.5 dpc, at which point expression declines. A low level is observed in Sertoli cells of the testis at 17.5 dpc. {ECO:0000269|PubMed:15042697}.'TISSUE SPECIFICITY: Expressed in Sertoli cells, prospermatogonia, early primary spermatocytes, and in oocytes at all stages of their growth. Expressed in embryonic stem (ES) and embryonic germ (EG) cells: expression is lost upon differentiation. {ECO:0000269|PubMed:15042697}.'SUBCELLULAR LOCATION: Nucleus {ECO:0000269|PubMed:15042697}. Chromosome {ECO:0000269|PubMed:23306437, ECO:0000269|PubMed:23306439, ECO:0000269|PubMed:23333305}. Chromosome, telomere {ECO:0000269|PubMed:15042697}. Cytoplasm, cytoskeleton, spindle {ECO:0000250|UniProtKB:Q5UIP0}. Note=Exhibits ATM- and TP53BP1-dependent localization to uncapped or aberrant telomeres and to DNA double strand breaks (DSBs). Following interaction with TP53BP1, recruited to sites of DNA damage, such as DSBs (PubMed:23333305, PubMed:23306437, PubMed:23306439). Localizes to microtubules of the midzone of the mitotic spindle during anaphase, and to condensed chromosomes in telophase (By similarity). While the majority of the protein appears nuclear and distinct from normal telomere structures, a small fraction may bind to telomeres in embryonic stem cells (PubMed:15042697). {ECO:0000250|UniProtKB:Q5UIP0, ECO:0000269|PubMed:15042697, ECO:0000269|PubMed:23306437, ECO:0000269|PubMed:23333305}.'MOD_RES 385; /note="Phosphoserine"; /evidence="ECO:0007744|PubMed:21183079"; MOD_RES 391; /note="Phosphoserine"; /evidence="ECO:0007744|PubMed:21183079"; MOD_RES 779; /note="Phosphoserine"; /evidence="ECO:0000250|UniProtKB:Q5UIP0"; MOD_RES 976; /note="Phosphoserine"; /evidence="ECO:0000250|UniProtKB:Q5UIP0"; MOD_RES 1005; /note="Phosphoserine"; /evidence="ECO:0000250|UniProtKB:Q5UIP0"; MOD_RES 1044; /note="Phosphothreonine"; /evidence="ECO:0000250|UniProtKB:Q5UIP0"; MOD_RES 1215; /note="Phosphothreonine"; /evidence="ECO:0000250|UniProtKB:Q5UIP0"; MOD_RES 1231; /note="Phosphoserine"; /evidence="ECO:0000250|UniProtKB:Q5UIP0"; MOD_RES 1233;

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splicing,Chromatin regulator,DNA-binding,Neurogenesis,Nucleus,Reference
proteome,Transcription,Transcription regulation','High motility group (HMG) box
superfamily','MDVRFYPPPAQPAAPCLGPSPCLDPYYCNKFDGENMYMSMTEPSQDYVPASQSYPGPSLES
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SGGMQRDKALYLT','526','57203','FUNCTION: Transcriptional regulator with a major role in neural stem
cell commitment and corticogenesis as well as in lymphoid cell development and lymphoid tissue
organogenesis (PubMed:25527292, PubMed:20818394, PubMed:11850626, PubMed:18195075,
PubMed:15078895, PubMed:25915732). Binds to GC-rich DNA sequences in the proximity of
transcription start sites and may alter chromatin structure, modifying access of transcription factors to
DNA (PubMed:25527292, PubMed:31207603, PubMed:31207604). During cortical development,
controls the neural stem cell pool by inhibiting the switch from proliferative to differentiating
progenitors. Beyond progenitor cells, promotes neurite outgrowth in newborn neurons migrating to
reach the cortical plate. May activate or repress critical genes for neural stem cell fate such as SOX2,
EOMES and ROBO2 (PubMed:25527292). Plays an essential role in the development of lymphoid
tissue-inducer (LTi) cells, a subset necessary for the formation of secondary lymphoid organs:
peripheral lymph nodes and Peyer's patches (PubMed:20818394). Acts as a developmental
checkpoint and regulates thymocyte positive selection toward T cell lineage commitment
(PubMed:11850626, PubMed:18195075). Required for the development of various T cell subsets,
including CD4-positive helper T cells, CD8-positive cytotoxic T cells, regulatory T cells and CD1D-
dependent natural killer T (NKT) cells (PubMed:18195075, PubMed:15078895). Required for the
differentiation of common lymphoid progenitors (CMP) to innate lymphoid cells (ILC). May regulate
the NOTCH-mediated gene program, promoting differentiation of the ILC lineage (PubMed:25915732).
Required at the progenitor phase of NK cell development in the bone marrow to specify NK cell lineage
commitment (PubMed:20818394). Upon chronic antigen stimulation, diverts T cell development by
promoting the generation of exhaustive T cells, while suppressing effector and memory T cell
programming. May regulate the expression of genes encoding inhibitory receptors such as PDCD1 and
induce the exhaustion program, to prevent the overstimulation of T cells and activation-induced cell
death (PubMed:31207603, PubMed:31207604). {ECO:0000269|PubMed:11850626,
ECO:0000269|PubMed:15078895, ECO:0000269|PubMed:18195075,
ECO:0000269|PubMed:20818394, ECO:0000269|PubMed:25527292,
ECO:0000269|PubMed:25915732, ECO:0000269|PubMed:31207603,
ECO:0000269|PubMed:31207604}.'Alternative sequence (2); Chain (1); Compositional bias (2); DNA
binding (1); Helix (4); Motif (1); Region (1); Sequence conflict (2)','SUBUNIT: Interacts with HBO1
complex composed at least of KAT7/HBO1, ING4, MEAF6, and JADE2; this complex is involved in
histone acetylation. Interacts with DNMT1, LEO1, PAF1, SAP130 and SIN3A; these interactors regulate
chromatin remodeling. Interacts with an array of proteins involved in RNA processing and translation
and DNA replication. {ECO:0000269|PubMed:31207603}.'DEVELOPMENTAL STAGE: In the developing
brain, expressed at embryonic day 9.5 dpc in neuroepithelium, displaying a rostral-high/ caudal-low
and lateral-high/medial-low expression pattern. Abundant at 15.5 dpc in progenitors of the ventricular
zone and differentiated neurons in the cortical plate. The lateral-medial gradient spread further in all

cells of the ventricular zone of the lateral cortex by 18.5 dpc (at protein level). {ECO:0000269|PubMed:25527292}.','TISSUE SPECIFICITY: Expressed in neurons of the subventricular zone (at protein level) (PubMed:25527292). Expressed in distinct subpopulations of thymocytes undergoing positive selection: double CD4-positive CD8-positive (DP) cells, CD4-positive CD8-low transitional cells and in single CD4-positive and CD8-positive cells (at protein level) (PubMed:11850626, PubMed:15078895). Expressed in ILC progenitors and mature ILC subsets: ILC1, ILC2 and ILC3 (at protein level) (PubMed:25915732). Expressed in lymphoid tissue-inducer cells and bone marrow NK cell subsets (PubMed:20818394). Abundant in thymus, liver and brain. Also detected in small intestine, spleen, stomach and testis (PubMed:11850626). Highly expressed in tumor-infiltrating CD8-positive T cells (at protein level) (PubMed:31207604). {ECO:0000269|PubMed:11850626, ECO:0000269|PubMed:15078895, ECO:0000269|PubMed:20818394, ECO:0000269|PubMed:25527292, ECO:0000269|PubMed:25915732, ECO:0000269|PubMed:31207604}.','SUBCELLULAR LOCATION: Nucleus {ECO:0000255|PROSITE-ProRule:PRU00267, ECO:0000269|PubMed:11850626}.'','',Atxn1'),('6','ENSMUSG00000050953','P23242','Gja1','protein _coding','Gap junction alpha-1 protein','UPI00000018B0','NP_034418.1','',',',A0A654ICD2','GO:0001937; GO:0002544; GO:0002931; GO:0003104; GO:0003158; GO:0005243; GO:0005741; GO:0005769; GO:0005771; GO:0005783; GO:0005794; GO:0005916; GO:0005922; GO:0007204; GO:0007267; GO:0007283; GO:0007507; GO:0009268; GO:0009749; GO:0010232; GO:0010649; GO:0010652; GO:0015867; GO:0017124; GO:0022898; GO:0030165; GO:0030308; GO:0032024; GO:0032355; GO:0032496; GO:0032526; GO:0034405; GO:0035437; GO:0042311; GO:0042981; GO:0043434; GO:0045121; GO:0045732; GO:0045836; GO:0045907; GO:0046697; GO:0048812; GO:0051924; GO:0060044; GO:0071253; GO:0071260; GO:0071374; GO:0097718; GO:0110053; GO:1904446; GO:1905867; GO:2000279; GO:2000810; GO:2000987','connexin complex [GO:0005922]; early endosome [GO:0005769]; endoplasmic reticulum [GO:0005783]; fascia adherens [GO:0005916]; Golgi apparatus [GO:0005794]; membrane raft [GO:0045121]; mitochondrial outer membrane [GO:0005741]; multivesicular body [GO:0005771]; connexin binding [GO:0071253]; disordered domain specific binding [GO:0097718]; gap junction channel activity [GO:0005243]; PDZ domain binding [GO:0030165]; SH3 domain binding [GO:0017124]; ATP transport [GO:0015867]; cell-cell signaling [GO:0007267]; cellular response to mechanical stimulus [GO:0071260]; cellular response to parathyroid hormone stimulus [GO:0071374]; chronic inflammatory response [GO:0002544]; decidualization [GO:0046697]; endothelium development [GO:0003158]; epididymis development [GO:1905867]; heart development [GO:0007507]; maintenance of protein localization in endoplasmic reticulum [GO:0035437]; negative regulation of cardiac muscle cell proliferation [GO:0060044]; negative regulation of cell growth [GO:0030308]; negative regulation of DNA biosynthetic process [GO:2000279]; negative regulation of endothelial cell proliferation [GO:0001937]; neuron projection morphogenesis [GO:0048812]; positive regulation of behavioral fear response [GO:2000987]; positive regulation of cell communication by chemical coupling [GO:0010652]; positive regulation of cytosolic calcium ion concentration [GO:0007204]; positive regulation of establishment of Sertoli cell barrier [GO:1904446]; positive regulation of glomerular filtration [GO:0003104]; positive regulation of insulin secretion [GO:0032024]; positive regulation of meiotic nuclear division [GO:0045836]; positive regulation of protein catabolic process [GO:0045732]; positive regulation of vasoconstriction [GO:0045907]; regulation of actin filament organization [GO:0110053]; regulation of apoptotic process [GO:0042981]; regulation of bicellular tight junction assembly [GO:2000810]; regulation of calcium ion transport [GO:0051924]; regulation of cell communication by electrical coupling [GO:0010649]; regulation of transmembrane transporter activity [GO:0022898]; response to estradiol [GO:0032355]; response to fluid shear stress [GO:0034405]; response to glucose [GO:0009749]; response to ischemia [GO:0002931]; response to

[illegible]

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membrane,Disulfide bond,Endoplasmic reticulum,Gap junction,Isopeptide
bond,Membrane,Phosphoprotein,Reference proteome,S-
nitrosylation,Transmembrane,Transmembrane helix,Ubl conjugation','Connexin family, Alpha-type
(group II)
subfamily','MGDWSALGKLLDKVQAYSTAGGKVWLSVLFIIRILLGTAVESAWGDEQSAFRCNTQQPGCENVCYD
KSPFISHVRFWVLQIIFVSVPTLLYLAHVYVMRKEEKLNKKEEELKVAQTDGVNVEMHLKQIEIKFKYGIEEHGKVK
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QNWANYSAEQNRMGOAGSTISNSHAQPFDFPDDSQNAKKVAAGHELQPLAIVDQRPSSRASSRASSRPRPDDLE
I','382','43004','FUNCTION: One gap junction consists of a cluster of closely packed pairs of
transmembrane channels, the connexons, through which materials of low MW diffuse from one cell
to a neighboring cell. {ECO:0000256|RuleBase:RU000630}.'','Compositional bias (1); Domain (2);
Region (1); Transmembrane (4)','SUBUNIT: A connexon is composed of a hexamer of connexins.
{ECO:0000256|RuleBase:RU000630}.'','SUBCELLULAR LOCATION: Cell junction, gap junction
{ECO:0000256|ARBA:ARBA00004610}. Cell membrane {ECO:0000256|ARBA:ARBA00004651,
ECO:0000256|RuleBase:RU000630}; Multi-pass membrane protein
{ECO:0000256|ARBA:ARBA00004651, ECO:0000256|RuleBase:RU000630}. Endoplasmic reticulum
{ECO:0000256|ARBA:ARBA00004240}. Membrane {ECO:0000256|ARBA:ARBA00004141}; Multi-pass
membrane protein
{ECO:0000256|ARBA:ARBA00004141}.'','Gja1,Tsg101,Nfkb1a,Usp2,Usp48,Was,Eed,Kalrn,Wdtdc1,Rgs
14,Src,Prkca,Prkce,Ppp1r9b,Usp9x,Htt,Cyfp2'),('7','ENSMUSG00000058589','AOA0R4J2A2','Anks1b','
protein_coding','Ankyrin repeat and sterile alpha motif domain containing
1B','UPI0001F795AF','218749','10090.ENSMUSP00000138539','GO:0005654; GO:0005813;
GO:0005829; GO:0005886; GO:0014069; GO:0043197; GO:0046875; GO:0048013; GO:0097120;
GO:0098685; GO:0098686; GO:0098978; GO:0099092; GO:0099523; GO:0099527; GO:0099565;
GO:1900383','centrosome [GO:0005813]; cytosol [GO:0005829]; dendritic spine [GO:0043197];
glutamatergic synapse [GO:0098978]; hippocampal mossy fiber to CA3 synapse [GO:0098686];
nucleoplasm [GO:0005654]; plasma membrane [GO:0005886]; postsynaptic density [GO:0014069];
postsynaptic density, intracellular component [GO:0099092]; presynaptic cytosol [GO:0099523];
Schaffer collateral - CA1 synapse [GO:0098685]; ephrin receptor binding [GO:0046875]; chemical
synaptic transmission, postsynaptic [GO:0099565]; ephrin receptor signaling pathway [GO:0048013];
postsynapse to nucleus signaling pathway [GO:0099527]; receptor localization to synapse
[GO:0097120]; regulation of synaptic plasticity by receptor localization to synapse
[GO:1900383]','Gene','ankyrin repeat and sterile alpha motif domain containing 1B [Source:MGI
Symbol;Acc:MGI:1924781]','Mus
musculus',10090,'GTAGAAGCTGCGCGGAGAGAAGGAGGACGGCGTGCTGCTCCCTGCGCGGGGCTGCAGG
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 of nucleoplasmic coilin protein interactions in neuronal and transformed cells.
 {ECO:0000250}.'Alternative sequence (7); Chain (1); Compositional bias (4); Domain (3); Modified
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 Isoform 2 interacts with COIL (By similarity). {ECO:0000250}.'','SUBCELLULAR LOCATION: Cytoplasm

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TTTTCTCTCACAGTAATCTCAAATATCATAAAAGAACCCATACTGGAGCAAAACCTTATGAATGTAATCAATGTGG
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AGTCTACTGGTGTCTTACCACCATGGAGAAGGCCGGGGCCCACTTGAAGGGTGGAGCCAAAAGGGTCATCAT
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CATCCCAGAGCTGAACGGGAAGCTCACTGGCATGGCCTTCCGTGTTCTACCCCCAATGTGTCCATCGTGGATCT
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1','122023844','122024845',NULL,NULL,NULL,NULL,NULL,NULL,NULL,NULL,NULL,NULL,NUL
L,'Ywhae');

```
/*!40000 ALTER TABLE `Summary` ENABLE KEYS */;
```

```
UNLOCK TABLES;
```

```
/*!40103 SET TIME_ZONE=@OLD_TIME_ZONE */;
```

```
/*!40101 SET SQL_MODE=@OLD_SQL_MODE */;
```

```
/*!40014 SET FOREIGN_KEY_CHECKS=@OLD_FOREIGN_KEY_CHECKS */;
```

```
/*!40014 SET UNIQUE_CHECKS=@OLD_UNIQUE_CHECKS */;
```

```
/*!40101 SET CHARACTER_SET_CLIENT=@OLD_CHARACTER_SET_CLIENT */;
```

```
/*!40101 SET CHARACTER_SET_RESULTS=@OLD_CHARACTER_SET_RESULTS */;
```

```
/*!40101 SET COLLATION_CONNECTION=@OLD_COLLATION_CONNECTION */;
```

```
/*!40111 SET SQL_NOTES=@OLD_SQL_NOTES */;
```

-- Dump completed on 2023-11-06 20:51:16