```
# Load required libraries
library(readxl)
                # For reading data from Excel files
## Warning: Paket 'readxl' wurde unter R Version 4.3.1 erstellt
library(multiMiR) # For querying validated miRNA-mRNA interactions
## Welcome to multiMiR.
## multiMiR database URL has been set to the
## default value: http://multimir.org/
## Database Version: 2.3.0 Updated: 2020-04-15
library(writexl) # For writing data to Excel files
## Warning: Paket 'writexl' wurde unter R Version 4.3.1 erstellt
# Read data from an Excel file named "miRNAmRNA.xlsx" and store it in the "new_list" variable.
new_list <- read_excel("C:/Users/Emre/Desktop/miRNAmRNA.xlsx")</pre>
mirnames <- new_list$miRNA
# Get validated miRNA-mRNA interactions using the "multiMiR" package.
# In this case, the interactions are queried for human (hsa) miRNAs (mirnames) from the "validated" tab
# The results will be summarized and stored in the "multimir_results" variable.
                                        = 'hsa',
multimir_results <- get_multimir(org</pre>
                                mirna = mirnames,
                                table = 'validated'.
                                summary = TRUE)
## Searching mirecords ...
## Searching mirtarbase ...
## Searching tarbase ...
# Display the first few rows of the "multimir_results" data to get an overview of the miRNA-mRNA intera
head(multimir_results@data)
     database mature_mirna_acc mature_mirna_id target_symbol target_entrez
## 1 mirecords MIMAT0000073 hsa-miR-19a-3p
                                                       PTEN
                                                                      5728
## 2 mirecords MIMAT0000073 hsa-miR-19a-3p
                                                        PTEN
                                                                      5728
## 3 mirecords MIMAT0000073 hsa-miR-19a-3p
                                                       PTEN
                                                                      5728
## 4 mirecords MIMAT0000073 hsa-miR-19a-3p
                                                        PTEN
                                                                      5728
## 5 mirecords MIMAT0000073 hsa-miR-19a-3p
                                                        PTEN
                                                                      5728
## 6 mirecords MIMAT0000073 hsa-miR-19a-3p
                                                        PTEN
                                                                      5728
     target_ensembl experiment support_type pubmed_id
## 1 ENSG0000171862
                                             14697198 validated
## 2 ENSG00000171862
                                             14697198 validated
## 3 ENSG0000171862
                                             14697198 validated
## 4 ENSG0000171862
                                             14697198 validated
## 5 ENSG00000171862
                                             14697198 validated
```

14697198 validated

6 ENSG00000171862

```
# Extract the results of miRNA-mRNA interactions from the "multimir_results" variable and store them in targets <- multimir_results@data</pre>
# Extract the results of miRNA-mRNA interactions from the "multimir_results" variable and store them in # Specify the Excel file name where the results will be saved.
excel_file <- "multimir_results.xlsx"

# Write the "targets" data to an Excel file with the specified file name.
write_xlsx(targets, path = excel_file)</pre>
```