

# RmiR.hsa

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RmiR.hsa_dbconn	<i>Collect information from different miRNA targets databases</i>
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## Description

A function to get a connection object to some miRNA targets databases.

## Usage

```
RmiR.hsa_dbconn()  
RmiR.hsa_dbfile()
```

## Details

RmiR.hsa\_dbconn returns a connection object to some miRNA targets databases. **IMPORTANT:** Do not call [dbDisconnect](#) on the connection object returned by RmiR.hsa\_dbconn or you will break all the [AnnDbObj](#) objects defined in this package!

RmiR.hsa\_dbfile returns the path (character string) to the package annotation DB (this is an SQLite v3 file).

## Value

RmiR.hsa\_dbconn  
A DBIConnection object representing an open connection to the miRNA targets database.

RmiR.hsa\_dbfile  
A character string with the path to the miRNA targets database.

## See Also

[dbGetQuery](#), [dbConnect](#), [dbconn](#), [dbfile](#)

**Examples**

```
## List all the tables of the database:
dbListTables(RmiR.hsa_dbconn())

## Count the number of rows in the "targetscan" table:
dbGetQuery(RmiR.hsa_dbconn(), "SELECT COUNT(*) FROM targetscan")

## List the contents of the "mirbase" tables:
dbListFields(RmiR.hsa_dbconn(), "mirbase")

## List all targets of "hsa-miR-21" in miranda database:
dbGetQuery(RmiR.hsa_dbconn(),
  "SELECT * FROM tarbase where mature_miRNA='hsa-miR-21'")

## The connection object returned by RmiR.hsa_dbconn() was created with:
dbConnect(SQLite(), dbname=RmiR.hsa_dbfile(), cache_size=64000, synchronous=0)
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