

# Package: GWASapi (via r-universe)

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**Version** 0.1-4

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**Title** NHGRI-EBI GWAS Catalog of Summary Statistics

**Description** Tools for connecting to the NHGRI-EBI API for GWAS summary statistics.

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**Depends** R (>= 3.1.0)

**Imports** httr, glue

**Suggests** testthat, devtools, roxygen2, knitr, rmarkdown

**License** MIT + file LICENSE

**URL** <https://github.com/rqtl/GWASapi>

**BugReports** <https://github.com/rqtl/GWASapi/issues>

**LazyData** true

**Encoding** UTF-8

**ByteCompile** true

**VignetteBuilder** knitr

**Roxygen** list(markdown=TRUE)

**Config/roxygen2/version** 8.0.0

**Config/pak/sysreqs** libssl-dev

**Repository** <https://rqtl.r-universe.dev>

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**RemoteRef** HEAD

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check_gwasapi	<i>Check if the GWAS Catalog is live</i>
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### Description

Check if the GWAS Catalog is live

### Usage

```
check_gwasapi()
```

### Value

Character string.

### Examples

```
check_gwasapi()
```

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get_asso	<i>Get GWAS associations for a given region</i>
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### Description

Get GWAS associations for a given region

**Usage**

```
get_asso(  
  chr,  
  bp_lower = NULL,  
  bp_upper = NULL,  
  study = NULL,  
  p_lower = NULL,  
  p_upper = NULL,  
  start = NULL,  
  size = NULL  
)
```

**Arguments**

chr	chromosome number
bp_lower	Lower endpoint of basepairs interval
bp_upper	Upper endpoint of basepairs interval
study	Restrict to a particular study
p_lower	Lower bound on p-values
p_upper	Upper bound of p-values
start	First record to retrieve (starting at 0)
size	Maximum number of results to retrieve

**Value**

Data frame of associations

**See Also**

[get\\_variant\(\)](#), [get\\_trait\\_asso\(\)](#)

**Examples**

```
result <- get_asso(chr=19, bp_lower=19200000, bp_upper=19300000)
```

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get_trait_asso	<i>Get GWAS associations for a particular trait</i>
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**Description**

Get GWAS associations for a particular trait

**Usage**

```
get_trait_asso(  
  trait = NULL,  
  study = NULL,  
  p_lower = NULL,  
  p_upper = NULL,  
  start = NULL,  
  size = NULL  
)
```

**Arguments**

trait	Restrict to a particular study
study	Restrict to a particular study
p_lower	Lower bound on p-values
p_upper	Upper bound of p-values
start	First record to retrieve (starting at 0)
size	Maximum number of results to retrieve

**Value**

Data frame of associations

**See Also**

[get\\_variant\(\)](#), [get\\_asso\(\)](#)

**Examples**

```
## Not run: result <- get_trait_asso("EFO_0001360", p_upper=1e-10)
```

---

get\_variant

*Get associations for a given variant*

---

**Description**

Get all associations for a given variant

**Usage**

```
get_variant(  
  rsnum,  
  chr = NULL,  
  p_lower = NULL,  
  p_upper = NULL,  
  study = NULL,
```

```
    start = NULL,  
    size = NULL  
  )
```

### Arguments

rsnum	RS number for a variant
chr	chromosome number if known
p_lower	Lower bound on p-values
p_upper	Upper bound of p-values
study	Restrict to a particular study
start	First record to retrieve (starting at 0)
size	Maximum number of results to retrieve

### Value

Data frame with associations as rows

### See Also

[get\\_asso\(\)](#), [get\\_trait\\_asso\(\)](#)

### Examples

```
# get associations for a given variant  
results <- get_variant("rs2228603")  
# use information about the chromosome it's on  
results <- get_variant("rs2228603", 19)  
# get the next 20 results  
next20 <- get_variant("rs2228603", 19, start=20)  
# get 100 results rather than just 20  
first100 <- get_variant("rs2228603", 19, size=100)  
# return just the associations with P < 1e-8  
top_results <- get_variant("rs2228603", 19, p_upper=1e-8)
```

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info\_study

*Information about a study*

---

### Description

Information about a particular study

### Usage

```
info_study(study)
```

**Arguments**

study            Study identifier

**Value**

List of meta-data

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list\_chr            *List chromosomes*

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**Description**

List chromosomes

**Usage**

```
list_chr()
```

**Value**

Vector of chromosome numbers (as integers)

**See Also**

[list\\_studies\(\)](#), [list\\_traits\(\)](#)

**Examples**

```
chr <- list_chr()
```

---

list\_studies        *List studies*

---

**Description**

List studies

**Usage**

```
list_studies(trait = NULL, start = NULL, size = NULL)
```

**Arguments**

trait            If provided, restrict search to studies that included the specified trait.  
start            First record to retrieve (starting at 0)  
size             Maximum number of results to retrieve

**Value**

Vector of study accessions

**See Also**

[list\\_chr\(\)](#), [list\\_traits\(\)](#)

**Examples**

```
first20 <- list_studies() # returns 20 studies
next20 <- list_studies(start=20) # returns the next 20 studies
first100 <- list_studies(size=100) # returns 100 studies
with_trait <- list_studies(trait="EFO_0001360")
```

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list_traits	<i>List traits</i>
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**Description**

List traits

**Usage**

```
list_traits(start = NULL, size = NULL)
```

**Arguments**

start	First record to retrieve (starting at 0)
size	Maximum number of results to retrieve

**Value**

Vector of trait IDs

**See Also**

[list\\_studies\(\)](#), [list\\_chr\(\)](#)

**Examples**

```
first20 <- list_traits() # first 20 traits
next20 <- list_traits(start=20) # the next 20 traits
first100 <- list_traits(size=100) # returns 100 traits
```

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