

# Package ‘myvariant’

January 20, 2026

**Type** Package

**Title** Accesses MyVariant.info variant query and annotation services

**Version** 1.40.0

**Date** 2025-07-22

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**Description** MyVariant.info is a comprehensive aggregation of variant annotation resources. myvariant is a wrapper for querying MyVariant.info services

**License** Artistic-2.0

**Depends** R (>= 3.2.1), VariantAnnotation

**Imports** httr, jsonlite, S4Vectors, Hmisc, plyr, magrittr, Seqinfo, GenomeInfoDb

**Suggests** BiocStyle

**biocViews** VariantAnnotation, Annotation, GenomicVariation

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/myvariant>

**git\_branch** RELEASE\_3\_22

**git\_last\_commit** 7fa4399

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.22

**Date/Publication** 2026-01-19

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| formatHgvs | <i>Get all HGVS IDs from Vcf object.</i> |
|------------|------------------------------------------|

---

**Description**

Read in a Vcf object created by [readVcf](#) to extract all HGVS IDs for querying MyVariant.info.

**Usage**

```
formatHgvs(vcf, variant_type = c("snp", "insertion", "deletion"))
```

**Arguments**

|              |                                                                                                 |
|--------------|-------------------------------------------------------------------------------------------------|
| vcf          | Vcf object created by <a href="#">readVcf</a> .                                                 |
| variant_type | Type of variant HGVS IDs to retrieve from Vcf object. Default c("snp", "insertion", "deletion") |

**Value**

vector

**References**

<https://myvariant.info> <http://www.hgvs.org/mutnomen/recs-DNA.html>

**See Also**

[formatSingleHgvs](#)

**Examples**

```
## return HGVS IDs for all snps in a Vcf
file.path <- system.file("extdata", "db SNP_mini.vcf", package="myvariant")
vcf <- readVcf(file.path, genome="hg19")
hgvs <- formatHgvs(vcf, variant_type="snp")
```

---

|                  |                                                                                     |
|------------------|-------------------------------------------------------------------------------------|
| formatSingleHgvs | <i>Get Hgvs HGVS ID from chromosome, position, reference and alternate alleles.</i> |
|------------------|-------------------------------------------------------------------------------------|

---

**Description**

Create a single HGVS ID for a variant from chromosome, position, reference and alternate alleles.

**Usage**

```
formatSingleHgvs(chrom, pos, ref, alt, mutant_type=FALSE)
```

**Arguments**

|             |                                                                                   |
|-------------|-----------------------------------------------------------------------------------|
| chrom       | Chromosome.                                                                       |
| pos         | Position of the variant on the reference genome (hg19).                           |
| ref         | Reference allele.                                                                 |
| alt         | Alternate allele.                                                                 |
| mutant_type | Logical indicating whether to return the type of mutation along with the HGVS ID. |

**Value**

returns a string

**References**

<https://myvariant.info> <http://www.hgvs.org/mutnomen/recs-DNA.html>

**See Also**

[formatHgvs](#)

**Examples**

```
## return HGVS ID for a variant
formatSingleHgvs(1, 35367, "G", "A")
```

---

|            |                                                         |
|------------|---------------------------------------------------------|
| getVariant | <i>Return the variant object for the given HGVS id.</i> |
|------------|---------------------------------------------------------|

---

**Description**

This is a wrapper for GET query of `"/variant/<hgvsid>"` service.

**Usage**

```
getVariant(hgvsid, fields=NULL,
           ..., return.as=c("records", "text"), myvariant)
```

**Arguments**

|           |                                                                                                                                                                                                                         |
|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| hgvsid    | HGVS id                                                                                                                                                                                                                 |
| fields    | Fields to return, a list of a comma-sep string. If <code>fields=="all"</code> , all available fields are returned.                                                                                                      |
| ...       |                                                                                                                                                                                                                         |
| return.as | "records" (list), "text" (JSON).                                                                                                                                                                                        |
| myvariant | A MyVariant object that describes how to connect to data resources. See <a href="#">MyVariant-class</a> . If missing, default object will be used that accesses the main MyVariant.info portal. Default is recommended. |

**Value**

returns a variant object containing the queried annotations

**References**

[http://docs.myvariant.info/en/latest/doc/variant\\_annotation\\_service.html#get-request](http://docs.myvariant.info/en/latest/doc/variant_annotation_service.html#get-request) <http://docs.myvariant.info/en/latest/parameters>

**See Also**

[getVariants](#) [queryVariant](#) [queryVariants](#)

**Examples**

```
## return the variant object for the given HGVS id
getVariant("chr7:g.55241707G>T")

## customize fields
getVariant("chr7:g.55241707G>T",
          fields=c("dbnsfp.cadd.phred", "dbnsfp.polyphen2"),
          return.as="text")
```

---

getVariants

*Return the list of variant objects for the given list of HGVS ids.*

---

**Description**

This is a wrapper for POST query of `"/variant"` service.

**Usage**

```
getVariants(hgvsids, fields=NULL, verbose=NULL, ...,
            return.as=c("DataFrame", "records", "text"), myvariant)
```

**Arguments**

|           |                                                                                                                                                                                                                         |
|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| hgvsids   | A vector, list, or comm-sep string HGVS ids                                                                                                                                                                             |
| fields    | A vector of fields to return. If <code>fields=="all"</code> , all available fields are returned.                                                                                                                        |
| verbose   | A logical turning on or off process status messages. Default = TRUE.                                                                                                                                                    |
| ...       |                                                                                                                                                                                                                         |
| return.as | "DataFrame" (default), "records" (list), "text" (JSON).                                                                                                                                                                 |
| myvariant | A MyVariant object that describes how to connect to data resources. See <a href="#">MyVariant-class</a> . If missing, default object will be used that accesses the main MyVariant.info portal. Default is recommended. |

**Value**

returns a variant object (DataFrame, list, or JSON text) containing the queried annotations

References

[http://docs.myvariant.info/en/latest/doc/variant\\_annotation\\_service.html#batch-queries-via-post](http://docs.myvariant.info/en/latest/doc/variant_annotation_service.html#batch-queries-via-post) [http://docs.myvariant.info/en/latest/doc/variant\\_annotation\\_service.html#batch-queries-via-post](http://docs.myvariant.info/en/latest/doc/variant_annotation_service.html#batch-queries-via-post)

See Also

[getVariants](#) [queryVariant](#) [queryVariants](#)

Examples

```
## given a list of HGVS ids
vars <- c('chr1:g.866422C>T',
'chr1:g.876664G>A',
'chr1:g.69635G>C',
'chr1:g.69869T>A',
'chr1:g.881918G>A',
'chr1:g.865625G>A',
'chr1:g.879368C>A',
'chr1:g.889226C>T',
'chr1:g.879492C>G',
'chr1:g.879423T>G',
'chr1:g.881602C>T',
'chr1:g.879115C>G',
'chr1:g.69892T>C',
'chr1:g.879381C>T',
'chr1:g.878330C>G')

## Return the list of variant object for the given list of HGVS ids.
df <- getVariants(vars, fields="dbsnp, welllderly")
```

---

|          |                 |
|----------|-----------------|
| metadata | <i>metadata</i> |
|----------|-----------------|

---

Description

Get metadata for MyVariant.info services.

Usage

```
metadata(x, ...)
```

Arguments

- xMyVariant object
- ...MyVariant object slot parameters

Value

returns the metadata including available databases and number of documents.

References

<http://myvariant.info/v1/metadata>

**Examples**

```
## Get metadata
myvariant<-MyVariant()
metadata(myvariant)
```

---

|           |                  |
|-----------|------------------|
| MyVariant | <i>MyVariant</i> |
|-----------|------------------|

---

**Description**

Construct a MyVariant object.

**Usage**

```
MyVariant(...)
```

**Arguments**

... See help page for MyVariant-class

**Value**

MyVariant object

**Examples**

```
MyVariant()
```

---

|           |                                                          |
|-----------|----------------------------------------------------------|
| myvariant | <i>Access MyVariant.info variant annotation services</i> |
|-----------|----------------------------------------------------------|

---

**Description**

MyVariant.Info provides REST web services to query/retrieve variant annotations. myvariant is an easy-to-use R wrapper to access MyVariant.info services.

**Details**

|          |                     |
|----------|---------------------|
| Package: | myvariant           |
| Type:    | Package             |
| Version: | 0.99.0              |
| Date:    | 2014-12-18          |
| License: | Artistic-2.0        |
| Depends: | httr jsonlite Hmisc |

**Author(s)**

Adam Mark

Maintainer: Adam Mark &lt;adammark@scripps.edu&gt;

**References**<https://github.com/Network-of-BioThings/myvariant.info/wiki>


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|                 |                   |
|-----------------|-------------------|
| MyVariant-class | Class "MyVariant" |
|-----------------|-------------------|

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**Description**

R Client to access MyVariant.Info annotation services

**Objects from the Class**

Objects can be created by calls of the form `MyVariant(base.url="http://myvariant.info/v1", delay=1, step=1000, version=version, verbose=TRUE, debug=FALSE)`.

**Slots**

`base.url`: "http://myvariant.info/v1". Object of class "character"  
`delay`: Sleep time between batch retrieval. Object of class "numeric"  
`step`: Batch limit. Object of class "numeric"  
`version`: httr package version. Object of class "character"  
`verbose`: Object of class "logical"  
`debug`: Object of class "logical"

**Methods**

`getVariant(hgvsid, fields=NULL, ..., return.as=c("records", "text"))`: Return the variant object for the given hgvsid

`getVariants(hgvsids, fields=NULL, ..., return.as=c("DataFrame", "records", "text"))`: Return the list of variant object for the given list of hgvsids.

`queryVariant(q, fields=NULL, ..., return.as=c("DataFrame", "records", "text"))`: Return the query result.

`queryVariants(qterms, scopes=NULL, fields=NULL, ..., return.as=c("DataFrame", "records", "text"))`, `r`: Return the batch query result.

**Author(s)**

Adam Mark

**References**<https://github.com/Network-of-BioThings/myvariant.info/wiki>**Examples**

```
showClass("MyVariant")
```

---

|              |                                 |
|--------------|---------------------------------|
| queryVariant | <i>Return the query result.</i> |
|--------------|---------------------------------|

---

**Description**

This is a wrapper for GET query of "/query?q=<query>" service.

**Usage**

```
queryVariant(q, ..., return.as=c("DataFrame", "records", "text"),
             myvariant)
```

**Arguments**

|           |                                                                                                                                                                                                                         |
|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| q         | query term(s).                                                                                                                                                                                                          |
| ...       | Commonly queried fields include fields, size as well as several other fields. View available fields by calling ?metadata.                                                                                               |
| return.as | "DataFrame" (default), "records" (list), or "text" (JSON).                                                                                                                                                              |
| myvariant | A MyVariant object that describes how to connect to data resources. See <a href="#">MyVariant-class</a> . If missing, default object will be used that accesses the main MyVariant.info portal. Default is recommended. |

**Value**

returns a variant object (DataFrame, list, or JSON text) containing the queried annotations

**References**

[http://docs.myvariant.info/en/latest/doc/variant\\_query\\_service.html#get-request](http://docs.myvariant.info/en/latest/doc/variant_query_service.html#get-request) <http://docs.myvariant.info/en/latest/doc/syntax>

**See Also**

[queryVariants](#) [getVariant](#) [getVariants](#)

**Examples**

```
## return the query result
queryVariant("dbnsfp.variantname:BRCA2")

queryVariant("chr1:1-1000000")
```



---

|               |                                       |
|---------------|---------------------------------------|
| queryVariants | <i>Return the batch query result.</i> |
|---------------|---------------------------------------|

---

## Description

This is a wrapper for POST query of "/query" service.

## Usage

```
queryVariants(qterms, scopes=NULL, ...,
              return.as=c("DataFrame", "records", "text"),
              myvariant)
```

## Arguments

|           |                                                                                                                                                                                                                                   |
|-----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| qterms    | A vector or list, or string of comma-separated query terms                                                                                                                                                                        |
| scopes    | Type of types of identifiers, either a list or a comma-separated fields to specify type of input qterms.                                                                                                                          |
| ...       | Commonly queried fields include fields, size as well as several other fields. returnall returns a list of all related data including duplicated and missing qterms. False by default. View available fields by calling ?metadata. |
| return.as | "DataFrame" (default), "records" (list), "text" (JSON).                                                                                                                                                                           |
| myvariant | A MyVariant object that describes how to connect to data resources. See <a href="#">MyVariant-class</a> . If missing, default object will be used that accesses the main MyVariant.info portal. Default is recommended.           |

## Value

returns a variant object (DataFrame, list, or JSON text) containing the queried annotations

## References

[http://docs.myvariant.info/en/latest/doc/variant\\_query\\_service.html#batch-queries-via-post](http://docs.myvariant.info/en/latest/doc/variant_query_service.html#batch-queries-via-post) <http://docs.myvariant.info/en/>

## See Also

[queryVariant](#) [getVariant](#) [getVariants](#)

## Examples

```
## return the batch query result
```

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