

# Package ‘cellbaseR’

April 21, 2026

**Type** Package

**Date** 2016-04-17

**Title** Querying annotation data from the high performance Cellbase web

**Version** 1.35.0

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**URL** <https://github.com/melsiddieg/cellbaseR>

**Description** This R package makes use of the exhaustive RESTful Web service API that has been implemented for the Cellbase database. It enable researchers to query and obtain a wealth of biological information from a single database saving a lot of time. Another benefit is that researchers can easily make queries about different biological topics and link all this information together as all information is integrated.

**License** Apache License (== 2.0)

**Depends** R(>= 3.4)

**Imports** methods, jsonlite, httr, data.table, pbapply, tidyr, R.utils, Rsamtools, BiocParallel, foreach, utils, parallel, doParallel

**Suggests** BiocStyle, knitr, rmarkdown, Gviz, VariantAnnotation

**RoxygenNote** 7.2.3

**biocViews** Annotation, VariantAnnotation

**Lazy** TRUE

**LazyData** TRUE

**Encoding** UTF-8

**Collate** 'commons.R' 'AllClasses.R' 'AllGenerics.R'  
'AnnotateVcf-methods.R' 'CellBaseParam-methods.R'  
'CellBaseR-methods.R' 'cellbase.R' 'getCellbase-methods.R'  
'getChromosomeInfo-methods.R' 'getClinical-methods.R'  
'getGene-methods.R' 'getMeta-methods.R' 'getProtein-methods.R'  
'getRegion-methods.R' 'getTranscript-methods.R'  
'getVariant-methods.R' 'getXref-methods.R' 'show-methods.R'  
'tools.R' 'user.R'

**VignetteBuilder** knitr

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

**git\_branch** devel  
**git\_last\_commit** 6f10847  
**git\_last\_commit\_date** 2025-10-29  
**Repository** Bioconductor 3.24  
**Date/Publication** 2026-04-21

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## Description

Querying annotation data from the high performance Cellbase web services

## Details

Documentation for the cellbaseR package

This R package makes use of the exhaustive RESTful Web service API that has been implemented for the Cellbase database. It enables researchers to query and obtain a wealth of biological information from a single database saving a lot of time. Another benefit is that researchers can easily make queries about different biological topics and link all this information together as all information is integrated. Currently Homo sapiens, Mus musculus and other 20 species are available and

many others will be included soon. Results returned from the cellbase queries are parsed into R data.frames and other common R data structures so users can readily get into downstream analysis.

**Author(s)**

Mohammed OE Abdallah

**See Also**

Useful links:

- <https://github.com/melsiddieg/cellbaseR>

---

AnnotateVcf,CellBaseR-method

*AnnotateVcf*

---

**Description**

This method is a convenience method to annotate bgzipped tabix-indexed vcf files. It should be ideal for annotating small to medium sized vcf files.

**Usage**

```
## S4 method for signature 'CellBaseR'  
AnnotateVcf(object, file, batch_size, num_threads, BPPARAM = bpparam())
```

**Arguments**

object	an object of class CellBaseR
file	Path to a bgzipped and tabix indexed vcf file
batch_size	integer if multiple queries are raised by a single method call, e.g. getting annotation info for several genes, queries will be sent to the server in batches. This slot indicates the size of each batch, e.g. 200
num_threads	number of asynchronous batches to be sent to the server
BPPARAM	a BiocParallel class object

**Value**

a dataframe with the results of the query

**See Also**

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinformatics.cam.ac.uk/cellbase/webservices/>

**Examples**

```
cb <- CellBaseR()  
f1 <- system.file("extdata", "hapmap_exome_chr22_200.vcf.gz",  
                 package = "cellbaseR" )  
res <- AnnotateVcf(object=cb, file=f1, BPPARAM = bpparam(workers=2),batch_size=100)
```

**Description**

CellBaseParam object is used to control what results are returned from the CellBaseR methods

**Usage**

```
CellBaseParam(
  assembly = character(),
  feature = character(),
  region = character(),
  rsid = character(),
  accession = character(),
  type = character(),
  mode_inheritance_labels = character(),
  clinsig_labels = character(),
  alleleOrigin = character(),
  consistency_labels = character(),
  so = character(),
  source = character(),
  trait = character(),
  include = character(),
  exclude = character(),
  limit = character()
)
```

**Arguments**

assembly	A character the assembly build to query, e.g.GRCh37(default)
feature	A character vector denoting the feature/s to be queried
region	A character vector denoting the region/s to be queried must be in the form 1:100000-1500000
rsid	A character vector denoting the rs ids to be queried
accession	A caharcter vector of Cinvar accessions
type	A caharcter vector of Variant types
mode_inheritance_labels	A character vector
clinsig_labels	A character vector
alleleOrigin	A character vector
consistency_labels	A character vector
so	A character vector denoting sequence ontology to be queried
source	A character vector
trait	A character vector denoting the trait to be queried
include	A character vector denoting the fields to be returned
exclude	A character vector denoting the fields to be excluded
limit	A number limiting the number of results to be returned

**Value**

an object of class CellBaseParam

**See Also**

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

**Examples**

```
cbParam <- CellBaseParam(assembly="GRCh38", feature=c("TP73", "TET1"))
print(cbParam)
```

---

CellBaseParam-class     *CellBaseParam Class*

---

**Description**

This class defines a CellBaseParam object to hold filtering parameters.

**Details**

This class stores parameters used for filtering the CellBaseR query and is available for all query methods. CellBaseParam object is used to control what results are returned from the CellBaseR methods

**Slots**

assembly A character the assembly build to query, e.g. GRCh37(default)  
 feature A character vector denoting the feature/s to be queried  
 region A character vector denoting the region/s to be queried must be in the form 1:100000-150000  
 rsid A character vector denoting the rs ids to be queried  
 accession A character vector of Clinvar accessions  
 type A character vector of Variant types  
 mode\_inheritance\_labels A character vector  
 clinsig\_labels A character vector  
 alleleOrigin A character vector  
 consistency\_labels A character vector  
 so A character vector denoting sequence ontology to be queried  
 source A character vector  
 trait A character vector denoting the trait to be queried  
 include A character vector denoting the fields to be returned  
 exclude A character vector denoting the fields to be excluded  
 limit A number limiting the number of results to be returned

**See Also**

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

---

 CellBaseR

*CellBaseR*


---

## Description

This is a constructor function for the CellBaseR object

## Usage

```
CellBaseR(
  host = "https://ws.zettagenomics.com/cellbase/webservices/rest/",
  version = "v5",
  species = "hsapiens",
  batch_size = 200L,
  num_threads = 8L
)
```

## Arguments

host	A character the default host url for cellbase webservices, e.g. "http://bioinfo.hpc.cam.ac.uk/cellbase/w
version	A character the cellbae API version, e.g. "V4"
species	a character specifying the species to be queried, e.g. "hsapiens"
batch_size	intger if multiple queries are raised by a single method call, e.g. getting annota- tion info for several genes, queries will be sent to the server in batches.This slot indicates the size of each batch,e.g. 200
num_threads	integer number of batches to be sent to the server

## Details

CellbaseR constructor function

This class defines the CellBaseR object. It holds the default configuration required by CellBaseR methods to connect to the cellbase web services. By default it is configured to query human data based on the GRCh37 genome assembly.

## Value

An object of class CellBaseR

## See Also

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

## Examples

```
cb <- CellBaseR()
print(cb)
```

---

CellBaseR-class	<i>CellBaseR Class</i>
-----------------	------------------------

---

### Description

This is an S4 class which defines the CellBaseR object

### Details

This S4 class holds the default configuration required by CellBaseR methods to connect to the cellbase web services. By default it is configured to query human data based on the GRCh37 assembly assembly.

### Slots

`host` a character specifying the host url. Default "http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/rest/"

`version` a character specifying the API version. Default "v4"

`species` a character specifying the species to be queried. Default "hsapiens"

`batch_size` if multiple queries are raised by a single method call, e.g. getting annotation info for several features, queries will be sent to the server in batches. This slot indicates the size of these batches. Default 200

`num_threads` the number of threads. Default 8

### See Also

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

---

<code>createGeneModel</code>	<i>createGeneModel</i>
------------------------------	------------------------

---

### Description

A convenience function to construct a genemodel

### Usage

```
createGeneModel(object, region = NULL)
```

### Arguments

`object` an object of class CellbaseResponse

`region` a character

### Details

This function create a gene model data frame, which can be then turned into a GeneRegionTrack for visualization by [GeneRegionTrack](#)

**Value**

A geneModel

**See Also**

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

**Examples**

```
cb <- CellBaseR()
test <- createGeneModel(object = cb, region = "17:1500000-1550000")
```

---

*getCellBase,CellBaseR-method*  
*getCellBase*

---

**Description**

The generic method for querying CellBase web services.

**Usage**

```
## S4 method for signature 'CellBaseR'
getCellBase(object, category, subcategory, ids, resource, param = NULL)
```

**Arguments**

object	an object of class CellBaseR
category	character to specify the category to be queried.
subcategory	character to specify the subcategory to be queried
ids	a character vector of the ids to be queried
resource	a character to specify the resource to be queried
param	an object of class CellBaseParam specifying additional param for the CellBaseR

**Details**

This method allows the user to query the cellbase web services without any predefined categories, subcategories, or resources.

**Value**

a dataframe holding the results of the query

**See Also**

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

**Examples**

```
cb <- CellBaseR()
res <- getCellBase(object=cb, category="feature", subcategory="gene",
ids="TET1", resource="info")
```

---

```
getCellBaseResourceHelp
      getCellBaseResourceHelp
```

---

**Description**

A function to get help about available cellbase resources

**Usage**

```
getCellBaseResourceHelp(object, subcategory)
```

**Arguments**

object            a cellBase class object  
subcategory      a character the subcategory to be queried

**Details**

This function retrieves available resources for each generic method like `getGene`, `getRegion`, `get-protein`, etc. It help the user see all possible resources to use with the `getGeneric` methods

**Value**

character vector of the available resources to that particular subcategory

**Examples**

```
cb <- CellBaseR()
# Get help about what resources are available to the getGene method
getCellBaseResourceHelp(cb, subcategory="gene")
# Get help about what resources are available to the getRegion method
getCellBaseResourceHelp(cb, subcategory="region")
# Get help about what resources are available to the getXref method
getCellBaseResourceHelp(cb, subcategory="id")
```

---

```
getChromosomeInfo, CellBaseR-method  
getChromosomeInfo
```

---

### **Description**

A method to query sequence data from Cellbase web services.

### **Usage**

```
## S4 method for signature 'CellBaseR'  
getChromosomeInfo(object, ids, resource, param = NULL)
```

### **Arguments**

object	an object of class CellBaseR
ids	a character vector of chromosome ids to be queried
resource	a character vector to specify the resource to be queried
param	a object of class CellBaseParam specifying additional param for the query

### **Details**

A method to query sequence data from Cellbase web services. This method retrieves information about chromosomes, including its size and detailed information about its different cytobands

### **Value**

a dataframe with the results of the query

### **See Also**

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

### **Examples**

```
cb <- CellBaseR()  
res <- getChromosomeInfo(object=cb, ids="22", resource="info")
```

---

getClinical,CellBaseR-method  
*getClinical*

---

## Description

A method to query Clinical data from Cellbase web services.

## Usage

```
## S4 method for signature 'CellBaseR'  
getClinical(object, param = NULL)
```

## Arguments

object	an object of class CellBaseR
param	a object of class CellBaseParam specifying the parameters limiting the Cell-BaseR

## Details

This method retrieves clinically relevant variants annotations from multiple resources including clinvar, cosmic and gwas catalog. Furthermore, the user can filter these data in many ways including trait, features, rs, etc.,.

## Value

a dataframe with the results of the query

## See Also

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

## Examples

```
cb <- CellBaseR()  
cbParam <- CellBaseParam(feature=c("TP73","TET1"), limit=100)  
res <- getClinical(object=cb,param=cbParam)
```

---

`getConservationByRegion`  
*getConservationByRegion*

---

**Description**

A convenience method to fetch conservation data for specific region/s

**Usage**

```
getConservationByRegion(object, id, param = NULL)
```

**Arguments**

<code>object</code>	an object of class <code>CellBaseR</code>
<code>id</code>	a character vector of genomic regions, eg 17:1000000-1100000
<code>param</code>	an object of class <code>CellBaseParam</code>

**Value**

a dataframe of the query result

**Examples**

```
cb <- CellBaseR()
res <- getConservationByRegion(cb, "17:1000000-1189811")
```

---

`getGene,CellBaseR-method`  
*getGene*

---

**Description**

A method to query gene data from Cellbase web services.

**Usage**

```
## S4 method for signature 'CellBaseR'
getGene(object, ids, resource, param = NULL)
```

**Arguments**

<code>object</code>	an object of class <code>CellBaseR</code>
<code>ids</code>	a character vector of gene ids to be queried
<code>resource</code>	a character vector to specify the resource to be queried
<code>param</code>	an object of class <code>CellBaseParam</code> specifying additional param for the <code>CellBaseR</code>

**Details**

This method retrieves various gene annotations including transcripts and exons data as well as gene expression and clinical data

**Value**

a dataframe with the results of the query

**See Also**

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

**Examples**

```
cb <- CellBaseR()
res <- getGene(object=cb, ids=c("TP73", "TET1"), resource="info")
```

---

getGeneInfo

*getGeneInfo*

---

**Description**

A convenience method to fetch gene annotations specific gene/s

**Usage**

```
getGeneInfo(object, id, param = NULL)
```

**Arguments**

object	an object of class CellBaseR
id	a character vector of HUGO symbol (gene names)
param	an object of class CellBaseParam

**Value**

a dataframe of the query result

**Examples**

```
cb <- CellBaseR()
res <- getGeneInfo(cb, "TET1")
```

---

getMeta,CellBaseR-method  
*getMeta*

---

### Description

A method for getting the available metadata from the cellbase web services

### Usage

```
## S4 method for signature 'CellBaseR'  
getMeta(object, resource)
```

### Arguments

object            an object of class CellBaseR  
resource          the resource you want to query it metadata

### Details

This method is for getting information about the available species and available annotation, assembly for each species from the cellbase web services.

### Value

a dataframe with the results of the query

### See Also

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinformatics.cam.ac.uk/cellbase/webservices/>

### Examples

```
cb <- CellBaseR()  
res <- getMeta(object=cb, resource="species")
```

---

getProtein,CellBaseR-method  
*getProtein*

---

### Description

A method to query protein data from Cellbase web services.

### Usage

```
## S4 method for signature 'CellBaseR'  
getProtein(object, ids, resource, param = NULL)
```

**Arguments**

object	an object of class CellBaseR
ids	a character vector of uniprot ids to be queried, should be one or more of uniprot ids, for example O15350.
resource	a character vector to specify the resource to be queried
param	a object of class CellBaseParam specifying additional param for the query

**Details**

This method retrieves various protein annotations including protein description, features, sequence, substitution scores, evidence, etc.

**Value**

an object of class CellBaseResponse which holds a dataframe with the results of the query

**Examples**

```
cb <- CellBaseR()
res <- getProtein(object=cb, ids="O15350", resource="info")
```

---

getProteinInfo	<i>getProteinInfo</i>
----------------	-----------------------

---

**Description**

A convenience method to fetch annotations for specific protein/s

**Usage**

```
getProteinInfo(object, id, param = NULL)
```

**Arguments**

object	an object of class CellBaseR
id	a character vector of Uniprot Ids
param	an object of class CellBaseParam

**Value**

a dataframe of the query result

**Examples**

```
cb <- CellBaseR()
res <- getProteinInfo(cb, "O15350")
```

getRegion, CellBaseR-method  
*getRegion*

---

### Description

A method to query features within a genomic region from Cellbase web services.

### Usage

```
## S4 method for signature 'CellBaseR'  
getRegion(object, ids, resource, param = NULL)
```

### Arguments

object	an object of class CellBaseR
ids	a character vector of the regions to be queried, for example, "1:1000000-1200000" should always be in the form 'chr:start-end'
resource	a character vector to specify the resource to be queried
param	a object of class CellBaseParam specifying additional param for the query

### Details

This method retrieves various genomic features from a given region including genes, snps, clinically relevant variants, proteins, etc.

### Value

a dataframe with the results of the query

### See Also

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

### Examples

```
cb <- CellBaseR()  
res <- getRegion(object=cb, ids="17:1000000-1200000", resource="gene")
```

---

```
getRegulatoryByRegion getRegulatoryByRegion
```

---

**Description**

A convenience method to fetch regulatory data for specific region/s

**Usage**

```
getRegulatoryByRegion(object, id, param = NULL)
```

**Arguments**

object	an object of class CellBaseR
id	a character vector of genomic regions, eg 17:1000000-1100000
param	an object of class CellBaseParam

**Value**

a dataframe of the query result

**Examples**

```
cb <- CellBaseR()
res <- getRegulatoryByRegion(cb, "17:1000000-1189811")
```

---

```
getTranscript, CellBaseR-method
getTranscript
```

---

**Description**

A method to query transcript data from Cellbase web services.

**Usage**

```
## S4 method for signature 'CellBaseR'
getTranscript(object, ids, resource, param = NULL)
```

**Arguments**

object	an object of class CellBaseR
ids	a character vector of the transcript ids to be queried, use ensemble transcript IDs eg, ENST00000380152
resource	a character vector to specify the resource to be queried
param	an object of class CellBaseParam specifying additional params for the query

**Details**

This method retrieves various genomic annotations for transcripts including exons, cDNA sequence, annotations flags, and cross references, etc.

**Value**

a dataframe with the results of the query

**See Also**

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

**Examples**

```
cb <- CellBaseR()
res <- getTranscript(object=cb, ids="ENST00000373644", resource="info")
```

---

<code>getTranscriptByGene</code>	<i>getTranscriptByGene</i>
----------------------------------	----------------------------

---

**Description**

A convenience method to fetch transcripts for specific gene/s

**Usage**

```
getTranscriptByGene(object, id, param = NULL)
```

**Arguments**

<code>object</code>	an object of class <code>CellBaseR</code>
<code>id</code>	a character vector of HUGO symbol (gene names)
<code>param</code>	an object of class <code>CellBaseParam</code>

**Value**

a dataframe of the query result

**Examples**

```
cb <- CellBaseR()
res <- getTranscriptByGene(cb, "TET1")
```

---

getVariant, CellBaseR-method  
*getVariant*

---

## Description

A method to query variant annotation data from Cellbase web services from Cellbase web services.

## Usage

```
## S4 method for signature 'CellBaseR'  
getVariant(object, ids, resource, param = NULL)
```

## Arguments

object	an object of class CellBaseR
ids	a character vector of the ids to be queried, must be in the following format 'chr:start:ref:alt', for example, '1:128546:A:T'
resource	a character vector to specify the resource to be queried
param	a object of class CellBaseParam specifying additional param for the query

## Details

This method retrieves extensive genomic annotations for variants including consequence types, conservation data, population frequencies from 1k genomes and Exac projects, etc. as well as clinical data and various other annotations

## Value

a dataframe with the results of the query

## See Also

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

## Examples

```
cb <- CellBaseR()  
res <- getVariant(object=cb, ids="19:45411941:T:C", resource="annotation")
```

---

```
getVariantAnnotation  getVariantAnnotation
```

---

**Description**

A convenience method to fetch variant annotation for specific variant/s

**Usage**

```
getVariantAnnotation(object, id, param = NULL)
```

**Arguments**

object	an object of class CellBaseR
id	a character vector of length < 200 of genomic variants, eg 19:45411941:T:C
param	an object of class CellBaseParam

**Value**

a dataframe of the query result

**Examples**

```
cb <- CellBaseR()
res <- getVariantAnnotation(cb, "19:45411941:T:C")
```

---

```
getXref,CellBaseR-method
  getXref
```

---

**Description**

A method to query cross reference data from Cellbase web services.

**Usage**

```
## S4 method for signature 'CellBaseR'
getXref(object, ids, resource, param = NULL)
```

**Arguments**

object	an object of class CellBaseR
ids	a character vector of the ids to be queried, any crossreferenceable ID, gene names, transcript ids, uniprot ids, etc.
resource	a character vector to specify the resource to be queried
param	an object of class CellBaseParam specifying additional param for the query

**Details**

This method retrieves cross references for genomic identifiers, eg ENSEMBL ids, it also provide starts\_with service that is useful for autocomplete services.

**Value**

a dataframe with the results of the query

**See Also**

<https://github.com/opencb/cellbase/wiki> and the RESTful API documentation <http://bioinfo.hpc.cam.ac.uk/cellbase/webservices/>

**Examples**

```
cb <- CellBaseR()
res <- getXref(object=cb, ids="ENST00000373644", resource="xref")
```

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