

# BioMartGOGeneSets

December 3, 2025

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|-------------------|---------------------------------------|
| BioMartGOGeneSets | <i>Version and source information</i> |
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## Description

Version and source information

## Usage

BioMartGOGeneSets

## Examples

BioMartGOGeneSets

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|                    |                              |
|--------------------|------------------------------|
| changeSeqnameStyle | <i>Change sequence names</i> |
|--------------------|------------------------------|

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## Description

Change sequence names

## Usage

```
changeSeqnameStyle(gr, dataset, seqname_style_from, seqname_style_to,  
  reformat_from = NULL, reformat_to = NULL)
```

**Arguments**

|                    |                                                                                                                                                                                                                                    |
|--------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| gr                 | The input regions                                                                                                                                                                                                                  |
| dataset            | A BioMart dataset or a taxon ID. For a proper value, please see <a href="#">supportedOrganisms</a> .                                                                                                                               |
| seqname_style_from | Value should be in c("Sequence-Name", "GenBank-Accn", "RefSeq-Accn").<br>If you are not sure which seqname style is in gr, use <a href="#">getBioMartGenomeInfo</a> to obtain list of examples.                                    |
| seqname_style_to   | Value should be in c("Sequence-Name", "GenBank-Accn", "RefSeq-Accn").                                                                                                                                                              |
| reformat_from      | A self-defined function to reformat the seqnames. The internal seqname style can be obtained via <code>getBioMartGenomeInfo(dataset)</code> . This function converts the internal "from" seqnames to fit the user's input regions. |
| reformat_to        | A self-defined function to reformat the seqnames.                                                                                                                                                                                  |

**Details**

Please the conversion is not one to one. For those sequences which cannot be corrected mapped to other styles, they are just removed.

**Value**

A [GRanges](#) object.

**Examples**

```
## Not run:
gr = getBioMartGenes("giant panda")
changeSeqnameStyle(gr, "giant panda", "Sequence-Name", "GenBank-Accn")

## End(Not run)
```

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getBioMartGOGeneSets    *Get GO gene sets*

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**Description**

Get GO gene sets

**Usage**

```
getBioMartGOGeneSets(dataset, ontology = "BP",
  as_table = FALSE, gene_id_type = "ensembl_gene")
```

**Arguments**

|              |                                                                                                                                                                                                                           |
|--------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| dataset      | A BioMart dataset or a taxon ID. For a proper value, please see <a href="#">supportedOrganisms</a> .                                                                                                                      |
| ontology     | The value should be "BP", "CC", or "MF".                                                                                                                                                                                  |
| as_table     | Whether to return the value as a data frame?                                                                                                                                                                              |
| gene_id_type | Since BioMart is from Ensembl database, the default gene ID type is Ensembl gene ID. Depending on different organisms, Entrez ID ("entrez_gene") or gene symbol ("gene_symbol") can also be selected as the gene ID type. |

**Details**

The gene sets are already compiled and are hosted on [https://github.com/jokergoo/BioMartGOGeneSets\\_data](https://github.com/jokergoo/BioMartGOGeneSets_data), This function just simply retrieves data from there.

**Value**

A list of gene IDs or a data frame.

**Examples**

```
lt = getBioMartGOGeneSets("hsapiens_gene_ensembl")
lt = getBioMartGOGeneSets("hsapiens_gene_ensembl", gene_id_type = "entrez")
tb = getBioMartGOGeneSets("hsapiens_gene_ensembl", as_table = TRUE)
```

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|                 |                               |
|-----------------|-------------------------------|
| getBioMartGenes | <i>Get genes from BioMart</i> |
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**Description**

Get genes from BioMart

**Usage**

```
getBioMartGenes(dataset, add_chr_prefix = FALSE)
```

**Arguments**

|                |                                                                                                                                               |
|----------------|-----------------------------------------------------------------------------------------------------------------------------------------------|
| dataset        | A BioMart dataset or a taxon ID. For a proper value, please see <a href="#">supportedOrganisms</a> .                                          |
| add_chr_prefix | Whether to add "chr" prefix to chromosome names? If it is true, it uses <code>GenomeInfoDb::seqlevelsStyle = "UCSC"</code> to add the prefix. |

**Details**

Note add\_chr\_prefix is just a helper argument. You can basically do the same as:

```
gr = getBioMartGenes("hsapiens_gene_ensembl")
seqlevelsStyle(gr) = "UCSC"
```

**Value**

A [GRanges](#) object.

**Examples**

```
gr = getBioMartGenes("hsapiens_gene_ensembl")
gr
gr = getBioMartGenes("hsapiens_gene_ensembl", add_chr_prefix = TRUE)
gr
```

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`getBioMartGenomeInfo`    *Get genome information*

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**Description**

Get genome information

**Usage**

```
getBioMartGenomeInfo(dataset)
```

**Arguments**

`dataset`                    A BioMart dataset or a taxon ID. For a proper value, please see [supportedOrganisms](#).

**Value**

A list.

**Examples**

```
getBioMartGenomeInfo(9606)
```

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```
print.BioMartGOGeneSets_info
```

*Print the BioMartGOGeneSets object*

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**Description**

Print the BioMartGOGeneSets object

**Usage**

```
## S3 method for class 'BioMartGOGeneSets_info'
print(x, ...)
```

**Arguments**

x                    A BioMartG0GeneSets\_info object.  
...                  Other arguments

**Value**

No value is returned.

**Examples**

```
BioMartG0GeneSets
```

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|                    |                                |
|--------------------|--------------------------------|
| supportedOrganisms | <i>All supported organisms</i> |
|--------------------|--------------------------------|

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**Description**

All supported organisms

**Usage**

```
supportedOrganisms(html = TRUE)
```

**Arguments**

html                Whether to open the table in the web browser?

**Value**

A data frame of supported organisms.

**Examples**

```
if(interactive()) {  
  supportedOrganisms()  
}
```

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