

# BioMartGOGeneSets

August 15, 2024

---

BioMartGOGeneSets      *Version and source information*

---

## Description

Version and source information

## Usage

BioMartGOGeneSets

## Examples

BioMartGOGeneSets

---

changeSeqnameStyle      *Change sequence names*

---

## 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)
```

---

getBioMartGOGeneSets *Get GO gene sets*

---

**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)
```

---

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

---

**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 ture, it uses GenomeInfoDb::seqlevelsStyle = "UCSC" 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
```

---

`getBioMartGenomeInfo` *Get genome information*

---

**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)
```

---

`print.BioMartGOGeneSets_info`  
*Print the BioMartGOGeneSets object*

---

**Description**

Print the BioMartGOGeneSets object

**Usage**

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

**Arguments**

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

**Value**

No value is returned.

**Examples**

```
BioMartGOGeneSets
```

---

`supportedOrganisms`     *All supported organisms*

---

**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()  
}
```

# Index

BioMartGOGeneSets, [1](#)

changeSeqnameStyle, [1](#)

getBioMartGenes, [3](#)

getBioMartGenomeInfo, [2, 4](#)

getBioMartGOGeneSets, [2](#)

GRanges, [2, 4](#)

print.BioMartGOGeneSets\_info, [4](#)

supportedOrganisms, [2–4, 5](#)