Package: IMPCdata (via r-universe)

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`getAlleles` *Method "getAlleles"*

Description

Returns alleles (MGI IDs or temporary IDs if the MGI ID is not assigned yet) that are processed for a specified combination of parameter, procedure, pipeline and phenotyping center. Temporary allele ID starts with "NULL".

Usage

```
getAlleles(PhenCenterName=NULL,PipelineID=NULL,ProcedureID=NULL,
ParameterID=NULL,StrainID=NULL)
```

Arguments

`PhenCenterName`	IMPC phenotyping center; mandatory argument
`PipelineID`	IMPC pipeline ID; mandatory argument
`ProcedureID`	IMPC procedure ID; mandatory argument
`ParameterID`	IMPC parameter ID; mandatory argument
`StrainID`	IMPC strain ID; optional argument

Value

Returns the list of IMPC alleles (IDS of alleles) that are processed measuring specified parameter within the procedure in the pipeline run by phenotyping center.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
listAlleles  <- getAlleles("RBRC","IMPC_001","IMPC_GRS_001","IMPC_GRS_003_001")
for (alleleIndex in 1:min(length(listAlleles), 5)) {
    print(paste(listAlleles[alleleIndex],"-",
                    getName("allele_accession_id","allele_symbol",
                    listAlleles[alleleIndex])))
}
```

getGenes *Method "getGenes"*

Description

Returns the genes (MGI IDs) that are reported for a specified combination of parameter, procedure, pipeline and phenotyping center.

Usage

```
getGenes(PhenCenterName=NULL,PipelineID=NULL,ProcedureID=NULL,ParameterID=NULL,StrainID=NULL)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
PipelineID	IMPC pipeline ID; mandatory argument
ProcedureID	IMPC procedure ID; mandatory argument
ParameterID	IMPC parameter ID; mandatory argument
StrainID	IMPC strain ID; optional argument

Value

Returns the list of IMPC genes (IDS of genes) that are processed measuring specified parameter within the procedure in the pipeline run by phenotyping center.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
listGenes  <- getGenes("RBRC","IMPC_001","IMPC_GRS_001","IMPC_GRS_003_001")
for (geneIndex in 1:min(length(listGenes), 5)) {
    print(paste(listGenes[geneIndex],"-",
                  getName("gene_accession_id","gene_symbol",listGenes[geneIndex])))
}
```

getIMPCDataset *Method "getIMPCDataset"*

Description

Returns the IMPC dataset for a knockout line for a specified combination of parameter, procedure, pipeline, phenotyping centre, allele and strain (genetic background) that is used within the data analysis pipeline implemented on the IMPC database.

Usage

```
getIMPCDataset(PhenCenterName=NULL,PipelineID=NULL,ProcedureID=NULL,ParameterID=NULL,
          AlleleID=NULL,StrainID=NULL)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
PipelineID	IMPC pipeline ID; mandatory argument
ProcedureID	IMPC procedure ID; mandatory argument
ParameterID	IMPC parameter ID; mandatory argument
AlleleID	IMPC allele ID; mandatory argument
StrainID	IMPC strain ID; optional argument

Value

Returns the IMPC dataset as a data frame. - metadata_group string a string indicating a group of experimental and control mice that have the same metadata (see also biological_sample_group)

- metadata list of strings list showing all relevant metadata in effect when the data was collected

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
df <- getIMPCDataset("WTSI","MGP_001","IMPC_CBC_001","IMPC_CBC_008_001","MGI:4433526")
```

getIMPCTable *Method "getIMPCTable"*

Description

Returns the IMPC dataset. There are optional arguments to subset the IMPC dataset. Be aware that without filters this file output will be very large and the query will be time intensive.

Usage

```
getIMPCTable(fileName="IMPCdata",PhenCenterName=NULL, PipelineID=NULL, ProcedureID=NULL, Parameter
       AlleleID=NULL, StrainID=NULL, multipleFiles=TRUE,recordsPerFile=10000)
```

Arguments

fileName	name of the file where to save resulting table with IMPC objects; mandatory argument; default value is set to 'IMPCdata'
PhenCenterName	IMPC phenotyping center
PipelineID	IMPC pipeline ID
ProcedureID	IMPC procedure ID
ParameterID	IMPC parameter ID
AlleleID	allele ID
StrainID	strain ID
multipleFiles	flag: "FALSE" value to get all records into one specified file; "TRUE" value (default) to split records across multiple files named starting with 'fileName'
recordsPerFile	number that specifies how many records to write into one file; default value is 10000

Value

Returns the IMPC dataset.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
getIMPCTable("./IMPCData_WTSI","WTSI","MGP_001","IMPC_CBC_001","IMPC_CBC_003_001","MGI:4431644")
```

getName *Method "getName"*

Description

Returns IMPC object name by its ID. An internal function, if called directly please use with caution.

Usage

```
getName(fieldNameFrom,fieldNameTo,fieldValueFrom)
```

Arguments

fieldNameFrom	name of the IMPC field for the object ID; mandatory argument
fieldNameTo	name of the IMPC field for the object name; mandatory argument
fieldValueFrom	actual IMPC object's ID to get the name for; mandatory argument

Value

Returns name of the object.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
getName("pipeline_stable_id","pipeline_name","MGP_001")
```

getParameters *Method "getParameters"*

Description

Returns the list of parameters (IMPReSS IDs) that are measured within specified procedure for a pipeline run by phenotyping center.

Usage

```
getParameters(PhenCenterName=NULL,PipelineID=NULL,ProcedureID=NULL)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
PipelineID	IMPC pipeline ID; mandatory argument
ProcedureID	IMPC procedure ID; mandatory argument

Value

Returns the list of IMPC parameters (IDS of parameters) that are measured within specified procedure in the pipeline run by phenotyping center.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
listParameters  <- getParameters("WTSI","MGP_001","IMPC_CBC_001")
for (parameterIndex in 1:min(length(listParameters), 5)) {
    print(paste(listParameters[parameterIndex],"-",
            getName("parameter_stable_id","parameter_name",listParameters[parameterIndex])))
}
```

---

getPhenCenters *Method "getPhenCenters"*

Description

Returns the list of IMPC phenotyping centers.

Usage

```
getPhenCenters(excludeLegacyPipelines=TRUE)
```

Arguments

excludeLegacyPipelines	flag: FALSE value to get all IMPC phenotyping centers that run all kind of pipelines including legacy pipelines; TRUE value (default) to get IMPC phenotyping centers excluding centers that run only legacy pipelines

Value

Returns the list of IMPC phenotyping centers.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
getPhenCenters()
```

getPipelines *Method "getPipelines"*

Description

Returns the list of IMPC pipelines (IMPReSS IDs) that are run by specified phenotyping center.

Usage

```
getPipelines(PhenCenterName=NULL,excludeLegacyPipelines=TRUE)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
excludeLegacyPipelines	flag: "FALSE" value to get all pipelines including legacy pipelines; "TRUE" value (default) to get current IMPC pipelines excluding legacy pipelines

Value

Returns the list of IMPC pipelines (IDS of pipelines) that are run by specified phenotyping center.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
listPipelines  <- getPipelines("WTSI")
for (pipelineIndex in 1:length(listPipelines)) {
    print(paste(listPipelines[pipelineIndex],"-",
          getName("pipeline_stable_id","pipeline_name",listPipelines[pipelineIndex])))
}
```

getProcedures *Method "getProcedures"*

Description

Returns the list of procedures (IMPReSS IDs) that are run for a specified phenotyping center and pipeline.

Usage

```
getProcedures(PhenCenterName=NULL,PipelineID=NULL)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
PipelineID	IMPC pipeline ID; mandatory argument

Value

Returns the list of IMPC procedures (IDS of procedures) that are run by specified phenotyping center and pipeline.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
 listProcedures  <- getProcedures("WTSI","MGP_001")
for (procedureIndex in 1:min(length(listProcedures), 5)) { # Print the name of 5 procedures
     print(paste(listProcedures[procedureIndex],"-",
             getName("procedure_stable_id","procedure_name",listProcedures[procedureIndex])))
 }
```

---

getStrains *Method "getStrains"*

Description

Returns the genetic background (MGI IDs) from which the knockout mice were derived for a specific combination of pipeline, procedure and paramater for a phenotyping center.

Usage

```
getStrains(PhenCenterName=NULL,PipelineID=NULL,ProcedureID=NULL,ParameterID=NULL)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
PipelineID	IMPC pipeline ID; mandatory argument
ProcedureID	IMPC procedure ID; mandatory argument
ParameterID	IMPC parameter ID; mandatory argument

Value

Returns the list of IMPC strains (IDS of strains) that are processed measuring specified parameter within the procedure in the pipeline run by phenotyping center.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
listStrains  <- getStrains("WTSI","MGP_001","IMPC_CBC_001","IMPC_CBC_003_001")
for (strainIndex in 1:length(listStrains)) {
    print(paste(listStrains[strainIndex],"-",
             getName("strain_accession_id","strain_name",listStrains[strainIndex])))
}
```

`getZygosities` *Method "getZygosities"*

Description

Returns the list of zygosities (homozygous, heterozygous and hemizygous) for mice that were measured for a gene/allele for a specificed combination of parameter, procedure, pipeline and phenotyping center.

Usage

```
getZygosities(PhenCenterName=NULL,PipelineID=NULL,ProcedureID=NULL,ParameterID=NULL,
         StrainID=NULL,GeneID=NULL, AlleleID=NULL)
```

Arguments

`PhenCenterName`	IMPC phenotyping center; mandatory argument
`PipelineID`	IMPC pipeline ID; mandatory argument
`ProcedureID`	IMPC procedure ID; mandatory argument
`ParameterID`	IMPC parameter ID; mandatory argument
`StrainID`	IMPC strain ID; optional argument
`GeneID`	IMPC gene ID; optional argument
`AlleleID`	IMPC allele ID; optional argument

Value

Returns the list of IMPC genes (IDS of genes) that are processed measuring specified parameter within the procedure in the pipeline run by phenotyping center.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
listZygosities <- getZygosities("WTSI","MGP_001","IMPC_CBC_001","IMPC_CBC_003_001",GeneID="MGI:1194894")
 for (zygosityIndex in 1:length(listZygosities)) {
     print(listZygosities[zygosityIndex])
 }
```

printAlleles *Method "printAlleles"*

Description

Prints out alleles (MGI IDs or temporary IDs if the MGI is not assigned yet and symbols) that are processed for a specified combination of parameter, procedure, pipeline and phenotyping center. Temporary allele ID starts with "NULL".

Usage

```
printAlleles(PhenCenterName=NULL,PipelineID=NULL,ProcedureID=NULL,
ParameterID=NULL,StrainID=NULL,n=NULL)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
PipelineID	IMPC pipeline ID; mandatory argument
ProcedureID	IMPC procedure ID; mandatory argument
ParameterID	IMPC parameter ID; mandatory argument
StrainID	IMPC strain ID; optional argument
n	print only first n alleles; optional argument

Value

Returns the character containing IMPC alleles (IDs and names of alleles)

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
printAlleles("RBRC","IMPC_001","IMPC_GRS_001","IMPC_GRS_003_001", n = 5)
```

printGenes *Method "printGenes"*

Description

Prints out genes (MGI IDs and symbols) that are reported for a specified combination of parameter, procedure, pipeline and phenotyping center.

Usage

```
printGenes(PhenCenterName=NULL,PipelineID=NULL,ProcedureID=NULL,
ParameterID=NULL,StrainID=NULL,n=NULL)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
PipelineID	IMPC pipeline ID; mandatory argument
ProcedureID	IMPC procedure ID; mandatory argument
ParameterID	IMPC parameter ID; mandatory argument
StrainID	IMPC strain ID; optional argument
n	print only first n genes; optional argument

Value

Returns the character containing IMPC genes (IDs and names of genes)

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
printGenes("RBRC","IMPC_001","IMPC_GRS_001","IMPC_GRS_003_001", n = 5)
```

printParameters *Method "printParameters"*

Description

Prints out the list of parameters (IMPReSS IDs and names) that are measured within specified procedure for a pipeline run by phenotyping center.

Usage

```
printParameters(PhenCenterName=NULL,PipelineID=NULL,ProcedureID=NULL,n=NULL)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
PipelineID	IMPC pipeline ID; mandatory argument
ProcedureID	IMPC procedure ID; mandatory argument
n	print only first n parameters; optional argument

Value

Returns the character containing IMPC parameters (IDs and names of parameters)

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
printParameters("WTSI","MGP_001","IMPC_CBC_001", n = 5)
```

---

printPhenCenters *Method "printPhenCenters"*

Description

Prints out the list of IMPC phenotyping centers.

Usage

```
printPhenCenters(n=NULL, excludeLegacyPipelines=TRUE)
```

Arguments

n	print only first n phenotyping centers; optional argument
excludeLegacyPipelines	flag: "FALSE" value to print all IMPC phenotyping centers that run all kind of pipelines including legacy pipelines; "TRUE" value (default) to print IMPC phenotyping centers excluding centers that run only legacy pipelines

Value

Returns the character with IMPC phenotyping centers.

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
printPhenCenters(excludeLegacyPipelines = FALSE)
```

printPipelines *Method "printPipelines"*

Description

Prints out the list of IMPC pipelines (IMPReSS IDs and names) that are run by specified phenotyping center.

Usage

```
printPipelines(PhenCenterName=NULL,n=NULL, excludeLegacyPipelines=TRUE)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
n	print only first n pipelines; optional argument
excludeLegacyPipelines	flag: "FALSE" value to print all pipelines including legacy pipelines; "TRUE" value (default) to print current IMPC pipelines excluding legacy pipelines

Value

Returns the character containing IMPC pipelines (IDs and names of pipelines)

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
printPipelines("WTSI")
```

printProcedures *Method "printProcedures"*

Description

Prints out the list of procedures (IMPReSS IDs and names) that are run for a specified phenotyping center and pipeline.

Usage

```
printProcedures(PhenCenterName=NULL,PipelineID=NULL,n=NULL)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
PipelineID	IMPC pipeline ID; mandatory argument
n	print only first n procedures; optional argument

Value

Returns the character containing IMPC procedures (IDs and names of procedures)

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
printProcedures("WTSI","MGP_001", 5)
```

---

printStrains *Method "printStrains"*

Description

Prints out the genetic background (MGI IDs and strain name) from which the knockout mice were derived for a specific combination of pipeline, procedure and paramater for a phenotyping center.

Usage

```
printStrains(PhenCenterName=NULL,PipelineID=NULL,ProcedureID=NULL,
ParameterID=NULL,n=NULL)
```

Arguments

PhenCenterName	IMPC phenotyping center; mandatory argument
PipelineID	IMPC pipeline ID; mandatory argument
ProcedureID	IMPC procedure ID; mandatory argument
ParameterID	IMPC parameter ID; mandatory argument
n	print only first n strains; optional argument

Value

Returns the character containing IMPC strains (IDs and names of strains)

Author(s)

Natalja Kurbatova, Jeremy Mason

Examples

```
printStrains("WTSI","MGP_001","IMPC_CBC_001","IMPC_CBC_003_001")
```

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