Package ‘ipdDb’

May 29, 2024

Title  IPD IMGT/HLA and IPD KIR database for Homo sapiens

Description  All alleles from the IPD IMGT/HLA
<https://www.ebi.ac.uk/ipd/imgt/hla/> and IPD KIR
<https://www.ebi.ac.uk/ipd/kir/> database for Homo sapiens.
Reference:
Robinson J, Maccari G, Marsh SGE, Walter L, Blokhuis J, Bimber B, Parham P,
De Groot NG, Bontrop RE, Guethlein LA, and Hammond JA
KIR Nomenclature in non-human species

Version  1.22.0

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Depends  R (>= 3.5.0), methods, AnnotationDbi (>= 1.43.1),
AnnotationHub

Imports  Biostrings, GenomicRanges, RSQLite, DBI, IRanges, stats,
assertthat

License  Artistic-2.0

URL  https://github.com/DKMS-LSL/ipdDb

BugReports  https://github.com/DKMS-LSL/ipdDb/issues/new

organism  Homo sapiens

species  Homo sapiens

biocViews  GenomicVariation, SequenceMatching, VariantAnnotation,
DataRepresentation,AnnotationHubSoftware

Suggests  knitr, rmarkdown, testthat

RoxygenNote  6.1.0

Encoding  UTF-8

VignetteBuilder  knitr

git_url  https://git.bioconductor.org/packages/ipdDb

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getAlleles,IpdpDb-method

Get alleles

Description
Get all alleles of a given locus.

Usage
getAlleles(x, locus)

Arguments
x The database connection; an IpdpDb object.
locus A single locus as a string.

Value
A character vector with all alleles of the give locus.

Examples
## Load the database
hla <- loadHlaData()
## Get the loci
loci <- getLoci(hla)
## Get alleles of a locus
alleles <- getAlleles(hla, loci[1])
getClosestComplete

*Description*

Get the sequence of the closest allele which for which a full-length sequence is available.

*Usage*

```r
getClosestComplete(x, allele, locus = NULL)
```

*Arguments*

- `x`: The database connection; an `IpdDb` object.
- `allele`: A single allele as a string.
- `locus`: optional parameter used if the allele identifier is not found.

*Value*

A `Biostrings:DNAStringSet` object with the sequence of the closest full-length allele.

*Examples*

```r
## Load the database
hla <- loadHlaData()
## Get the loci
loci <- getLoci(hla)
## Get alleles of a locus
alleles <- getAlleles(hla, loci[1])
alleleOfInterest <- alleles[1]
## Get the closest complete sequence
seqs <- getClosestComplete(hla, alleleOfInterest, loci[1])
```

getLoci

*Description*

Get all available loci of the KIR or HLA database

*Usage*

```r
getLoci(x)
```
Arguments

x  The database connection; an IpdDb object.

Value

A vector of available loci in the database.

Examples

## Load the database
hla <- loadHlaData()
## Get the loci
loci <- getLoci(hla)

# Load the database
hla <- loadHlaData()
# Get the loci
loci <- getLoci(hla)
# Get alleles of a locus
alleles <- getAlleles(hla, loci[1])
allelesOfInterest <- alleles[1:10]
# Get the sequences
seqs <- getReference(hla, allelesOfInterest)
getStructure,IpdDb-method

Get gene structures

Description
Get the gene structures for alleles.

Usage
getStructure(x, allele)

Arguments
x
The database connection; an IpdDb object.

allele
The alleles of interest as a character vector.

Value
A GenomicRanges:GRanges object with all gene structures.

Examples
## Load the database
hla <- loadHlaData()
## Get the loci
loci <- getLoci(hla)
## Get alleles of a locus
alleles <- getAlleles(hla, loci[1])
allelesOfInterest <- alleles[1:10]
## Get the structures
seqs <- getStructure(hla, allelesOfInterest)

IpdDb-class

The database class for storing allele data from IPD.

Description
This class extends the AnnotationDbi::AnnDbObj-class object by higher level methods for sequence and annotation retrieval. blubb
Usage

columns(x)
keytypes(x)
keys(x, keytype, ...)
select(x, keys, columns, keytype, ...)

Arguments

x the IpdDb object
keytype The keytype for which the keys are retrieved
... Additional arguments. Not used now.
keys The keys for which columns should be selected by select()
columns The columns to retrieve by select

Value

character vector (keys, columns, keytypes) or a data.frame (select).

Slots

ggetDbVersion() Get the version of the original ipd database
getLoci() get all loci from a database, see getLoci.
ggetReference(alleles) Get the reference sequence for alleles, see getReference.
getStructure(alleles) Get the structures of alleles, see getStructure.
getClosestComplete(allele) Get the closest full-length reference sequence of one allele, see getClosestComplete.
getAlleles(locus) Get all alleles of a locus, see getAlleles.

See Also

AnnotationDbi::AnnDbObj-class

Examples

## load the data
hla <- loadHlaData()
## get all valid keytypes
kts <- keytypes(hla)
## get all valid columns
cols <- columns(hla)
## get the keys of one keytype
kt <- kts[[1]]
keys <- keys(hla, kt)
## Get data of the two first columns for the first 10 keys
cols <- cols[1:10]
res <- select(hla, keys, cols, kt)

loadHlaData(version = "Latest")

version

Value

an IpdDb object containing the database.
**Examples**

```r
## Load the HLA database
hla <- loadHlaData()
```

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**loadKirData**  
*Load the IPD KIR database*

**Description**

Load the IPD KIR database

**Usage**

```r
loadKirData(version = "Latest")
```

**Arguments**

- `version`  
  Either a valid version of the IPD KIR database or "Latest" to fetch the latest version

**Value**

an `IpdDb` object containing the database.

**Examples**

```r
## Load the KIR database
kir <- loadKirData()
```
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