Package ‘ipdDb’

February 2, 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

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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,Ipdb-method

Get alleles

Description
Get all alleles of a given locus.

Usage
getAlleles(x, locus)

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

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

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

Get closest full-length sequence

Description

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

Usage

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, IpdDb-method

Get loci

Description

Get all available loci of the KIR or HLA database

Usage

getLoci(x)
getReference.IpdDb-method

Arguments

x
The database connection; an IpdDb object.

Value

A vector of available loci in the database.

Examples

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

getReference.IpdDb-method

Get reference sequences

Description

Get the reference sequences for alleles.

Usage

getReference(x, allele)

Arguments

x
The database connection; an IpdDb object.

allele
The alleles of interest as a character vector.

Value

A Biostrings:DNAStringSet object with all references.

Examples

```r
## 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**

```r
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**

```r
## 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 IpDb 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

- `getDbVersion()` Get the version of the original ipd database
- `getLoci()` Get all loci from a database, see `getLoci`.
- `getReference(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

```r
## 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)

ipdDbPackage

Get allele information from IPD

Description
This package holds the IPD IMGT/HLA and IPD KIR database. All alleles are accessible using the select, columns, keys and keytypes methods of the AnnotationDbi package of bioconductor.

Details
Included data are:
Allele names
p-groups
g-groups
cwd_status
completeness status
gene structure
reference sequences
closest full-length allele

loadHlaData
Load the IPD IMGT/HLA database

Description
Load the IPD IMGT/HLA database

Usage
loadHlaData(version = "Latest")

Arguments
version Either a valid version of the IPD IMGT/HLA database or "Latest" to fetch the latest version

Value
an IpdDb object containing the database.
Examples

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

loadKirData

Load the IPD KIR database

Description

Load the IPD KIR database

Usage

`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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