Package ‘ipdDb’

May 28, 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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Author  Steffen Klasberg
Maintainer  Steffen Klasberg <klasberg@dkms-lab.de>
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AnnotationHub
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assertthat
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BugReports  https://github.com/DKMS-LSL/ipdDb/issues/new
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**getAlleles, IpdDb-method**

*Get alleles*

**Description**

Get all alleles of a given locus.

**Usage**

```r
getAlleles(x, locus)
```

**Arguments**

- `x`: The database connection; an `IpdDb` object.
- `locus`: A single locus as a string.

**Value**

A character vector with all alleles of the give locus.

**Examples**

```r
## Load the database
hla <- loadHlaData()
## Get the loci
loci <- getLoci(hla)
## Get alleles of a locus
alleles <- getAlleles(hla, loci[1])
```
**getClosestComplete,IpDb-method**  
*Get closest full-length sequence*

**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 `Ipdb` 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,IpDb-method**  
*Get loci*

**Description**

Get all available loci of the KIR or HLA database.

**Usage**

```r
getLoci(x)
```
getReference.IpdDb-method

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)

## 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
```
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 AnnoatationDbi 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()
```

---

## 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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