Package ‘ipdDb’

May 17, 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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AnnotationHub
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assertthat
License   Artistic-2.0
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BugReports   https://github.com/DKMS-LSL/ipdDb/issues/new
organism   Homo sapiens
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getAlleles.IpdDb-method

Get alleles

Description

Get all alleles of a given locus.

Usage

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 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
## 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)
**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)

## Get alleles of a locus
alleles <- getAlleles(hla, loci[1])
allelesOfInterest <- alleles[1:10]
## Get the sequences
seqs <- getReference(hla, allelesOfInterest)
```

---

**getDescription.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

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

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

## 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**

```r
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()
```

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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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