Package ‘ipdDb’

March 22, 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.
De Groot NG, Bontrop RE, Guethlein LA, and Hammond JA
KIR Nomenclature in non-human species

Version  1.20.0

Author  Steffen Klasberg

Maintainer  Steffen Klasberg <klasberg@dkms-lab.de>

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

git_branch  RELEASE_3_18

git_last_commit  91c41ad
getAlleles.IpdDb-method

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 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, 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

## 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
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.
## 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()
```
Index

.IpdDb (IpdDb-class), 5
Biostrings:DNAStringSet, 3, 4
columns (IpdDb-class), 5
columns, IpdDb-method (IpdDb-class), 5
GenomicRanges:GRanges, 5
getAlleles, 6
getAlleles (getAlleles, IpdDb-method), 2
getAlleles, IpdDb-method, 2
getClosestComplete, 6
getClosestComplete
   (getClosestComplete, IpdDb-method), 3
getClosestComplete, IpdDb-method, 3
getLoci, 6
getLoci (getLoci, IpdDb-method), 3
getLoci, IpdDb-method, 3
getReference, 6
getReference
   (getReference, IpdDb-method), 4
getReference, IpdDb-method, 4
getStructure, 6
getStructure
   (getStructure, IpdDb-method), 5
getStructure, IpdDb-method, 5
IpdDb, 2–5, 7, 8
IpdDb (IpdDb-class), 5
IpdDb-class, 5
ipdDbPackage, 7
ipdDbPackage-package (ipdDbPackage), 7
keys (IpdDb-class), 5
keys, IpdDb-method (IpdDb-class), 5
keytypes (IpdDb-class), 5
keytypes, IpdDb-method (IpdDb-class), 5
loadHlaData, 7
loadKirData, 8