Package ‘ipdDb’

January 18, 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

Get alleles

Description
Get all alleles of a given locus.

Usage
get Alleles(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

## 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

## 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 se-
quence 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.

getAddress(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]

## 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

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

## Load the KIR database
```r
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
ggetReference, 6
ggetReference
  (getReference, IpdDb-method), 4
ggetReference, 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