Package ‘ipdDb’

March 20, 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, Blokhuys 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

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URL https://github.com/DKMS-LSL/ipdDb

BugReports https://github.com/DKMS-LSL/ipdDb/issues/new

organism Homo sapiens

species Homo sapiens

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  DataRepresentation,AnnotationHubSoftware

Suggests knitr, rmarkdown, testthat

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getAlleles,IpdpDb-method

Get alleles

Description
Get all alleles of a given locus.

Usage
getAlleles(x, locus)

Arguments
x The database connection; an IpdpDb 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,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

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

## 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

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)

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

## 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,IpDb-method

Get gene structures

Description

Get the gene structures for alleles.

Usage

getStructure(x, allele)

Arguments

x
The database connection; an IpDb 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.
getAddress(alleles) Get the reference sequence for alleles, see getAddress.
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 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

## Load the KIR database
kir <- loadKirData()
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