Package ‘ipdDb’

May 3, 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

Version  1.22.0

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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

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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 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

getchClosestComplete(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

getchLoci(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)
```
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 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

```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
```
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

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**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.
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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