Package ‘ipdDb’

March 6, 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
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,
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getAlleles,Ipdb-method

Get alleles

Description

Get all alleles of a given locus.

Usage

getAlleles(x, locus)

Arguments

x
The database connection; an Ipdb 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**

```r
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**

```r
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)
```

```r
generateReference,IpdpDb-method

Get reference sequences

Description

Get the reference sequences for alleles.

Usage

generateReference(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 <- generateReference(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

  ## 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.
Examples

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

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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