

Package ‘ipdDb’

May 29, 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

Immunogenetics (2018), in preparation.

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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, IpdDb-method
Get alleles

Description

Get all alleles of a given locus.

Usage

```
getAlleles(x, locus)
```

Arguments

| | |
|-------|--|
| x | The database connection; an <code>IpdDb</code> 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)
```

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, 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 | <i>Get allele information from IPD</i> |
|--------------|--|

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 | <i>Load the IPD IMGT/HLA database</i> |
|-------------|---------------------------------------|

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  
hla <- loadHlaData()
```

| | |
|-------------|----------------------------------|
| loadKirData | <i>Load the IPD KIR database</i> |
|-------------|----------------------------------|

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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