

Package ‘ipdDb’

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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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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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getAlleles, IpdDb-method
<i>Get alleles</i>

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, 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

<code>x</code>	the IpdDb object
<code>keytype</code>	The keytype for which the keys are retrieved
<code>...</code>	Additional arguments. Not used now.
<code>keys</code>	The keys for which columns should be selected by <code>select()</code>
<code>columns</code>	The columns to retrieve by <code>select</code>

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)
```

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 `AnnoatationDbi` 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  
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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