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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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

biocViews GenomicVariation, SequenceMatching, VariantAnnotation, 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 `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

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 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` *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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