

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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Author Steffen Klasberg

Maintainer Steffen Klasberg <klasberg@dkms-lab.de>

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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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Contents

getAlleles,IpDb-method	2
getClosestComplete,IpDb-method	3
getLoci,IpDb-method	3
getReference,IpDb-method	4
getStructure,IpDb-method	5
IpDb-class	5
ipDbPackage	7
loadHlaData	7
loadKirData	8

Index	9
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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 <code>IpDb</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 *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

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

loadKirData	<i>Load the IPD KIR database</i>
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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
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Value

an [IpdDb](#) object containing the database.

Examples

```
## Load the KIR database  
kir <- loadKirData()
```


Index

.IpdDb (IpdDb-class), 5

Biostrings:DNAStrngSet, 3, 4

columns (IpdDb-class), 5
columns, IpdDb-method (IpdDb-class), 5

GenomicRanges:GRanges, 5
getAlleles, 6
getAlleles (getAlleles, IpdDb-method), 2
getAlleles, IpdDb-method, 2
getClosestComplete, 6
getClosestComplete
 (getClosestComplete, IpdDb-method),
 3
getClosestComplete, IpdDb-method, 3
getLoci, 6
getLoci (getLoci, IpdDb-method), 3
getLoci, IpdDb-method, 3
getReference, 6
getReference
 (getReference, IpdDb-method), 4
getReference, IpdDb-method, 4
getStructure, 6
getStructure
 (getStructure, IpdDb-method), 5
getStructure, IpdDb-method, 5

IpdDb, 2–5, 7, 8
IpdDb (IpdDb-class), 5
IpdDb-class, 5
ipdDbPackage, 7
ipdDbPackage-package (ipdDbPackage), 7

keys (IpdDb-class), 5
keys, IpdDb-method (IpdDb-class), 5
keytypes (IpdDb-class), 5
keytypes, IpdDb-method (IpdDb-class), 5

loadHlaData, 7
loadKirData, 8

select (IpdDb-class), 5
select, IpdDb-method (IpdDb-class), 5