

# Package ‘ipdDb’

April 15, 2020

**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

**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

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DataRepresentation

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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**

```
getClosestComplete(x, allele, locus = NULL)
```

**Arguments**

x	The database connection; an <a href="#">IpdDb</a> 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 <a href="#">IpdDb</a> 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 <a href="#">IpdDb</a> 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)
```

**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>
-------------	----------------------------------

---

**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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