

# Package ‘ipdDb’

December 18, 2025

**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.

**Version** 1.29.0

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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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Contents

|                                           |          |
|-------------------------------------------|----------|
| getAlleles,IpdDb-method . . . . .         | 2        |
| getClosestComplete,IpdDb-method . . . . . | 3        |
| getLoci,IpdDb-method . . . . .            | 3        |
| getReference,IpdDb-method . . . . .       | 4        |
| getStructure,IpdDb-method . . . . .       | 5        |
| IpdDb-class . . . . .                     | 5        |
| ipdDbPackage . . . . .                    | 7        |
| loadHlaData . . . . .                     | 7        |
| loadKirData . . . . .                     | 8        |
| <b>Index</b>                              | <b>9</b> |

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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 <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 [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 <a href="#">IpdDb</a> 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 | <i>The database class for storing allele data from IPD.</i> |
|-------------|-------------------------------------------------------------|

---

### 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> |
|-------------|----------------------------------|

---

**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()
```



# Index

.IpdDb (IpdDb-class), [5](#)

Biostrings:DNASTringSet, [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](#)