

# Package ‘ipdDb’

September 3, 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.

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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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|                          |
|--------------------------|
| 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 <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 | <i>Load the IPD IMGT/HLA database</i> |
|-------------|---------------------------------------|

---

**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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