# Package 'ipdDb'

November 19, 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`
*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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