

# Package ‘immReferent’

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**Title** An Interface for Immune Receptor and HLA Gene Reference Data

**Version** 0.99.7

**Description** Provides a consistent interface for downloading, storing, and accessing immune receptor (TCR/BCR) and HLA sequences from IMGT, IPD-IMGT/HLA, and OGRDB (AIRR-C). Supports export to popular analysis tools including MiXCR, TRUST4, Cell Ranger, and IgBLAST. This package serves as a core dependency for immunogenomics packages, ensuring reliable and high-quality sequence access with local caching for reproducibility.

**License** MIT + file LICENSE

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immReferent-package     *immReferent: An Interface for Immune Receptor and HLA Gene Reference Data*

---

### Description

**immReferent** provides a stable, reproducible, and lightweight interface to reference sequences for immune receptors (TCR/BCR) and HLA genes sourced from IMGT, IPD-IMGT/HLA, and the AIRR-C's OGRDB. It centralizes downloading, caching, and querying of curated nucleotide and protein sequences, and plays a foundational role in computational immunology workflows.

### Details

The package is designed as a common reference layer across immunoinformatics tools, ensuring consistent provenance and offline reproducibility via caching.

#### Core functionality

- Download and parse receptor and HLA sequences from IMGT and OGRDB
- Local caching to support offline, reproducible analysis
- Query by gene, allele, species, locus, and sequence type/format
- Export to popular analysis tools (MiXCR, TRUST4, Cell Ranger, IgBLAST)
- Interoperability with Bioconductor classes such as [DNAStrngSet](#) and [AAStrngSet](#)

#### Data retrieval functions

- [getIMGT](#): Download sequences from IMGT
- [getOGRDB](#): Download sequences from OGRDB

- `loadIMGT`, `loadOGRDB`: Load cached sequences
- `refreshIMGT`, `refreshOGRDB`: Force re-download

### Export functions

- `exportMiXCR`: Export for MiXCR analysis
- `exportTRUST4`: Export for TRUST4 analysis
- `exportCellRanger`: Export for 10x Cell Ranger VDJ
- `exportIgBLAST`: Export for IgBLAST analysis

### Supported data sources

- IMGT: The international ImMunoGeneTics information system (<https://www.imgt.org/>)
- IPD-IMGT/HLA: The HLA Database (<https://www.ebi.ac.uk/ipd/imgt/hla/>)
- OGRDB: Open Germline Receptor Database (AIRR-C) (<https://ogrdb.airr-community.org/>)

### Getting started

```
browseVignettes("immReferent")
```

### Attribution and Licensing

Data obtained from IMGT and OGRDB must be cited according to their terms. IMGT data are distributed under a [CC BY-NC-ND 4.0](#) license. Proper attribution is required, and derivative or commercial use is restricted per IMGT policy. Always review the current licensing and citation requirements of each resource prior to use.

### Author(s)

**Maintainer:** Nick Borcharding <[ncborch@gmail.com](mailto:ncborch@gmail.com)>

### See Also

<https://github.com/BorchLab/immReferent>

---

exportCellRanger

*Export Reference Sequences to Cell Ranger VDJ Format*

---

### Description

Exports a `DNAStringSet` to FASTA format suitable for creating a custom Cell Ranger VDJ reference. The function generates a FASTA file with properly formatted headers for use with `cellranger mkvdjref`.

### Usage

```
exportCellRanger(sequences, output_file, gene_type = NULL)
```

**Arguments**

sequences	A <a href="#">DNAStrngSet</a> object containing immune receptor sequences. Sequence names must follow standard IG/TR gene nomenclature (e.g., "IGHV1-2*01"). Can be obtained from <a href="#">getIMGT</a> or <a href="#">getOGRDB</a> .
output_file	Character string specifying the path to the output FASTA file. The parent directory will be created if it does not exist.
gene_type	Character string specifying the type of gene region. One of "V", "D", "J", or "C". If NULL (default), the function will attempt to infer the type from sequence names.

**Details**

Cell Ranger's `mkvdjref` command expects FASTA files with specific header formats. This function creates a FASTA file that can be used as input to build a custom VDJ reference.

**Note:** For a complete Cell Ranger VDJ reference, you also need a GTF file with gene annotations. This function only creates the FASTA component.

This function works with sequences from both **IMGT** (via [getIMGT](#)) and **OGRDB** (via [getOGRDB](#)).

**Value**

Character string with the path to the created file, returned invisibly.

**See Also**

[getIMGT](#), [getOGRDB](#) for obtaining sequences

[exportMiXCR](#), [exportTRUST4](#), [exportIgBLAST](#) for other export formats

<https://www.10xgenomics.com/support/software/cell-ranger/latest/analysis/inputs/cr-5p-references> for Cell Ranger documentation

**Examples**

```
# Create a small example DNAStrngSet
seqs <- Biostrings::DNAStrngSet(c(
  "ATGCGATCGATCGATCG",
  "ATGCGATCGATCG"
))
names(seqs) <- c("IGHV1-2*01", "IGHV1-3*01")

# Export to temporary file
output_file <- tempfile(fileext = ".fa")
exportCellRanger(seqs, output_file)

# View the result
cat(readLines(output_file), sep = "\n")

# Clean up
unlink(output_file)
```

---

exportIgBLAST                      *Export Reference Sequences to IgBLAST Format*

---

### Description

Exports a [DNAStrngSet](#) to FASTA files formatted for use with IgBLAST. The function creates separate FASTA files for V, D, and J gene segments with simplified headers compatible with IgBLAST's requirements.

### Usage

```
exportIgBLAST(
  sequences,
  output_dir,
  organism = "custom",
  receptor_type = c("ig", "tcr")
)
```

### Arguments

sequences	A <a href="#">DNAStrngSet</a> object containing immune receptor sequences. Sequence names must follow standard IG/TR gene nomenclature (e.g., "IGHV1-2*01"). Can be obtained from <a href="#">getIMGT</a> or <a href="#">getOGRDB</a> .
output_dir	Character string specifying the directory where output files will be written. The directory will be created if it does not exist.
organism	Character string specifying the organism name for the output files. Used in file naming. Default is "custom".
receptor_type	Character string specifying the receptor type. One of "ig" for immunoglobulin or "tcr" for T-cell receptor. Default is "ig".

### Details

IgBLAST requires FASTA files with simplified headers containing only the gene/allele name. This function mimics the output of IgBLAST's `edit_imgt_file.pl` script, which truncates IMGT headers to keep only the allele designation.

Output files follow the naming convention used by IgBLAST:

- <organism>\_<receptor\_type>\_v.fasta
- <organism>\_<receptor\_type>\_d.fasta
- <organism>\_<receptor\_type>\_j.fasta

After exporting, use `makeblastdb` with the `-parse_seqids` flag to create the BLAST database:

```
makeblastdb -parse_seqids -dbtype nucl -in <fasta_file> -out <db_name>
```

This function works with sequences from both **IMGT** (via [getIMGT](#)) and **OGRDB** (via [getOGRDB](#)).

**Value**

A named list containing the paths to the created files, returned invisibly. The list may contain elements `v_genes`, `d_genes`, and `j_genes` depending on which segment types were found in the input sequences.

**See Also**

[getIMGT](#), [getOGRDB](#) for obtaining sequences

[exportMiXCR](#), [exportTRUST4](#), [exportCellRanger](#) for other export formats

<https://ncbi.github.io/igblast/> for IgBLAST documentation

**Examples**

```
# Create a small example DNASTringSet
seqs <- Biostrings::DNASTringSet(c(
  "ATGCCGATCGATCGATCG",
  "ATGCCGATCGATCG",
  "ATGCCGATC"
))
names(seqs) <- c("IGHV1-2*01", "IGHD1-1*01", "IGHJ1*01")

# Export to temporary directory
output_dir <- tempdir()
files <- exportIgBLAST(seqs, output_dir, organism = "human", receptor_type = "ig")
print(files)

# Clean up
unlink(unlist(files))
```

---

exportMiXCR

*Export Reference Sequences to MiXCR Format*

---

**Description**

Exports a [DNASTringSet](#) or [AAStringSet](#) to FASTA files formatted for use with MiXCR's `buildLibrary` command. The function creates separate FASTA files for V, D, J, and C gene segments.

**Usage**

```
exportMiXCR(
  sequences,
  output_dir,
  chain = c("IGH", "IGK", "IGL", "TRA", "TRB", "TRD", "TRG")
)
```

## Arguments

sequences	A <a href="#">DNAStrngSet</a> or <a href="#">AAStringSet</a> object containing immune receptor sequences. Sequence names must follow standard IG/TR gene nomenclature (e.g., "IGHV1-2*01", "TRBJ2-1*01"). Can be obtained from <a href="#">getIMGT</a> or <a href="#">getOGRDB</a> .
output_dir	Character string specifying the directory where output files will be written. The directory will be created if it does not exist.
chain	Character string specifying the chain type for the output files. Must be one of "IGH", "IGK", "IGL", "TRA", "TRB", "TRD", or "TRG".

## Details

MiXCR expects FASTA files with simple headers containing only the gene name. The function filters sequences by gene type (V, D, J, C) based on the gene name pattern and writes separate files for each segment type.

Output files follow the naming convention:

- v-genes.<chain>.fasta
- d-genes.<chain>.fasta
- j-genes.<chain>.fasta
- c-genes.<chain>.fasta

This function works with sequences from both **IMGT** (via [getIMGT](#)) and **OGRDB** (via [getOGRDB](#)).

## Value

A named list containing the paths to the created files, returned invisibly. The list may contain elements `v_genes`, `d_genes`, `j_genes`, and `c_genes` depending on which segment types were found in the input sequences.

## See Also

[getIMGT](#), [getOGRDB](#) for obtaining sequences

[exportTRUST4](#), [exportCellRanger](#), [exportIgBLAST](#) for other export formats

<https://mixcr.com/mixcr/guides/create-custom-library/> for MiXCR documentation

## Examples

```
# Create a small example DNAStrngSet
seqs <- Biostrings::DNAStrngSet(c(
  "ATGCCGATCGATCGATCG",
  "ATGCCGATCGATCG",
  "ATGCCGATC",
  "ATGCCGATCGATCGATCGATCG"
))
names(seqs) <- c("IGHV1-2*01", "IGHD1-1*01", "IGHJ1*01", "IGHC*01")

# Export to temporary directory
output_dir <- tempdir()
```

```
files <- exportMiXCR(seqs, output_dir, chain = "IGH")
print(files)

# Clean up
unlink(unlist(files))
```

---

 exportTRUST4

*Export Reference Sequences to TRUST4 Format*


---

## Description

Exports a [DNAStrngSet](#) to a FASTA file formatted for use with TRUST4. The output follows the format produced by TRUST4's `BuildImgtAnnot.pl` script.

## Usage

```
exportTRUST4(sequences, output_file, include_constant = TRUE)
```

## Arguments

sequences	A <a href="#">DNAStrngSet</a> object containing immune receptor sequences. Sequence names must follow standard IG/TR gene nomenclature (e.g., "IGHV1-2*01"). Can be obtained from <a href="#">getIMGT</a> or <a href="#">getOGRDB</a> .
output_file	Character string specifying the path to the output FASTA file. The parent directory will be created if it does not exist.
include_constant	Logical. If TRUE (default), include constant region sequences. TRUST4's <code>IMGT+C.fa</code> file includes constant regions.

## Details

TRUST4 expects FASTA files with headers containing only the allele name (e.g., >IGHV1-2\*01). The function reformats sequence headers to match the output of TRUST4's `BuildImgtAnnot.pl` script.

TRUST4 uses this reference for the `--ref` parameter in its analysis pipeline.

This function works with sequences from both **IMGT** (via [getIMGT](#)) and **OGRDB** (via [getOGRDB](#)).

## Value

Character string with the path to the created file, returned invisibly.

## See Also

[getIMGT](#), [getOGRDB](#) for obtaining sequences

[exportMiXCR](#), [exportCellRanger](#), [exportIgBLAST](#) for other export formats

<https://github.com/liulab-dfci/TRUST4> for TRUST4 documentation

**Examples**

```
# Create a small example DNASTringSet
seqs <- Biostrings::DNASTringSet(c(
  "ATGCCGATCGATCGATCG",
  "ATGCCGATCGATCG",
  "ATGCCGATC"
))
names(seqs) <- c("IGHV1-2*01", "IGHJ1*01", "IGHC*01")

# Export to temporary file
output_file <- tempfile(fileext = ".fa")
exportTRUST4(seqs, output_file)

# View the result
cat(readLines(output_file), sep = "\n")

# Clean up
unlink(output_file)
```

---

getIMGT	<i>Download and Load Immune Receptor and HLA Sequences from IMGT</i>
---------	--

---

**Description**

This is the main function to download and load reference sequences from IMGT and the IPD-IMGT/HLA database. It handles caching of downloaded files.

**Usage**

```
getIMGT(
  species = "human",
  gene,
  type = c("NUC", "PROT"),
  refresh = FALSE,
  suppressMessages = FALSE
)
```

**Arguments**

species	Character string specifying the species for which to download data. Required for TCR/BCR queries. Currently supported species: "human", "mouse", "rat", "rabbit", "pig", "dog", "rhesus_monkey", "cyno_monkey". Defaults to "human" for HLA queries.
gene	Character string specifying the gene or locus to download. For TCR/BCR, this can be a specific chain (e.g., "IGHV", "TRBJ") or a group (e.g., "IGH", "TCR"). For HLA, use "HLA".

type	Character string specifying the type of sequence to retrieve. Either "NUC" for nucleotide or "PROT" for protein sequences. This primarily distinguishes between VDJ nucleotide and V-region amino acid sequences for TCR/BCR genes.
refresh	Logical. If TRUE, forces a re-download of the data even if it exists in the cache. Default is FALSE.
suppressMessages	Logical. If TRUE, suppresses the license and other informational messages. Default is FALSE.

**Value**

A [DNAStrngSet](#) object (when type = "NUC") or [AAStringSet](#) object (when type = "PROT") containing the requested sequences.

**See Also**

[loadIMGT](#), [refreshIMGT](#) for convenience wrappers

[getOGRDB](#) for OGRDB/AIRR-C germline sequences

[exportMiXCR](#), [exportTRUST4](#), [exportCellRanger](#), [exportIgBLAST](#) for exporting sequences to analysis tools

**Examples**

```
if(is_imgt_available()) {
  # Download human IGHV nucleotide sequences
  ighv_nuc <- getIMGT(species = "human",
                    gene = "IGHV",
                    type = "NUC")

  # Download all HLA protein sequences
  hla_prot <- getIMGT(gene = "HLA",
                    type = "PROT")

  # Download all mouse TRB genes
  trb_mouse <- getIMGT(species = "mouse",
                      gene = "TRB",
                      type = "NUC")
}
```

---

getOGRDB

*Download and Load Immune Receptor Germline Sequences from OGRDB*

---

**Description**

Downloads AIRR-compliant germline sets (or FASTA) from OGRDB (Open Germline Receptor Database) and returns sequences as a [DNAStrngSet](#) or [AAStringSet](#).

**Usage**

```

getOGRDB(
  species = "human",
  locus = c("IGH", "IGK", "IGL"),
  set_name = NULL,
  type = c("NUC", "PROT"),
  format = c("FASTA_GAPPED", "FASTA_UNGAPPED", "AIRR"),
  version = c("published", "latest"),
  species_subgroup = NULL,
  refresh = FALSE,
  suppressMessages = FALSE
)

```

**Arguments**

species	Character string specifying the species. Accepts "human", "Homo sapiens", "mouse", or "Mus musculus". Default is "human".
locus	Character string specifying the locus short code. One of "IGH", "IGK", or "IGL". Can be NULL if you pass a set_name explicitly.
set_name	Optional character string specifying an explicit OGRDB set name (e.g., "IGH_VDJ"). If provided, overrides locus.
type	Character string specifying the sequence type. Either "NUC" (default) for nucleotide or "PROT" for protein. "PROT" will translate V-gene CDS; only supported for FASTA or AIRR records that include a valid CDS.
format	Character string specifying the download format. One of "FASTA_GAPPED" (default), "FASTA_UNGAPPED", or "AIRR".
version	Character string specifying the version. Either "published" (default) or "latest".
species_subgroup	Optional character string specifying a subgroup (e.g., a mouse strain like "C57BL/6"). If it contains /, OGRDB requires it encoded as %252f.
refresh	Logical. If TRUE, forces re-download even if cached. Default is FALSE.
suppressMessages	Logical. If TRUE, suppresses informational messages. Default is FALSE.

**Details**

OGRDB (Open Germline Receptor Database) is the AIRR Community's curated repository of germline receptor sequences. It complements IMGT with additional species support and standardized AIRR JSON format.

The function supports multiple download formats:

- FASTA\_GAPPED: FASTA with IMGT gaps preserved
- FASTA\_UNGAPPED: FASTA without gaps
- AIRR: AIRR-C compliant JSON format

**Value**

A `DNAStrngSet` object (when `type = "NUC"`) or `AAStringSet` object (when `type = "PROT"`) containing the requested sequences.

**See Also**

`loadOGRDB`, `refreshOGRDB` for convenience wrappers

`getIMGT` for IMGT sequences

`exportMiXCR`, `exportTRUST4`, `exportCellRanger`, `exportIgBLAST` for exporting sequences to analysis tools

<https://ogrdb.airr-community.org/> for OGRDB documentation

**Examples**

```
if (is_ogrdb_available()) {
  # Download human IGH nucleotide sequences (gapped FASTA)
  igh_nuc <- getOGRDB(species = "human",
                     locus   = "IGH",
                     type    = "NUC",
                     format  = "FASTA_GAPPED")

  # Download human IGK sequences in AIRR JSON format
  igk_airr <- getOGRDB(species = "human",
                      locus   = "IGK",
                      type    = "NUC",
                      format  = "AIRR")

  # Download human IGL sequences and translate to AA
  igl_prot <- getOGRDB(species = "human",
                      locus   = "IGL",
                      type    = "PROT",
                      format  = "FASTA_UNGAPPED")

  # Example using an explicit set name (instead of locus)
  igh_explicit <- getOGRDB(species = "human",
                          set_name = "IGH_VDJ",
                          type    = "NUC",
                          format  = "FASTA_GAPPED")
}
```

---

is\_imgt\_available

*Check if IMGT Website is Available*

---

**Description**

Sends a lightweight HEAD request to the main IMGT page to check if the service is online and accessible. This function is used to conditionally run examples and tests that require an internet connection.

**Usage**

```
is_imgt_available()
```

**Value**

A logical value: TRUE if the IMGT website is accessible, FALSE otherwise.

**See Also**

[is\\_ogrdb\\_available](#) for checking OGRDB availability  
[getIMGT](#) which uses this function

**Examples**

```
is_imgt_available()
```

---

<code>is_ogrdb_available</code>	<i>Check if OGRDB Website is Available</i>
---------------------------------	--

---

**Description**

Sends a lightweight HEAD request to the OGRDB API to check if the service is online and accessible. This function is used to conditionally run examples and tests that require an internet connection.

**Usage**

```
is_ogrdb_available()
```

**Value**

A logical value: TRUE if the OGRDB website is accessible, FALSE otherwise.

**See Also**

[is\\_imgt\\_available](#) for checking IMGT availability  
[getOGRDB](#) which uses this function

**Examples**

```
is_ogrdb_available()
```

---

listIMGT	<i>List Datasets in the Local Cache</i>
----------	---

---

**Description**

Scans the cache directory and returns a list of available datasets that have been downloaded.

**Usage**

```
listIMGT()
```

**Value**

A character vector of absolute file paths for the cached datasets. Returns an empty character vector if the cache directory does not exist or contains no files.

**See Also**

[getIMGT](#) for downloading sequences

[listOGRDB](#) for listing OGRDB cached files

**Examples**

```
# List all files in the cache
cached_files <- listIMGT()

# To see the structure, you can print the first few
head(cached_files)
```

---

listOGRDB	<i>List OGRDB Datasets in Local Cache</i>
-----------	---

---

**Description**

Scans the cache directory and returns a list of available OGRDB datasets that have been downloaded.

**Usage**

```
listOGRDB()
```

**Value**

A character vector of absolute file paths to cached OGRDB files. Returns an empty character vector if no OGRDB files have been cached. Paths are typically under the package cache directory (e.g., `~/.immReferent/<Species>/ogrdb/`).

**See Also**

[getOGRDB](#) for downloading sequences

[listIMGT](#) for listing IMGT cached files

**Examples**

```
# List cached OGRDB files
cached_files <- listOGRDB()
head(cached_files)
```

---

loadIMGT

*Load Cached IMGT/HLA Sequences*


---

**Description**

Loads sequences from the local cache without attempting to download. This function is a convenience wrapper for `getIMGT(refresh = FALSE)`. If the data is not found in the cache, it will be downloaded unless an internet connection is unavailable.

**Usage**

```
loadIMGT(
  species = "human",
  gene,
  type = c("NUC", "PROT"),
  suppressMessages = FALSE
)
```

**Arguments**

<code>species</code>	Character string specifying the species for which to download data. Required for TCR/BCR queries. Currently supported species: "human", "mouse", "rat", "rabbit", "pig", "dog", "rhesus_monkey", "cyno_monkey". Defaults to "human" for HLA queries.
<code>gene</code>	Character string specifying the gene or locus to download. For TCR/BCR, this can be a specific chain (e.g., "IGHV", "TRBJ") or a group (e.g., "IGH", "TCR"). For HLA, use "HLA".
<code>type</code>	Character string specifying the type of sequence to retrieve. Either "NUC" for nucleotide or "PROT" for protein sequences. This primarily distinguishes between VDJ nucleotide and V-region amino acid sequences for TCR/BCR genes.
<code>suppressMessages</code>	Logical. If TRUE, suppresses the license and other informational messages. Default is FALSE.

**Value**

A `DNAStrngSet` object (when `type = "NUC"`) or `AAStringSet` object (when `type = "PROT"`) containing the requested sequences.

**See Also**

`getIMGT` for the main download function

`refreshIMGT` to force re-download

**Examples**

```
if(is_imgt_available()) {
  # First, download a file to ensure it's in the cache
  getIMGT(species = "human", gene = "IGHV", type = "NUC", suppressMessages = TRUE)
  # Now, load it from the cache
  ighv_cached <- loadIMGT(species = "human", gene = "IGHV", type = "NUC")
}
```

---

loadOGRDB

*Load Cached OGRDB Sequences*


---

**Description**

Loads sequences from the local cache without attempting to download. This function is a convenience wrapper for `getOGRDB(refresh = FALSE)`. If the data is not found in the cache, it will be downloaded unless an internet connection is unavailable.

**Usage**

```
loadOGRDB(
  species = "human",
  locus = c("IGH", "IGK", "IGL"),
  set_name = NULL,
  type = c("NUC", "PROT"),
  format = c("FASTA_GAPPED", "FASTA_UNGAPPED", "AIRR"),
  version = c("published", "latest"),
  species_subgroup = NULL,
  suppressMessages = FALSE
)
```

**Arguments**

<code>species</code>	Character string specifying the species. Accepts "human", "Homo sapiens", "mouse", or "Mus musculus". Default is "human".
<code>locus</code>	Character string specifying the locus short code. One of "IGH", "IGK", or "IGL". Can be NULL if you pass a <code>set_name</code> explicitly.

set_name	Optional character string specifying an explicit OGRDB set name (e.g., "IGH_VDJ"). If provided, overrides locus.
type	Character string specifying the sequence type. Either "NUC" (default) for nucleotide or "PROT" for protein. "PROT" will translate V-gene CDS; only supported for FASTA or AIRR records that include a valid CDS.
format	Character string specifying the download format. One of "FASTA_GAPPED" (default), "FASTA_UNGAPPED", or "AIRR".
version	Character string specifying the version. Either "published" (default) or "latest".
species_subgroup	Optional character string specifying a subgroup (e.g., a mouse strain like "C57BL/6"). If it contains /, OGRDB requires it encoded as %252f.
suppressMessages	Logical. If TRUE, suppresses informational messages. Default is FALSE.

**Value**

A [DNAStrngSet](#) object (when type = "NUC") or [AAStringSet](#) object (when type = "PROT") containing the requested sequences.

**See Also**

[getOGRDB](#) for the main download function

[refreshOGRDB](#) to force re-download

**Examples**

```
if (is_ogrdb_available()) {
  # First, ensure the file is cached
  getOGRDB(species = "human", locus = "IGH",
           type = "NUC", format = "FASTA_GAPPED",
           suppressMessages = TRUE)

  # Now load from cache only
  igh_cached <- loadOGRDB(species = "human",
                        locus = "IGH",
                        type = "NUC",
                        format = "FASTA_GAPPED")
}
```

---

refreshIMGT

*Force Re-download of IMGT/HLA Sequences*


---

**Description**

A convenience wrapper for `getIMGT(..., refresh = TRUE)` to ensure that the local cache is updated with the latest versions of the requested sequences.

## Usage

```
refreshIMGT(  
  species = "human",  
  gene,  
  type = c("NUC", "PROT"),  
  suppressMessages = FALSE  
)
```

## Arguments

species	Character string specifying the species for which to download data. Required for TCR/BCR queries. Currently supported species: "human", "mouse", "rat", "rabbit", "pig", "dog", "rhesus_monkey", "cyno_monkey". Defaults to "human" for HLA queries.
gene	Character string specifying the gene or locus to download. For TCR/BCR, this can be a specific chain (e.g., "IGHV", "TRBJ") or a group (e.g., "IGH", "TCR"). For HLA, use "HLA".
type	Character string specifying the type of sequence to retrieve. Either "NUC" for nucleotide or "PROT" for protein sequences. This primarily distinguishes between VDJ nucleotide and V-region amino acid sequences for TCR/BCR genes.
suppressMessages	Logical. If TRUE, suppresses the license and other informational messages. Default is FALSE.

## Value

A [DNAStrngSet](#) object (when type = "NUC") or [AAStringSet](#) object (when type = "PROT") containing the requested sequences.

## See Also

[getIMGT](#) for the main download function

[loadIMGT](#) to load from cache without downloading

## Examples

```
if(is_imgt_available()) {  
  # Force a re-download of human IGHV protein sequences  
  ighv_prot_fresh <- refreshIMGT(species = "human", gene = "IGHV", type = "PROT")  
}
```

---

refreshOGRDB	<i>Force Re-download of OGRDB Sequences</i>
--------------	---

---

### Description

A convenience wrapper for `getOGRDB(..., refresh = TRUE)` to ensure that the local cache is updated with the latest versions of the requested sequences.

### Usage

```
refreshOGRDB(
  species = "human",
  locus = c("IGH", "IGK", "IGL"),
  set_name = NULL,
  type = c("NUC", "PROT"),
  format = c("FASTA_GAPPED", "FASTA_UNGAPPED", "AIRR"),
  version = c("published", "latest"),
  species_subgroup = NULL,
  suppressMessages = FALSE
)
```

### Arguments

species	Character string specifying the species. Accepts "human", "Homo sapiens", "mouse", or "Mus musculus". Default is "human".
locus	Character string specifying the locus short code. One of "IGH", "IGK", or "IGL". Can be NULL if you pass a set_name explicitly.
set_name	Optional character string specifying an explicit OGRDB set name (e.g., "IGH_VDJ"). If provided, overrides locus.
type	Character string specifying the sequence type. Either "NUC" (default) for nucleotide or "PROT" for protein. "PROT" will translate V-gene CDS; only supported for FASTA or AIRR records that include a valid CDS.
format	Character string specifying the download format. One of "FASTA_GAPPED" (default), "FASTA_UNGAPPED", or "AIRR".
version	Character string specifying the version. Either "published" (default) or "latest".
species_subgroup	Optional character string specifying a subgroup (e.g., a mouse strain like "C57BL/6"). If it contains /, OGRDB requires it encoded as %252f.
suppressMessages	Logical. If TRUE, suppresses informational messages. Default is FALSE.

### Value

A [DNAStrngSet](#) object (when type = "NUC") or [AAStringSet](#) object (when type = "PROT") containing the requested sequences.



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