# LowMACAAnnotation

November 6, 2026

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`getLowMACAAnnotationData` *Retrieve Data from LowMACAAnnotation Package*

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## Description

Functions to retrieve protein level, Pfam level and aliases data from LowMACAAnnotation Package.

## Usage

```
## Retrieve the dataset containing protein level information
getMyUni()

## Retrieve the dataset containing Pfam level information
getMyPfam()

## Retrieve the dataset containing Gene Symbols aliases
getMyAlias()
```

## Value

All the functions return dataframes

## See Also

`myUni` `myPfam` `myAlias`

## Examples

```
myUni <- getMyUni()
myPfam <- getMyPfam()
myAlias <- getMyAlias()
```

## myAlias *Gene Symbol aliases for LowMACA package*

### Description

A simple parsing of the HGNC database to map aliases and previous symbols to correct official Gene Symbols

### Usage

```
data("myAlias")
```

### Format

A data frame with the following 2 variables.

`Alias` a character vector representing all the possible aliases and previous symbols for official Gene Symbols

`Official_Gene_Symbol` a character vector representing the approved and official Gene Symbol for HGNC database

`Locus_Group` a character vector representing all the possible locus groups in HGNC database, like protein coding, RNA, pseudogene etc.

`Locus_Type` a character vector representing all the possible locus types in HGNC database. It is a specification of locus group

`MappedByLowMACA` a character vector of yes and no if the gene is included in myUni.RData

### Source

HGNC

### Examples

```
#Load myAlias and show its structure
myAlias <- getMyAlias()
str(myAlias)
```

## myPfam *Pfam-A for LowMACA package*

### Description

This dataset comprises all the Pfam-A entries mapped for LowMACA

### Usage

```
data("myPfam")
```

### Format

A data frame with the following 11 variables.

**Entry** a character vector of Uniprot entries

**Envelope_Start** a numeric vector of starts of the pfam domain relative to the reference protein

**Envelope_End** a numeric vector of ends of the pfam domain relative to the reference protein

**Pfam_ID** a character vector of Pfam IDs in the form of PF###### supported by LowMACA

**Pfam_Name** a character vector of full Pfam domain names

**Type** a character vector. One of the following: "Domain" "Family" "Repeat" or "Motif"

**Clan_ID** a numeric vector of Clan IDs, a sort of families of Pfam domains

**Entrez** a numeric vector of Entrez IDs

**UNIPROT** a character vector of Uniprot entries in format "name_HUMAN"

**Gene_Symbol** a character vector of official Gene Symbols

**Pfam_Fasta** a character vector of amino acid sequences of corresponding Pfam

### Details

This is the result of a merge between Pfam-A, Uniprot, HGNC databases

### Source

Pfam website

### Examples

```
#Load and show contents of myPfam
data(myPfam)
str(myPfam)
```

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## myUni *Uniprot database for LowMACA*

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### Description

This dataset comprises all the Uniprot entries mapped for LowMACA

### Usage

```
data("myUni")
```

### Format

A data frame with 9 variables.

**Gene_Symbol** a character vector of official Gene Symbols

**Entrez** a numeric vector of Entrez IDs

**UNIPROT** a character vector of Uniprot entries in "name_HUMAN" format

**Entry** a character vector of Uniprot entries

**HGNC** a character vector of gene names as HGNC numbers

**Approved_Name** a character vector of approved extended gene names

**Protein.name** a character vector of approved extended protein names

**Chromosome** a character vector of chromosomic cytoband positions

**AMINO_SEQ** a character vector of amino acid sequences for Uniprot entries

## Details

This dataset is a 1 to 1 mapping of genes to their canonical proteins or main proteins

## Source

Uniprot

## Examples

```
#Load dataset and show its structure
data(myUni)
str(myUni)
```

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