**getLowMACAAnnotationData**  
*Retrieve Data from LowMACAAnnotation Package*

**Description**

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

**Usage**

```r
## 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**

```r
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")
**myUni**

**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**

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

---

**myUni**  
Uniprot database for LowMACA

**Description**

This dataset comprises all the Uniprot entries mapped for LowMACA

**Usage**

```r
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
**myUni**

**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)
Index

*Topic datasets
  * myAlias, 2
  * myPfam, 2
  * myUni, 3

getLowMACAAnnotationData, 1
getMyAlias(getLowMACAAnnotationData), 1
getMyPfam(getLowMACAAnnotationData), 1
getMyUni(getLowMACAAnnotationData), 1

myAlias, 1, 2
myPfam, 1, 2
myUni, 1, 3