

# Package ‘pfamAnalyzeR’

December 20, 2025

**Type** Package

**Title** Identification of domain isotypes in pfam data

**Version** 1.11.0

**Description** Protein domains is one of the most import annoation of proteins we have with the Pfam database/tool being (by far) the most used tool. This R package enables the user to read the pfam prediction from both webserver and stand-alone runs into R. We have recently shown most human protein domains exist as multiple distinct variants termed domain isotypes. Different domain isotypes are used in a cell, tissue, and disease-specific manner. Accordingly, we find that domain isotypes, compared to each other, modulate, or abolish the functionality of a protein domain. This R package enables the identification and classification of such domain isotypes from Pfam data.

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**Depends** R (>= 4.3.0), readr, stringr, dplyr

**Imports** utils, tibble, magrittr

**Encoding** UTF-8

**LazyData** false

**RoxygenNote** 7.2.1

**Suggests** BiocStyle, knitr, rmarkdown

**VignetteBuilder** knitr

**biocViews** AlternativeSplicing, TranscriptomeVariant,  
BiomedicalInformatics, FunctionalGenomics, SystemsBiology,  
Annotation, FunctionalPrediction, GenePrediction, DataImport

**BugReports** <https://github.com/kvittingseerup/pfamAnalyzeR/issues>

**git\_url** <https://git.bioconductor.org/packages/pfamAnalyzeR>

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|-----------------------|---------------------------------|
| analyse_pfam_isotypes | <i>Determine domain isotype</i> |
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Description

Determine domain isotype

Usage

```
analyse_pfam_isotypes(pfamRes, fracCutoff = 0.1)
```

Arguments

- |            |                                                                                                     |
|------------|-----------------------------------------------------------------------------------------------------|
| pfamRes    | A data frame with pfam augmneted with indel and truncation info (as produced by augment_pfam).      |
| fracCutoff | The fraction of a protein domain that must be affected before classifying it a truncation or indel. |

Value

The data.frame with the Pfam results now augmented with info about domain domain isotype

Examples

```
### Load pfam data
pfamResultFile <- system.file("extdata/pfam_results.txt", package = "pfamAnalyzeR")
pfamRes <- read_pfam(pfamResultFile)

### Augment the pfam data
pfamRes <- augment_pfam(pfamRes)

### Predict domain isotype
pfamRes <- analyse_pfam_isotypes(pfamRes)
```

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|              |                                                                |
|--------------|----------------------------------------------------------------|
| augment_pfam | <i>Augment pfam domains with truncation/indel calculations</i> |
|--------------|----------------------------------------------------------------|

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**Description**

Augment pfam domains with truncation/indel calculations

**Usage**

```
augment_pfam(pfamRes)
```

**Arguments**

pfamRes            A data frame with pfam results as produced by read\_pfam.

**Value**

The data.frame with the Pfam results now augmented with info on trunkation and indel sizes

**Examples**

```
### Load pfam data
pfamResultFile <- system.file("extdata/pfam_results.txt", package = "pfamAnalyzeR")
pfamRes <- read_pfam(pfamResultFile)

### Augment the pfam data
pfamRes <- augment_pfam(pfamRes)
```

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|              |                                                  |
|--------------|--------------------------------------------------|
| pfamAnalyzeR | <i>Read in and analyze pfam domains isotypes</i> |
|--------------|--------------------------------------------------|

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**Description**

Read in and analyze pfam domains isotypes

**Usage**

```
pfamAnalyzeR(path, fracCutoff = 0.1)
```

**Arguments**

path            A string indicating the full path to the Pfam result file

fracCutoff      The fraction of a protein domain that must be affected before classifying it a truncation or indel.

**Value**

The data.frame with the Pfam results now augmented with info about domain structural variation

**Examples**

```
### Predict domain isotypes in pfam results
pfamResultFile <- system.file("extdata/pfam_results.txt", package = "pfamAnalyzeR")
pfamRes <- pfamAnalyzeR(pfamResultFile)
```

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|           |                              |
|-----------|------------------------------|
| read_pfam | <i>Read Pfam file into R</i> |
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**Description**

Read Pfam result file into R. Supports both result files from local and web-server

**Usage**

```
read_pfam(path)
```

**Arguments**

path                      A string indicating the full path to the Pfam result file

**Details**

The pfam webserver can be found at <https://www.ebi.ac.uk/Tools/hmmer/search/hmmscan>.

**Value**

A data.frame with the Pfam results

**Examples**

```
pfamResultFile <- system.file("extdata/pfam_results.txt", package = "pfamAnalyzeR")
pfamRes <- read_pfam(pfamResultFile)
```

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