

# Package: pfamAnalyzeR (via r-universe)

June 15, 2024

**Type** Package

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

**Version** 1.5.0

**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>

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/pfamAnalyzeR>

**RemoteRef** HEAD

**RemoteSha** b38e61b1a7b02acfef39a64e129255e489bd3cc9

## Contents

analyse_pfam_isotypes . . . . .	2
augment_pfam . . . . .	3
pfamAnalyzeR . . . . .	3
read_pfam . . . . .	4
<b>Index</b>	<b>5</b>

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analyse\_pfam\_isotypes *Determine domain isotype*

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### Description

Determine domain isotype

### Usage

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

### Arguments

pfamRes	A data frame with pfam augmented 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 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)
```

# Index

`analyse_pfam_isotypes`, [2](#)

`augment_pfam`, [3](#)

`pfamAnalyzeR`, [3](#)

`read_pfam`, [4](#)