

# Package ‘pepXMLTab’

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**Type** Package

**Title** Parsing pepXML files and filter based on peptide FDR.

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**Description** Parsing pepXML files based one XML package.

The package tries to handle pepXML files generated from different softwares.

The output will be a peptide-spectrum-matching tabular file.

The package also provide function to filter the PSMs based on FDR.

**License** Artistic-2.0

**Depends** R (>= 3.0.1)

**Imports** XML(>= 3.98-1.1)

**Suggests** RUnit, BiocGenerics

**biocViews** ImmunoOncology, Proteomics, MassSpectrometry

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pepXML2tab

*Generate a data frame objects from a pepXML file.*

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## Description

The pepXML2tab() function generates a data frame from a pepXML file.

## Usage

```
pepXML2tab(pepxml, ...)
```

## Arguments

|        |                                                         |
|--------|---------------------------------------------------------|
| pepxml | a character contains the path and name of a pepXML file |
| ...    | additional arguments                                    |

## Details

Read peptide identification from pepXML file into an data frame object.

## Value

a data frame object, each row represent a PSM (peptide spectrum match) from the pepXML file

## Author(s)

Xiaojing Wang

## Examples

```
## MyriMatch example
pepxml <- system.file("extdata/pepxml", "Myrimatch.pepXML",
  package="pepXMLTab")
tttt <- pepXML2tab(pepxml)

## Mascot example
pepxml <- system.file("extdata/pepxml", "Mascot.pepXML",
  package="pepXMLTab")
tttt <- pepXML2tab(pepxml)

## SEQUEST example
pepxml <- system.file("extdata/pepxml", "SEQUEST.pepXML",
  package="pepXMLTab")
tttt <- pepXML2tab(pepxml)

## XTandem example
pepxml <- system.file("extdata/pepxml", "XTandem.pepXML",
  package="pepXMLTab")
tttt <- pepXML2tab(pepxml)
```

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PSMfilter*Filter the peptide identification.*

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**Description**

The PSMfilter() function filter the peptide identification based on user chosen paramter.

**Usage**

```
PSMfilter(PSMtab, pepFDR = 0.01, scorecolumn = "mvh", hitrank = 1,  
          minpeplen = 6, decoyprefix = "rev_", ...)
```

**Arguments**

|             |                                                                                                                           |
|-------------|---------------------------------------------------------------------------------------------------------------------------|
| PSMtab      | a data frame contain peptide identification from a pepXML file                                                            |
| pepFDR      | filter the peptides based on this chosen FDR, default is 0.01.                                                            |
| scorecolumn | which column is chosen to calculate FDR                                                                                   |
| hitrank     | an integer indicates how many peptides to retain for a spectrum. A spectrum can match to multiple peptides. Default is 1. |
| minpeplen   | an integer of minimum peptide length                                                                                      |
| decoyprefix | a character indicates decoy sequence in the 'protein' column. Usually is 'rev_' or 'DECOY_'.                              |
| ...         | additional arguments                                                                                                      |

**Details**

Filter the peptide identification based on FDR, hit rank, or peptide length.

**Value**

a data frame object, contain PSMs (peptide spectrum match) passed the filters.

**Author(s)**

Xiaojing Wang

**Examples**

```
##MyriMatch example  
pepxml <- system.file("extdata/pepxml", "Myrimatch.pepXML",  
                      package="pepXMLTab")  
tttt <- pepXML2tab(pepxml)  
passed <- PSMfilter(tttt, pepFDR=0.01, scorecolumn='mvh', hitrank=1,  
                   minpeplen=6, decoyprefix='rev_')
```

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