

# Package ‘shinyTANDEM’

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**Type** Package

**Title** Provides a GUI for rTANDEM

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## Description

This package provides a GUI interface for rTANDEM. The GUI is primarily designed to visual-  
ize rTANDEM result object or result xml files. But it will also provides an interface for creating pa-  
rameter objects, launching searches or performing conversions between R objects and xml files.

**biocViews** MassSpectrometry, Proteomics

**License** GPL-3

**Depends** rTANDEM (>= 1.3.5), shiny, mixtools, methods, xtable

**NeedsCompilation** no

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## Description

The function `shinyTANDEM(dataset, port)` launch a shiny GUI running on the given port. The shiny GUI will use the default browser. A rTANDEM result object can be passed as an argument. In this case, the dataset will be loaded as the GUI opens. The dataset can be changed later on by loading another dataset either from an xml or an Rdata file. If a dataset is loaded from an Rda file that contains more than one object, the name of the object to be loaded must be specified.

**Usage**

```
shinyTANDEM(dataset=NULL, port=8100,...)
```

**Arguments**

dataset	An optional rTANDEM result object (class rTResult) that will be loaded as the GUI opens.
port	Shiny's default port is 8100. The port parameter lets you specify a different one.
...	Arguments can be passed to shiny::runApp().

**Value**

This function does not return. Interrupt R to stop the GUI (usually by pressing Ctrl+C or Esc).

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**Examples**

```
# The package contains a RDS file with a rTResult object. Load it into  
# memory and pass it to the call to shinyTANDEM.  
# To exit the GUI, press your interrupt command  
# (usually Ctrl+C or Esc) in the R window.  
  
my.result <- readRDS(system.file("extdata/result.RDS", package="shinyTANDEM"))  
if(interactive()){ shinyTANDEM(dataset=my.result) }
```

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