

Package ‘crisprseekplus’

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Type Package

Title crisprseekplus

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Description Bioinformatics platform containing interface to work with
offTargetAnalysis and compare2Sequences in the CRISPRseek
package, and GUIDEseqAnalysis.

Depends R (>= 3.3.0), shiny, shinyjs, CRISPRseek

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LazyData true

Imports DT, utils, GUIDEseq, GenomicRanges, GenomicFeatures,
BiocInstaller, BSgenome, AnnotationDbi, hash

RoxygenNote 5.0.1

Suggests testthat, rmarkdown, knitr, R.rsp

VignetteBuilder knitr, R.rsp

URL <https://github.com/UMMS-Biocore/crisprseekplus>

BugReports <https://github.com/UMMS-Biocore/crisprseekplus/issues/new>

biocViews GeneRegulation, SequenceMatching, Software

NeedsCompilation no

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cspServer	<i>cspServer</i>
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Description

Sets up shinyServer to be able to run crisprseekplus interactively.

Usage

```
cspServer(input, output)
```

Arguments

input,	input params from UI
output,	output params to UI

Value

the panel for main plots;

Note

cspServer

Examples

```
cspServer
```

cspUI	<i>cspUI</i>
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Description

Creates a shinyUI to be able to run crsiprseekplus interactively.

Usage

```
cspUI()
```

Value

the panel for the UI;

Note

cspUI

Examples

```
x<-cspUI()
```

disableDownload	<i>disableDownload</i>
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Description

Enable or disable to download button depending on if analysis is complete

Usage

```
disableDownload(input = NULL)
```

Arguments

input, disable the download button

Value

the download button either enabled or disabled;

Note

disableDownload

Examples

```
x<- disableDownload()
```

fileInputFunc	<i>fileInputFunc</i>
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Description

If input file is empty, use sample file

Usage

```
fileInputFunc(input = NULL, sampleFile = NULL)
```

Arguments

input, enter correct files
sampleFile, sampleFile

Value

If no file is uploaded, use sample file

Note

fileInputFunc

Examples

```
x<- fileInputFunc()
```

getLoadingMsg

getLoadingMsg

Description

getLoadingMsg

Usage

```
getLoadingMsg()
```

Value

loading msg

Note

getLoadingMsg

Examples

```
x <- getLoadingMsg()
```

getLogo

getLogo

Description

getLogo

Usage

```
getLogo()
```

Value

return logo

Note

getLogo

Examples

```
x <- getLogo()
```

<code>installpack</code>	<i>installpack</i>
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Description

install packages if they don't exist display.

Usage

```
installpack(package_name = NULL)
```

Arguments

package_name, package name to be installed

Value

install package

Note

installpack

Examples

```
x<- installpack()
```

<code>startcrisprseekplus</code>	<i>startcrisprseekplus</i>
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Description

Starts the crisprseekplus to be able to run.

Usage

```
startcrisprseekplus()
```

Value

the app

Note

startcrisprseekplus

Examples

```
startcrisprseekplus()
```

trueFalseFunc

trueFalseFunc

Description

If radio button input == 1, the function returns true and if the radio button value is 2, the function returns false

Usage

```
trueFalseFunc(input = NULL)
```

Arguments

input, user inputs

Value

true or false depending on input

Note

trueFalseFunc

Examples

```
x<- trueFalseFunc()
```

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