

# Package ‘crisprseekplus’

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**Type** Package

**Title** crisprseekplus

**Version** 1.14.0

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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

**License** GPL-3 + file LICENSE

**LazyData** true

**Imports** DT, utils, GUIDEseq, GenomicRanges, GenomicFeatures,  
BiocManager, 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

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

**git\_branch** RELEASE\_3\_11

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cspServer

*cspServer*


---

**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`*cspUI*

---

**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`*disableDownload*

---

**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            *fileInputFunc*

---

**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()
```

---

`installpack`                      *installpack*

---

**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()
```

startcrisprseekplus    *startcrisprseekplus*

---

**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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