

# 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

**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-Biocode/crisprseekplus>

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

**biocViews** GeneRegulation, SequenceMatching, Software

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

**git\_branch** RELEASE\_3\_17

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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`*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	<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	<i>getLoadingMsg</i>
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---

**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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