

# Package ‘crisprVerse’

August 28, 2025

**Title** Easily install and load the crisprVerse ecosystem for CRISPR  
gRNA design

**Version** 1.11.0

**Description** The crisprVerse is a modular ecosystem of R packages developed for the design and manipulation of CRISPR guide RNAs (gRNAs). All packages share a common language and design principles. This package is designed to make it easy to install and load the crisprVerse packages in a single step. To learn more about the crisprVerse, visit <<https://www.github.com/crisprVerse>>.

**Depends** R (>= 4.2.0)

**Imports** BiocManager, cli, crisprBase, crisprBowtie, crisprScore, crisprScoreData, crisprDesign, crisprViz, rlang, tools, utils

**Suggests** BiocStyle, knitr, testthat

**biocViews** CRISPR, FunctionalGenomics, GeneTarget

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.2.1

**VignetteBuilder** knitr

**BugReports** <https://github.com/crisprVerse/crisprVerse/issues>

**URL** <https://github.com/crisprVerse/crisprVerse>

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

**git\_branch** devel

**git\_last\_commit** 0a4abad

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-08-28

**Author** Jean-Philippe Fortin [aut, cre]

**Maintainer** Jean-Philippe Fortin <[fortin946@gmail.com](mailto:fortin946@gmail.com)>

## Contents

|                                |   |
|--------------------------------|---|
| crisprVerse-package . . . . .  | 2 |
| crisprVerse_deps . . . . .     | 2 |
| crisprVerse_packages . . . . . | 3 |
| crisprVerse_update . . . . .   | 3 |

**Index****4**


---

|                     |                                                                                              |
|---------------------|----------------------------------------------------------------------------------------------|
| crisprVerse-package | <i>crisprVerse: Easily install and load the crisprVerse ecosystem for CRISPR gRNA design</i> |
|---------------------|----------------------------------------------------------------------------------------------|

---

**Description**

The crisprVerse is a modular ecosystem of R packages developed for the design and manipulation of CRISPR guide RNAs (gRNAs). All packages share a common language and design principles. This package is designed to make it easy to install and load the crisprVerse packages in a single step. To learn more about the crisprVerse, visit <https://www.github.com/crisprVerse>.

**Author(s)**

**Maintainer:** Jean-Philippe Fortin <fortin946@gmail.com>

**See Also**

Useful links:

- <https://github.com/crisprVerse/crisprVerse>
- Report bugs at <https://github.com/crisprVerse/crisprVerse/issues>

---

|                  |                                          |
|------------------|------------------------------------------|
| crisprVerse_deps | <i>List all crisprVerse dependencies</i> |
|------------------|------------------------------------------|

---

**Description**

List all crisprVerse dependencies

**Usage**

```
crisprVerse_deps(recursive = FALSE)
```

**Arguments**

**recursive**      If TRUE, will also list all dependencies of crisprVerse packages.

**Value**

A data.frame describing crisprVerse dependencies

**Examples**

```
if (interactive()){
  crisprVerse_deps()
}
```

---

`crisprVerse_packages`    *List all packages in the crisprVerse*

---

**Description**

List all packages in the crisprVerse

**Usage**

```
crisprVerse_packages(include_self = TRUE)
```

**Arguments**

`include_self`    Include crisprVerse in the list?

**Value**

A character vector of packages in the crisprVerse

**Examples**

```
crisprVerse_packages()
```

---

`crisprVerse_update`    *Update crisprVerse packages*

---

**Description**

This will check to see if all crisprVerse packages (and optionally, their dependencies) are up-to-date, and will install after an interactive confirmation.

**Usage**

```
crisprVerse_update(recursive = FALSE)
```

**Arguments**

`recursive`    If TRUE, will also list all dependencies of crisprVerse packages.

**Value**

Print messages to console as a side effect.

**Examples**

```
if (interactive()){  
  crisprVerse_update()  
}
```

# Index

## \* **internal**

    crisprVerse-package, [2](#)

crisprVerse (crisprVerse-package), [2](#)

crisprVerse-package, [2](#)

crisprVerse\_deps, [2](#)

crisprVerse\_packages, [3](#)

crisprVerse\_update, [3](#)