

# crisprVerse: ecosystem of R packages for CRISPR gRNA design

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2022-10-17

## 1 Installation and getting started

The [crisprVerse](#) is a collection of packages for CRISPR guide RNA (gRNA) design that can easily be installed with the `crisprVerse` package. This provides a convenient way of downloading and installing all `crisprVerse` packages with a single R command.

The package can be installed from the Bioconductor devel branch using the following commands in an R session:

```
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")

BiocManager::install(version="devel")
BiocManager::install("crisprVerse")
```

The core `crisprVerse` includes the packages that are commonly used for gRNA design, and are attached when you attach the `crisprVerse` package:

```
library(crisprVerse)
```

```
## Warning: multiple methods tables found for 'aperm'
```

```
## Warning: replacing previous import 'BiocGenerics::aperm' by
## 'DelayedArray::aperm' when loading 'SummarizedExperiment'
```

You can check that all `crisprVerse` packages are up-to-date with the function `crisprVerse_update()`.

## 2 Components

The following packages are installed and loaded with the `crisprVerse` package:

- [crisprBase](#) to specify and manipulate CRISPR nucleases.
- [crisprBowtie](#) to perform gRNA spacer sequence alignment with Bowtie.
- [crisprScore](#) to annotate gRNAs with on-target and off-target scores.
- [crisprDesign](#) to design and manipulate gRNAs with `GuideSet` objects.

## 3 Reproducibility

```
sessionInfo()
```

```
## R version 4.2.1 (2022-06-23)
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Catalina 10.15.7
##
```

```

## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] crisprViz_0.99.22      crisprDesign_0.99.176  crisprScore_1.1.15
## [4] crisprScoreData_1.1.3  ExperimentHub_2.5.0     AnnotationHub_3.5.1
## [7] BiocFileCache_2.5.0    dbplyr_2.2.1           BiocGenerics_0.43.4
## [10] crisprBowtie_1.1.1     crisprBase_1.1.8       crisprVerse_0.99.9
##
## loaded via a namespace (and not attached):
## [1] backports_1.4.1          Hmisc_4.7-1
## [3] lazyeval_0.2.2          splines_4.2.1
## [5] BiocParallel_1.31.12    GenomeInfoDb_1.33.7
## [7] ggplot2_3.3.6           digest_0.6.29
## [9] ensemblDb_2.21.4        htmltools_0.5.3
## [11] fansi_1.0.3             checkmate_2.1.0
## [13] magrittr_2.0.3          memoise_2.0.1
## [15] BSgenome_1.65.2         cluster_2.1.4
## [17] tzdb_0.3.0              Biostrings_2.65.3
## [19] readr_2.1.2             matrixStats_0.62.0
## [21] prettyunits_1.1.1       jpeg_0.1-9
## [23] colorspace_2.0-3        blob_1.2.3
## [25] rappdirs_0.3.3          xfun_0.32
## [27] dplyr_1.0.10            crayon_1.5.1
## [29] RCurl_1.98-1.8          jsonlite_1.8.0
## [31] survival_3.4-0          VariantAnnotation_1.43.3
## [33] glue_1.6.2              gtable_0.3.1
## [35] zlibbioc_1.43.0         XVector_0.37.1
## [37] DelayedArray_0.23.1     scales_1.2.1
## [39] DBI_1.1.3               Rcpp_1.0.9
## [41] htmlTable_2.4.1         xtable_1.8-4
## [43] progress_1.2.2          reticulate_1.26
## [45] foreign_0.8-82          bit_4.0.4
## [47] Formula_1.2-4           stats4_4.2.1
## [49] htmlwidgets_1.5.4       httr_1.4.4
## [51] dir.expiry_1.5.1        RColorBrewer_1.1-3
## [53] ellipsis_0.3.2          pkgconfig_2.0.3
## [55] XML_3.99-0.10           Gviz_1.41.1
## [57] nnet_7.3-17             deldir_1.0-6
## [59] utf8_1.2.2             tidyselect_1.1.2
## [61] rlang_1.0.5             later_1.3.0
## [63] AnnotationDbi_1.59.1    munsell_0.5.0
## [65] BiocVersion_3.16.0      tools_4.2.1
## [67] cachem_1.0.6            cli_3.4.0
## [69] generics_0.1.3          RSQLite_2.2.16
## [71] evaluate_0.16           stringr_1.4.1
## [73] fastmap_1.1.0           yaml_2.3.5

```

```

## [75] knitr_1.40 bit64_4.0.5
## [77] purrr_0.3.4 randomForest_4.7-1.1
## [79] AnnotationFilter_1.21.0 KEGGREST_1.37.3
## [81] Rbowtie_1.37.0 mime_0.12
## [83] xml2_1.3.3 biomaRt_2.53.2
## [85] BiocStyle_2.25.0 compiler_4.2.1
## [87] rstudioapi_0.14 filelock_1.0.2
## [89] curl_4.3.2 png_0.1-7
## [91] interactiveDisplayBase_1.35.0 tibble_3.1.8
## [93] stringi_1.7.8 basilisk.utils_1.9.3
## [95] GenomicFeatures_1.49.6 lattice_0.20-45
## [97] ProtGenerics_1.29.0 Matrix_1.4-1
## [99] vctrs_0.4.1 pillar_1.8.1
## [101] lifecycle_1.0.1 BiocManager_1.30.18
## [103] data.table_1.14.2 bitops_1.0-7
## [105] httpuv_1.6.5 rtracklayer_1.57.0
## [107] GenomicRanges_1.49.1 R6_2.5.1
## [109] BiocIO_1.7.1 latticeExtra_0.6-30
## [111] promises_1.2.0.1 gridExtra_2.3
## [113] IRanges_2.31.2 codetools_0.2-18
## [115] dichromat_2.0-0.1 assertthat_0.2.1
## [117] SummarizedExperiment_1.27.2 rjson_0.2.21
## [119] GenomicAlignments_1.33.1 Rsamtools_2.13.4
## [121] S4Vectors_0.35.3 GenomeInfoDbData_1.2.8
## [123] parallel_4.2.1 hms_1.1.2
## [125] rpart_4.1.16 grid_4.2.1
## [127] basilisk_1.9.6 rmarkdown_2.16
## [129] MatrixGenerics_1.9.1 biovizBase_1.45.0
## [131] Biobase_2.57.1 shiny_1.7.2
## [133] base64enc_0.1-3 interp_1.1-3
## [135] restfulr_0.0.15

```