<https://www.bioconductor.org/packages/release/bioc/vignettes/BiocStyle/inst/doc/LatexStyle2.R>

at console

bioconductor.sty = readLines(BiocStyle:::bioconductor.sty)

pattern = "^\\\\RequirePackage(\\[.\*\\])?\\{([[:alnum:]]+)\\}.\*"

pkgs = sub(pattern, "\\2", grep(pattern, bioconductor.sty, value = TRUE))

# add hyperref which is not captured by the regex

pkgs = c(pkgs, "hyperref")

# list sorted and unique names

pkgs = sort(unique(pkgs))

latexpkgs = paste0("\\\\latex{", pkgs, "}", collapse=", ")

https://cran.r-project.org/web/packages/BiocManager/vignettes/BiocManager.html#installing-bioconductor-cran-or-github-packages