

Package ‘openPrimeR’

December 3, 2025

Title Multiplex PCR Primer Design and Analysis

Version 1.33.0

Description An implementation of methods for designing, evaluating, and comparing primer sets for multiplex PCR. Primers are designed by solving a set cover problem such that the number of covered template sequences is maximized with the smallest possible set of primers. To guarantee that high-quality primers are generated, only primers fulfilling constraints on their physicochemical properties are selected. A Shiny app providing a user interface for the functionalities of this package is provided by the 'openPrimeRui' package.

Depends R (>= 4.0.0)

License GPL-2

Encoding UTF-8

RoxygenNote 7.3.2

Imports Biostrings (>= 2.38.4), palign, XML (>= 3.98-1.4), scales (>= 0.4.0), reshape2 (>= 1.4.1), seqinr (>= 3.3-3), IRanges (>= 2.4.8), GenomicRanges (>= 1.22.4), ggplot2 (>= 2.1.0), plyr (>= 1.8.4), dplyr (>= 0.5.0), stringdist (>= 0.9.4.1), stringr (>= 1.0.0), RColorBrewer (>= 1.1-2), DECIPHER (>= 1.16.1), lpSolveAPI (>= 5.5.2.0-17), digest (>= 0.6.9), Hmisc (>= 3.17-4), ape (>= 3.5), BiocGenerics (>= 0.16.1), S4Vectors (>= 0.8.11), foreach (>= 1.4.3), magrittr (>= 1.5), unqiqt (>= 1.0), openxlsx (>= 4.0.17), grid (>= 3.1.0), grDevices (>= 3.1.0), stats (>= 3.1.0), utils (>= 3.1.0), methods (>= 3.1.0)

Suggests testthat (>= 1.0.2), knitr (>= 1.13), rmarkdown (>= 1.0), devtools (>= 1.12.0), doParallel (>= 1.0.10), pandoc (>= 0.6.0), learnr (>= 0.9)

SystemRequirements MAFFT (>= 7.305), OligoArrayAux (>= 3.8), ViennaRNA (>= 2.4.1), MELTING (>= 5.1.1), Pandoc (>= 1.12.3)

biocViews Software, Technology, Coverage, MultipleComparison

VignetteBuilder knitr

