

Package ‘qPCRtools’

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Version 0.1.1

Title Tools for qPCR

Description A set of tools for qPCR data process.

URL <https://github.com/lixiang117423/qPCRtools>

BugReports <https://github.com/lixiang117423/qPCRtools/issues>

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Imports broom, data.table, dplyr, ggplot2, ggpmisc, magrittr,
multcomp, readxl, reshape2, sjmisc, stringr, xlsx

RoxygenNote 7.2.0

NeedsCompilation no

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CalCurve	<i>Standard Curve Calculation.</i>
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Description

Standard Curve Calculation.

Arguments

cq.table	The data frame of the position and Cq value.
concen.table	The data frame of the position and concentration.
highest.concen	The highest concentration.
lowest.concen	The lowest concentration.
dilution	Dilution factor of cDNA template.
by.mean	Calculation by mean Cq value or not.

Value

A list.

Author(s)

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Examples

```
df.1.path <- system.file("examples", "calsc.cq.txt", package = "qPCRtools")
df.2.path <- system.file("examples", "calsc.info.txt", package = "qPCRtools")
df.1 <- data.table::fread(df.1.path)
df.2 <- data.table::fread(df.2.path)
CalCurve(
  cq.table = df.1,
  concen.table = df.2,
  lowest.concen = 4,
  highest.concen = 4096,
  dilu = 4,
  by = "mean"
) -> p

p[["table"]]
p[["figure"]]
```

CalRTable

Calculate volume.

Description

Calculate RNA and other reagent volume required for reverse transcription.

Arguments

data	A data.frame contained the sample names and the concentration value. The default unit of concentration is ng/uL.
template	A data.frame contained the information of reverse transcription.
RNA.weight	RNA weight required for reverse transcription. Default is 1 ug.

Value

A data frame.

Author(s)

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Examples

```
df.1.path <- system.file("examples", "crtv.data.txt", package = "qPCRtools")
df.2.path <- system.file("examples", "template", package = "qPCRtools")
df.1 <- data.table::fread(df.1.path)
df.2 <- data.table::fread(df.2.path)
result <- CalRTable(data = df.1, template = df.2, RNA.weight = 2)
head(result)
```

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