

# Package: rutledge (via r-universe)

September 19, 2024

**Type** Package

**Title** Real-Time PCR Data Sets by Rutledge et al. (2004)

**Version** 0.1.1

**Description** Real-time quantitative polymerase chain reaction (qPCR) data by Rutledge et al. (2004) <[doi:10.1093/nar/gnh177](https://doi.org/10.1093/nar/gnh177)> in tidy format. The data comprises a six-point, ten-fold dilution series, repeated in five independent runs, for two different amplicons. In each run, each standard concentration is replicated four times. For the original raw data file see the Supplementary Data section:  
<<https://academic.oup.com/nar/article/32/22/e178/2375678#supplementary-data>>.

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**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 2.10)

**RoxygenNote** 7.3.1

**Roxygen** list(markdown = TRUE)

**Imports** tibble

**URL** <https://github.com/ramiromagno/rutledge>,  
<https://rmagno.eu/rutledge/>

**BugReports** <https://github.com/ramiromagno/rutledge/issues>

**Repository** <https://patterninstitute.r-universe.dev>

**RemoteUrl** <https://github.com/ramiromagno/rutledge>

**RemoteRef** HEAD

**RemoteSha** c997f9d8eb20d24bb5a0b563734a603b1bc0df38

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rutledge

*qPCR data set by Rutledge et al. (2004)*

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### Description

Each data set comprises a six-point, ten-fold dilution series, repeated in five independent runs, for two different amplicons: K1/K2, 102 bp, and K3/K2, 218 bp. Fluorescence readings were exported after background subtraction via baseline averaging of the 5 cycles immediately preceding the cycles in which fluorescence was first detected. Please read the Materials and Methods section of Rutledge et al. (2004) for more details.

### Format

A `tibble` with 10,800 rows and 10 variables:

`plate` Plate identifier. Because one plate (run) was used per dilution series, `plate` values are simply numbered 1 thru 5.

`well` Well identifier. Values are always NA (not available). This variable is kept nevertheless to be coherent with other data sets from other similar R data packages.

`dye` The type of dye used. In this data set the values are always "SYBR", meaning SYBR Green I master mix (Roche).

`target` Target identifier: the amplicon used, K1/K2 or K3/K2.

`sample_type` Sample type (all curves are standards, i.e. "std").

`replicate` Replicate identifier: 1 thru 4.

`copies` Standard copy number.

`dilution` Dilution factor. Higher number means greater dilution.

`cycle` PCR cycle.

`fluor` Raw fluorescence values.

### Source

[doi:10.1093/nar/gnh177](https://doi.org/10.1093/nar/gnh177)

### Examples

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