

Package ‘sisti’

July 23, 2025

Title Real-Time PCR Data Sets by Sisti et al. (2010)

Version 0.0.1

Description This data package contains four datasets of quantitative PCR (qPCR) amplification curves that were used as supplementary data in the research article by Sisti et al. (2010), <[doi:10.1186/1471-2105-11-186](https://doi.org/10.1186/1471-2105-11-186)>. The primary dataset comprises a ten-fold dilution series spanning copy numbers from 3.14×10^7 to 3.14×10^2 , with twelve replicates per concentration. These samples are based on a pGEM-T Promega plasmid containing a 104 bp fragment of the mitochondrial gene NADH dehydrogenase 1 (MT-ND1), amplified using the ND1/ND2 primer pair. The remaining three datasets contain qPCR results in the presence of specific PCR inhibitors: tannic acid, immunoglobulin G (IgG), and quercetin, respectively, to assess their effects on the amplification process. These datasets are useful for researchers interested in PCR kinetics. The original raw data file is available as Additional File 1:
<https://static-content.springer.com/esm/art%3A10.1186%2F1471-2105-11-186/MediaObjects/12859_2009_3643_MOESM1_ESM.XLS>.

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Encoding UTF-8

RoxygenNote 7.3.1

Imports tibble

Depends R (>= 2.10)

LazyData true

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

BugReports <https://github.com/ramiromagno/sisti/issues>

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-04-28 11:00:02 UTC

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sisti	<i>qPCR data sets by Sisti et al. (2010)</i>
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Description

One single tabular tidy data set in long format, encompassing four data sets of amplification curves: (i) six-point, ten-fold dilution series, (ii) tannic acid inhibition, (iii) IgG inhibition and (iv) quercitin inhibition. The target amplicon consisted of a 104 bp fragment of the mitochondrial gene NADH dehydrogenase 1 (MT-ND1). Please read the Methods section of Sisti et al. (2010) for more experimental details.

Dilution series:

A six-point, ten-fold dilution series spanning an amplicon copy number range 3.14×10^7 thru 3.14×10^2 . Each concentration is replicated twelve times. Each reaction has been amplified through 50 cycles.

```
dplyr::filter(sisti, plate == "calibration")
#> # A tibble: 3,600 x 13
#>   plate    well target dye  sample sample_type inhibitor inhibitor_conc
#>   <fct>    <fct> <fct> <fct> <fct>  <fct>      <fct>      <dbl>
#> 1 calibration <NA> MT-ND1 SYBR  pGEM-T std      none          0
#> 2 calibration <NA> MT-ND1 SYBR  pGEM-T std      none          0
#> 3 calibration <NA> MT-ND1 SYBR  pGEM-T std      none          0
#> 4 calibration <NA> MT-ND1 SYBR  pGEM-T std      none          0
#> 5 calibration <NA> MT-ND1 SYBR  pGEM-T std      none          0
#> 6 calibration <NA> MT-ND1 SYBR  pGEM-T std      none          0
#> 7 calibration <NA> MT-ND1 SYBR  pGEM-T std      none          0
#> 8 calibration <NA> MT-ND1 SYBR  pGEM-T std      none          0
#> 9 calibration <NA> MT-ND1 SYBR  pGEM-T std      none          0
#> 10 calibration <NA> MT-ND1 SYBR  pGEM-T std      none          0
#> # i 3,590 more rows
#> # i 5 more variables: replicate <fct>, copies <int>, dilution <int>,
#> #   cycle <int>, fluor <dbl>
```

Tannic acid inhibition:

A series of reactions subjected to inhibition by tannic acid with concentrations: 0.000391, 0.000781, 0.00156, 0.00312, 0.00625, 0.0125, 0.025, 0.05 and 0.1 mg/mL. Each tannic acid concentration sample is replicated six times. Each reaction has been amplified through 40 cycles.

```
dplyr::filter(sisti, plate == "tannic acid")
#> # A tibble: 2,160 x 13
#>   plate    well target dye  sample sample_type inhibitor inhibitor_conc
#>   <fct>    <fct> <fct> <fct> <fct>  <fct>      <fct>      <dbl>
```

```
#> 1 tannic acid <NA> MT-ND1 SYBR pGEM-T std tannic acid 0.1
#> 2 tannic acid <NA> MT-ND1 SYBR pGEM-T std tannic acid 0.1
#> 3 tannic acid <NA> MT-ND1 SYBR pGEM-T std tannic acid 0.1
#> 4 tannic acid <NA> MT-ND1 SYBR pGEM-T std tannic acid 0.1
#> 5 tannic acid <NA> MT-ND1 SYBR pGEM-T std tannic acid 0.1
#> 6 tannic acid <NA> MT-ND1 SYBR pGEM-T std tannic acid 0.1
#> 7 tannic acid <NA> MT-ND1 SYBR pGEM-T std tannic acid 0.1
#> 8 tannic acid <NA> MT-ND1 SYBR pGEM-T std tannic acid 0.1
#> 9 tannic acid <NA> MT-ND1 SYBR pGEM-T std tannic acid 0.1
#> 10 tannic acid <NA> MT-ND1 SYBR pGEM-T std tannic acid 0.1
#> # i 2,150 more rows
#> # i 5 more variables: replicate <fct>, copies <int>, dilution <int>,
#> # cycle <int>, fluor <dbl>
```

Immunoglobulin G (IgG) inhibition:

A series of reactions subjected to inhibition by IgG with concentrations: 0.00781, 0.0156, 0.0312, 0.0625, 0.125, 0.25, 0.5, 1 and 2 mg/mL. Each IgG concentration sample is replicated six times. Each reaction has been amplified through 40 cycles.

```
dplyr::filter(sisti, plate == "IgG")
#> # A tibble: 2,160 x 13
#>   plate well target dye sample sample_type inhibitor inhibitor_conc
#>   <fct> <fct> <fct> <fct> <fct> <fct> <fct> <dbl>
#> 1 IgG <NA> MT-ND1 SYBR pGEM-T std IgG 2
#> 2 IgG <NA> MT-ND1 SYBR pGEM-T std IgG 2
#> 3 IgG <NA> MT-ND1 SYBR pGEM-T std IgG 2
#> 4 IgG <NA> MT-ND1 SYBR pGEM-T std IgG 2
#> 5 IgG <NA> MT-ND1 SYBR pGEM-T std IgG 2
#> 6 IgG <NA> MT-ND1 SYBR pGEM-T std IgG 2
#> 7 IgG <NA> MT-ND1 SYBR pGEM-T std IgG 2
#> 8 IgG <NA> MT-ND1 SYBR pGEM-T std IgG 2
#> 9 IgG <NA> MT-ND1 SYBR pGEM-T std IgG 2
#> 10 IgG <NA> MT-ND1 SYBR pGEM-T std IgG 2
#> # i 2,150 more rows
#> # i 5 more variables: replicate <fct>, copies <int>, dilution <int>,
#> # cycle <int>, fluor <dbl>
```

Quercetin inhibition:

A series of reactions subjected to inhibition by quercetin with concentrations: 0.000312, 0.000625, 0.00125, 0.0025, 0.005, 0.01, 0.02, and 0.04 mg/mL. Each quercetin concentration sample is replicated six times. Each reaction has been amplified through 40 cycles.

```
dplyr::filter(sisti, plate == "quercetin")
#> # A tibble: 1,920 x 13
#>   plate well target dye sample sample_type inhibitor inhibitor_conc
#>   <fct> <fct> <fct> <fct> <fct> <fct> <fct> <dbl>
#> 1 quercetin <NA> MT-ND1 SYBR pGEM-T std quercetin 0.04
#> 2 quercetin <NA> MT-ND1 SYBR pGEM-T std quercetin 0.04
#> 3 quercetin <NA> MT-ND1 SYBR pGEM-T std quercetin 0.04
```

```
#> 4 quercitin <NA> MT-ND1 SYBR pGEM-T std quercitin 0.04
#> 5 quercitin <NA> MT-ND1 SYBR pGEM-T std quercitin 0.04
#> 6 quercitin <NA> MT-ND1 SYBR pGEM-T std quercitin 0.04
#> 7 quercitin <NA> MT-ND1 SYBR pGEM-T std quercitin 0.04
#> 8 quercitin <NA> MT-ND1 SYBR pGEM-T std quercitin 0.04
#> 9 quercitin <NA> MT-ND1 SYBR pGEM-T std quercitin 0.04
#> 10 quercitin <NA> MT-ND1 SYBR pGEM-T std quercitin 0.04
#> # i 1,910 more rows
#> # i 5 more variables: replicate <fct>, copies <int>, dilution <int>,
#> # cycle <int>, fluor <dbl>
```

Format

A [tibble](#) providing amplification curve data in long format. Each row is for an amplification curve point.

plate Plate identifier. There is one identifier for each of the four data sets.

well Well identifier, i.e. the position within a PCR plate. This information was not available from the original publication, thus all values are NA.

target Target identifier. In all data sets the target is an amplicon consisting of a 104 bp fragment of the mitochondrial gene NADH dehydrogenase 1 (MT-ND1), thus the values are all "MT-ND1".

dye Type of fluorescence dye, in this data set it is always SYBR Green I master mix (Roche) ("SYBR").

sample Name of the biological sample. All samples are based on a pGEM-T Promega plasmid, so all values are "pGEM-T".

sample_type Sample type. All reactions are standard curves, i.e. "std".

inhibitor Name of the molecule used as PCR inhibitor. In the case of the dilution series the value is "none".

inhibitor_conc Inhibitor concentration in mg/mL.

replicate Replicate identifier.

copies Standard copy number of the amplicon.

dilution Dilution factor. Higher number means greater dilution, e.g. 10 means a 1:10 (ten-fold) dilution.

cycle PCR cycle.

fluor Raw fluorescence values.

Source

[doi:10.1186/1471210511186](https://doi.org/10.1186/1471210511186)

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