

# Package ‘karlen’

May 8, 2026

**Title** Real-Time PCR Data Sets by Karlen et al. (2007)

**Version** 0.0.2

**Description** Real-time quantitative polymerase chain reaction (qPCR) data sets by Karlen et al. (2007) <[doi:10.1186/1471-2105-8-131](https://doi.org/10.1186/1471-2105-8-131)>. Provides one single tabular tidy data set in long format, encompassing 32 dilution series, for seven PCR targets and four biological samples. The targeted amplicons are within the murine genes: Cav1, Ccn2, Eln, Fn1, Rpl27, Hspg2, and Serpine1, respectively. Dilution series: scheme 1 (Cav1, Eln, Hspg2, Serpine1): 1-fold, 10-fold, 50-fold, and 100-fold; scheme 2 (Ccn2, Rpl27, Fn1): 1-fold, 10-fold, 50-fold, 100-fold and 1000-fold. For each concentration there are five replicates, except for the 1000-fold concentration, where only two replicates were performed. Each amplification curve is 40 cycles long. Original raw data file is Additional file 2 from ``Statistical significance of quantitative PCR" by Y. Karlen, A. McNair, S. Perseguers, C. Mazza, and N. Mermoud (2007) <[https://static-content.springer.com/esm/art%3A10.1186%2F1471-2105-8-131/MediaObjects/12859\\_2006\\_1503\\_MOESM2\\_ESM.ZIP](https://static-content.springer.com/esm/art%3A10.1186%2F1471-2105-8-131/MediaObjects/12859_2006_1503_MOESM2_ESM.ZIP)>.

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**Encoding** UTF-8

**RoxygenNote** 7.3.1

**Imports** tibble

**Depends** R (>= 2.10)

**LazyData** true

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

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

**NeedsCompilation** no

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### Description

One single tabular tidy data set in long format, encompassing 32 dilution series, for seven PCR targets and four biological samples. The targeted amplicons are within the murine genes: Cav1, Ccn2, Eln, Fn1, Rpl27, Hspg2, and Serpine1, respectively. Dilution series: scheme 1 (Cav1, Eln, Hspg2, Serpine1): 1-fold, 10-fold, 50-fold, and 100-fold; scheme 2 (Ccn2, Rpl27, Fn1): 1-fold, 10-fold, 50-fold, 100-fold and 1000-fold. For each concentration there are five replicates, except for the 1000-fold concentration, where only two replicates were performed. Each amplification curve is 40 cycles long. Please read the sections *Experimental set of qPCR data* and *Quantitative PCR assays* of Karlen et al. (2007) for more details.

### Format

A [tibble](#) providing amplification curve data in long format.

`plate` Plate identifier. This corresponds, loosely, to the name of the targets. In the original publication the amplicons are indicated by gene symbol synonyms which we do use here for naming each plate. This differs from the names used in the column `target` where actual murine gene symbols are used.

`well` Well identifier, i.e. the position within the 96-well plate.

`target` Target identifier: murine gene symbol where the amplicon maps to.

`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.

`sample_type` Sample type. Most reactions in this data set are standard curves, i.e. "std", but a few no template controls ("ntc") are also included.

`replicate` Replicate identifier: 1 thru 5.

`copies` Standard copy number.

`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:10.1186/147121058131](https://doi.org/10.1186/147121058131)

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