

## **LinRegPCR update history**

The most recent updates can be found on the [LinRegPCR](#) website.

### **LinRegPCR version 2012.0** released April 2012

In this version the following features have been implemented:

- This version is fully RDML compatible

- Data can be read from an RDML file

- Results can be saved to an RDML file

- Saved results can be imported in [qbasePLUS](#) for normalisation and statistical analysis

### **LinRegPCR version 12.18** released March 2012

- Release in preparation of the full RDML compatible release

- Added tab page for assignment of Tissue Samples per reaction

- Added option to read amplicon group, tissue sample and baseline from Excel

- Note that spaces will be removed from the given identifiers

- Moved user choices to separate tab page 'User Settings'

- Note that the LinRegPCR\_help.pdf is not yet updated

- When you want to test the RDML input and output: please contact us at [info@linregpcr.nl](mailto:info@linregpcr.nl)

### **LinRegPCR version 12.17** released November 2011

- Enabled the import of data from Excel files with column codes AAA and further.

- Previous versions were restricted to ZZ.

### **LinRegPCR version 12.16** released September 2011

- Corrected visibility of Amplicon Group Tab when baseline-corrected data are read (this error was introduced in version 12.13).

- Added option to read baseline values that were saved in an earlier analysis of the data set.

- Corrected a bug that occurred when the plateau phase data were not fully continuously increasing. This then resulted in a two plateau phase points being selected and the sample being excluded. Note that this correction can lead to changed results when data are re-analysed.

### **LinRegPCR version 12.15** released August 2011

- Repaired an error in placing of the Legends column that was introduced when adding the Tissue sample column in version 12.13.

- This change has no effect on the results.

### **LinRegPCR version 12.14** released August 2011

- Repaired an error that sometimes occurred in setting of Window-of-Linearity: when the variation between curves decreased close to the baseline, the W-o-L was set too low (see Manual for details). NOTE: this change can lead to different results when data are re-analysed.

### **LinRegPCR version 12.13** released August 2011

Release of second (test) version for RDML output.

Lay-out of Read data dialog was changed to accomodate future RDML input.

Added Tab-page for annotation of tissue samples.

Added functionality to read Amplicon groups and Tissue sample annotation from Excel.

Changes have no effect on calculations.

**LinRegPCR version 12.12** released June 2011

Release of first (test) version for RDML output. No other changes were implemented

**LinRegPCR version 12.11** released April 2011

Improved the handling of different decimal separators used by different Regional Settings of Windows

**LinRegPCR version 12.10** released March 2011

Added handling of fully negative samples to Step-One-Plus format. Was already implemented for Eppendorf Realplex. When fully negative samples occur processing stops, the user is notified, given the well numbers and the program waits for new input.

**LinRegPCR version 12.9** released March 2011

Added input format for the new Applied Biosystems export format with 5 leading columns. Ignore the first lines: given range should start at cell with content 'Well'. The empty 'Rn' column has to be included. See the manual for further details.

A menu item 'Open Manual (pdf)' was added to the 'Help' menu. LinRegPCR.pdf should be stored in the program directory

**LinRegPCR version 12.8** released February 2011

Added input format for Eppendorf Realplex. Ignore the first lines: given range should start at cell with content 'Position'.

From this version onwards LinRegPCR writes its version number to the Windows Registry. When, sometime in the future, your system manager has installed a newer version you will be notified

**LinRegPCR version 12.7** released November 2010

Corrected error in browsing though groups that was introduced in version 12.6. This error had no effect on the output

**LinRegPCR version 12.6** released November 2010

Solved 'floating point division by zero' error that occurred when all samples in an amplicon group were excluded from the calculation of the mean efficiency

**LinRegPCR version 12.5** released August 2010

Updated Read-from-Excel dialog to deal with different targets for hydrolysis probes

Adjusted Cq correction to handle different targetting as well as different input (see 12.3)

**LinRegPCR version 12.4** released July 2010

Bug fix in baseline estimation. Bug caused a crash but had no effect on estimated baselines.

Bug fix in import of Step-One Plus output: Rn column is used, delta-Rn column is ignored.

**LinRegPCR version 12.3** released May 2010

Restricted application of Cq-shift correction to hydrolysis probe monitored qPCR with input of ds-DNA.

**LinRegPCR version 12.2** released March 2010

Updated manual released.

Tuomi et al reference completed.

**LinRegPCR version 12.1** released February 2010

Correction of an error in the display of flagged samples.

Exclusion of deviating PCR efficiency values was adapted to handle skewed distributions.

**LinRegPCR version 12.0** released February 2010

Update because of acceptance of the paper in Methods ([Tuomi et al.](#))

This paper describes how to deal with cumulative fluorescence data like those obtained with TaqMan hydrolysis probes.

**LinRegPCR version 11.5**

Updated Rotor-Gene input format to include raw and baseline-corrected data

Raw data are exported with the "Excel data sheet" option of Rotor-Gene

The LinReg export format exports baseline-corrected data (constant baseline per sample)

**LinRegPCR version 11.4**

not released

**LinRegPCR version 11.3**

Updated the code to read the Step-One Plus format to allow for different output versions

Enabled a 'relaxed' baseline estimation for datasets with a short continuous log-linear phase due to measurement noise

Extended 'Legends' column in output with list of choices made by the User

**LinRegPCR version 11.2**

Added import formats to Read-from-Excel dialog:

- Step-One Plus system (ABI)
- LightCycler 480, 2 columns per sample
- Rotor-Gene (Corbett Reseach; LinRegPCR export)

Corrected program flow after detection of noisy samples

Enabled easier handling of baseline error samples

**LinRegPCR version 11.1**

Removed 'overflow' error that occurred sometimes when empty wells were included in the data

**LinRegPCR version 11.0** released January 2009.

Version number was increased because of the acceptance of the paper in Nucleic Acids Research ([Ruijter et al.](#)).

Added input format for Stratagene systems (Format 1, Vertically Grouped data)

Added export of input data in '1 row per sample, 1 column per cycle' format

### **LinRegPCR version 10.3**

Detection of noisy datasets

Extended quality check with 'noisy sample'

Removed error that lead to crash in the setting of the window-of-linearity in noisy datasets

Help on the handling of noisy data

### **LinRegPCR version 10.2**

Corrected error in the setting of the Ct value

Corrected assignment of upper W-o-L limit for first amplicon group

Implemented full reset of the values when 'determine baseline' is pressed twice

### **LinRegPCR version 10.1**

'division by zero' error that occurred when not enough data were present at low W-o-L settings was captured and handled

Freezing of the tab pages when a grouping error occurred was removed

### **LinRegPCR version 10.0** fully updated version. Released March 2008.

In this version the following features have been implemented:

import of raw data files

estimation of baseline fluorescence

new approaches to determine the window-of-linearity and fluorescence threshold

definition of sample groups per amplicon

calculation of the mean PCR efficiency per amplicon group

calculation of starting concentrations based on mean efficiency and individual Ct values

reports on data quality for each sample

### **LinRegPCR versions 8 and 9**

Non-released. these versions were intermediate versions while implementing baseline subtraction and amplicon grouping.

### **LinRegPCR version 7.4**

Version released with Ramakers et al Neurosci Lett 2003.

The use of this version is no longer recommended and its distribution was discontinued in March 2008