analytikjena
An Endress+Hauser Company

Operating Manual

qPCRsoft touch
Software for Real-Time PCR-Thermocycler

Manufacturer

Analytik Jena GmbH+Co. KG
Konrad-Zuse-Straße 1
07745 Jena / Germany
Phone: +49 3641 77 70
Fax: +49 3641 77 9279
Email: info@analytik-jena.com

Technical Service

Analytik Jena GmbH+Co. KG
Konrad-Zuse-Straße 1
07745 Jena / Germany
Phone: +49 3641 77 7407
Fax: +49 3641 77 9279
Email: service@analytik-jena.com

For a proper and safe use of this product follow the instructions. Keep the operating manual for future reference.

General Information

http://www.analytik-jena.com

Documentation Number

/

Edition

B (04/2024)

Technical Documentation

Analytik Jena GmbH+Co. KG

Table of contents

1 Software overview

The qPCRsoft touch software is used to control real-time PCR thermal cyclers and to create and analyze qPCR experiments.

Software version described

The information in this manual are based on qPCRsoft touch 4.0.1.0.

Supported devices

The software supports the device control and data analysis of the following devices:

- qTOWER iris

Notes on this operating manual

This manual uses the following typographical marks:

- Software terms are marked in **bold.**
- In the software, functions are divided into tabs and menu items. Tabs and menu items are separated by a vertical bar "|", e.g. **Templates** | **New Template** | **Thermal cycler**.
- Work steps for operating the software are denoted by a triangle:

▸ Open the **Templates** page.

1.1 Starting and exiting the software

Starting the software

When the thermal cycler is switched on, the integrated tablet automatically starts up and the software is started.

▸ Switch on the thermal cycler by the mains switch.
  ✓ The integrated tablet is switched on.
  ✓ The software starts automatically.

▸ Alternatively, the software can also be launched from the start screen.

Exiting the software

Exiting the software from the start page

▸ On the start page: Exit the software by tapping  .
  ✓ The software has been exited.
  ✓ The operating system can be used.
  ✓ The tablet can be shut down via the operating system.
  ✓ The thermal cycler can be switched off after the tablet has been shut down. When switching it off, observe the information provided in the operating manual of the thermal cycler.

Exiting the software from the settings

▸ Open the settings by tapping  .

▸ Exit the software by tapping  .
  ✓ The software has been exited.
  ✓ The operating system can be used.
  ✓ The tablet can be shut down.

✓ The thermal cycler can be switched off after the tablet has been shut down. When switching it off, observe the information provided in the operating manual of the thermal cycler.

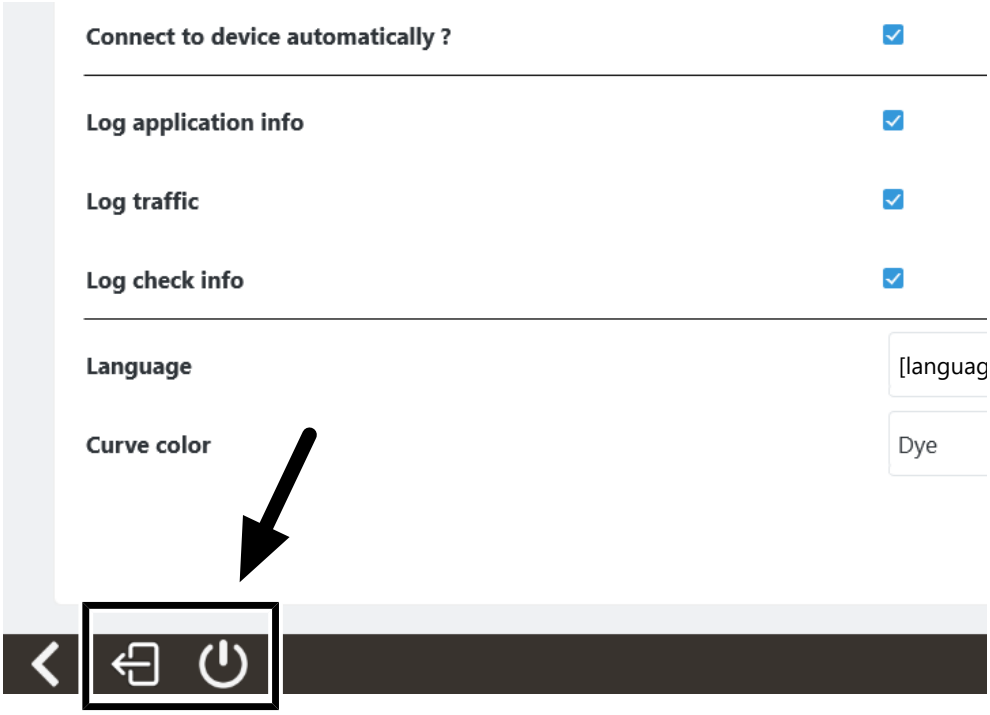

Fig. 1 Closing the software from General Settings

Exiting the software via the operating system

- Open up the Action Center of the Windows operating system: Swipe your finger from the right edge of the screen to the left.
- Activate tablet mode in the Action Center.
- Open up the taskbar of the Windows operating system: Swipe your finger from the bottom edge of the screen upward.
- Click on the icon to see the active applications.
- In the active applications view, close the software by clicking on ✕.
  - ✓ The software has been exited.
  - ✓ The tablet can be shut down.
  - ✓ The thermal cycler can be switched off. When switching it off, observe the information provided in the operating manual of the thermal cycler.

Shutting down the tablet

Shutting down the tablet via the settings

- Open the settings via the icon: exit the software with .
  - ✓ The software has been exited and the tablet is shut down.
  - ✓ The thermal cycler can be switched off. When switching it off, observe the information provided in the operating manual of the thermal cycler.

Shutting down the tablet via the operating system

⇨ The software has been exited.

- Open up the taskbar of the Windows operating system: Swipe your finger from the bottom edge of the screen upward.
- Click **Start** | **On/Off** | **Shut down**.
  - ✓ The tablet is shut down.
  - ✓ The thermal cycler can be switched off. When switching it off, observe the information provided in the operating manual of the thermal cycler.

1.2 Using the software

Frequently used icons

The following icons/functions are frequently used in the software:

Icon	Function
	Access help
	Open settings
	Return to previous page.

Enable a function

Software functions are enabled by tapping. For input fields, an alphanumeric or numeric keypad is opened depending on the type of input.

Keypads

Fig. 2 Alphanumeric keypad

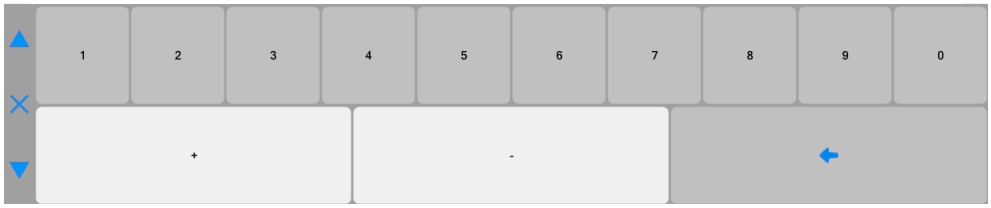

Fig. 3 Numeric keypad

The alphanumeric keypad appears for entering texts. The numeric keypad is displayed for entering numerical values. The keypads contain the following function keys:

Key	Description
	Alphanumeric: Switch to uppercase Numeric: Switch to arithmetic operators
	Move cursor

Key	Description
	Delete characters to the left of the cursor
	Delete character to the right of the cursor
 	Jump to the beginning of the line or selection Jump to the end of the line or selection
	Move keypad to the bottom or top of the screen.
	Hide keypad

Use help

Help can be displayed for each program page, containing information about the available parameters, options and icons on the page.

- Tap ⓘ on the software interface.
  - ✓ Help is displayed.
- Tap anywhere on the tablet screen to return to the program.

1.3 Home screen

Fig. 4 Home screen

Menus

The start page appears after the software starts. All basic functions of the software can be accessed via the menus displayed on this page.

Menu	Functions
Templates	Create new templates for experiments Enable a saved template for the qPCR run Start qPCR run
Results	Open saved results file

Icons

Icon	Description
	Exit the software and switch off the tablet The device must then be switched off at the mains switch. Observe the information provided in the operating manual of the device.
	Open help

NOTICE! You can specify in the settings whether the start page should be displayed when the software is started. If the function is disabled, the template page appears when the software is started.

1.4 Templates page

Experiments are started in the software using a template. All information about the experiment is stored in the template.

You can use the **Templates** page to search for templates, start an experiment with an existing template, or create a new template.

NOTICE! If a large number of templates have been created in the selected storage location, it may take a moment to load the list of templates. A loading bar above the list of templates indicates how far loading the list has progressed. The number above the loading bar indicates the number of templates loaded.

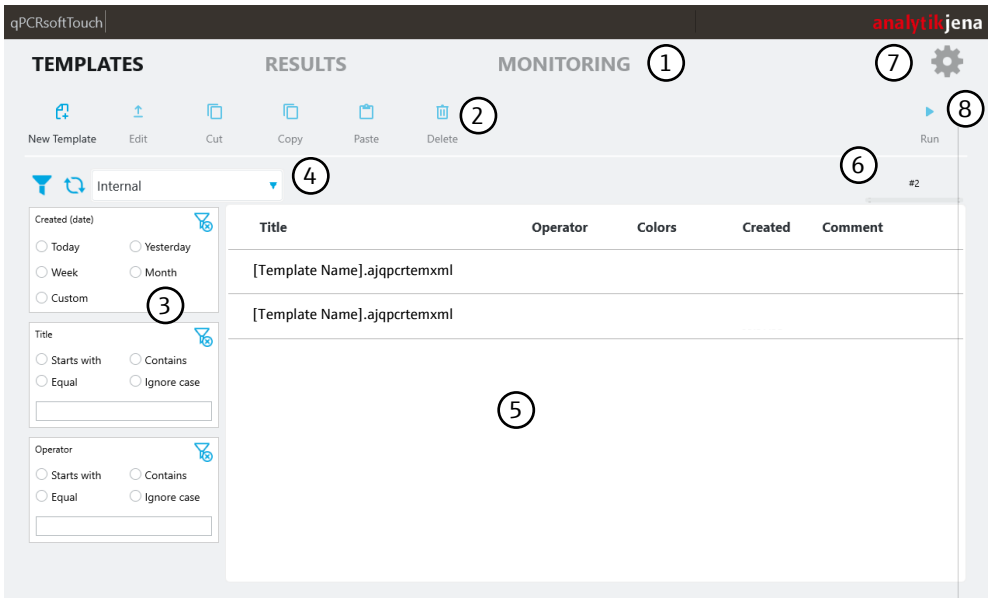

Fig. 5 Page Templates

Elements

The templates area of the **Templates** page contains the following elements:

No.	Element	Description
1	Header	The tabs make it easy to switch between the function pages of the software.
2	Icon bar	Functions for editing existing templates and creating new ones. The templates can also be moved between different storage locations.
3	Filter	Allows filtering according to selected criteria. The filter is applied when one of the radio buttons or the icon is selected. The filter can be reset via the icon.
4	Selecting the storage location	If an external data storage device is connected to the device and configured, in this drop-down menu you can choose between the tablet's internal memory and the external data storage device.
5	List of templates	The table shows all templates in the selected storage location. Details about the templates, such as **Operator**, **Colors**, **Created** or **Comment** are also displayed.
6	Loading bar	Shows the loading progress for the list of templates.
7	Configuration	■ Make general software and device settings for the thermal cycler. ■ Manage color modules. ■ Insert the transport lock. ■ Start the software update.
8	▶ **Run**	Start an experiment with the selected template

1.5 Template pages

The **New Template** area is used to enter the PCR protocol, define the fluorescence measurement, enter the samples, and start the qPCR run.

Main elements in the template area

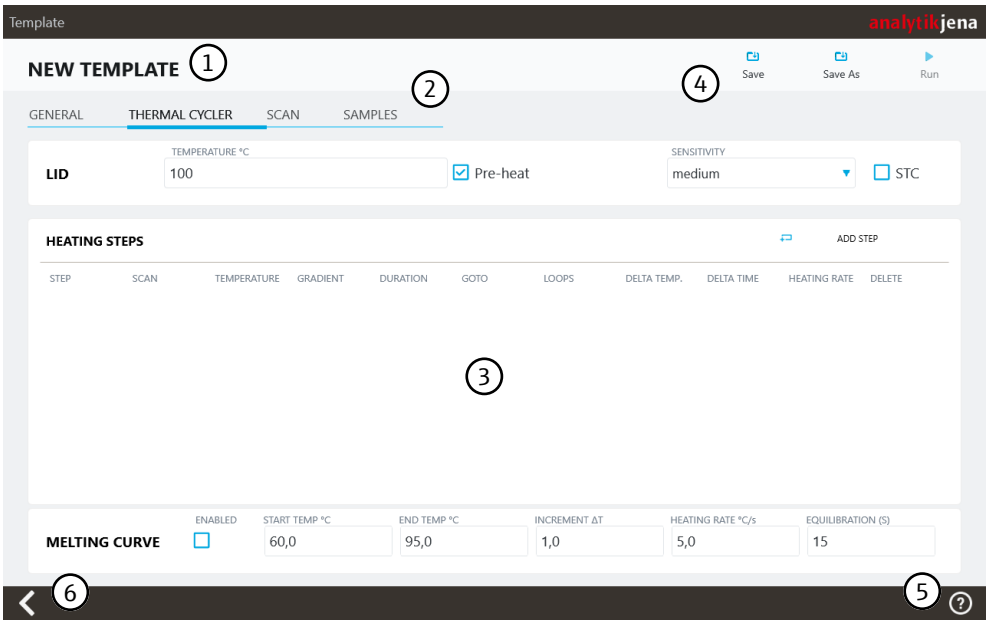

Fig. 6 Template area using the example of Thermal cycler

The template area contains the following elements:

No.	Element	Description
1	Header	Information about the page names, the name of the template file
2	Screen selection	Jump to the template page
3	Template page	Editing area for the qPCR protocol
4	Icon bar	Function icons The functions and their icons vary according to the content of the current page.
5	Help	Open help
6	Close	Close the **New Template** page and return to the **Templates** page.

The template pages contain all parameters for conducting a real-time PCR experiment. The views of the template pages appear:

- when creating a new template via the button on the **New Template** page **Templates**
- when editing an already created template by selecting it on the **Templates** page and clicking the button **Edit**

1.5.1 General template page

The inputs on the **General** page are optional.

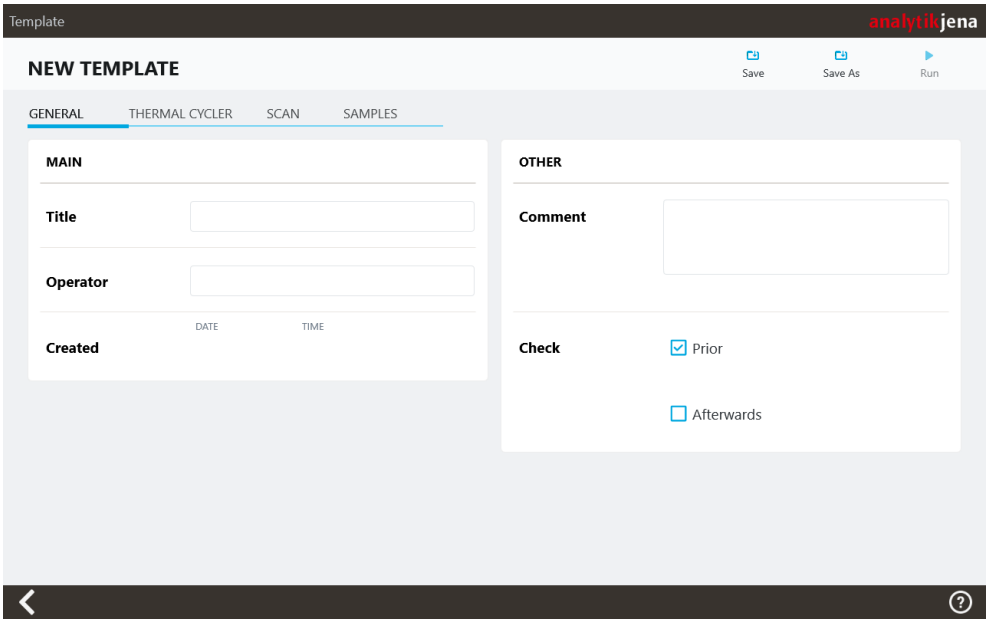

Fig. 7 Page General

Elements

The following information can be entered on the **General** page:

Option	Description
Title	Name of the template
Operator	Name of the template author
Created	Time and date the template was created The information is entered automatically by the software.
Comment	Additional information
Check	Perform a technical check. Can optionally be carried out before and after the experiment.

Icons

Icon	Description
	Save a template Save a template as
	Start run
	Return to the **Templates** page, entries will be lost.
	Open help

1.5.2 Thermal cycler template page

The **Thermal cycler** page contains all parameters for the PCR protocol. You can define up to 28 heating steps.

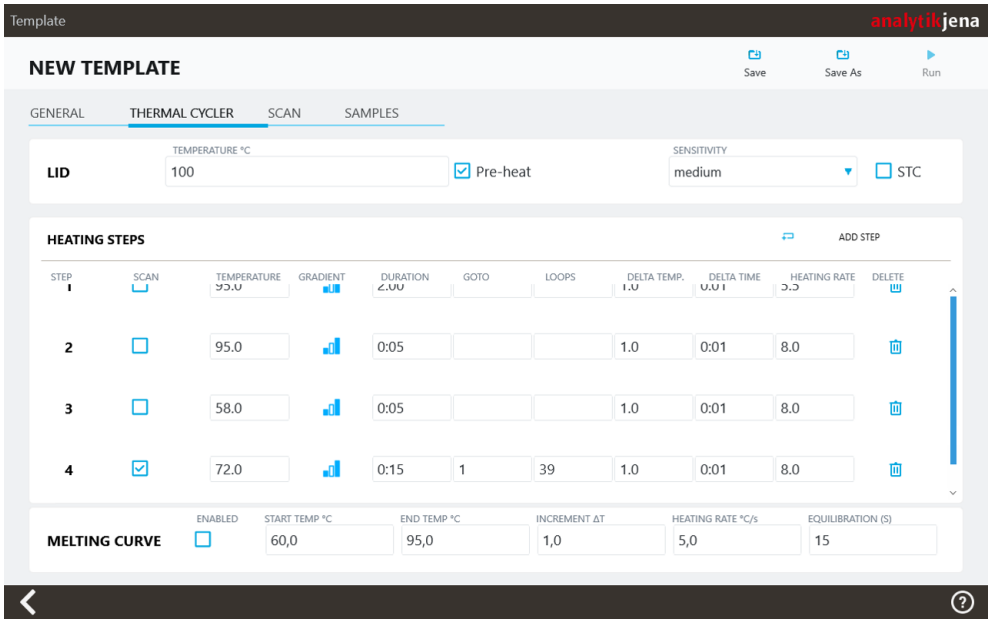

Fig. 8 Page Thermal cycler

LID

Option	Description
Temperature	Lid temperature The lid temperature should be approx. 5 °C above the maximum block temperature to prevent liquids from evaporating from the reaction mixture and condensing at the walls or lid of the reaction cups. Input range: 30 to 110 °C
Pre-heat	The heated lid is preheated to the set temperature before the actual program starts. The preheating creates a homogeneously tempered air cushion between the sample vessels, which ensures better temperature uniformity between the samples. While the lid is being heated, the block is kept at a constant 25°C. If the option is disabled, the PCR program starts while the lid is still being heated.
SENSITIVITY	Basic sensitivity of the detection system This setting affects all dyes and should only be changed if particularly weak or intense samples are to be measured. Default setting: **medium**
STC (Simulated Tube Control)	If enabled, the temperature in the sample is pre-calculated with the measured block temperature and the temperature is controlled to the sample temperature. This method is particularly recommended for fast protocols and high sample volumes. If disabled, the block temperature is controlled according to the selected temperature program. Particularly if the heating and cooling rates are high and the hold times are short the actual sample temperature can differ from the desired temperature.

HEATING STEPS

Edit the PCR protocol in the table area.

Melting curve

When this function is enabled, the melt is connected to the completed product amplification.

You can configure the melting curve in the table area.

Icons

Icons	Description
	Save a template Save a template as
	Start run
	Delete heating step
	Return to the **Templates** page, entries will be lost.
	Open help

1.5.3 Scan template page

The product accumulation is measured in the real-time PCR by the increases in fluorescence. The colors to be measured are defined on the **Scan** page.

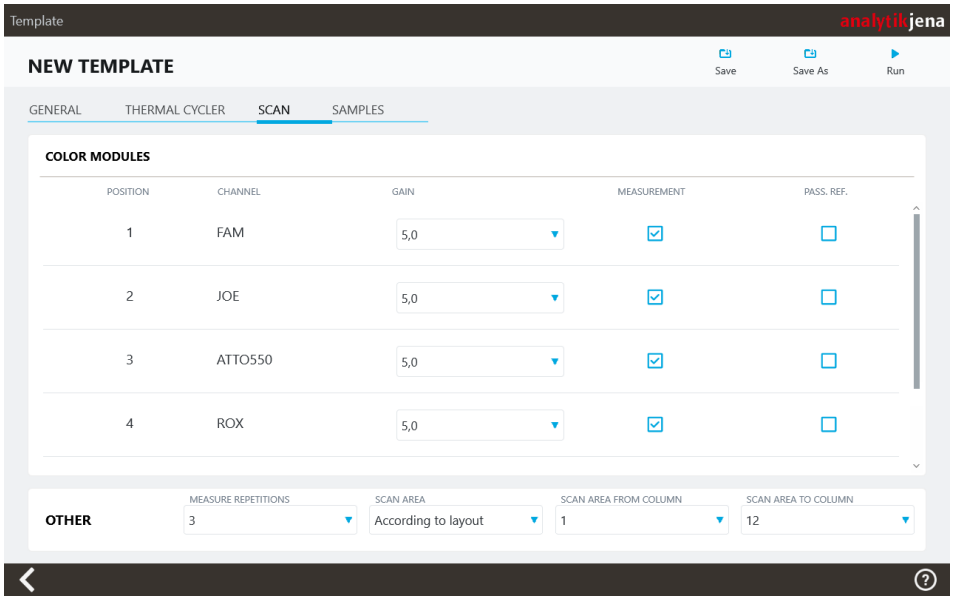

Fig. 9 Page Scan

Elements/parameters

Elements	Description
POSITION	Position of the color modules on the color module wheel of the thermal cycler
CHANNEL	Installed dye modules Up to 6 different color modules can be installed in the thermal cycler. The installed color modules are specified in the software options.
GAIN	Adjustment of signal intensities The intensity is in steps in the range 0.1 to 10.0 and should be selected such that the intensity of a positive sample is at least 10000 at the end of the PCR run.

Elements	Description
	The default setting is 5.0. This setting is recommended and ideal for most experiments. You can change the default setting at any time in the options.
MEASUREMENT	Measurement of the dye The fluorescences of the dyes marked with a tick ☑ are measured during the qPCR run.
PASS.REF.	Reference dye The LED technology used does not require a passive reference. If you wish to measure a reference dye anyway, you must place a check mark in this column.

Icons

Icon	Description
	Save a template Save a template as
▶	Start run
‹	Return to the **Templates** page, entries will be lost.
?	Open help

1.5.4 Samples template page

The sample layout is displayed and edited on the **Samples** page with the sample properties and sample positions in the plate diagram. Each sample can be assigned properties such as name and sample type. In addition, samples from different experimental preparations can be combined into groups.

Each dye can be assigned the corresponding detected gene and its concentration, which is hidden behind the measured dye fluorescence.

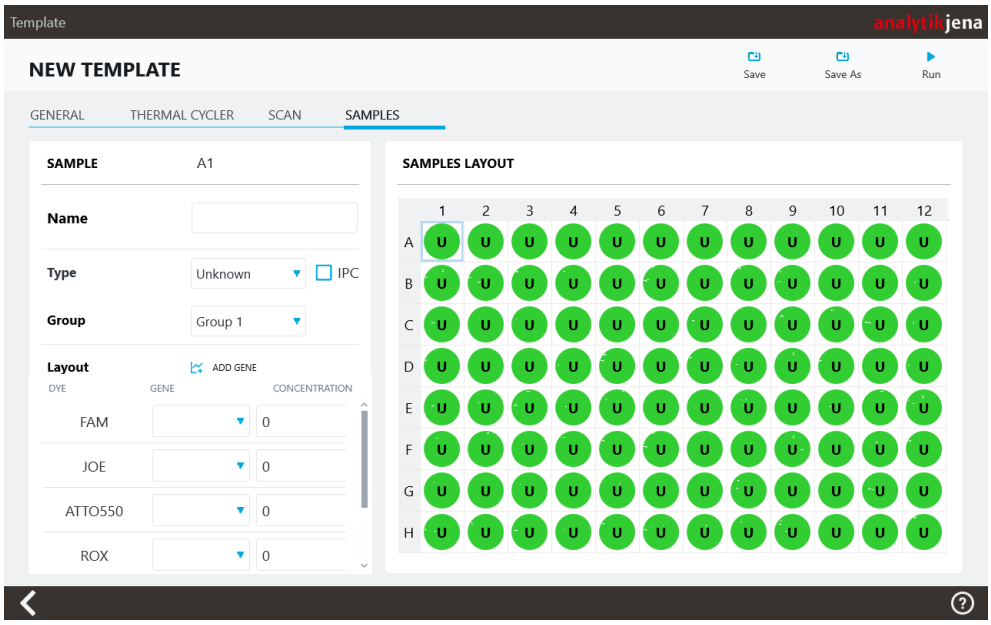

Fig. 10 Samples page with the sample layout in plate format

Elements/parameters

Element	Description
SAMPLE	The entered sample properties are displayed in this field for the well framed in blue (highlighted). If several wells are marked, the properties of the sample located in the selected area at the top left are displayed.
SAMPLES LAYOUT	Overview of the occupied positions in the layout with brief information on the sample properties The sample cell is marked with the icon of the sample type.
Layout	During amplification, the genes to be examined are marked with specified dyes. A dye is detected by a specific color module. The genes behind the measured dye fluorescence can be assigned to the color modules under **Layout**. For **Standard** sample type: Enter the concentration of the gene to be analyzed.

Icons

Icon	Function
	Add a gene for selection in the drop-down menu. Added genes can be assigned to the dyes.
	Save a template Save a template as
	Start run
	Return to the **Templates** page, entries will be lost.
	Open help

1.6 MONITORING page

The **MONITORING** page is displayed when a new experiment is started with a selected or created template. You can monitor the qPCR run with the settings defined in the template on the **MONITORING** page.

After the qPCR run, the measured results are summarized in a results file. In the results file, starting from the **MONITORING** page, you can analyze the fluorescence curves and determine the Ct value and the melting temperature Tm.

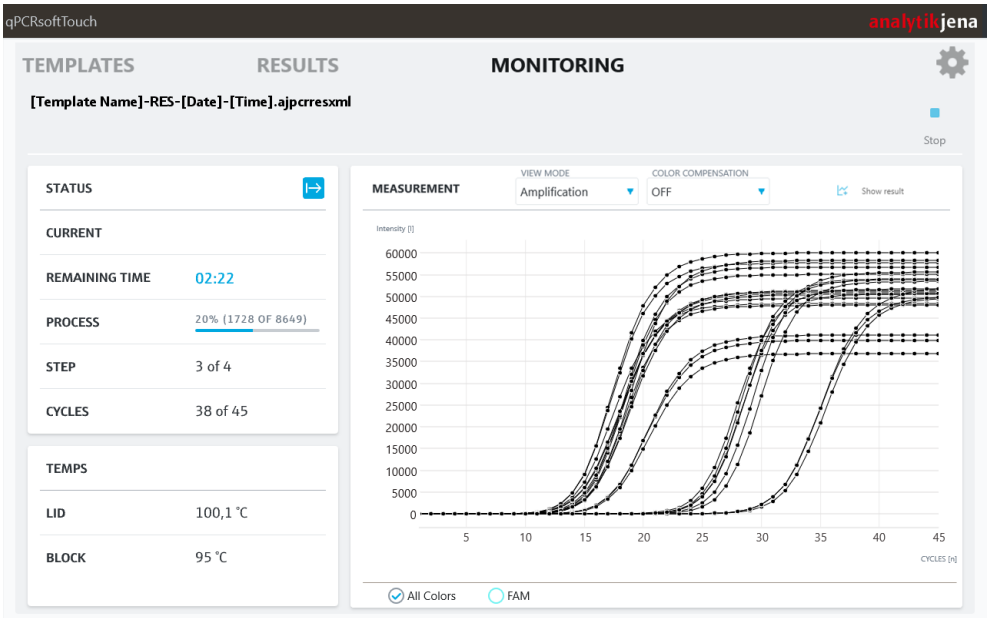

Fig. 11 The MONITORING page with display of the fluorescence curves

Elements

Element	Description
Graph	Display of amplification curves or melting curves (fluorescence measurement data) The curve colors can be selected in the options under **General Settings**. Open the options with ⚙.
VIEW MODE	List with display options: ■ **Raw data** (Amplification without baseline subtraction) ■ **Amplification** ■ **Melting curve**
Color compensation	List with color compensation options
Dyes below the graph	Select target gene / dye combination for display The display can be switched between the fluorescence intensity for the selected dye (gene) or all dyes (**All Colors**).

Icons

Icon	Description
■	Stop qPCR run The data recorded so far must be saved and can then be analyzed. NOTICE! It is not recommended to analyze data from aborted measurements!
↦	Status of the measurement Current status: Start of measurement Further statuses are explained in the "Monitor display" chapter.
Radio buttons ○ ⊘	Select target gene / dye combination for display Selection between the following displays: ■ **All Colors** ■ Target gene/dye combinations
Show result	Open results Displays the results of the performed and completed measurement in the results file. Can only be selected after the measurement has finished.

1.7 Results page

Completed experiments are saved in a results file.

You can use the **Results** page to search for and open results files.

NOTICE! If a large number of results files have been saved in the selected storage location, it may take a moment to load the list of results files. A loading bar above the list of results files indicates how far loading the list has progressed. The number above the loading bar indicates the number of results files loaded.

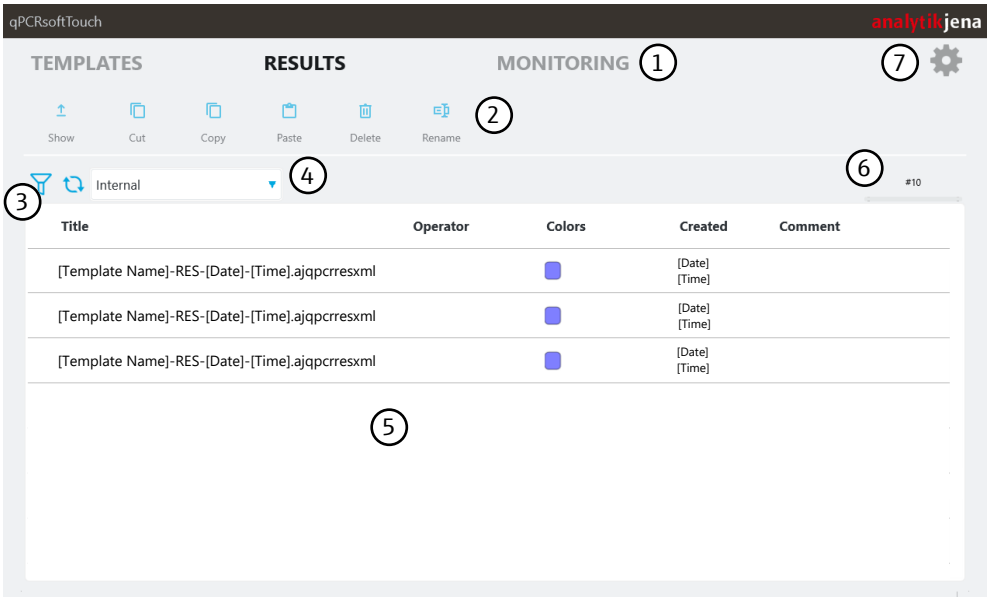

Fig. 12 Page Results

Elements

The templates area of the **Results** page contains the following elements:

No.	Element	Description
1	Header	The tabs make it easy to switch between the function pages of the software.
2	Icon bar	Functions for: ■ Displaying results ■ Moving results between different storage locations
3	Filter	Allows filtering according to selected criteria. The filter is applied when one of the radio buttons or the icon is selected. The filter can be reset via the icon.
4	Selecting the storage location	If an external data storage device is connected to the device and configured, in this drop-down menu you can choose between the tablet's internal memory and the external data storage device.
5	List with results files	The table shows all results in the selected storage location. Details about the results, such as **Operator**, **Colors**, **Created** or **Comment** are also displayed.
6	Loading bar	Shows the loading progress for the list of templates.
7	Configuration	■ Make general software and device settings for the thermal cycler. ■ Manage color modules. ■ Insert the transport lock. ■ Start the software update.

1.8 Results pages

1.8.1 Info results page

The **Info** results page contains basic information on the PCR settings configured for the results file displayed.

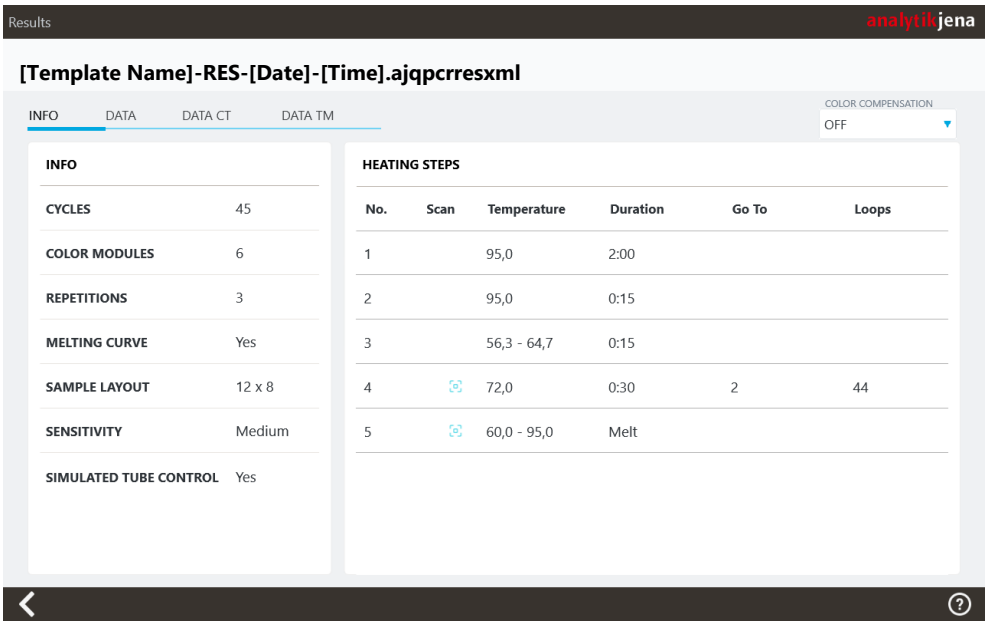

Fig. 13 Page Info

Info

Option	Description
CYCLES	Number of cycles
COLOR MODULES	Number of color modules used
REPETITIONS	Number of repeat measurements
Melting curve	Indicates whether a melting curve was performed. If a melting curve was performed, the information on this is also displayed in the table under **HEATING STEPS**.
SAMPLE LAYOUT	Number of samples in the sample layout (columns x rows)
SENSITIVITY	Basic sensitivity of the detector system
SIMULATED TUBE CONTROL	Indicates whether the **SIMULATED TUBE CONTROL** method was enabled. If enabled, the temperature in the sample is pre-calculated with the measured block temperature and the temperature is controlled to the sample temperature. This method is particularly recommended for fast protocols and high sample volumes.

HEATING STEPS

Option	Description
No.	Step of the temperature protocol
Scan	Indicates the step in which a scan is performed
Temperature	Configured temperature of the step
Goto	Indicates the step to which the programmed loop returns.
Loops	Number of repetitions of the cycle
Color compensation	List with color compensation options

Icons

Option	Description
	Scan takes place in this step of the PCR protocol.
	Return to the **Results** page.
	Open help

1.8.2 DATA, DATA CT and DATA TM results pages

The **DATA** results page shows all measurement results of the measurement.

The **DATA CT** and **DATA TM** results pages allow the Ct values and melting temperatures to be determined.

The basic structure of the three results pages is explained in the sections below. Differences are indicated at the appropriate point.

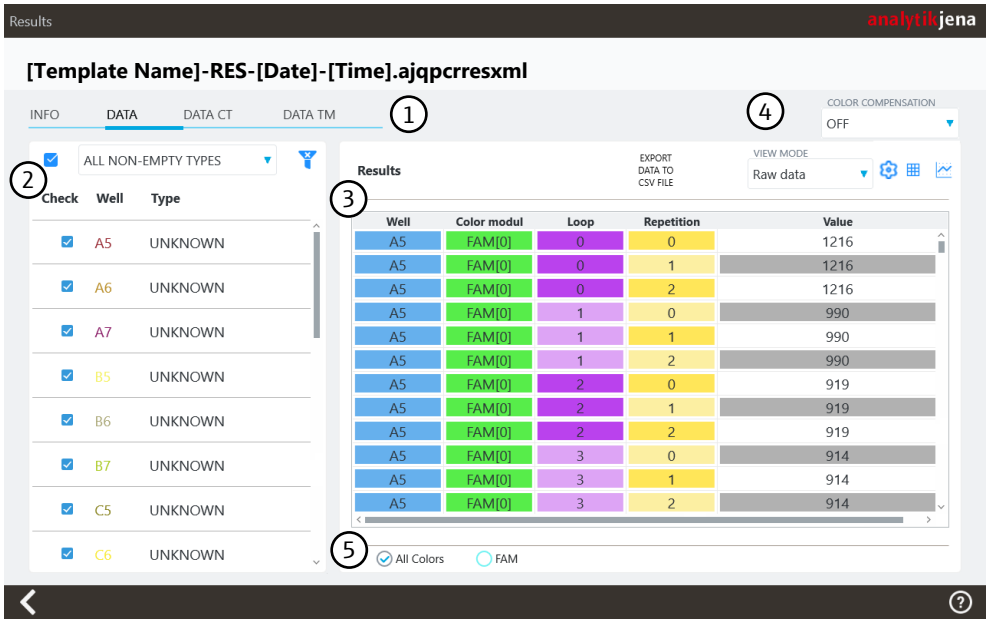

Fig. 14 Elements on the page DATA

1 Navigation tab
2 Table with sample selection
3 Results, as table or graph in the view
4 Customization options, data export, and switch between list and chart view
5 Radio buttons

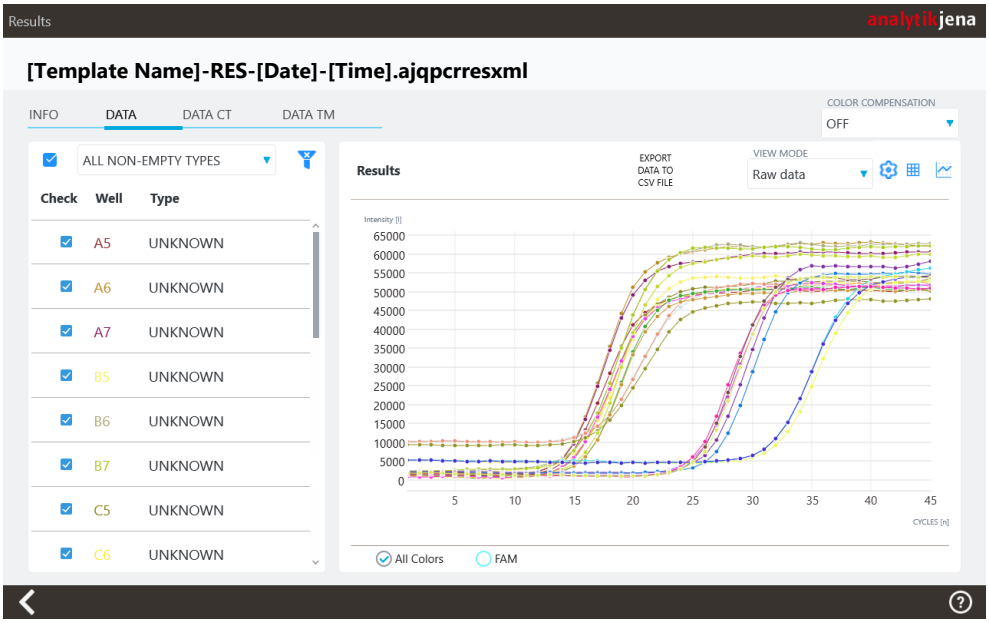

Fig. 15 DATA page as a chart in the view

NOTICE! In the chart view, you can click on individual points in the curves. The software automatically highlights the corresponding sample in the sample selection table on the left-hand side of the screen.

Navigation tab

You can switch between the following pages using the navigation tabs:

- **Info**: shows general information and settings configured for the measurement
- **DATA**: provides an overview of the measurement results
- **DATA CT**: allows you to calculate and display the Ct values
- **DATA TM**: allows you to calculate and display the melting temperatures (only appears when a melting curve is performed in the experiment)

Table with sample selection

Option	Description
Drop-down menu	A filter can be defined via the drop-down menu. The filter determines which results are selected and deselected with the checkbox.
	Select or deselect all samples
	Clear filter
Check	Select and deselect individual results
Well	■ Well position of the measured sample ■ Curve color of the measured sample in the graph
Type	Sample type

NOTICE! You can customize the assignment of the curve color in the general software options.

Results

The results of the measurement are displayed in the **Results** section. The calculated results of the Ct values and the melting temperatures are displayed in the **DATA CT** and **DATA TM** tabs in this section.

The table view contains the following information in this section:

Tab	Options and description
DATA	■ **Well**: Well position of the measured sample ■ **Color modul**: Color module used for the measurement ■ **Loop**: Cycle in which the measurement was performed ■ **Repetition** ■ **Value**: Measured value
DATA CT	■ **Well**: Well position of the measured sample ■ **Sample Name**: Assigned sample name ■ **Sample Type**: Assigned sample type ■ **Dye**: Measured dye ■ **Gene**: Assigned gene ■ **Ct**: Ct value ■ **Mean Ct**: Mean Ct value of replicates If no replicates have been created, the mean value is equal to the value under **Ct**. ■ **Std. dev. Ct**: Standard deviation of the mean Ct value of replicates If no replicates have been created, this value is omitted.
DATA TM	■ **Well**: Well position of the measured sample ■ **Sample Name**: Assigned sample name ■ **Sample Type**: Assigned sample type ■ **Dye**: Measured dye ■ **Gene**: Assigned gene ■ **Tm**: Melting temperature value ■ **Mean Tm**: Mean melting temperature of replicates If no replicates have been created, the mean value is equal to the value under **Tm**. ■ **Std. dev. mean Tm**: Standard deviation of the mean melting temperature of replicates If no replicates have been created, this value is omitted.

Customization options and data export

Option	Description
VIEW MODE (only for **DATA**)	List with display options: ■ **Amplification** ■ **Raw data** ■ **Melting curve**
EXPORT DATA TO CSV FILE	Export results as .CSV file
GENE OF INTEREST (GOI) (only for **DATA TM**)	Select target gene / dye combination
THRESHOLD	Enter threshold manually (For **DATA CT**: only when selecting a gene/dye combination) (For **DATA TM**: only when selecting **Derivative**)
AUTO	Determine threshold automatically (For **DATA CT**: only when selecting a gene/dye combination) (For **DATA TM**: only when selecting **Derivative**)
Color compensation	List with color compensation options
	Display results as a list
	Display results as a chart
	Customize the display and mathematical calculation of the results

Radio buttons

Option	Description
Radio buttons 	Select target gene / dye combination for display Selection between the following displays on the **DATA** and **DATA CT** pages ■ **All Colors** ■ Gene/dye combinations Selection between the following displays on the **DATA TM** page: ■ **Derivative** ■ **GOI** (Gene of Interest)

Other elements

Option	Description
	Return to the **Results** page.
	Open help

2 Templates and results

Results

The software saves all experiments in results files. A results file contains the following information:

- General information about the experiment (**Info** page)
- Measurement results (**DATA** page)
- Ct value calculation results (**DATA CT** page)
- Melting curve calculation results (**DATA TM** page)

No further qPCR experiments can be started from a results file.

Results files are saved as .AJQPCRRESXML files (AJ qPCR Result XML).

Templates

A template contains the information entered beforehand for carrying out an experiment, but does not contain any measurement data. New qPCR experiments can be carried out over and over again with saved templates. All parameters of a template can be edited.

Templates are saved as .AJQPCRTEMXML files (AJ qPCR Template XML).

2.1 Create templates

You can add a template to the software from 3 different sources:

- Create a new template from **New Template**
- Create a template in the qPCRsoft desktop software and import it into the qPCRsoft touch software
- Import templates from an older software version in .RTSX format

See also

Save templates [▶ 25]

2.2 Save templates

Save templates

You can save the parameters on the template pages as a template. Not all template pages have to be filled out completely. For example, you can define the qPCR protocol and save it as a template and later add to the current sample layout.

▶ After entering the parameters on the template pages, tap .

▶ Select the storage medium: **Internal** or an external storage location

▶ Enter the file name.

▶ Tap **OK**.

✓ The template is saved and is now available on the **Templates** page.

NOTE! The internal folder for saving data on the tablet is always **C:\User\qTOWER iris\Documents\Analytik-Jena\qPCRsoft touch\files**.

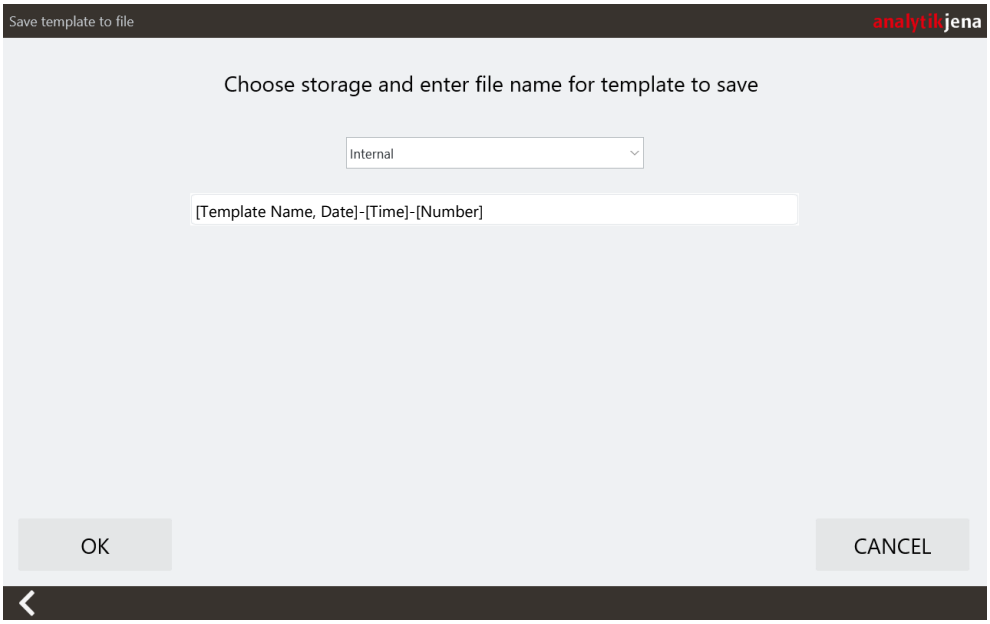

Fig. 16 Saving a template

See also

Opening results files [▶ 27]

2.3 Open templates

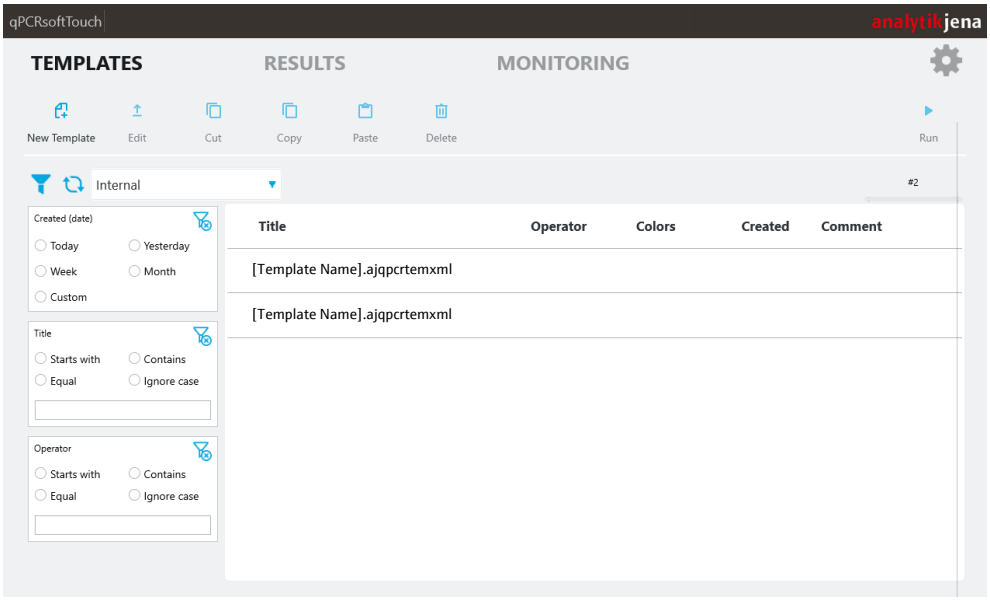

Fig. 17 Templates page with expanded filter options

You can use a saved template to start an experiment.

- Open the **Templates** page.
- Select the storage location from the drop-down menu: **Internal** or an external storage location

- If required, search for a template using the filter.
  - Use one or more filter options.
  - The selected filter is applied when you click on a radio button or click on .
  - Clear individual or all filters as required with .
- Select a template and choose one of the following actions:
- Edit the selected template with **Edit**.
- Start a qPCR run with the selected template with **Run**.

NOTICE! If a large number of templates have been created in the selected storage location, it may take a moment to load the list of templates. A loading bar above the list of templates indicates how far loading the list has progressed. The number above the loading bar indicates the number of templates loaded.

2.4 Saving results files

At the end of the qPCR run, the software automatically saves the data as a results file in the tablet's internal memory.

You can retrieve and view the results files on the **Results** page. You can also move or copy the results files from the internal memory to an external storage location. You can find more information on data management in the corresponding chapter of this manual.

See also

Data management [▶ 28]

2.5 Opening results files

You can open and recalculate a saved results file:

- Open the **Results** page.
- Select the storage location from the drop-down menu: **Internal** or an external storage location
- If required, search for a template using the filter.
  - Use one or more filter options.
  - The selected filter is applied when you click on a radio button or click on .
  - Clear individual or all filters as required with .
- Select the results file.
- Open the selected results file with .
  - ✓ The results file is loaded and the experiment data is displayed.

NOTICE! If a large number of templates have been created in the selected storage location, it may take a moment to load the list of templates. A loading bar above the list of templates indicates how far loading the list has progressed. The number above the loading bar indicates the number of templates loaded.

2.6 Data management

Within the software, you can move files between the device tablet and an external data storage device. The external data storage device can be connected via the USB port on the front of the device or via a network.

File formats

The following file formats are available in the software:

File type/ File extension	Description
.AJQPCRRESXML	Results file with real-time PCR data
.AJQPCRTEMXML	Template for real-time PCR experiment
.RTSX	Template for real-time PCR experiment from previous software versions

NOTE! The internal folder for saving data on the tablet is always **C:\User\qTOWER iris\Documents\Analytik-Jena\qPCRsoft touch\files**.

Exchanging files between the tablet and an external data storage device

You can exchange files between the internal data storage and an external data storage device in the following ways:

- Open the **Templates** or **Results** page.
- Select the source directory from the drop-down menu:
  - **Internal**: Internal storage location on the tablet.
  - Drive name of the external storage location
- Tap the desired file.
  - ✓ The file is highlighted in blue.
- Copy the file to the clipboard by tapping **Copy** or cut it by tapping **Cut**.
- Select the target directory from the drop-down menu.
- Paste the file into the target folder by tapping **Paste**.
  - ✓ The file has now been transferred.

Deleting files

- Open the **Templates** or **Results** page.
- Select the source directory from the drop-down menu:
  - **Internal**: Internal storage location on the tablet.
  - Drive name of the external storage location
- Tap the desired file.
  - ✓ The file is highlighted in blue.
- Delete the selected file by tapping on **Delete**.
- The file is deleted.

Renaming results files

- Open the **Results** page.
- Select the source directory from the drop-down menu:
  - **Internal**: Internal storage location on the tablet.
  - Drive name of the external storage location
- Tap the desired file.
  - ✓ The file is highlighted in blue.
- Rename the file by tapping on **Rename**.

Exporting Ct values and melting temperatures

You can export the results as a .CSV file from the **DATA** and **DATA CT** results pages.

You can find more information about the procedure under (→ "Export results" 52).

See also

Export results [▶ 52]

2.6.1 Setting up an external data storage device

NOTICE

All additional modifications or add-ons, in particular the installation of additional software, that go beyond the procedure described here and were not carried out by Analytik Jena or Analytik Jena service personnel are no longer subject to the warranty and responsibility of Analytik Jena.
Malfunctions caused by additional modifications or add-ons are not subject to the warranty and responsibility of Analytik Jena.

The user is responsible for implementing and complying with measures to meet safety requirements.

You can save, move or load templates and results files to or from connected USB sticks, hard disks, and network drives.

NOTICE! Make sure that the external storage devices are connected before you launch the software so that they are detected by the software. Connected networks must also be defined as storage paths so that they are recognized by the software.

What to do if an external storage device that has already been defined as a storage path is not recognized and does not appear in the drop-down menus on the **Templates** and **Results** pages: Close the software and restart it.

USB port on the front of the device

You can connect an external data storage device, such as a USB stick or a hard disk, to the USB port on the front of the device.

The software automatically detects the external data storage device after it starts. The external data storage device appears in the drop-down menus on the **Templates** and **Results** pages and in the dialog box for saving templates.

Network connection on the back of the device lid

You can connect a network cable to the integrated tablet via the network connection on the back of the lid. This connection allows you to access folders and drives in the connected network as storage locations.

You must first connect these external storage locations as networks and define them as storage paths to be able to use them as storage locations in the software.

NOTICE! Make sure that the external storage location is shared. If this is not the case, the software cannot access the storage location.

- Activate tablet mode:
  - Open up the Action Center of the Windows operating system: Swipe your finger from the right edge of the screen to the left.
  - Activate tablet mode in the Action Center.
  - ✓ Tablet mode has been activated.
- Open up the taskbar of the Windows operating system: Swipe your finger from the bottom edge of the screen upward.
- Click on Start .
- Open the Windows Explorer by clicking on **Documents**.
- Connect the network:
  - Open the following file path using the Windows Explorer: **\\[IP address of the external network]\[shared folder]**
  - Open the context menu.
  - **Select** Connect Network.
  - ✓ The network has been connected.
- Define the storage path:
  - Open the following file path using the Windows Explorer: **C:\Users\qTOWER iris\Documents\Analytik-Jena\qPCRsoft touch**
  - Open the .INI file under the specified storage path.
  - In the .INI file under **UserDataSources**, define the storage path of the desired external storage location as follows: **UserDataSources=[Display Name]=[IP address of the external network]\[shared folder]**
  - Example of a shared folder: **UserDataSources=Result on network=\\123.456.789.123\Results**
  - Example of a connected data storage device: **UserDataSources=hard disk=\\123.456.789.123\M:**
  - Save and close the .INI file.
  - ✓ The storage path has been defined.
  - ✓ The connected network can be used as a storage location.

Configuring multiple external storage paths

If a network cable is connected to the network port, you can also define several external storage paths in the .INI file using the above method.

You can use this method to define different storage locations.

Multiple storage paths are separated from each other by the | character, without spaces between the storage paths.

- Example of multiple storage paths: **UserDataSources=Results User 1=\\123.456.789.123\User\User1\Results|Results User2=\\123.456.789.123\User\User2\Results**

2.6.2 Exchanging data with the qPCRsoft desktop software

You can exchange data with the qPCRsoft desktop software via a connected data carrier or an external data storage device.

You can use the desktop software to:

- Create templates
- Analyze results files

3 Settings for a real-time PCR experiment

At the beginning of a real-time PCR experiment, you create or load a template.

The template contains the following settings:
- Parameters of the qPCR protocol
- Optical measurement parameters
- Sample layout of the PCR plate

Start input

To create a new template, tap the **New Template** button on the **Templates** page.

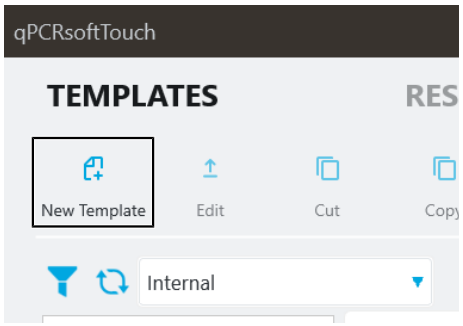

Fig. 18 Button for creating a new template

Pages for creating templates

On the individual template pages, you can enter the required information for a new template or change the settings of an existing template.

There is a menu at the top of the template area that you can use to quickly get to the individual template pages.

Template page	Description
Page **General**	General information Inputs on this page are optional.
Page **Thermal cycler**	Enter PCR protocol
Page **Scan**	Select color modules and dyes for the optical scan
Page **Samples**	Enter plate layout with sample properties (can also be done after the qPCR run)

3.1 General information on the real-time PCR experiment

All entries on the template page **General** are optional. The following information can be entered:

Option	Description
Title	Name of the template
Operator	Name of the template author
Created	Time and date the template was created The information is entered automatically by the software.
Comment	Additional information
Check	Perform a technical check. Can optionally be carried out before and after the experiment.

NOTICE! The software only issues a message after performing a technical check if a fault was detected during this check. If the software has completed the technical check without any faults, no separate message is displayed. In the settings, you can enable the option to log the result of the technical check. Please note the information in the corresponding chapter of this manual.

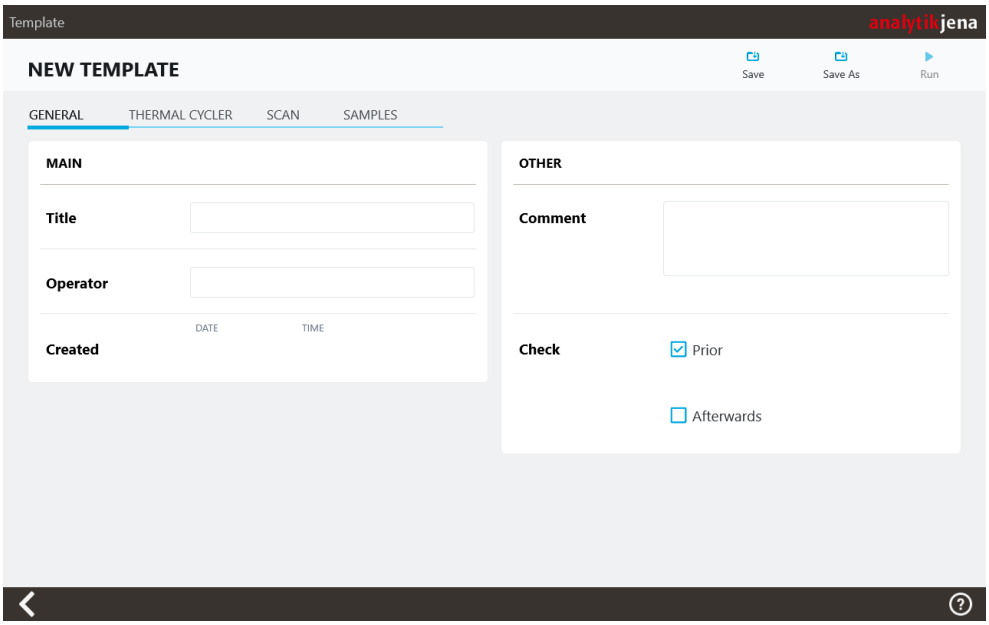

Fig. 19 General page with information on the real-time PCR experiment

3.2 Program qPCR-protocol

Enter the qPCR protocol in the input mask on the **Thermal cycler** page.

You can define up to 28 heating steps for the qPCR protocols and freely configure all parameters within the device specifications.

Functions on the Thermal cycler page

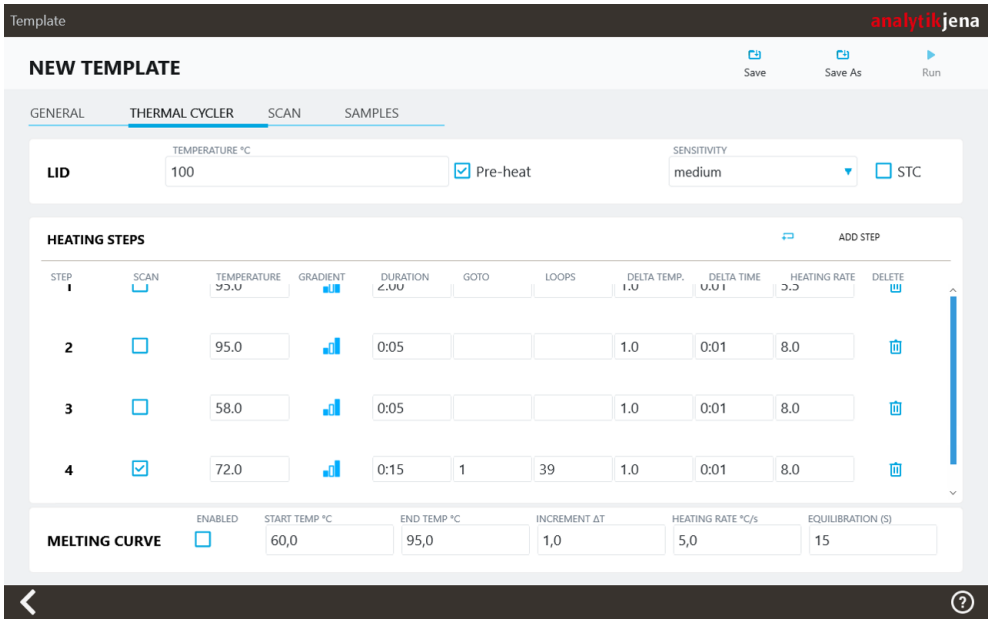

Fig. 20 Control elements on page Thermal cycler

Option	Description
LID	■ Set the lid temperature ■ Activate the preheating function ■ Adjust measurement sensitivity ■ Activate STC (Simulated Tube Control)
HEATING STEPS	Enter protocol parameters
Melting curve	Next, record a DNA melting curve following the qPCR run
	Save a template Save a template as

Programming the lid heater

Set the lid temperature in the **LID** field in the **TEMPERATURE °C** box
Adjustable lid temperature: **30 ... 110 °C**

If the **Pre-heat** option is enabled, the heated lid is preheated to the set temperature before the actual PCR protocol starts. While the lid is being pre-heated, the block is kept at a constant 25 °C. If **Pre-heat** is disabled, the PCR protocol starts already while the lid is still being heated.

NOTICE! Preheating of the lid is enabled by default.

Basic sensitivity of the detection system

Select the basic sensitivity of the detection system in the drop-down menu. The options are **high**, **medium** and **low**.

The default setting is **medium**.

NOTICE! The basic sensitivity setting affects all dyes. Only change the setting if you want to measure particularly weak or intense samples.

STC (Simulated Tube Control)

Enable the **STC** function if you want to pre-calculate the temperature in the sample using the measured block temperature and regulate the temperature to the sample temperature.

NOTICE! Enabling this function is particularly recommended for fast protocols and high sample volumes.

If disabled, the block temperature is controlled according to the selected temperature program. Particularly if the heating and cooling rates are high and the hold times are short the actual sample temperature can differ from the desired temperature.

Adding or removing heating steps

- Append a heating step to a protocol:
  Tap the **ADD STEP** button.
  ✓ The heating step is appended to the previous protocol.
- Remove a heating step:
  Tap in the column of the heating step you want to delete.
  ✓ The selected heating step is removed.

Entering the target temperature, hold time, and heating rate

- Enter the target temperature for each heating step in °C in the **Temperature** column.
- In the **Duration** column, enter the hold time for each heating step in the format "mm:ss" (minutes:seconds).
- Enter the heating rate or cooling rate for each heating step in °C/s in the **Heating rate (°C/s)** column.

NOTICE! The default setting is 8.0 °C/s for heating rates and 5.5 °C/s for cooling rates.

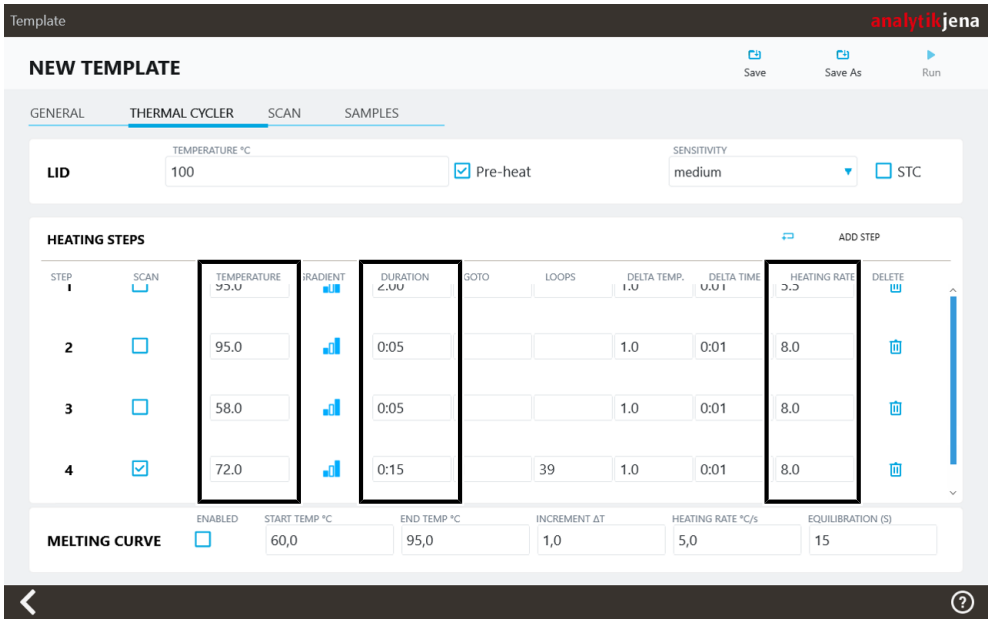

Fig. 21 Programming Temperature, Duration and Heating rate (°C/s)

Program florescence measurement

- In the **Scan** column, check the box next to the heating step in which the fluorescence measurement is to take place. The fluorescence measurement can only be carried out in one heating step.

NOTICE! During the DNA melt, an optical measurement is performed at each step.

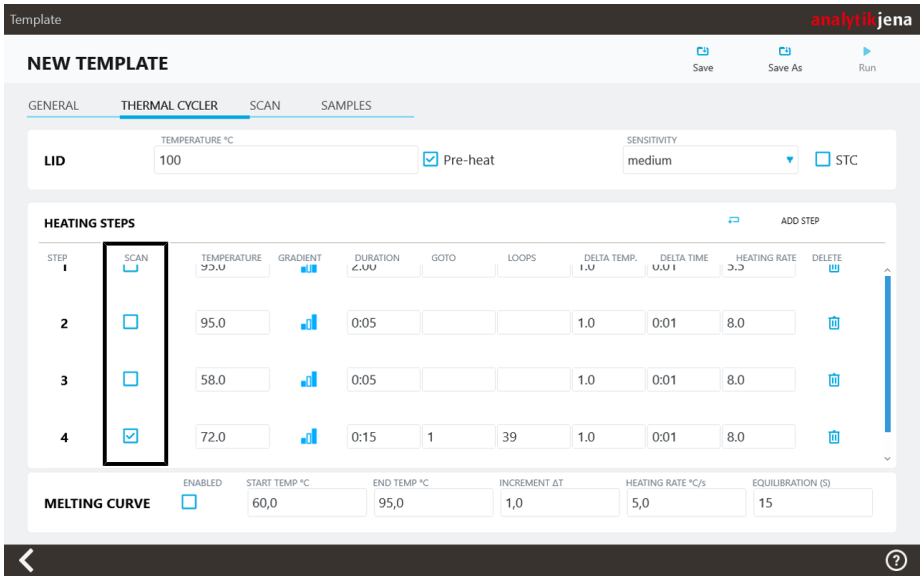

Fig. 22 Program florescence measurement

Program a loop

Cycles in which a number of consecutive temperature heating steps are iterated are called a loop. The loop is defined by a target step for the return (**Goto**) and the number of iterations (**Loops**):

- In the last heating step of the future loop: enter the number of the target step for the return to the start of the loop in the **Goto** column.
- Also in the last heating step of the future loop: enter the number of iterations in the **Loops** column.

  ✓ The programmed loop has been configured.

NOTICE! The total number of loops is the sum of programmed iterations plus 1, as the sequence of steps prior to reaching the loop has already cycled through once. Example: Program 39 iterations for 40 loops.

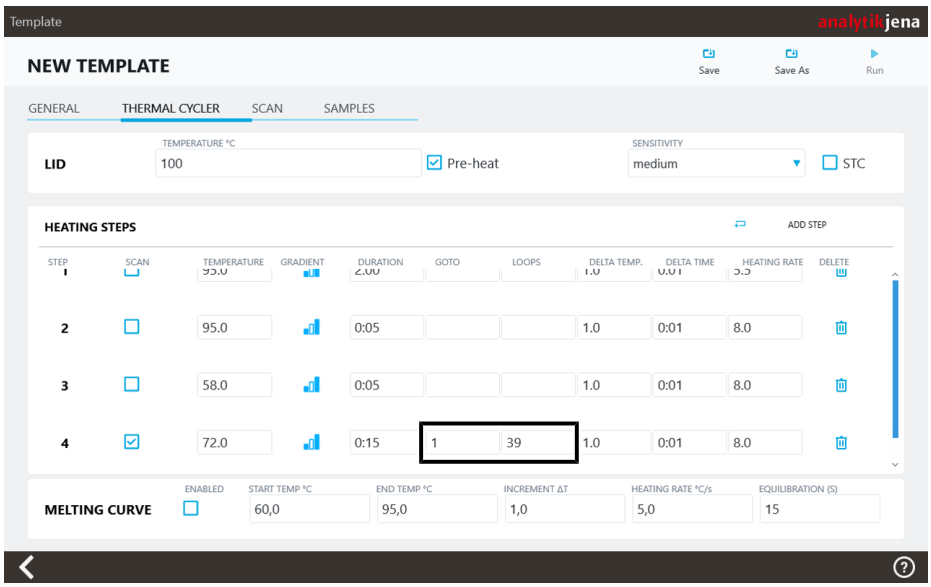

Fig. 23 Program loop in the PCR protocol

Program increment/decrement for temperature and hold times

Within a loop, the target temperature can be changed with increments/decrements and the hold time with increments can be changed step by step from cycle to cycle by a certain amount. A decrement is stipulated with the "-" prefix, i.e. the temperature is gradually reduced by this amount. Absence of a prefix or a "+" indicates an increment at which the parameter increases step by step by that amount.

- Gradual change of the target temperature:
  Enter the change in the **DELTA TEMP.** column.
- Gradual change in hold time:
  Enter the change in the **DELTA TIME** column.

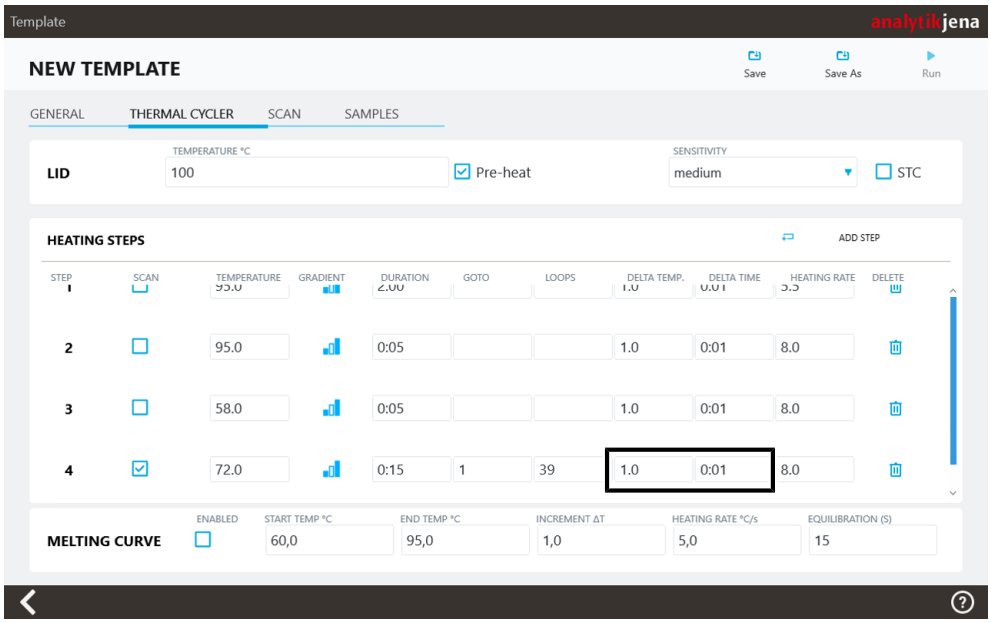

Fig. 24 Program increment/decrement for target temperature and hold time in the PCR protocol

Program DNA melt

For experiments with intercalating dyes, it is recommended to check the specificity of the products by measuring a melting curve. To do this, a corresponding step must be programmed.

⇨ The qPCR protocol is programmed and contains a heating step with enabled fluorescence measurement.

- Enable DNA melt in the **ENABLED** column.
- Edit options for the DNA melt.

  ✓ The DNA melt is appended to the end of the PCR protocol. The fluorescence measurement is automatically enabled for the melt.

NOTICE! A heating step with enabled fluorescence measurement must have been carried out before the DNA melt. If you only want to carry out a DNA melt without a previous temperature protocol, be sure to create a single heating step and enable the fluorescence measurement by checking the "Scan" box.

The following options can be edited:

Option	Description
ENABLED	If enabled, the melt will be appended to the PCR protocol. If disabled, the melt will be removed from the PCR protocol; however, the parameters will remain.
START TEMP °C	Starting temperature of the melt
END TEMP °C	Final temperature of the melt
INCREMENT ΔT	Temperature difference between two heating steps at which a fluorescence measurement is performed
HEATING RATE °C/s	Rate of increase in temperature
EQUILIBRATION (S)	Time to equilibrate the sample before the fluorescence is measured

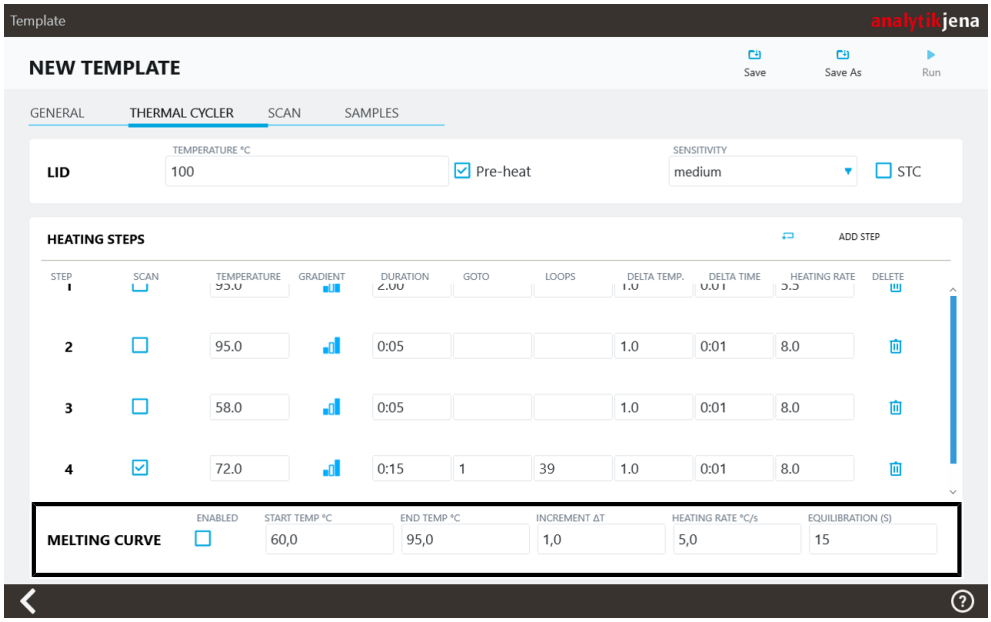

Fig. 25 Program DNA melt

See also

Program block temperature gradients [▶ 38]

3.2.1 Program block temperature gradients

You can program a temperature gradient for the thermal block. The gradient can lie within a range of up to 40 °C in the temperature range 4 to 99 °C.

You can choose between two options for programming the gradient:

- **Margins**: You can specify the temperatures for columns 1 and 12. The software automatically determines the temperature steps between the columns.
- **linear**: You can specify the temperature for column 6 (middle column) and an increment. The software reduces the temperature toward column 1 and increases the temperature toward column 12 from column to column.

The gradient can be programmed individually for each heating step of the qPCR protocol.

Opening the gradient function

▶ Click on the  icon in the line of the heating step for which you want to program a gradient.

✓ A page appears with details of the heating step.

Programming a gradient

The gradient is displayed in the qPCR protocol by the two temperature values separated by a dash. In this way, the gradient can also be entered directly in the table of the qPCR protocol.

▶ Select the type of gradient input in **Gradient**: **Margins** or **linear**.

▶ When selecting **Margins**:

– Enter the temperature for column 1 under **First column temperature**.

– Enter the temperature for column 12 under **Last column temperature**.

▶ When selecting **linear**:

– Enter the temperature for column 6 under **Middle temperature**.

– Enter the increment under **Increment of temperature**.

✓ The software calculates the individual temperature steps and displays the temperature for each column visually.

▶ Click **OK**.

✓ The software applies the programmed gradient to the qPCR protocol.

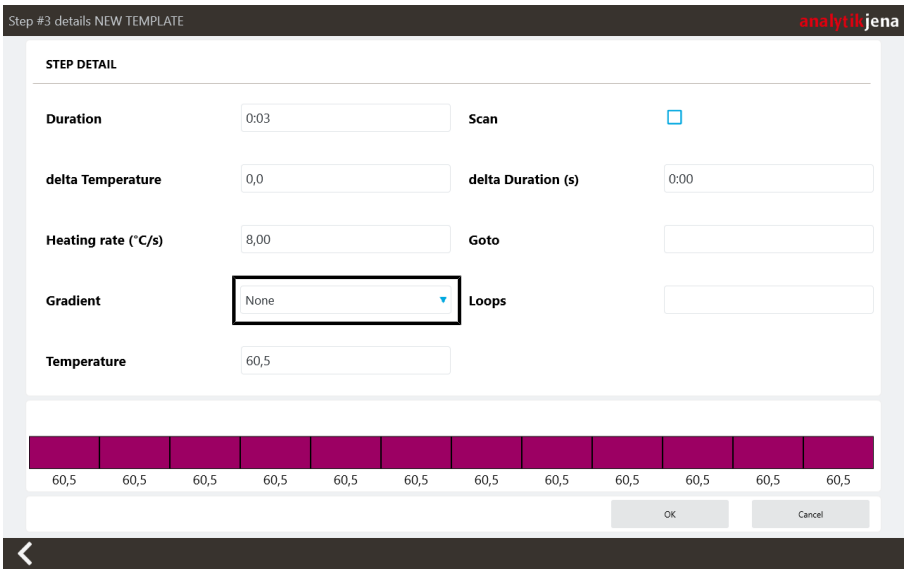

Fig. 26 Page with details of the heating step and settings for the gradient function; gradient entered via the first and last columns

3.3 Program parameters for the fluorescence measurement

The product amplification is measured in the real-time PCR by the increases in fluorescence. The following parameters must be defined on the **Scan** page:

- Dyes that are measured
- Settings for the dyes
- Area of the PCR plate that is scanned

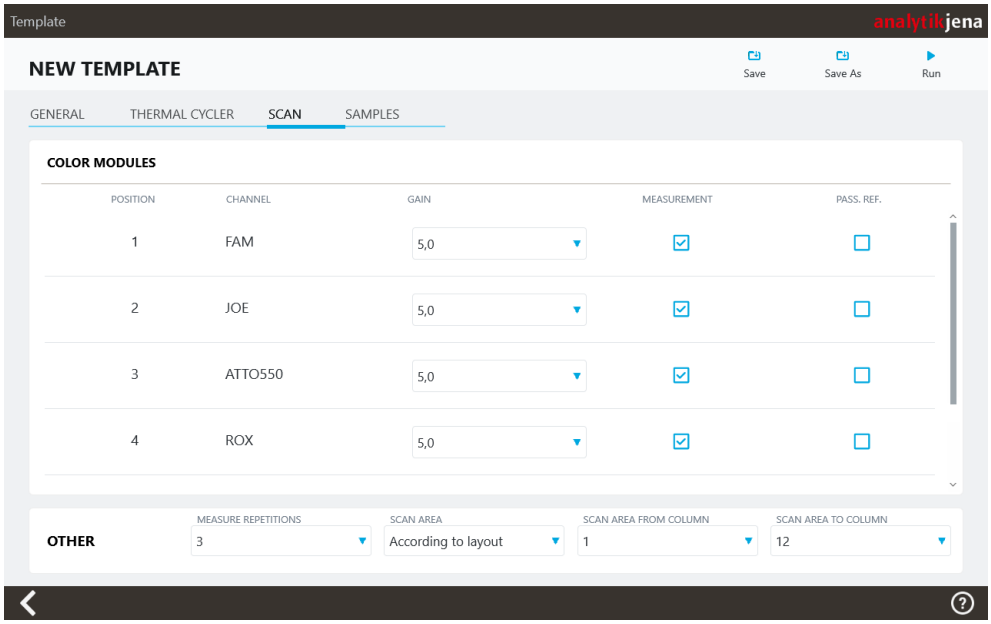

Fig. 27 Page Scan

Configure the parameters

▶ Enable the fluorescence measurement for the required color module:
Touch the appropriate field in the **MEASUREMENT** column next to the color module.
Enabled color measurements are marked with a check mark.

NOTICE! The number of dyes to be measured has no influence on the duration of the fluorescence measurement.

▶ Optionally: Change the gain. A value can be set for **GAIN** in the range 0.1 to 10.0.
The recommended setting is 5.0.

NOTE! You can change the default value for the gain in the settings. Click on ⚙ under **Templates** or **Results**. In the **Device settings** tab, you can define a separate default setting for the gain for each color module.

▶ If a reference dye is used, enable the **PASS.REF.** option of the color module.

✓ The basic parameters for the fluorescence measurement are thus defined.

Set scan range and measurement iterations

The scanning range can be defined in accordance with the plate layout in the sample table (pre-setting) or manually. The scan region for the thermal cycler is always defined per column. It must always consist of connected columns.

The number of measurement iterations can be varied for the fluorescence measurement. A higher number of measurement iterations can improve the signal-to-noise ratio with weak fluorescence; however, it increases the measurement time.

▶ Set the number of measurement iterations in the **OTHER** row under **MEASURE REPETITIONS**. Preset value: 3

- Define the scan area under **SCAN AREA**.
  - **According to layout**: The software defines the scan area based on the sample layout. The scan starts at column 1 and ends at the last column in which samples have been created in the sample layout. All columns in between are scanned, regardless of whether they contain samples or not.
  - **Define manually**: Select this option if you want to define the scan area manually under **SCAN AREA FROM COLUMN** and **SCAN AREA TO COLUMN**. Here too, as with **According to layout**, all columns in between are scanned as well.

3.4 Enter sample properties in the layout

The sample layout is required for the analysis of the experiments and describes the allocation in the sample block. Each well in the block can be assigned a sample with a name, a sample type, genes to be analyzed and concentrations (for standards).

You can edit the sample layout on the **Samples** page.

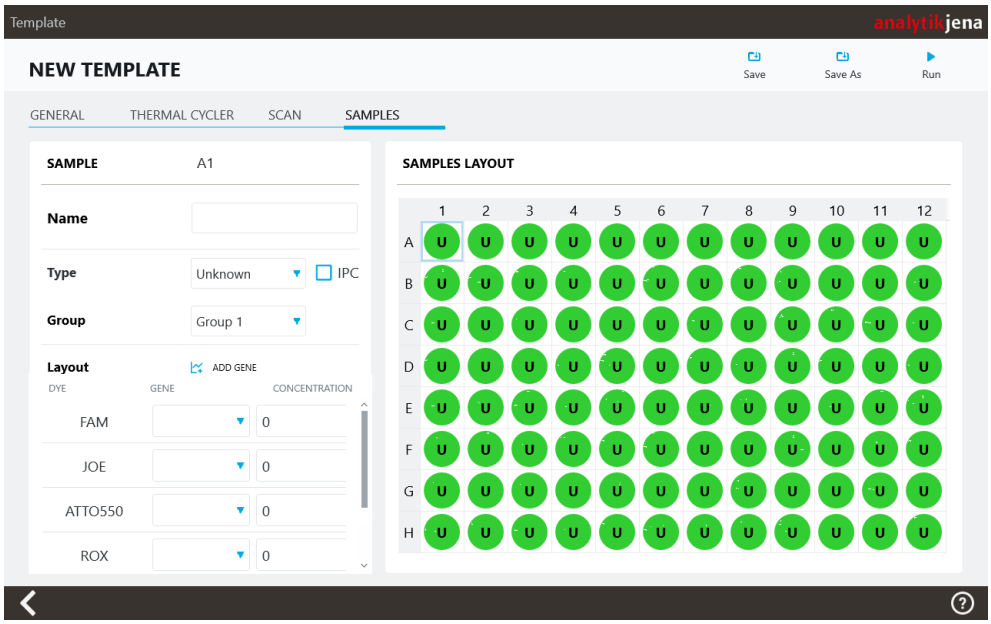

Fig. 28 Page Samples

Elements of the Samples page

Element	Description
Name	Enter sample name
Type	Select the sample type
IPC	Define internal positive control
Group	Assign sample to a sample group. The samples can be divided into up to 12 groups.
Layout	Assign a gene from the selection list to a dye. ■ **Add Gene**: Add a gene to the selection list. ■ **Gene** / **Concentration**: Enter gene and concentration/unit (for sample standards)
Selected areas in the sample layout	The sample properties are assigned to the selected areas in the sample layout. Individual samples or sample areas can be marked.

Sample types in the software

The following sample types can be assigned:

Sample type	Icon	Description
Empty	-	Empty position on the PCR plate / in the layout There is no analysis for empty positions.
Unknown	U	Sample of unknown concentration or dilution (measuring sample)
Standard	S	Sample of known concentration or dilution
Calibrator	K	Sample whose target gene expression level is set as 1
NTC	N	Complete reaction set without matrix strand (No Template Control)
Positive control	+	Positive control preparation for which a reaction product is expected
Negative control	-	Negative control preparation for which no reaction product is expected

Mark samples in the layout

Specimens must be marked for entering the properties:

- Mark individual samples by tapping them.
- To mark multiple samples in adjacent fields, swipe across the area diagonally or horizontally/vertically.
  - ✓ Selected samples or areas in the layout are outlined in blue.

Edit samples

Samples with identical sample properties (sample name, sample type, same gene-dye-assignments) are viewed as replicates. The individual values of these samples are averaged and their mean value is used for the remaining calculations.

With a singleplex assay, samples can have the same sample name and sample type; however, the differ as far as the gene-dye-assignment is concerned. These samples are identified as associated samples due to the same name. The analysis, however, is performed individually.

- Mark samples with the same properties in the layout.
- Assign sample type: Select the sample type from the drop-down menu under **Type**.
- Enter the sample name: Enter the name in the field under **Name**.
- Enter gene and concentration under **Layout**:
  - Select the gene sought in the **Gene** drop-down menu or add a new gene name with the **Add Gene** function.
  - For **Standard** sample type: Enter the concentration of the gene to be analyzed in the **Concentration** field.
  - ✓ The properties are assigned to the marked samples.
- Process all other samples in the same manner.

Arrange experiments in groups

Several experiments can run simultaneously in the thermal block with the same thermal cycler settings during a qPCR run. Samples that belong to an experiment are grouped together. All reaction preparations of a group are analyzed together. A maximum of 12 groups can be defined.

All samples in the layout are assigned to Group 1 in the pre-setting.

- Mark all samples of an experiment in the layout.
- Select the group number from the drop-down menu in the sample properties under **Name**.
  - ✓ The group number is assigned to the selected samples.
- Process all other samples in the same manner.
  - ✓ The groups are created.

4 Monitoring

The functions required to start and monitor a real-time PCR experiment are summarized on the **MONITORING** page.

4.1 Execute qPCR run

Prerequisites for starting

A template is required to start a qPCR run. You can select an existing template on the **Templates** page or create a new template.

Start qPCR run

- Insert the samples into the thermal cycler. When inserting samples, observe the information provided in the operating manual of the thermal cycler.
- Select an existing template on the **Templates** page or create a new template.
- Tap the ▶ **Run** button to start the PCR run with the selected template.
  - ✓ The **MONITORING** page opens automatically.
  - ✓ The qPCR run starts. The progress is displayed on the **MONITORING** page.

Ending a qPCR run

At the end of the qPCR run, the software automatically saves the measurement results in a results file.

You can retrieve the results file via the **Results** page.

The results file is named as follows:

[Template Name]-RES-[Date]-[Time].ajqpcrresxml

Stop qPCR run

- Tap ■ **Stop** on the **MONITORING** page.
  - ✓ The qPCR run stops and cannot be continued again.

See also

Program parameters for the fluorescence measurement [▶ 39]

4.2 Monitor display

During the qPCR run, the fluorescence curves (fluorescence intensity versus cycle number) are plotted in the graph on the **MONITORING** page.

Amplification curves

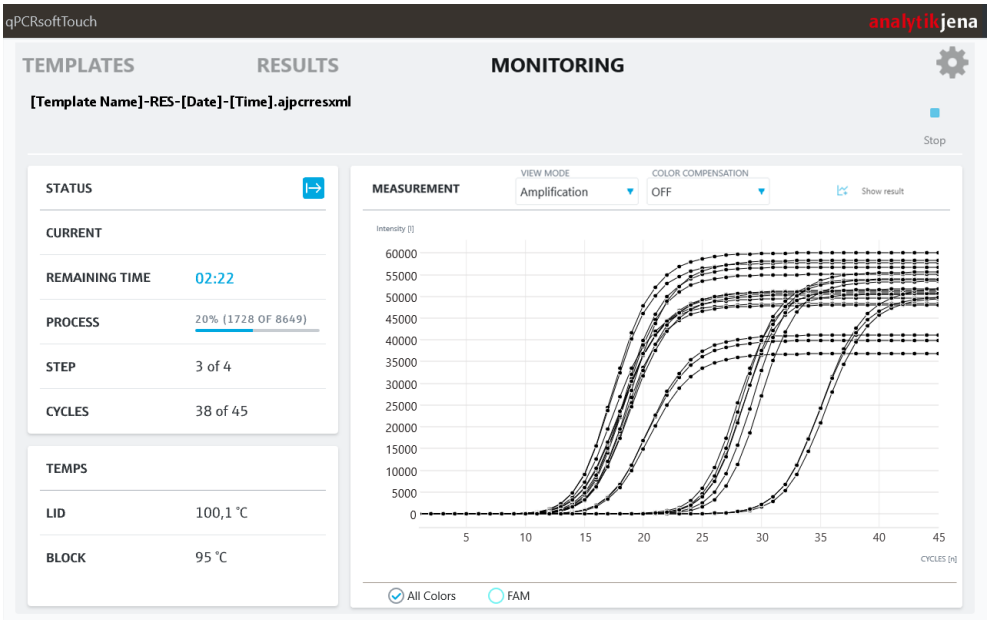

Fig. 29 Amplification curves on page MONITORING

By selecting the dyes below the graph, you can choose between the superimposed display of the measurement results with all dyes or the display of the individual dyes.

The display of **Raw data** , **Amplification** and **Melting curve** are available from the **VIEW MODE** drop-down menu.

The assignment of the curve colors can be configured in the software options.

Color compensation

If several fluorescent dyes are used in one sample (multiplexing), spectral overlay of the fluorescence can occur, which can be corrected by color compensation. You can select a color compensation from the **Color compensation** drop-down menu.

- **Off**
  The default setting for the color compensation is Off, because for the most frequent applications (only one active measuring channel or dyes with a large spectral distance, such as FAM and ROX) color compensation is not required.
- **Device-specific color compensations**
  When selecting a color compensation, a compensation matrix is applied to the measurement data, which facilitates sufficient overlay compensation in all colors with a gain setting of 5.0.
  Select one of the color compensations available for your device model. Experiment to see which of the standard color compensations is more suitable for your experiments.
- **Import color compensation**
  You can record color compensations in the **qPCRsoft** desktop software and import them into the software. Imported color compensations appear in the drop-down menu.
  Please note the information on importing color compensations in the Options section.

Status icons

You can read the status of the measurement from the following icons.

Icon	Description
	Start of the measurement
	Device initialization
	System tests
	Technical check in progress
	Measurement of references in progress
	Measurement of sample in progress
	Cleaning after the measurement
	Post-processing is being carried out
	Measurement finished You can end the experiment and display the results with  **Show result**.

The following icons indicate special states outside the measurement process:

Icon	Description
	The measurement is aborted.
	An error message has occurred.
	No action in progress. You can start a new measurement.

See also

- Options – General software settings [▶ 53]

5 Results

The results of a measurement are summarized in results files. The results files can be retrieved via the **Results** page.

5.1 Customizing the display and mathematical calculation of the results

On the **DATA**, **DATA CT** and **DATA TM** pages, you can customize the results via the **Color compensation** drop-down menu and via the options by clicking on .

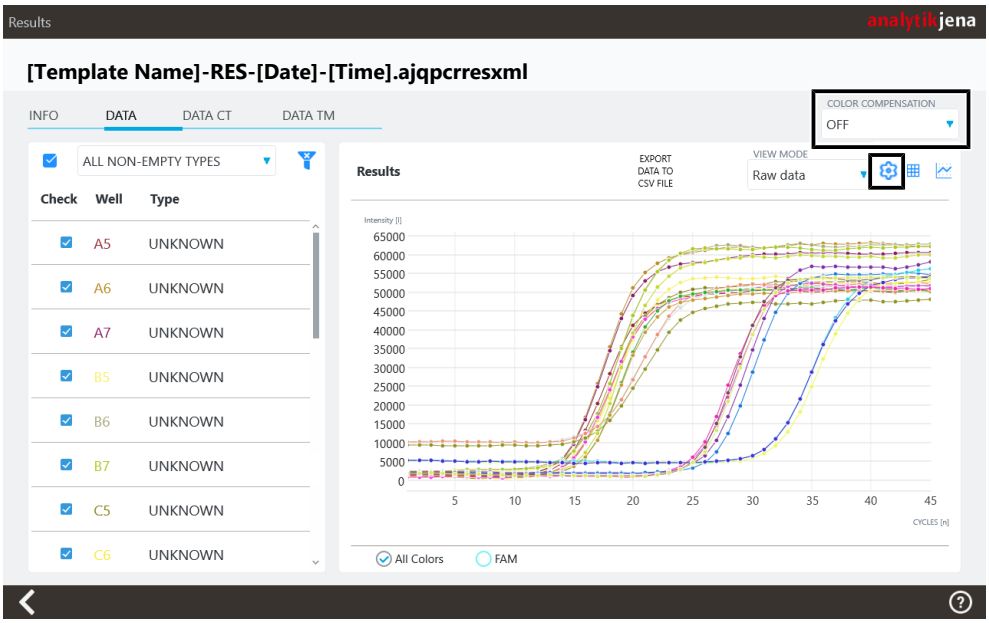

Fig. 30 Off drop-down menu and icon for the options

Color compensation

If several fluorescent dyes are used in one sample (multiplexing), spectral overlay of the fluorescence can occur, which can be corrected by color compensation. You can select a color compensation from the **Color compensation** drop-down menu.

Please also note the information under (→ "Monitor display" 44) on the individual color compensations.

Change display options

The graphical display of the amplification curves can be customized on the **DATA**, **DATA CT** and **DATA TM** pages using the icon.

The display options influence the graphical display of the measurement data in the **Amplification** view.

Option	Description
Smoothing	Smoothing of the measurement data ■ **none** ■ **[...]points** The smoothing is calculated using the selected number of points. Input range: 2 ... 12
Scaling	Scaling of the intensity axis: **linear**

Option	Description
Baseline correction	**For all samples** Determine the baseline for each sample in the same range Enter the lower and upper limit of the range in the **From cycle** and **To cycle** fields. **Sample specific** This correction is recommended for samples with different Ct values. Enter the lower range limit in the **Crop first cycles:** field. The upper range limit is determined separately for each sample using an algorithm.

- Tap ⚙ on the **DATA**, **DATA CT** or **DATA TM** pages. The display options appear.
- Edit the parameters on the page.
- Exit the page with ‹. The parameters are applied.
  - ✓ The graphical representation under **Amplification** is updated.

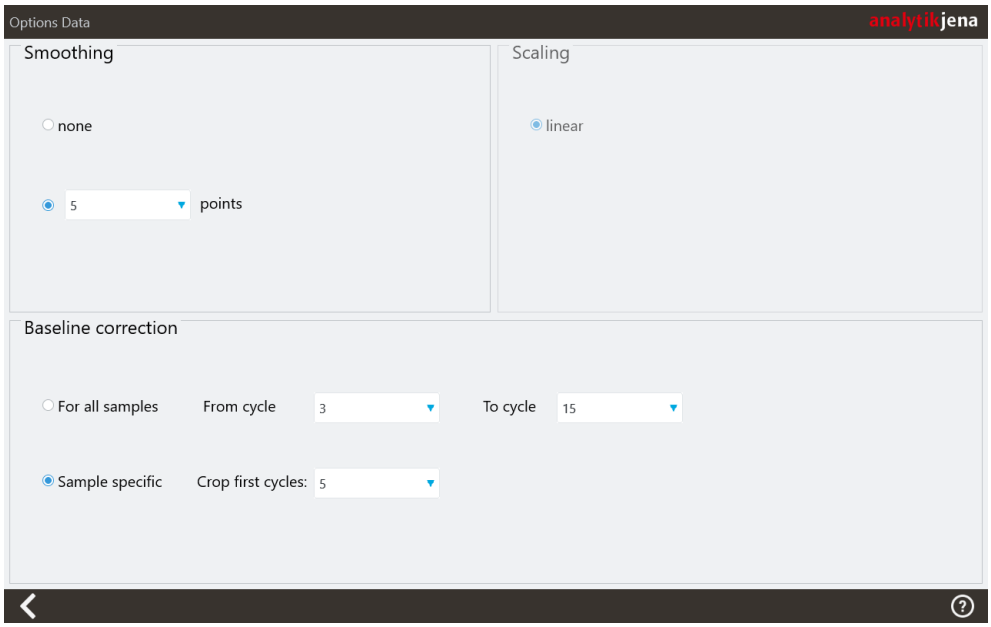

Fig. 31 Display options

See also

- Monitor display [▶ 44]
- Options – General software settings [▶ 53]
- Monitor display [▶ 44]

5.2 Calculate Ct value

You can calculate the Ct values on the **DATA CT** page.

Elements for calculating the Ct values

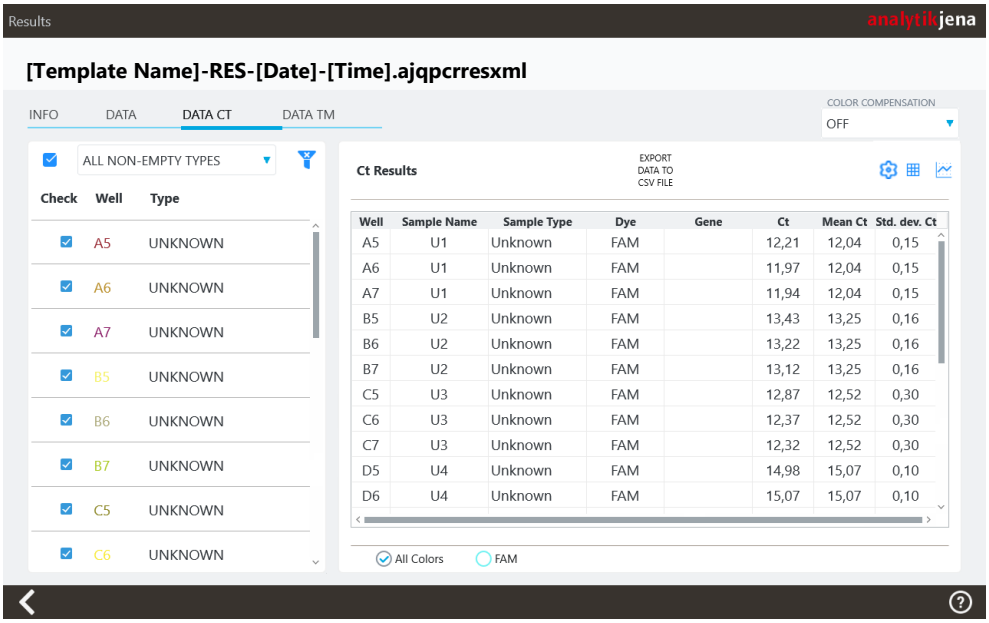

Fig. 32 DATA CT page, table view

Element	Description
Table	List of samples according to the sample selection
Graph and results area	Display of the amplification curves Display of the measured values as a table
THRESHOLD	Only if ✓ gene/dye combination is selected below the graph and table area. Only those curves whose maximum ddRn/dT is greater than the threshold are analyzed. ■ Enter threshold manually: Enter value in the **THRESHOLD** input field Determine threshold automatically: Tap **AUTO**
EXPORT DATA TO CSV FILE	Export results as .CSV file
⚙	Options for calculating the Ct values Display options
▦ and 📈	Switch between the view as a results table and as a graph
Radio buttons ○ ✓	Select gene/dye combination for display Selection between the following displays: ■ **All Colors**: Derivation of the melting curve ■ **Gene/dye combination**: Melting curve of the selected target gene/dye combination

Calculate Ct value

The Ct values of the analyzed samples can be calculated and displayed in tabular form.

- Open the **DATA CT** page in an open results file.
- Optionally: Tap and edit the options for calculating the Ct values (see above).
- Optional: Select a color compensation from the **Color compensation** drop-down menu.
- Tap .
  - ✓ The Ct values of the individual samples are given in the table of results.

The table of results contains the following information:

Column	Description
Well	Position of the sample in the sample layout.
Sample Name	Name of sample
Sample Type	Type of the sample
Dye	Fluorescent dye used
Gene	Name of the gene analyzed in the sample
Ct	Ct value of the sample
Mean Ct	Mean Ct value of replicates If no replicates have been created, the mean value is equal to the value under **Ct**.
Std. dev. Ct	Standard deviation of the Ct values of replicates If no replicates have been created, this value is omitted.

NOTE! Click on to switch to the graph view.

5.3 Calculate melting temperature

Elements of the DATA TM page

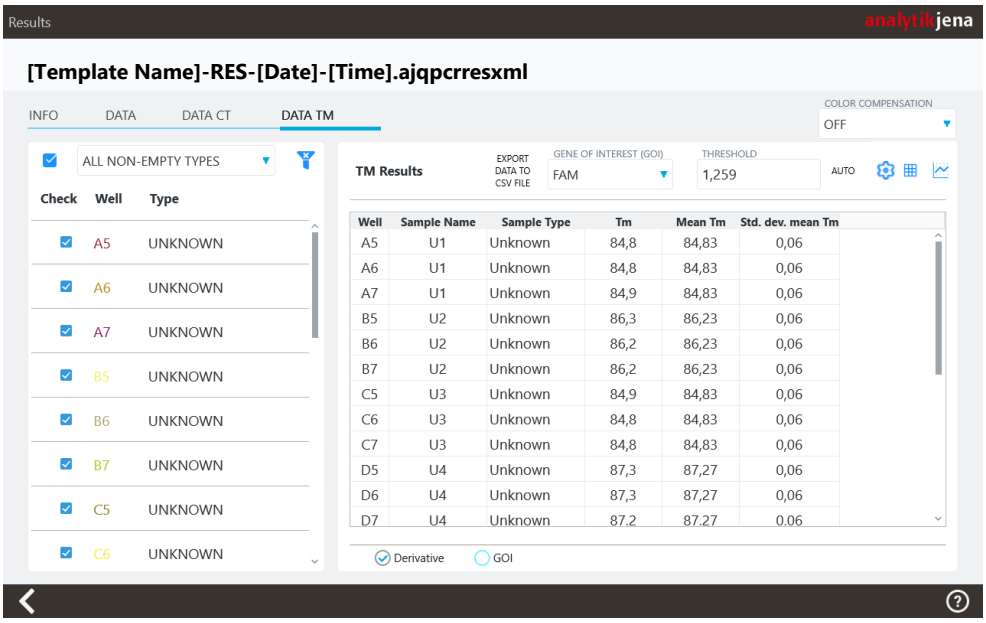

Fig. 33 Page DATA TM

Element	Description
Table	List of samples according to the sample selection
GENE OF INTEREST (GOI)	Select target gene / dye combination The target gene/dye combination is then displayed in the table and the graph, if ⊙ **GOI** is selected below the graph. Generally, an intercalating dye must be selected for the target gene for the melting curve analysis.
THRESHOLD	Only if ⊙ **Derivative** is selected below the graph and table area. Only those curves whose maximum ddRn/dT is greater than the threshold are analyzed. ■ Enter threshold manually: Enter value in the **THRESHOLD** input field ■ Determine threshold automatically: Tap **AUTO**
EXPORT DATA TO CSV FILE	Export results as .CSV file
⚙	Options for calculating the Ct values Display options
▦ and 📈	Switch between the view as a results table and as a graph
Radio buttons ○ ⊙	Select gene/dye combination for display Selection between the following displays: ■ **Derivative**: Derivation of the melting curve ■ **GOI**: Melting curve of the selected target gene/dye combination

NOTICE! You can visually define the melting point and any non-specific amplifications using the derivation of the melting curve.

Calculate melting temperature

- Open the **DATA TM** page in an open results file.
- Select the dye (the gene) from the **GENE OF INTEREST (GOI)** drop-down menu.
- Adjust the threshold. The threshold is used to distinguish significant peaks from insignificant peaks. The threshold can be set in two ways:
  - Set the threshold in the **THRESHOLD** field.
  - Click the **AUTO** button to have the threshold set automatically by the software
- Tap  .
  - ✓ The melting temperatures of the individual samples are given in the table of results.

NOTE! The threshold value is updated and displayed in the **THRESHOLD** input field for both manual determination and automatic calculation.

The table of results contains the following information:

Column	Description
Well	Position of the sample in the sample layout.
Sample Name	Name of sample
Sample Type	Type of the sample
Tm	Melting temperature of the sample
Mean Tm	Mean melting temperature of the replicates If no replicates have been created, the mean value is equal to the value under **Tm**
Std. dev. mean Tm	Standard deviation of the melting temperature of replicates If no replicates have been created, this value is omitted.

NOTE! Click on  to switch to the graph view.

5.4 Analyzing results files in the desktop software

You can open and analyze the results files in the **qPCRsoft** desktop software.

You can also view other measurement settings in the desktop software. For example, the desktop software shows which gain was configured or whether the **STC** function was enabled.

- Transfer the desired results files to an external data storage device. To transfer them, follow the instructions in the "Data management" chapter in this user manual.
- Connect the external data storage device containing results files to the PC.
- Open the **qPCRsoft** software.
- Open the desired results file in the software.
- The results file can be analyzed in the desktop software. The analyses can be saved as .RTPX files.

NOTICE! Follow the instructions for use in the user manual for the qPCRsoft desktop software.

5.5 Export results

The results in the **DATA** and **DATA CT** tabs can be exported as a .CSV file (*.csv):

- Open **DATA** or **DATA CT**.
- Click on **EXPORT DATA TO CSV FILE** above the results table.
- Select the storage medium: **Internal** or an external storage location
- Enter the file name.
- Tap **OK**.
  - ✓ The result data is exported and written to the selected storage location.

6 Options – General software settings

The icon takes you to the basic settings for the software. On the associated pages, you can configure settings for the software itself and for the color modules. You can also run a program update.

Setting general software options

To set the software options, tap **General Settings**. The following subitems are available:

Option	Description
System info	Software version number
Device info	Information on the device, such as serial number and device type
Show Start Dialog ?	**Activated**: the start page is displayed when starting the software. **Deactivated**: the **Templates** page is displayed when starting the software.
Connect to device automatically ?	This option is activated by default. **Activated**: the software automatically connects to the thermal cycler when the thermal cycler is switched on and the integrated tablet and the software have been started. ▪ The thermal cycler can be controlled via the software on the integrated tablet. **Deactivated**: the software does **not** connect to the thermal cycler automatically. ▪ When the thermal cycler is switched on, the integrated tablet and the software start up as usual. However, the thermal cycler cannot be controlled via the software on the integrated tablet. The software is in demo mode. ▪ The thermal cycler can be controlled directly via the control software on a connected PC. Exiting the software on the integrated tablet is not necessary. ▪ The **Connect device** button is displayed on the **Templates** page. The software on the integrated tablet can be connected to the thermal cycler by clicking on the button.
Log application info	Creates a log file of the software actions. The log is stored under: **C:\Users\[user name]\Documents\Analytik-Jena\qPCRsoft touch\log**
Log traffic	Creates a log file of the device communication actions. The log is stored under: **C:\Users\[user name]\Documents\Analytik-Jena\qPCRsoft touch\log\traffic**
Log check info	Creates a log file of the technical test actions. The log is stored under: **C:\Users\[user name]\Documents\Analytik-Jena\qPCRsoft touch\log\fibercheck**
Language	Select the language of the program interface NOTE! Changing the language setting is only applied after restarting the application. Close the software via the operating system and restart the software to use it in the language selected.
Curve color	Select the curve color assignment: ▪ **Well** ▪ **Sample Type**

Option	Description
	■ Dye ■ Replicates
	Exit the software and shut down the tablet.

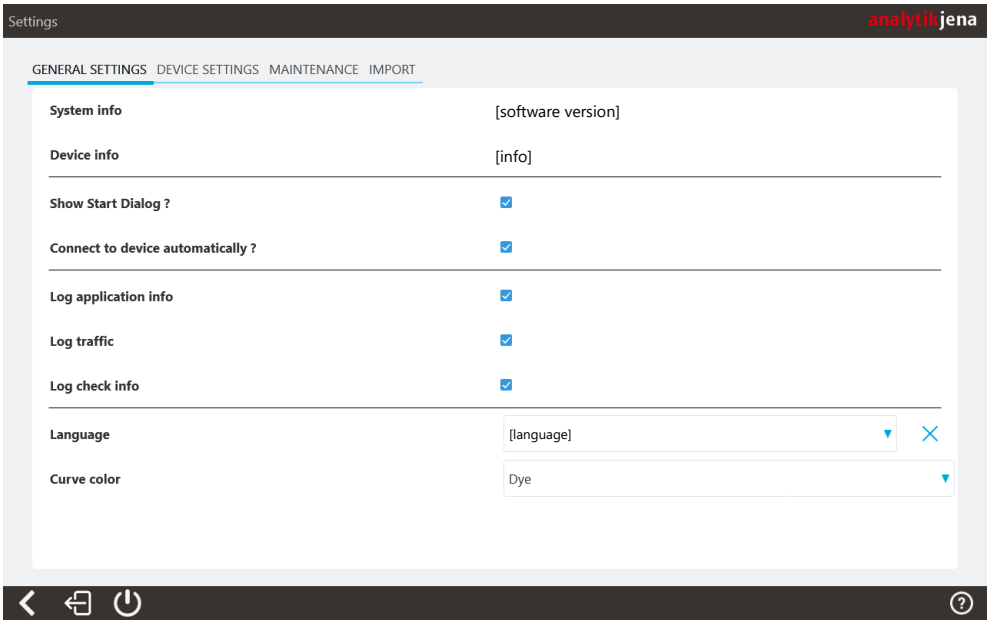

Fig. 34 General Settings page with basic software settings

Set color modules

Define the positions of the color modules used in the device under **Device settings**.

- In the first column: In the drop-down menu, select the color module that is installed at this point.
- In the second column (optional): Enter the name of the dye that you are measuring with this color module. This name will then appear in the color channel names below the graphs next to **MONITORING** and **Results**.
- In the third column: Set the default setting for the gain. The default setting is displayed under **New Template** | **Scan** when creating a new template. A value in the range 0.1 to 10.0 can be set for the gain; the recommended setting is 5.0.

  ✓ The settings are applied when you exit the **Device settings** page.

NOTICE! Use the default gain setting to define a value that you use regularly. The default setting saves you several clicks when creating a new template. If the default value is not right for your current measurement, you can simply adjust the value.

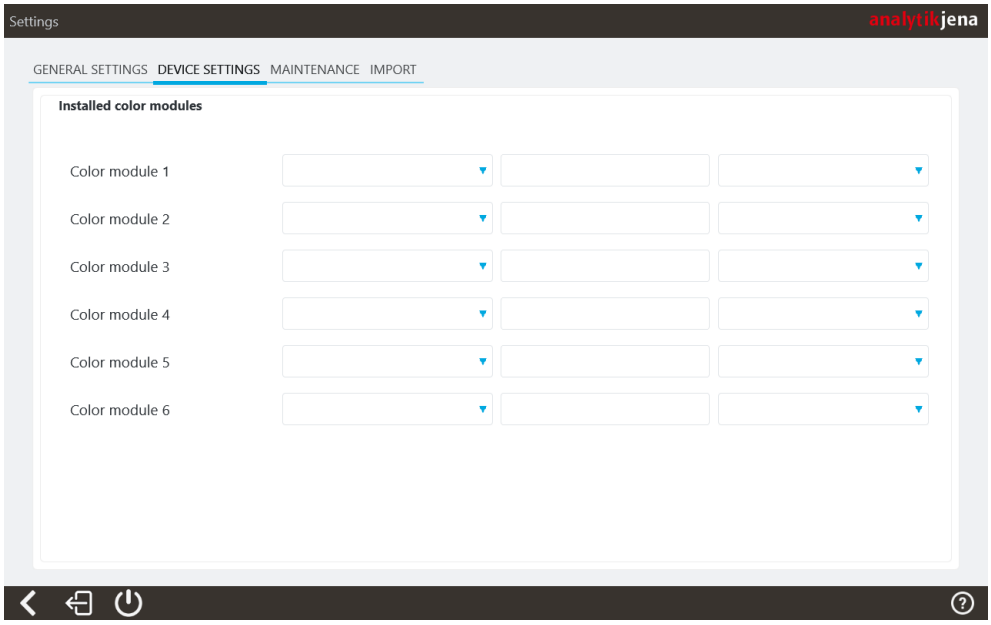

Fig. 35 Device settings page with settings for the color modules

Attaching and removing the transport lock

Before transporting or shipping the device, e.g., for servicing purposes, you must use the transport lock and enable it under **Settings** | **Maintenance**.

- Place the red shipping lock or an empty PCR plate in the thermal block and tap **Lock now for transport**. Switch off the device afterwards.
  - ✓ The sample block and the sensitive optics in the lid are secured now.
- The transport lock gets unlocked automatically when the device is switched on. You can also unlock the transport lock manually by tapping **Unlock device from transport state** on the **Maintenance** page.

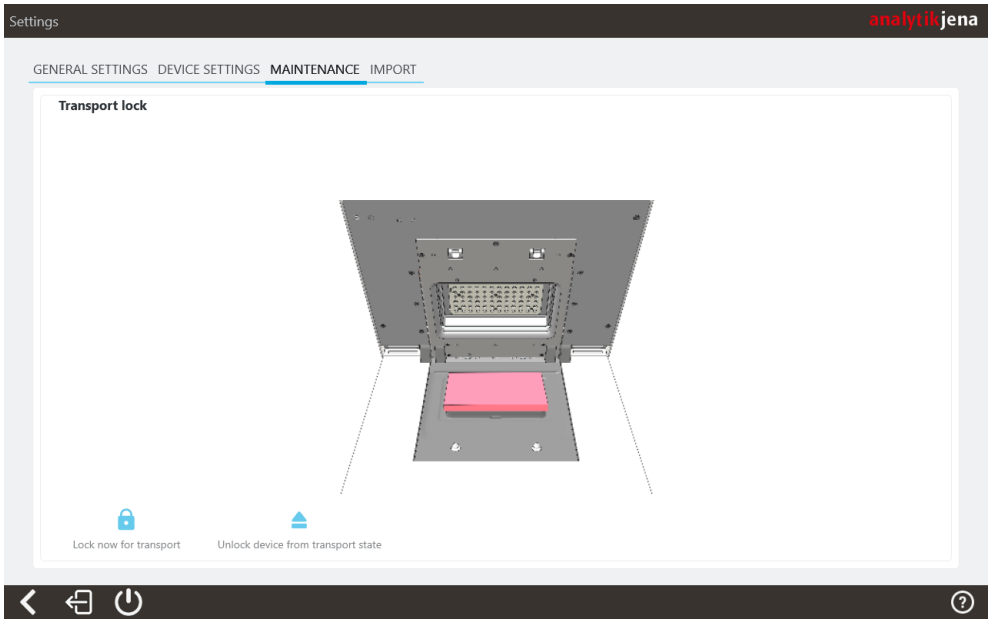

Fig. 36 Page Maintenance

Importing color compensations

You can record color compensations in the qPCRsoft desktop software and import them into the qPCRsoft touch tablet software.

To do this, proceed as follows:

- Record a color compensation using the qPCRsoft desktop software.

- Export the color compensation to an external storage location.

NOTICE! Follow the instructions in the desktop software user manual for recording and exporting color compensations.

- Connect the external storage to the device. Establish the connection either via the USB port on the front or the network connection on the rear of the cover. To configure the external storage location, follow the instructions in the corresponding chapter of this manual.
- Open the software.
- Open the **Settings** | **Import** page.
- Select the external storage location from the drop-down menu.
  - ✓ The color compensations of the external storage location appear in the selection field on the right.
- Select the desired color compensation.
- Click on to import the color compensation.
  - ✓ The color compensation appears in the left-hand selection field and is now available as a selection in the software.

You can remove color compensations from the left-hand selection field by clicking on .

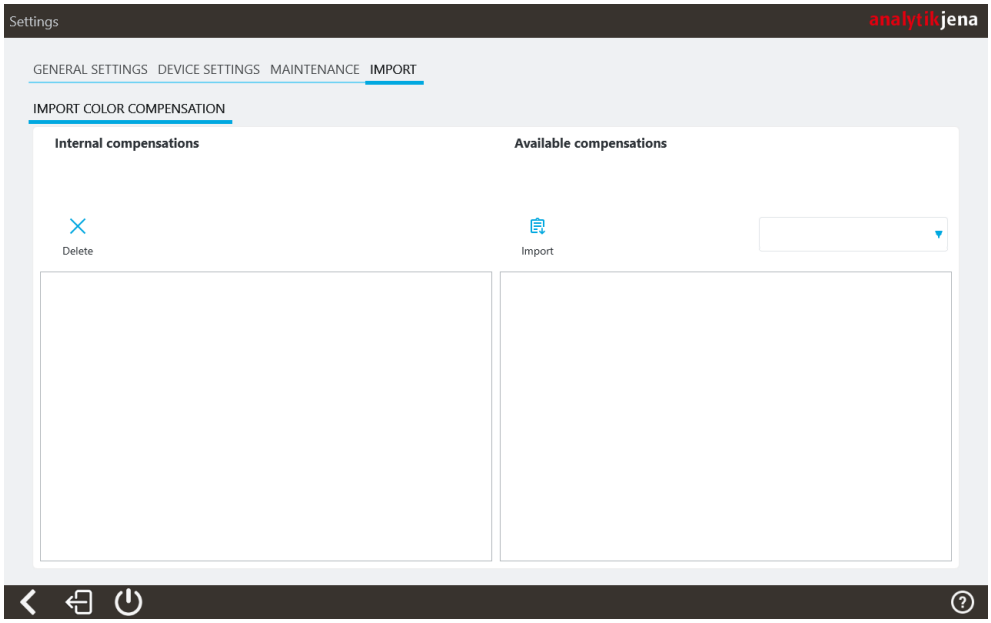

Fig. 37 Import | Import color compensation