DRAWELL
Artist of Science

Drawell Real-Time qPCR System
Drawell-X4 / X6

The quantitative polymerase chain reaction (qPCR) is an established method for the highly sensitive detection and quantification of DNA or RNA. The measuring principle is based on fluorescent signals, which, cycle by cycle, captures the presence of the existing target sequence in real time. The key features of this detection method are outstanding high-performance optics as well as excellent temperature uniformity over 96 samples.

Drawell products guarantee well-founded real-time PCR results as it benefits from peerless temperature control precision in the sample block regardless of the number of samples used. The patented high-performance optics guar- antee the outstanding homogeneous excitation and illumination of all individual samples.

Multiple Applications

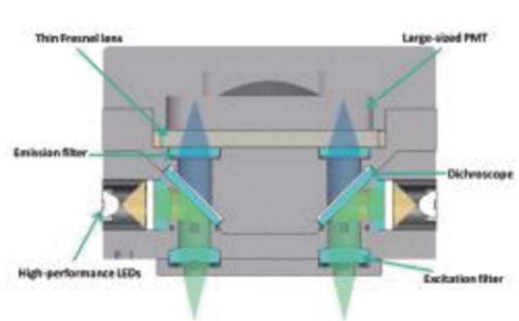
- Gene Expression Analysis
- Genotyping
- Gene Mutation Analysis
- Pathogen Detection/Quantification
- GMO Detection
- Protein Stability Screening
- miRNA Analysis
- Genetic Variation Analysis

Features:

- **Innovative Optical Design - Higher Sensitivity, Less Cross-talk**

As for the core detector, the Drawell system further improves the detection sensitivity by using Fresnel lens combined with large size PMT, a patented new optical detection system. High quality PMT is used to ensure the detection sensitivity of the system. Meanwhile, it combines the advantages of thin Fresnel lens with short focal length to make the detector closer to the sample, thus effectively reducing the loss of optical signal as well as optical cross-talk between samples, and fifinally improves the detection sensitivity. Further, the matching of high frequency LED and PMT makes the detection time of each well and each fluorescent channel very short, so that effectively reduce flfluorescence quenching.

In terms of scanning methods, the Drawell innovatively adopts the time-resolved well-by-well scanning technology. Through the setting of interlaced scanning heads, the problem of cross-talk between wells is signifificantly reduced from the perspective of spatial distribution. Meanwhile, high-precision scanning heads are used to detect signals of different fluorescent channels in different wells in time sequence (time-resolved), thus eliminating the cross-talk in principle.



The state of the art optics shuttle of the Archimed system

- **Outstanding Thermal Cycler-Superior Uniformity, Precision, Speed**

The Drawell system uses the latest Peltier components through strict screening and testing for excellent performance and stable quality, the unique hollow-out thermal block which has higher ramp rates than standard blocks by reducing the overall mass of metal block, the edge temperature compensation technology based on thermal conductive carbon fifilm and auxiliary heating plate for maintaining tight temperature uniformity throughout the entire sample plate, and the precise temperature control algorithm for fast time to target temperature and faster protocol run times.

As a result, the Drawell is distinguished by excellent temperature control precision and uniformity of ± 0.2 °C (over 96 wells) and fifirst-class heating rates of up to 6 °C/s. In addition, to ensure the highest specifificity for different assays, the device is equipped with a gradient function with a spread of up to 36 °C. This combination makes the entire system absolutely ideal for any real-time PCR application.

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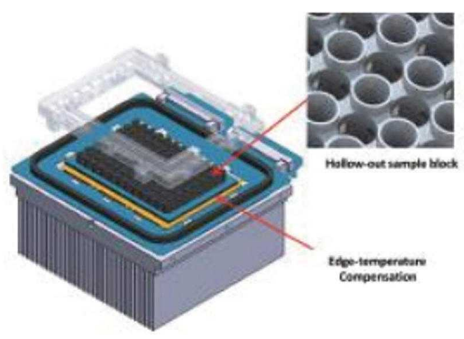
QPCR in the proven 0.1 ml fonnat with 96 wells

Precise temperature control of ± 0.2 °C across the entire sample block

Innovative thermal block with outstanding ramping rates of up to 6 °C

Gradient function over 12 columns with a 36 °C spread



Special hollow-out thermal block for reliable, consistent results

Features:

◆ **Impressive performance you can trust to generate high-quality data**

The combination of innovative optics and unique thermal cycler with incomparably precise temperature control ensures ideal amplification results. This makes the Drawell a trustworthy partner for quantitative real-time PCR applications.

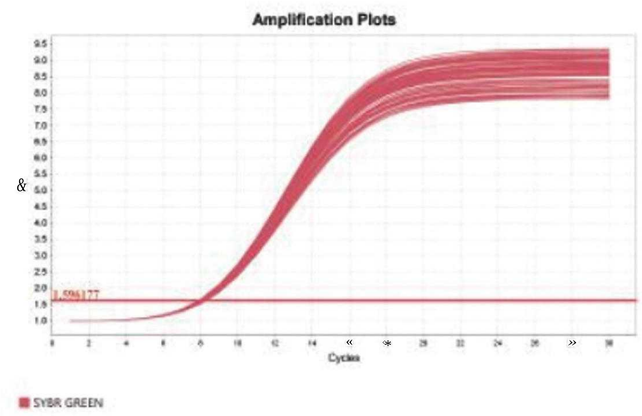
Excellent reproducibility and 10-log dynamic range

Precise quantification with 1.33-fold discrimination

True Five-Target Multiplexing

Excellent reproducibility for reliable results.

Amplifification of a plasmid template in 96 wells. The mean ct value of 11.86 with a standard deviation of 0.05 was determined automatically, illustrating highly homogeneous amplifification results obtained by the Drawell.



Sensitive detection and high-confifi- dence target discrimination down to 1.33-fold.

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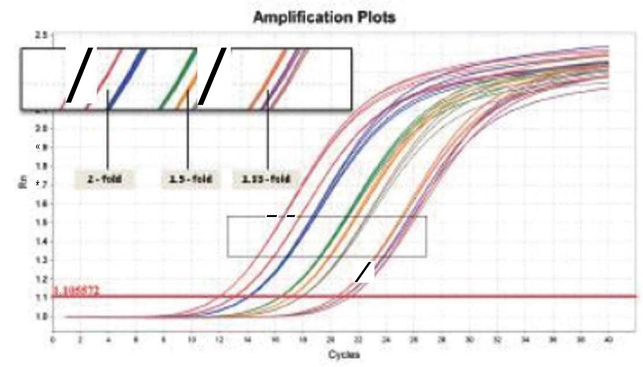
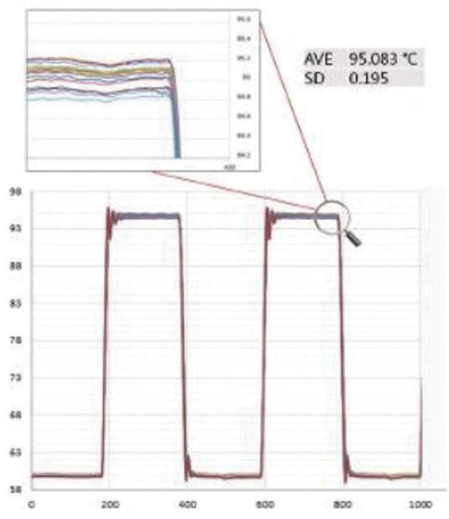


Superior Uniformity, Precision and Speed.

The Drawell thermal cycler exhibits high average ramp rates, rapid setting time, and tight thermal uniformity. This graph shows the temperature measured by probes in 20 wells across a sample block. The traces are nearly indistinguishable due to the tight unifonnity with <±0.2℃ temperature flfluctuation.



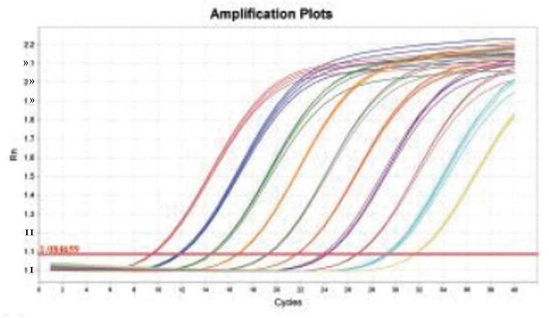
Broad linear dynamic range ensuring accurate quantifification.

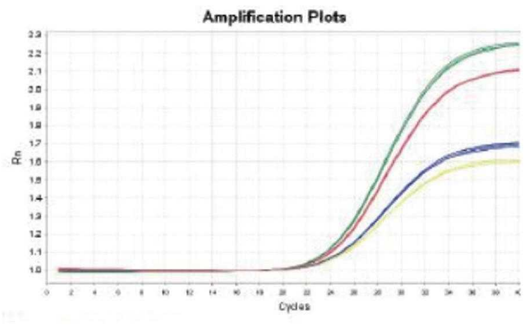
The example of plasmid DNA amplifification shows an optimal linearity over 10 orders of magnitude from 2.5 ng/μl to 0.12 fg/pl, illustrating the broad linear dynamic range of the system

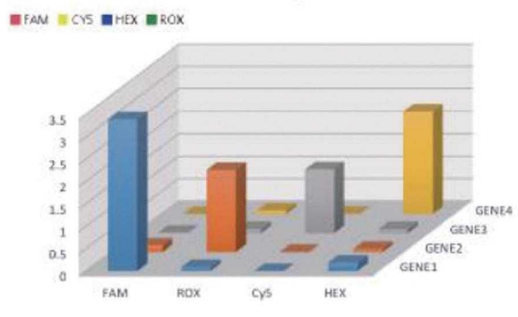
Multiplexing for richer datasets.

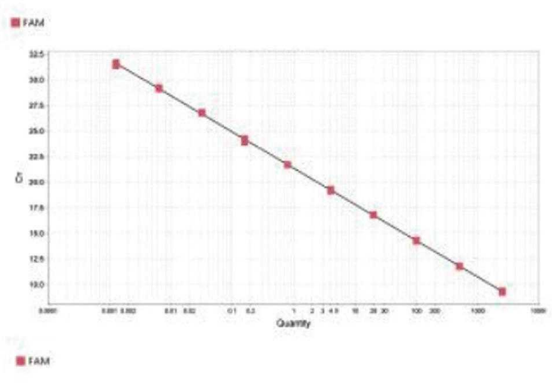
The Drawell system can discriminate up to fifive

targets in a single reaction well. The fluorescent data from four FAM-HEX-ROX-Cy5 channels of four different target genes in a single well showing there is almost no cross-talk between different channels.









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Parameters

Thermal Cycler		Optical Detection	
Block capacity	96	Excitation source	6 long-life, high-performance LEDs
Sample volume	1-50μl	Detector	Highly sensitive PMT (photo multiplier tube) with Fresnel lens
Heating/cooling method	Peltier	Scanning principle	Time-resolved scanning technology
Maximum ramp rate	6 °C/s	Detector position	Top of the block
Temperature setting range	4-100 °C	Excitation/detection range	455-650nm/510-715nm
Heated lid	Electronic automatic lid	Fluorescence channel	4 channels / 6 channels
Temperature accuracy	±0.2℃	Dye compatibility	FAM/SYBR Green, VIC/JOE/HEX/TET, NED/TAMRA/Cy3(6 channel), JUN, ROX/Texas Red, Mustang Purple, Cy5/LIZ
Temperature uniformity	±0.2°C	Detection sensitivity	1 copy of the target sequence
Gradient zone	12 columns	System sensitivity	Detect differences as small as 1.33-fold in target quantities in singleplex reactions
Gradient range	1-36°C	Dynamic range	10 orders of magnitude
Data Analysis Modes			
Absolute quantification Relative quantification Endpoint qualitative analysis Melt curve analysis Protein Stability Screening Genotyping			
Data Export			
Customizable reports containing run settings, data graphs, and spreadsheets can be directly exported or saved as Excel, txt, PDFs			

◆ Drawell Analyzer Software

Drawell Analyzer Software is powerful software for a powerful instrument. It accommo- dates user needs and different types of experi- ments with intuitive navigation and customizable settings. The logical, clear arrangement of all the tools, the intuitive handling, and last but not least the parameter-oriented memory and programming concept make the software easier to use.

User-friendly and clearly structured
Intuitive navigation and customizable settings
Integrated analysis algorithms with automatic analysis
Comprehensive analysis modules for multiple applications
License-free, free updates

Intuitive navigation and customizable settings

To further speed up your process, get the experiment started with the quick plate feature, and then enter or edit well information on your own schedule - before, during , or after the run has finished.

Intelligent Analysis

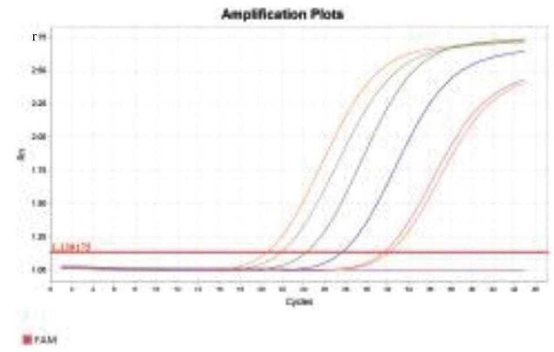
To ensure that operation is as simple as possible, many of the steps occur automatically – such as perfonning normalized gene expression analysis (ddCt), you take your results a step further without having to export data and set up your own analysis macro.

Personalized Data Export

The software allows you to save predefined analysis settings for auto-exporting run data into their format of choice, including Excel, PDF, txt export format.

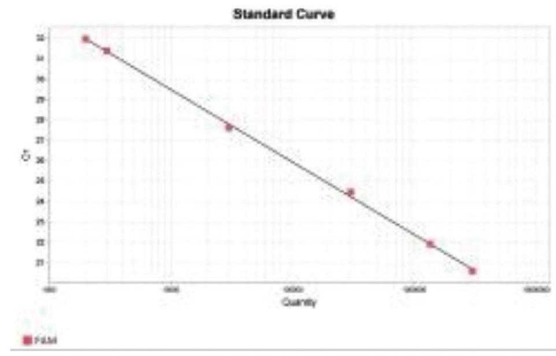
◆ **Comprehensive Function**

The software has built-in data analysis modules with automatic baseline subtraction and threshold calculation for determining Ct values or possible standard curves and PCR efficiencies. Further analyses can likewise be conducted automatically, such as absolute or relative quantifications. The software also includes analysis methods for probe-based allelic discrimination and the use of a positive/negative analysis via the end-point detection of samples.



Absolute quantifification.

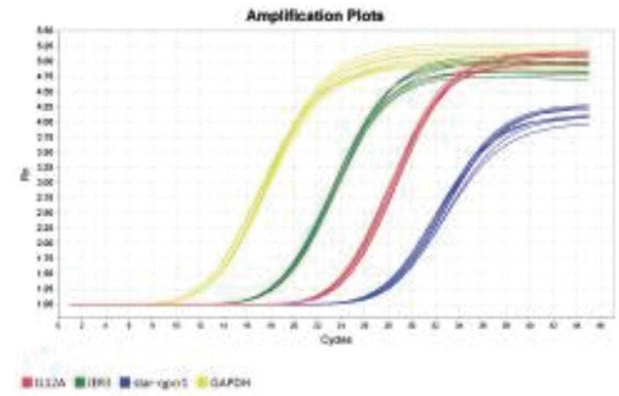
The module enables analysis of genes of interest with the use of a standard curve. Additional flexibility is achieved by importing standard curves from other experiments.



Relative quantification.

With this module, you can customize groupings of data within projects for a thorough comparison of data. The module also includes integrated correlation, volcano, and cluster plot analysis, with the ability to drill down to amplification plots.

Positive/Negative Analysis. The fifigure shows that the positive and negative African swine fever vims samples are well differentiated.



Melt curve analysis. in this experiment, 96 replicates of human genomic DNA were amplifified followed by a dissociation step with a melting temperature (Tm) of 77.9°C (SD 0.07°C), showing good specifificity of the reaction.

Protein Stability Screening. The fifigure shows that the protein exhibits different Tm values when binding with ligands of different concentrations (ImM, 0.lmM, OmM), which indicates that the protein thermal stability changed.