

## Leverage and revolutionize the way you work with the newest Absolute Q Digital PCR system

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Digital PCR is a robust technique that overcomes variability and low accuracy by allowing absolute quantification of DNA/RNA targets without the need for a standard curve. Dividing the bulk reaction into thousands of smaller independent reactions (micro-chambers) is the basis of dPCR and allows numerous advantages such as high resistance to inhibitors present in particularly difficult samples.

The Applied Biosystems QuantStudio Absolute Q Digital PCR System is a plate-based digital PCR (dPCR) platform powered by proprietary microfluidic array plate (MAP) technology that allows to deliver highly accurate dPCR results. The MAP has 16 dPCR reaction units, made up of 20,480 fixed array microchambers. Once the reagents have been compartmentalized into the microchambers, PCR amplification then proceeds, and the number of microchambers with successful DNA amplification are counted.

This state of the art technology allowed to overcome most of the main limitations of other existing digital PCR platforms. With this technology there is:

- less sample/reagent waste (95% of the sample is effectively analyzed)
- high consistency in the analysis (a minimum of 20000 independent reactions are analyzed per array)
- high confidence (through an auto false-positive rejection algorithm).
- MAP technology enables all the necessary steps for dPCR—compartmentalizing, thermal cycling, and data acquisition to be conducted on a single instrument.
- The QuantStudio Absolute Q dPCR workflow is identical to the qPCR workflow to improve ease of use, minimize hands on steps, and maximize consistency
- Fast time-to-results in just 90 minutes.
- Multiplexing capabilities with up to 4 targets being amplified in the same Array.
- High flexibility allowing from 4 to 16 samples per run

The QuantStudio Absolute Q Digital PCR System advantages make it the ideal platform when quick and reliable absolute quantification, rare target detection/quantification and SNP discrimination, high confidence copy number variation or very sensitive gene expression are needed. Come learn more about this technology and be part of the (R)evolution.