

qbase^{PLUS} features

Quantification models

- delta-delta-Ct (no efficiency correction, normalization with a single reference gene)
- Pfaffl model (efficiency correction, normalization with a single reference gene)
- qBase model (efficiency correction & multi-gene normalization)

Efficiency correction

- one amplification efficiency for the entire experiment
- assay specific amplification efficiencies
- assay and run specific amplification efficiencies
- user defined or calculated from dilution series
- calculation and propagation of the error on the estimated amplification efficiency (e.g. 95.4% ± 2.3%)

Normalization

- one reference gene
- multiple reference genes

Inter run calibration

- on normalized relative quantities (highest flexibility, fewest calculations)

Error propagation




- PCR replicates
- amplification efficiency
- normalization
- inter-run calibration

Data import

- specific importers for over 25 real-time PCR instruments
- support for ABI relative quantification studies with data from multiple runs
- support of the generic simple & qBase formats
- compatible with the universal RDML data format

Data management

- store data in a workspace folder with hierarchical organization into projects and experiments

-  unlimited number of experiments and runs per experiment
- experiments store raw Cq values, annotation and settings
-  exchange of analyzed projects and experiments
-  exchange of RDML files

MIQE compliancy

- sample information
- assay information
- RDML compatibility



The qbase^{PLUS} feeling

- calculations on the fly (no start or calculate button)
- from Cq tables to results in 24 seconds
- advanced window management
- alert bar with warnings and tips


Quality control

- detect and exclude bad data to improve result quality
- replicates
- negative controls
- positive controls
- reference gene stability (geNorm M value & coefficient of variation on the normalized relative quantities of reference genes)

Run annotation

- taken from instrument files
- custom editing of run layout in visual run editor
-  import of large sample and target lists
-  exchange of sample, target or run layouts between runs

Graphs

- single target bar chart
-  multi target bar chart
- normalization factor histogram
- standard curves

Platform independent

- Windows, Mac and Linux
- 32-bit and 64-bit support

Trust

- based on peer-reviewed and proven geNorm and qBase technology
- developed by Jo Vandesompele and Jan Hellemans with a 10 year track record on qPCR innovations

* Items marked with  are only available in qbase^{PLUS} with a license (full or demo)