



qBasePlus: import file guidelines

qBase



General information

Import files should contain a list of Quantification Cycle (**Cq**) values. Depending on the instrument software that generates the data, Cq values might have alternative names such as Ct, CP, TOP, etc. Cq is the official abbreviation in the Real-time PCR Data Markup Language (more info on <http://www.rdml.org>). The qBasePlus calculation engine is based on Cq values. Raw amplification curve data are not (yet) supported.

Import file formats should be either a tab delimited text file (.txt), a comma or semicolon separated value file (.csv) or a Microsoft Excel file (.xls). Microsoft Excel 2007 (.xlsx), OpenOffice.org Calc (.ods) and proprietary or binary instrument files are not supported.

In qBasePlus, there are restrictions on sample, target and run names. Only the following characters are allowed: all alphanumerical characters (0-9, a-z, A-Z), space, _, -, \$, #, :, ^, . and the greek letter mu (μ). **Illegal characters** such as brackets and slashes should be removed or replaced.

Utility of qBase files

qBase files (*.xls) can be used to get your data from the phased out qBase into qBasePlus. It is also a simple, instrument independent, and self-explanatory file format that contains most of the data that qBasePlus can process and store. This might be useful if you encounter problems importing data from any of the many file formats that are available. Most file types (provided they are in a tabular format containing Cq values) can be relatively easy transformed into qBase files (see Creating qBase files yourself).

Extracting qBase run files from qBase

Biogazelle provides a *qBase Run Extraction tool* to automatically extract the run data of all your old qBase projects and experiments into individual qBase run files (the tool can be downloaded from <http://www.biogazelle.com/resources/tools>).

Generated files using the tool described above may fail to import into qBasePlus, because:

1. You have very old qBase files that do not contain an exclusion column. Adding the header "Exclusion" to column G will solve this problem.
2. Illegal characters are used in the qBase file. Perform a find-and-replace action on the sample and target columns, and correct the filename if required.



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Creating qBase files yourself

qBase files contain one data table starting with a header row. This header row must match the following items exactly and in the same order (from column A to G):

- Well
- Type
- Sample
- Gene
- Ct
- Quantity
- Exclusion

If you start from another import file type, you should reorder your columns so they match exactly with the required column positions in a qBase file. After reordering, header names should be corrected according to the guidelines (see above). Well positions should be like A1, H12, P24. The following sample types are recognized: UNKN (for unknowns), STD (for standards), NTC (for negative controls - no template). Mind invalid characters in the Sample and Gene columns. The Ct and Quantity columns can contain only numerical values or should be left empty. The Exclusion column should be left blank or contain the value TRUE if the data point is to be excluded from calculations.