

# Import file guidelines - qBase



qbase<sup>PLUS</sup>



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## Subject

This chapter explains how to create a qBase file for import into qbase<sup>PLUS</sup>.

## Summary

qBase files (.xls or .xlsx) can be used to get your data from the discontinued Ghent University qBase software into qbase<sup>PLUS</sup>. It is also a simple, instrument independent, and self-explanatory file format. The qBase file type proves useful if you encounter problems importing your data from using one of the many file formats that are supported. Most file types (provided they are in a tabular format containing Cq values) can relatively easy be transformed into qBase files.

The qBase file type is supported as of qbase<sup>PLUS</sup> version 1.0.

## General information

Import files should contain a list of Quantification Cycle (Cq) values. Depending on the instrument software that generates the data, Cq values may have alternative names such as Ct, Cp, or TOP. Cq is the official abbreviation in the Real-time PCR Data Markup Language (more info on <http://www.rdml.org>).

The qbase<sup>PLUS</sup> calculation engine starts with Cq values. Sigmoidal amplification curve data are not supported.

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

### qBase Run Extractor tool

Biogazelle provides the qBase Run Extractor tool (for Microsoft Excel 2000/XP/2003) to automatically extract the run data from 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 qbase<sup>PLUS</sup>, because the qBase files may not contain an exclusion column. Adding the header "Exclusion" to column G will solve this problem.

## qBase data table format

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
- Cq (Ct is also accepted)
- Quantity
- Exclusion

If you start from another import file type, you should reorder your columns so that 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 letter-number combinations like A1, H12, P24, or plain numbers. When using numbers as well identifiers, the data will be imported as an ordered list instead of a plate format (96-well or 384-well). The following sample types are recognized: UNKN (for unknowns), STD (for standards), NTC (for negative controls – no template), POSITIVE\_CONTROL, MINUS\_RT, NO\_AMPLIFICATION.

The Ct and Quantity columns should only contain 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.

## Import qBase files into qbase<sup>PLUS</sup>

Detailed information on the import functionality within qbase<sup>PLUS</sup> can be found in the dedicated manual chapter 'data import' (<http://www.biogazelle.com/support/qbaseplus/manual>).