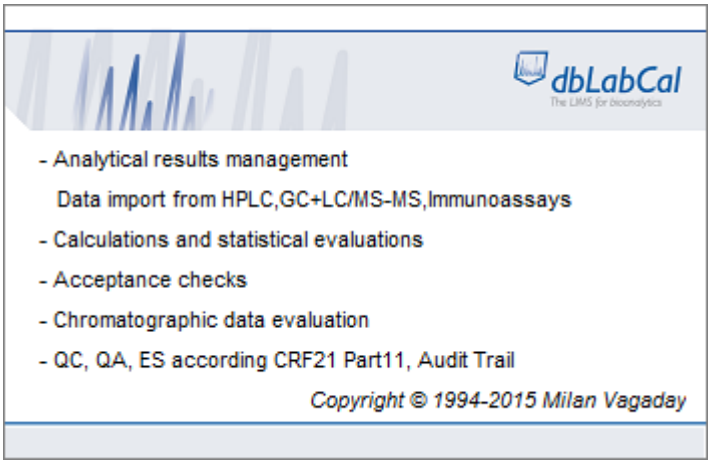
dbLabCal

Manual



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Introduction

The aim of DBLABCAL is the management of analytical data and results generated during bioanalytical studies (e.g. bioavailability, bioequivalence study). It is compatible with a wide variety of analytical methods and instruments (HPLC, LC/MS, GC/MS etc.).

DBLABCAL is an interface to a database in which the information on analytical studies, on the batches of the studies and, lastly, "all" data of the individual chromatograms are stored. DBLABCAL sends the user's commands or questions (selected from the individual menu items) to the database and then displays/prints/exports the answers from the database in a formatted and meaningfully arranged way. In addition, many plausibility tests are performed to support the user.

All data of a chromatographic run (batch) are imported into the database by an ASCII file.

DBLABCAL monitors the data for any irregularities and provides information/hints about certain situations. Furthermore, the program contains user management functions and only actions which are meaningful at that particular time and for which the user has access authority can be performed

All actions (commands) of the user which modify the data/results of a project are documented in the audit trail. DBLABCAL fulfils the CFR21Part11 requirements.

The chromatographic source data (retention times, peak heights, peak areas, calculated concentration, etc.) cannot be modified with DBLABCAL once they have been imported.

It is also possible in DBLABCAL, based on the analytical data stored in the DBLABCAL database, to extract management information data such as project status or number of samples analyzed in a specific period of time in a specific department, etc.

In order to work with the database the user must comply with certain rules for assigning sample names. Then, all data of the project are available immediately, free of errors, for further processing (e.g. biometric evaluation, export into other programs for report generation or for further statistical analyses, etc.).

This version of DBLABCAL works with all Oracle database versions. Versions from 8i to 11gR2 as well as Oracle XE versions were tested.

DBLABCAL works in two different languages. The user can freely switch between the two. Furthermore, the administrator can modify and adapt all annotations, messages, texts and system texts at any time.

This manual describes only the most important points. There may therefore be some situations in which the program returns questions or messages to the user that are not explicitly described herein.

Program Tasks

The major tasks of DBLABCAL can be summarized as follows:

Administration:

Project Administration
Permission Administration
Display, printing and export of project results
Export of subject results into ASCII files for further processing
Release of project results

Import of chromatographic batch data
Display, printing and export of data from individual batches
Release of individual batches

Editing of sample names
Release of individual chromatograms

Long Term Stability Planning

Calculations:

Calibration curves
Concentration of unknown samples
(QCs, subject samples, validation samples, etc. ...)
Statistical evaluation of project results

Monitoring of all results for correctness:

Verifying the correctness of project results
Verification that batch data meet acceptance criteria

Chromatography data analysis:

Display of retention times and peak widths for peaks of all project chromatograms
e.g. for verifying the correctness of integration, peak assignment, etc.
Selection of specific data from the database
e.g. peak areas of all QCs to demonstrate their stability throughout the duration of measurements...

Audit trail / Electronic Signature

Management information

Typical Workflow

DBLABCAL is generally used as follows:

	Person	Action	Comment
BEFORE SAMPLE MEASUREMENT			
1	PI/Study Director (Analyst)	defines new project	Define project code, comment, access authority for analyst, analyte, IS name(s), matrix, parameters, model, weighting, conc. unit(s) analytical method(s), project type, if routine project: number of samples to be analyzed see page 15
DURING SAMPLE MEASUREMENT			
2	Analyst	analyzes batches	Writes batch lists Runs batches
3	Analyst	checks chromatograms BEFORE data export into dbLabCal	Checks chromatography data for analyte(s) and ISs Sets the acceptance on the chromatograms (flags)
4	Analyst	creates export ASCII files (*.lca, *.xls, *.asc, *.csv…)	Using the chromatography software (Analyst, Xcalibur, Empower Magellan, etc.)
5	Analyst	imports ASCII files into DBLABCAL	see page 57
6	Analyst	sets chromatogram flags in dbLabCal if necessary *Chromatogram release*	In accordance with the notes on the chromatograms see page 67
7	Analyst	sets batch status (to “batch accepted” or “not accepted”) *Batch release*	depending on the acceptance criteria check results see page 64
8	PI/Study Director	reviews batch data<->chromatograms	informs the analyst if necessary (possible also via the batch memo) sets R / C flag if required
		continue at 2	
AFTER SAMPLE MEASUREMENT			
9	Analyst	sets project status to ‘finished’ *Project release*	see page 34
10	PI/Study Director	sets project status to ‘released’ (it also locks all batches, batches remain locked even after project status is reset) *Project release/lock*	see page 34
11	QC-Check	QC check of the whole project	Consistency and correctness re. project plan, chromatographic data etc…
12	QM/QA	Documents the quality audit in the QM/QA department	
13	Any user	prints, exports batch data prints, exports project results	as required for documentation and report

Data are released/locked in three steps:

- release of individual chromatograms (flag)
- release of individual batches (batch status), “batch lock”
- release of whole project (project status), “project lock”

User Authorization

The following permission levels exist:

ReadOnly	No permission to edit data
Analyst	may modify data of "own" projects
PI/Study Director	PI/Study director may modify data of "own" projects
QC/QA Reviewer	permission to document QC/QA work otherwise like ReadOnly
Department Manager	PI/Study director permissions for all projects in the department
Administrator	permissions for all projects

Action	ReadOnly	Analyst	PI/Study Director	QC/QA	Comment
Create new project		+	+		Analyst cannot assign other user
Edit project data		+	+		if project ”released” add new analyte(s) only allowed
Grant permissions for project			+		
Change model, weighting and readings		+	+		if project type “validation”
Change acceptance criteria			+		as long as project not ”released”
Change settings and output texts	(+)	+	+		ReadOnly-User only for current session, save not possible
Print/export of data	+	+	+	+	
Finish project		+	+		
Release project, Reset project status			+		
Data export in ASCII			+		if project ”released”
Import batch		+	+		as long as project not ”released”
Change unit, batch number, start date		+	+		Analyst only if project „started“ PI/study director only as long not ”released”
Change batch status		+	+		Analyst only if project „started“ AND to a batch status in accordance with batch acceptance criteria
Final result selection (from re-assays)		+	+		Analyst only as long as project „started“
Change chromatogram flag		+	+		Analyst only as long as batch status “not set yet”
Change sample name		+	+		Analyst only as long as batch status “not set yet”
QC check, QA				+	after project was ”released”

+ permitted

Naming Conventions

Batches:

A batch file (ASCII file for import into DBLABCAL) can have any name. The file extension describes the ASCII file format

Extension *.lca created by Analyst (Sciex)
*.xls created by Xcalibur, LabX, MultiLab Pilot, SearchLight
*.rep created by Elan-ICP
*.csv created by Access2, FACS, Mesoscale (MSD)
*.asc created by Magellan (ELISA)
*.txt created by SoftMax Pro

It is recommended to use ASCII file names consisting of any 2 letters and 2 numbers which define the batch number, e.g. aa01.lca, mn17.xls, xy99.rep, de5an01.csv and de5an02.asc etc.

Samples:

<table>
<tr><th>Sample Type</th><th>Code</th><th colspan="3">Further Information</th><th>Example</th></tr>
<tr><td>System Suitability Sample</td><td>SSS</td><td colspan="3"></td><td>SSS</td></tr>
<tr><td>Standards</td><td>CAL</td><td colspan="3">Nominal concentration</td><td>CAL 10.0 ng/mL
CAL 10.0/25.0 ng/mL</td></tr>
<tr><td>QC’s</td><td>QCS</td><td colspan="3">Nominal concentration</td><td>QCS 150 ng/mL
QCS 150/450 ng/mL</td></tr>
<tr><td rowspan="2">Unknown samples</td><td rowspan="2">SUB</td><td colspan="3">Number,
Period,
Sampling time (ALL VALUES MUST BE NUMERIC!)</td><td>SUB01DG01TP2d4h30m
SUB15DG02TP2.5h
SUB99DG03TP5</td></tr>
<tr><td colspan="3">Number or name</td><td>SUB123456
SUBMD44_F01</td></tr>
<tr><td rowspan="3">Validation samples</td><td rowspan="2">VAL</td><td colspan="3">Nominal concentration</td><td rowspan="2"></td></tr>
<tr><td>“Matrix”-Group *)</td><td>“Temp”-Group *)</td><td>Duration</td></tr>
<tr><td>E extracts
N matrix
P thawing cycles
A other (whole blood)
B n/a</td><td>R room temp.
K refrigerator
G freezer
T deep-freezer</td><td>given in hours or _d_h_m format</td><td>VAL ET4d 10/50/100
VAL PR8w 150 ng/mL
VAL BT2h 10 ng/mL</td></tr>
<tr><td>QCS</td><td colspan="3">Nominal concentration and dilution factor (df)</td><td>QCS 1000 ng/mL
df in the chromatography software</td></tr>
</table>

*) The codes for “Matrix” group (E, N, P, A) or “Temp” group (R, K, G, T), respectively, are assigned by default to the matrix type and storage conditions as shown in table.
It is possible to assign any description to any “Matrix”-“Temp” combination.
E.g., VAL **AT** 2h xxx pg/mL may belong to the validation/stability samples group: „Plasma stabilized with X and kept cool in ice water during sample collection”.

It is required for CAL, QCS, and VAL samples to enter the nominal concentration after one or more blanks. Nominal concentrations should be entered in the order of their retention times separated by '/' in case the CAL, QCS, or VAL sample contains more than one analyte with different nominal concentrations.
Examples:
CAL 500 ng/mL, VAL NG48 10/20/20 ng/mL, QCS 5/10 ng/mL etc. If all analytes are of the same nominal concentration it is sufficient to enter the nominal concentration just once.

dbLabCal read nominal concentrations from Analyst, Empower2 and Xcalibur DIRECTLY. Nominal concentrations in the sample name are ignored for Analyst, Empower2 and Xcalibur. They are used ONLY if this information was missing in the chromatography software.

In the case of SUB samples, it must be decided before starting the measurements whether the samples should be named SUBxxxxDGxxTPxxx or only SUBxxxxx as both modes are not allowed simultaneously in one project.
It is possible to switch between the SUB naming modes (SUBxxxxDGxxTPxxx or SUBxxxxx). Potentially missing Period and Sampling Time data may need to be completed.

The SUBxxxxDGxxTPxxx naming is appropriate only when the samples are indeed samples from a bioequivalence study with "real" periods and time points.
If, for example, samples from a Phase II study or a toxicological study are to be analyzed, the sample names will probably better be coded in such a way that the results appear in RESULTS / SUBJECT SAMPLES in the desired order (the results are sorted alphabetically) and consequently, can easily be processed further (e.g. in Excel).
Subject Samples Results are sorted in alphabetical order. That means that also the numbers are sorted in alphabetical order. (example: 1, 10, 11, 2, 222, 3 etc.).
In case the samples should be sorted as: 1, 2, 3, 10, 11, 222 etc, it is necessary to write numbers in SUBxxxxxx as SUB0001, SUB0002, SUB0003, SUB0010, SUB0011, SUB0222, etc.

For instance, a sample from a female rat no. 118, dosage 10 mg/kg i.v. obtained on day 7, 12 hours, could be identified as follows: SUBIV_D010_F_D07H12_NO0118 (or short, e.g., SUBI_010_F_07_12_118). The results will then be shown sorted by type of dosage, dosage, sex, time and animal number. If it were necessary to separately report the results first by sex and then by dosage, the samples would be identified as follows: SUBF_IV_D010_D07H12_NO0118. The separator '_' is useful for improving readability and facilitating the later extraction of individual data with SEARCH AND REPLACE into Excel where they will be written into separate columns.
The determining factor for naming samples is the way of subsequent result data processing and reporting.

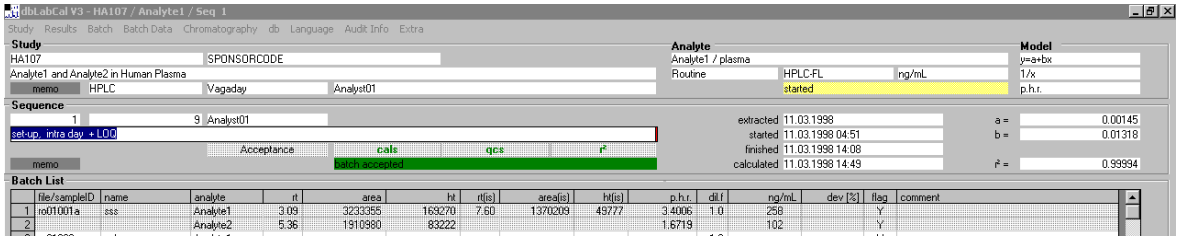
Operation

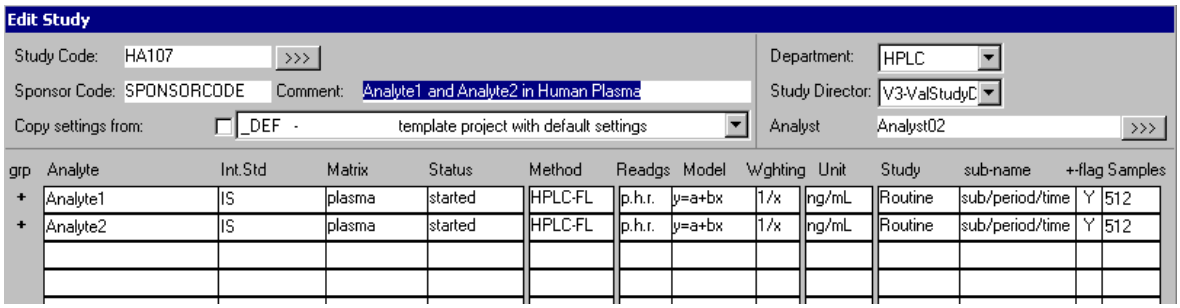
General
Keyboard and Mouse

Both keyboard and mouse operations follow the Windows conventions.
Menus, availability of certain commands, etc. are adapted dynamically to the current data and the access authority of the user. Furthermore, certain menus and commands are disabled if their use is not meaningful or not allowed at that particular point in time.
Whenever the OK and CANCEL buttons are shown on the screen, the ENTER and ESCAPE keys are available for use. Pressing the ENTER key is equivalent to clicking on the OK button and, similarly, pressing the ESCAPE key has the same effect as clicking on the CANCEL button.
To terminate an input and jump to the next element (e.g. to the next text field of the current dialog), the TAB key and not the ENTER key is used in Windows.
The mouse is used in very much the same way as it is in Windows:

Left mouse button:	Click:	Select
	Double-click:	Select with confirmation (OK)
Right mouse button:	Click:	Selection menu / context menu, where available

Some inputs can be performed by more than one way. For example, the project comment can be entered via the menu PROJECT | NEW... or PROJECT | EDIT… or by double-clicking on COMMENT ON THE PROJECT.





dbLabCal accept following shortcuts:

ENTER/ESCAPE	Default keys for clicking on OK or CANCEL buttons, respectively
CTRL-INS or CTRL-C SHFT-INS or CTRL-V	In addition to the menu-driven export (see below) it is possible at any time to export (marked) data and/or graphics from the active window into other programs via the Windows clipboard (as generally done in Windows).
STRG+L, +P, +E	Laden, Drucken, Export des Projekts, bzw. der aktuellen Sequenz
CTRL - +/- (NUMERIC KEYPAD)	loads next / previous batch
SHFT+CTRL+C, +Q, +V, +S, +K, +D	Sample type filter on/off (in batch view)
SHFT+CTRL +R	Current batch is immediatelly re-calculated
CTRL-R	(un)marks „Random Repeats“/IncurredSamples ISR are marked by yellow background color
press SHIFT while changing the concentration unit in PROJECT | EDIT...	nominal concentrations of all until now analyzed CAL, QC and VAL samples will be re-calculated according new concentration unit. (factor 1000, 1 000 000 etc.)
press CTRL while changing the concentration unit, readings or regression model in PROJECT | EDIT...	changes parameter for CURRENT ANALYTE ONLY (default behavior is to do changes the parameter for all analytes in one chromatographic run)
press CTRL at program start...	Project load dialog will always be displayed
press CTRL while clicking on the user name (status line, right side)...	Login dialog will be displayed for re-login
press CTRL while changing chromatogram flag...	chromatogram flag will instantly be changed for all analytes of the chromatogram
press CTRL while double clicking on a value or batch number in any results table or in the chromatography menue... (or press CTRL+G)	dbLabCal “jumps” to the chosen batch and chromatogram return to original view by pressing the ESCAPE key
CTRL while certain actions gives the PI/study director more freedom than normally available, e.g. before selecting final results from re-assays *(the so-called ‘study director special wish key’)*	

Screen

Title bar: Shows the current information for
program name / version - project code / analyte name / batch number

Menus:

Status line: The status line shows the following information:

left: progress display or time

center: - messages to current actions of the program
- explanations to the significance of the fields under the mouse pointer, and
- tips to possible user actions
- name of current data base

right: name of current user

Between the menus and the status line the screen is hierarchically divided into three segments:

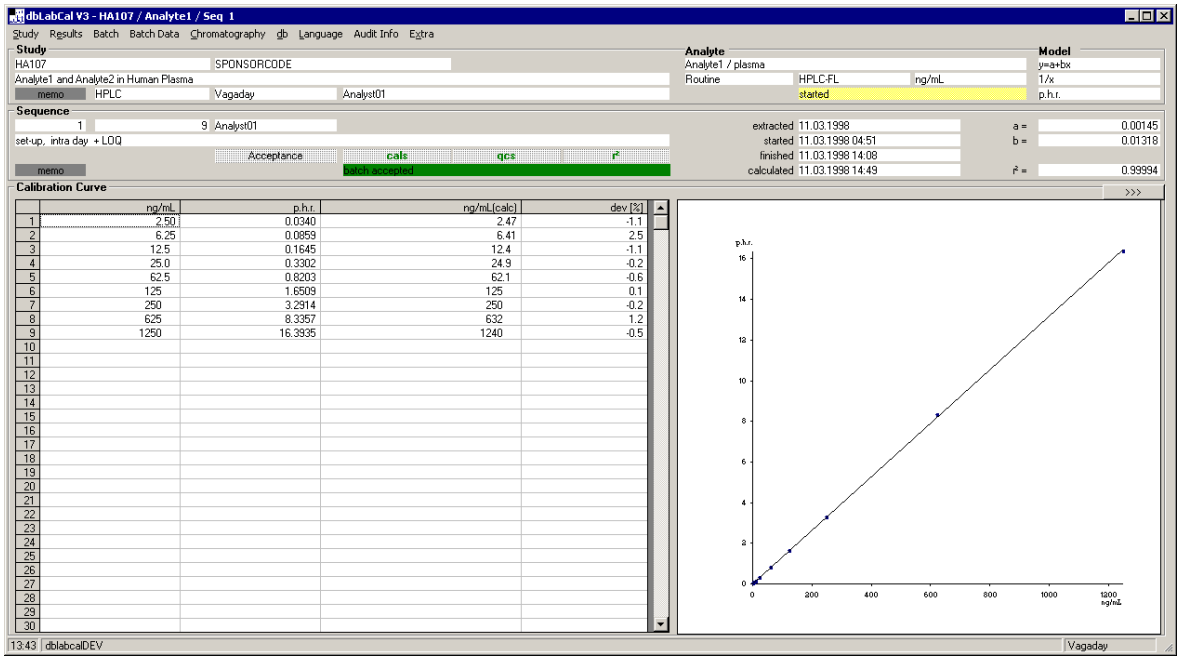
top: information to current project and to analyte

center: information to current batch (if batch data view was chosen)

bottom: data of current batch in the selected view
or data (results) of current project

The MEMO fields allow for entering comments or notes to results or to the individual batches. They are also suitable vehicles information exchange. The MEMO field displays green if there is content, otherwise they are dark gray.

Occasionally the button >>> is displayed. Clicking on this button opens a dialog offering more settings available for the current display.



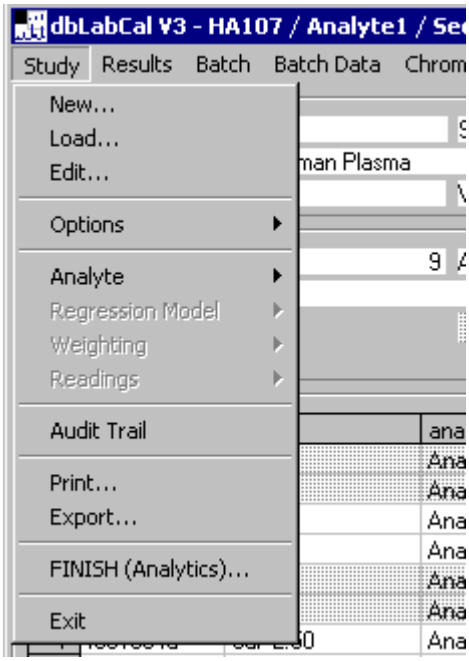
Login

At program start the following Login Dialog appears:

User can log into DBLABCAL even if another user is logged into Windows. The user is locked after a specific inactivity time period.

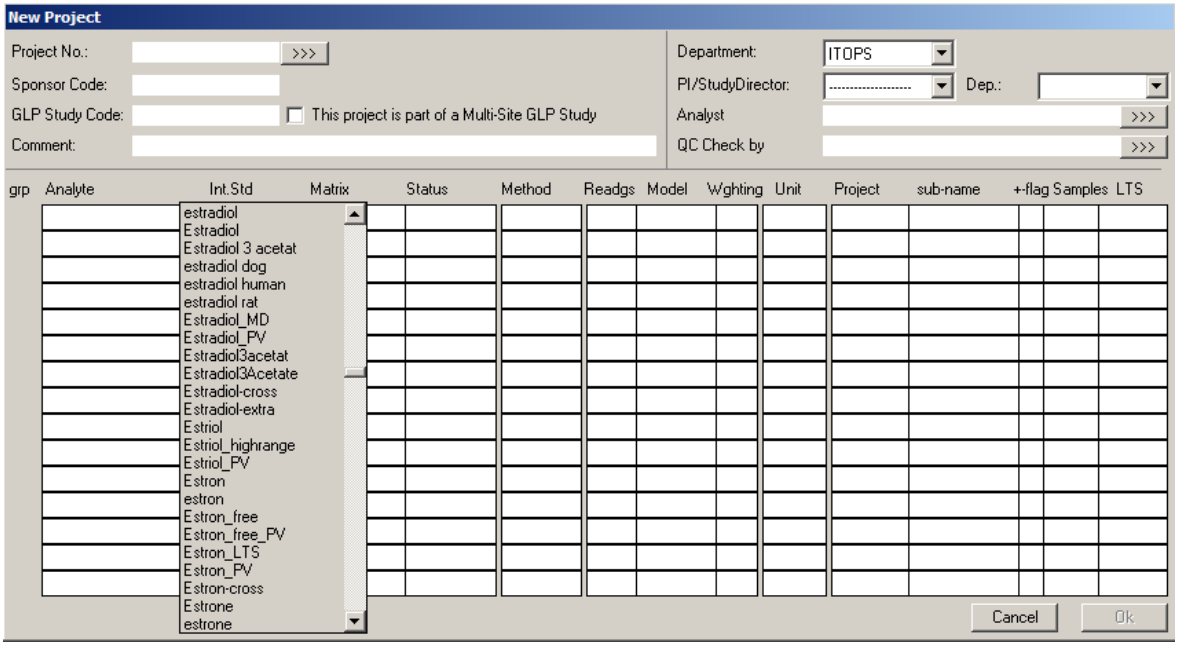
Project Menu

Studies are managed through this menu



New...

A new dialog for entering all required information for a new project appears:



- Project code

By default a project code is allowed just once (per department). In certain situations, however, it may be advantageous to subdivide a project into, for instance, a validation part and a routine part, or subdivide by matrix etc. In such a case the department manager, after acknowledging the security prompt, can create another project with an existing project code in the data base.

- GLP code for the project
- Sponsor code for the project
- Comment to project - usually the analyte(s) name and the matrix
- Department, analyst and PI/study director, deputy of the PI
- Analyte names measured in the current project, plus other details such as project types, analytical method, matrix, readings, concentration unit, model, weighting, and, if used, name of internal standard and decision whether the program will or will not set the '+' flag in chromatograms of pre-dose samples. (see page 67 for more information about flags)

If the current project is a “routine” project the number of samples to be measured must be entered in the last column and the used SUB naming type can be chosen

User can select in last column (right mouse) if long term stability is due for the selected analyte/matrix. He/she will be reminded 2 weeks before the due date to perform the stability evaluations.

It is possible to copy all analytes and their settings from another project by clicking  on next to PROJECT-NO. into current project.
Furtermore, it is possible with COPY ALL SETTINGS FROM: to copy all settings (submenu PROJECT | SETTINGS) from another project into the current project.

If several analytes are measured in a project not all analytes in a chromatogram have to be determined. It is thus possible, for instance, to measure analyte X and metabolites 1, 2 and 3 in plasma in one 'run' with analyte X in urine and, perhaps, analyte X (total) in urine being part of the project XY001 as well. This example would lead to 6 analyte entries.

If a project includes several chromatographic methods and/or different matrices it is more reasonable to create a separate projects (PI or administrator are allowed to create dbLabCal projects with identical project codes) for each of the chromatographic method and/or matrix in DBLABCAL.

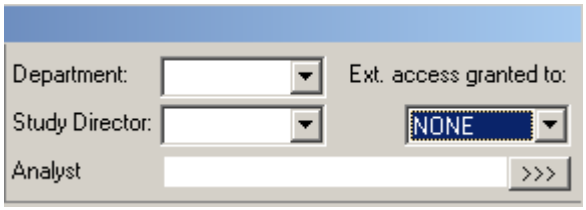
A list with all analytes stored in dbLabCal appears after double-click in the text field ANALYTE or INT.STD. Double-click on analyte name select that analyte for the new project. This saves typing work as well as using exact the same names for same analytes makes any further evaluation of analyte data beyond ‘project limits’easier.

When entering an analyte the fields for internal standard, matrix, readings, model, weighting etc. will automatically be filled with the contents of the upper line.

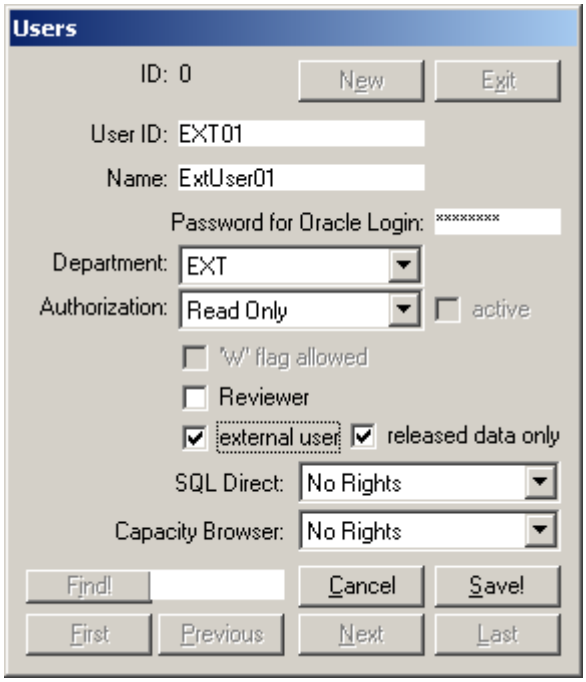
By clicking on >>> in the list of analysts the PI/study director can name up to 10 analysts (use SHFT or CTRL key) who will also be granted access to the newly created project. By clicking on the <<< list of analysts will be closed again.

Furthermore, up to 10 user with the QC permission (ReadOnly) may be defined. Analysts and QC check user must not be identical.

If admin has set the database external access option, the user may grant or revoke access to the project also to one external user.



An external user has to be defined first in dbLabCal through the db users dialog (page 81) in the same way as the “internal” user. Only the checkbox “external user” has to be selected. An external user may get access to the released data only or to all data.



The program always checks all user entries for plausibility and automatically corrects non-plausible entries. If, for instance, you select ‘p.a.r.’ for readings without having entered internal standard before, readings is automatically corrected to ‘area’. The dialog cannot be closed by selecting OK before all required data are entered.

Load...

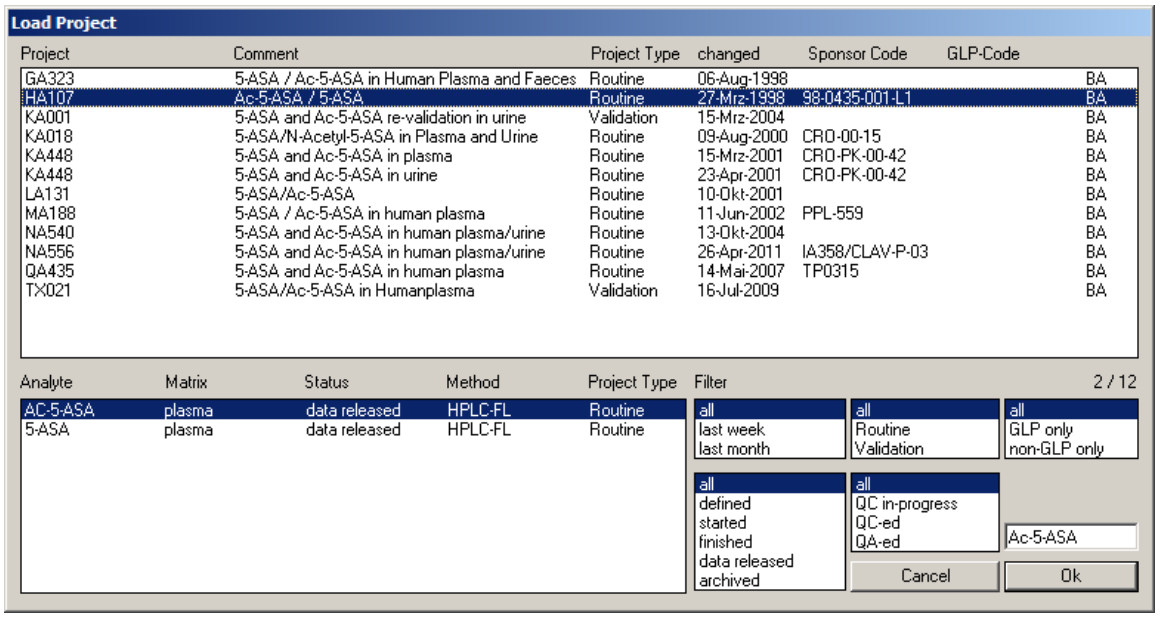
A list of all projects sorted by project code appears. 'Filter' allows selection of projects to be displayed in the project load dialog.

Each user only sees his/her own studies. All project's analytes are listed below the project list together with their status. After selecting the project and the analyte the user can load the data by clicking on OK. (or by double-click on the project or the analyte)

Quick access to dialog: Double-click anywhere within the screen area 'Project'.

The dialog LOAD PROJECT is also displayed at program start if automatic display of the last project data was not selected at the time of the last program exit (see section EXIT). The LOAD PROJECT dialog always displays if the CTRL key is pressed and held down during program start.

Keeping CTRL key pressed while opening the dialog let open PROJECT LOAD dialog in ReadOnly Modus. It mean that user see all projects and that loaded project also opened in ReadOnly modus. User cannot edit such projects independently of the actual users permissions.



After clicking on OK the data for the selected project and the analyte are loaded.
If another user already works on the selected project the corresponding user name is shown to the right of the analyte name. However, in this case the project data cannot be edited.

Project data can only be edited by one user at a time.
Other users always are in 'ReadOnly' mode.

If the authorized user has made any modifications to the project data a message is displayed for all other users, logged in the project. After double-click on the message New Data! the new data will be re-loaded.

Edit...

The same dialog as in the menu PROJECT | NEW is displayed.
This dialog allows for subsequent modifications to some project information, such as sponsor code, comment etc. The PI/study director is also authorized to change the project code.
The name(s) of the analyte(s) and the matrix can also be modified - the assignments of data acquired so far remains the same - or additional new analytes can be entered into the project. Existing analytes can be deleted from the list as long as the analyte status is 'applied'.

If readings, regression model and weighting are changed the complete project will be recalculated according to the new settings after exiting the dialog. Modifications to readings, regression model and weighting are automatically applied to all analytes measured in a chromatogram.

Rows for all analytes measured in a chromatogram with the current analyte (current analyte is displayed in the title bar and in the „project" frame) have white back color. The other rows are grey.

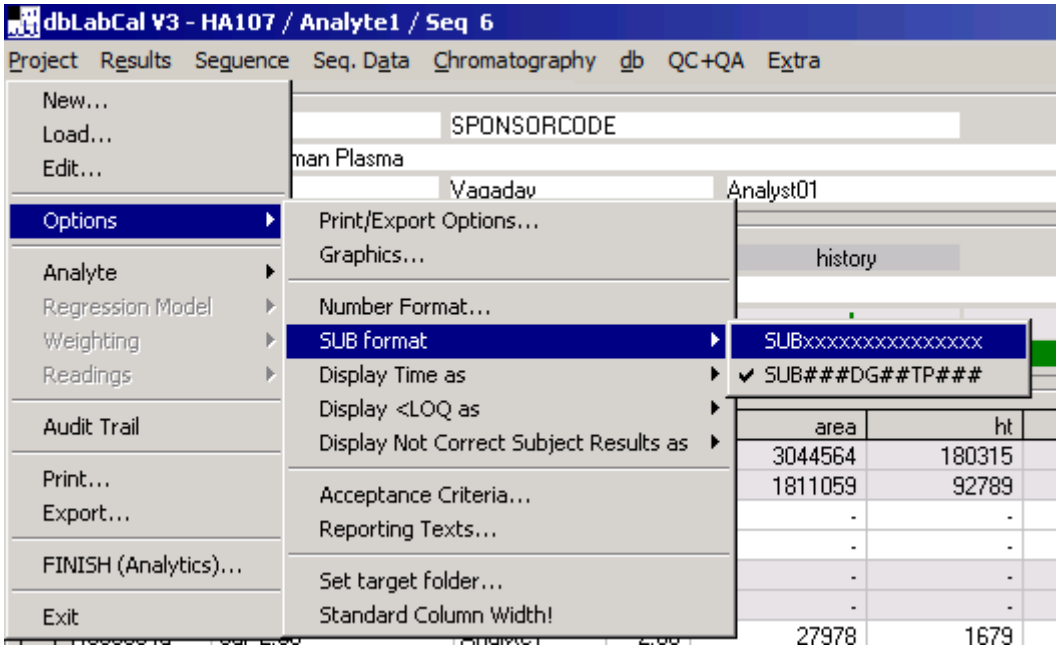
The decision whether DBLABCAL should set or not set the '+' flag can also be changed. The complete project will be recalculated after closing the dialog.

The concentration unit can be changed as well. There are two possible scenarios. Either only the concentration unit (concentration unit text only) is changed or - if the SHFT key is pressed when selecting the new concentration unit - the nominal concentrations of the calibration, QC and validation samples measured so far can be recalculated according to the new concentration unit as well.

By default, concentration unit, readings and regression model etc. will be changed for all analytes measured in a chromatogram simultaneously. To change the parameter for one analytes only, keep the CTRL key pressed.
See also page 12 for SHIFT and CTRL keys.

All setting (all data in menu Project | Settings) can be copied from an existing project. See also page 16.

Options Menu

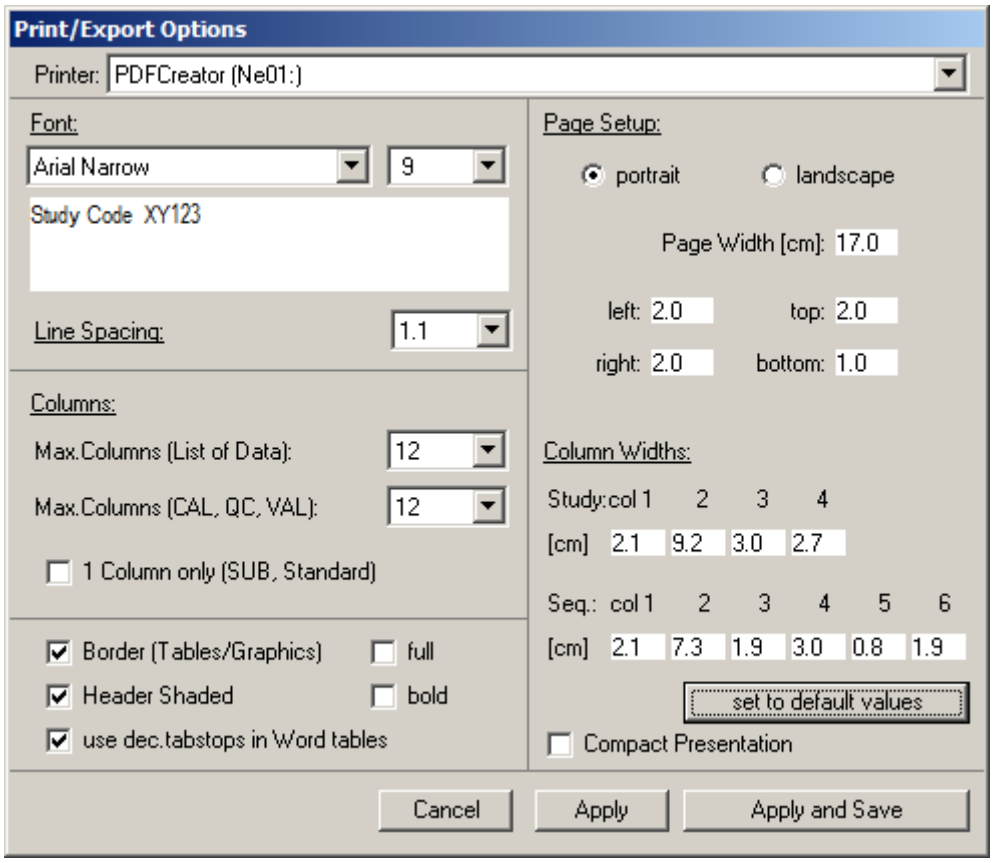


Various settings applicable to the current project are selected through the options in this menu.
Acceptance criteria can only be changed by the PI/study director. Analysts and visitors are only allowed to view them but can modify other settings. However, modifications done by visitors are not saved and therefore only apply to the current session.

All setting (all data in menu Project | Settings) can be copied from an existing project in the Project | New... or Project | Edit... menu. See also page 16.

Print/Export Options...

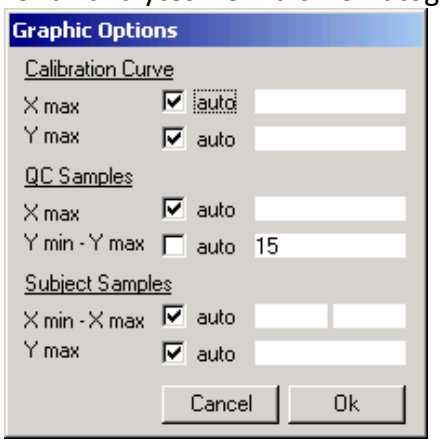
The dialog Print/Export Options... allows for changing the appearance (and the content) of the data to be printed or exported. The appearance of the printout can also be modified (frame.... header shaded..).
The number of columns/page can be set via MAX.COLUMNS (LIST OF DATA) for printing the subject results in the LIST OF DATA format for standardizing the appearance of all printouts. For instance, if 30 subjects have been measured, a good setting would be 10, or 15 (or maybe 6... try it out...).
Subject results in the STANDARD format are usually printed with 2 columns/page. However, if some of the comments to the results take up more space and extend into the next column in the printout it is better to print with 1 COLUMN ONLY (SUB, STANDARD) to generate a one-column printout. 1 COLUMN ONLY is the default setting.



The settings for margins, font, font size and line spacing allow for adapting the appearance of the DBLABCAL printouts to the report. The user should ”play” with these settings to find the optimum configuration.
Via HEADER COLUMN WIDTHS the user can modify the appearance (column widths) of the project and/or sequence headers on the printout and in the formatted export file to MS Word. The page width to be used can also be set for the formatted export into MS Word. Changing page width standardizes the individual column widths to the new page width.

Graphics...

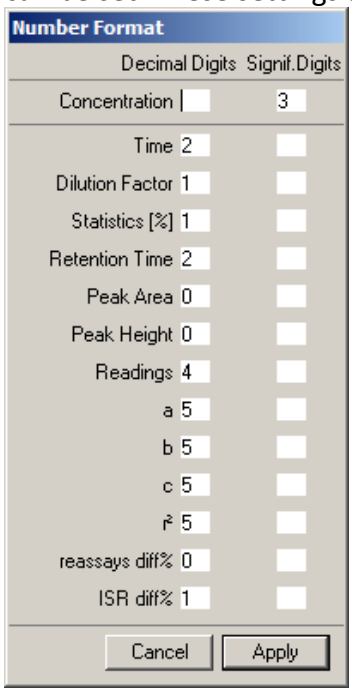
DBLABCAL adapts the scaling of all graphics to the current data by default. As desired, all or only some of the axis parameters can be set to fixed values.
These settings are accepted for all analytes in a chromatogram if they have not been individually set before. In other words, scaling can be but does not have to be the same for all analytes from a chromatogram.



Quick access: double-click on the graphic.

Number Format...

For each reading either the number of decimal digits or the number of significant digits can be set. These settings apply to all analytes from a chromatogram.



Quick access for number of decimal digits: right mouse button in the respective header row in VIEW.

SUB Format...

It is possible to switch between the 2 possible SUB sample display formats: SUBxxxxxxxx or SUB###DG###TP###..

Display Time as...

Times (for SUB and VAL samples) are given either in hours or in the _d_h_m or in „hh:mm“ format (50.5h = 2d2h30m = 50:30) format.

Display LOQ as…

<LOQ	‘<LOQ’ as text (or another text defined in the Reporting Texts dialog)
<LOQ (NUMERIC)	Instead of <LOQ the results show the LOQ as value taking the respective dilution factor into account. Example: if LOQ is 0.5 for DF=1: <0.5, or for DF=2 correspondingly <1.0, or for DF=0.5: <0.25 etc.
VALUE	the found concentration is displayed

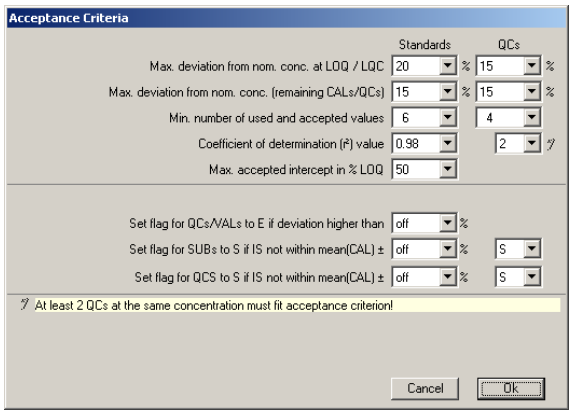
Display Not Correct SUB results as...

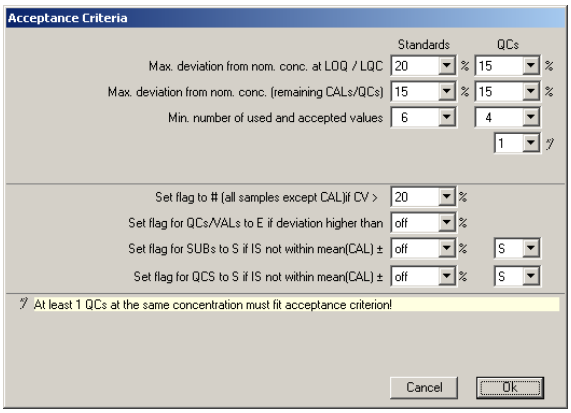
There are three ways to display (yet) not correct SUB results:
:

- Result is in red color only
- Result is in red color with added **X** character
- Result is displayed as text „n.correct“ or „n.report“

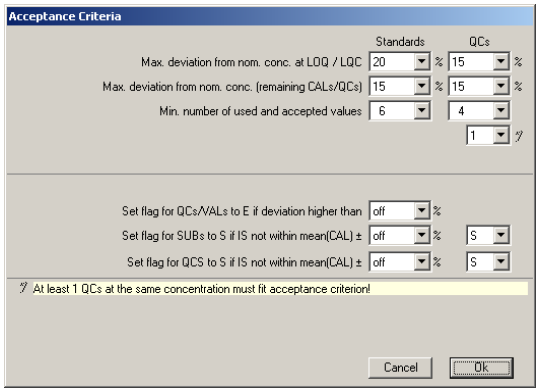
Acceptance Criteria...

The following figure shows the default values for the acceptance criteria in the individual batches. If other acceptance criteria are to be applied to the current project, they must be entered here.





or

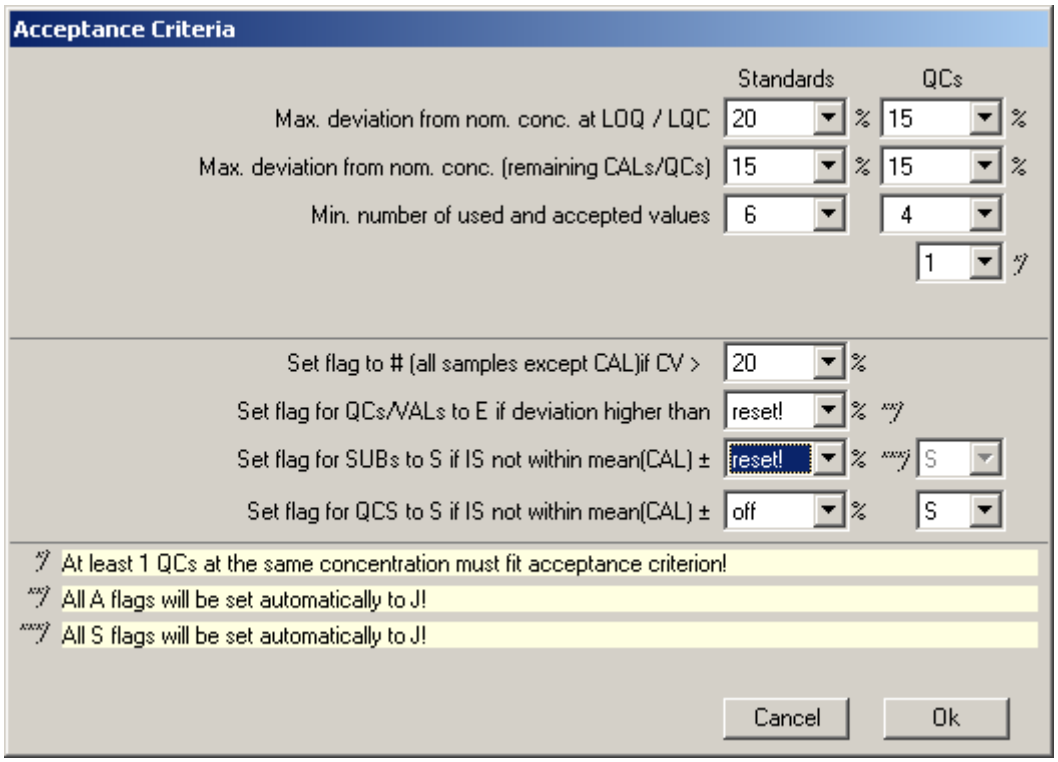


After a change, all batches of the current project are checked for compliance with the new acceptance criteria. If one or more analytes do not meet the new acceptance criteria the corresponding batch number is displayed with an exclamation mark ‘!’ after the number. According to the acceptance criteria check results the respective batch tags are displayed (in the batch view) green or red. Further details on the acceptance checks are logged in the Audit Trail.

dbLabCal is able to set the E chromatogram flag and/or the S chromatogram flags automatically according to the respective users settings. This function is an extension of the acceptance criteria functionality.

User chooses the percent value of the accepted deviation. DBLABCAL checks all unknown samples (SUB) and set the flag automatically.

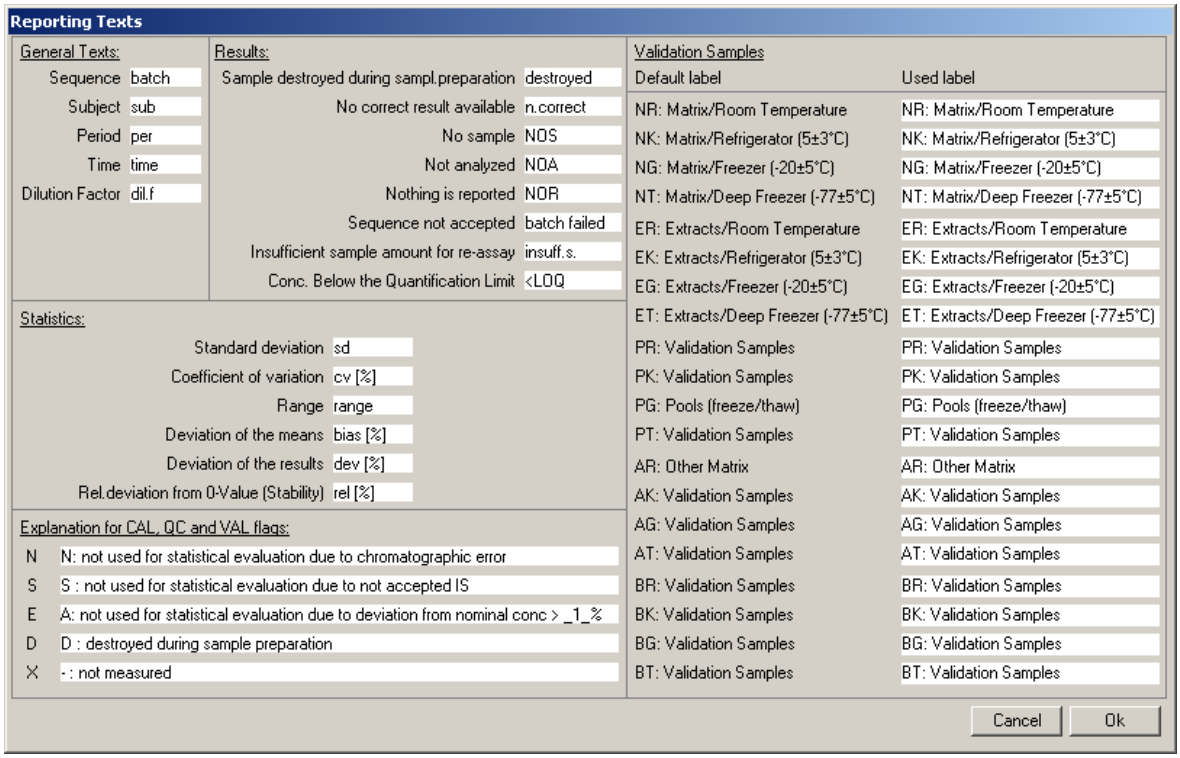
All E or S flags in the project can be set back to Y with the „reset!“ option. If the option is set to “off” only, current E/S flag will be NOT reset.



Quick access: double-click on the acceptance status display in batch area.

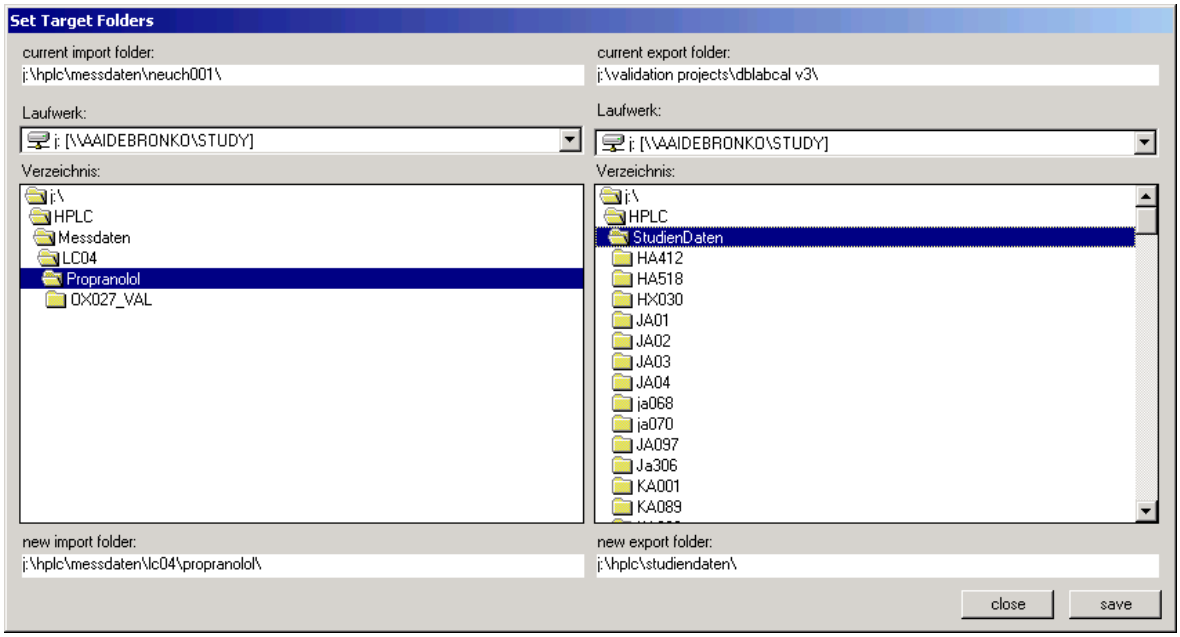
Reporting Texts...

The following dialog is available for adapting the output of the various texts to the current project.



The placeholder _1_ is replaced by the valid value upon printout/export.
It is the value chosen for the automatic E flag setting in the acceptance criteria dialog. If it is set to „off“, the chosen values for LOQ and lowest QC are used (see previous page).

Set Target Folders...



DBLABCAL expects a folder structure like:

example

folder	*i:\unit01*	*content (example)*	
⎿ Project01	⎿ *XX001*		
⎿ batch01	⎿ *SP01*	*Chromatograms of 1st batch in plasma*	
⎿ batch02	⎿ *SP02*	*Chromatograms of 2nd batch in plasma*	
⎿ batch03	⎿ *SU01*	*Chromatograms of 1st batch in urine*	
⎿ etc...			
⎿ Project02	⎿ *XX002*		
⎿ batch01	⎿ *AB01*		
⎿ batch02	⎿ *AB02*		
⎿ etc...			
⎿ Project03	⎿ *XX003*		
etc...			

and tries to „jump“ into the folder e.g. during the import accordingly.

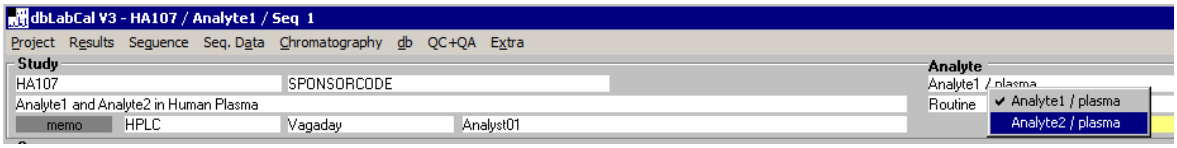
This folder structure is not required by DBLABCAL. Well organized folder structure makes the daily work much easier and is strongly recommended anyway.

Standard Column Width!

The column widths in the tables can be changed if required (with the mouse). By clicking on this menu option the original column widths are restored.

Analyte

This menu option is only offered when more than one analyte was measured in a project. The project data of the selected analyte are loaded.



Quick access: click with right mouse button on the name of the analyte.

Regression Model, Weighting, Readings

These menu options are accessible only if the project is a validation.
After any changes to readings, weighting or regression model the data for the whole project are recalculated based on the new settings.

These changes automatically affect all analytes that were measured in the same chromatogram! If it is necessary to change the parameter for just one analyte, it has to be done via PROJECT | EDIT...

It is possible to change only one parameter each here. In case one has to change more/all regression parameters at once, it is more reasonable to do it in the dialog PROJECT | EDIT... See page 20. The whole project is re-calculated only once in such case

Quick access: click with right mouse button on the corresponding terms.

In order to make changes to regression model, weighting or readings in a routine project the project type must first be changed from 'routine' to 'validation'. (via PROJECT | Edit... or by clicking with the right mouse button on the project type name)

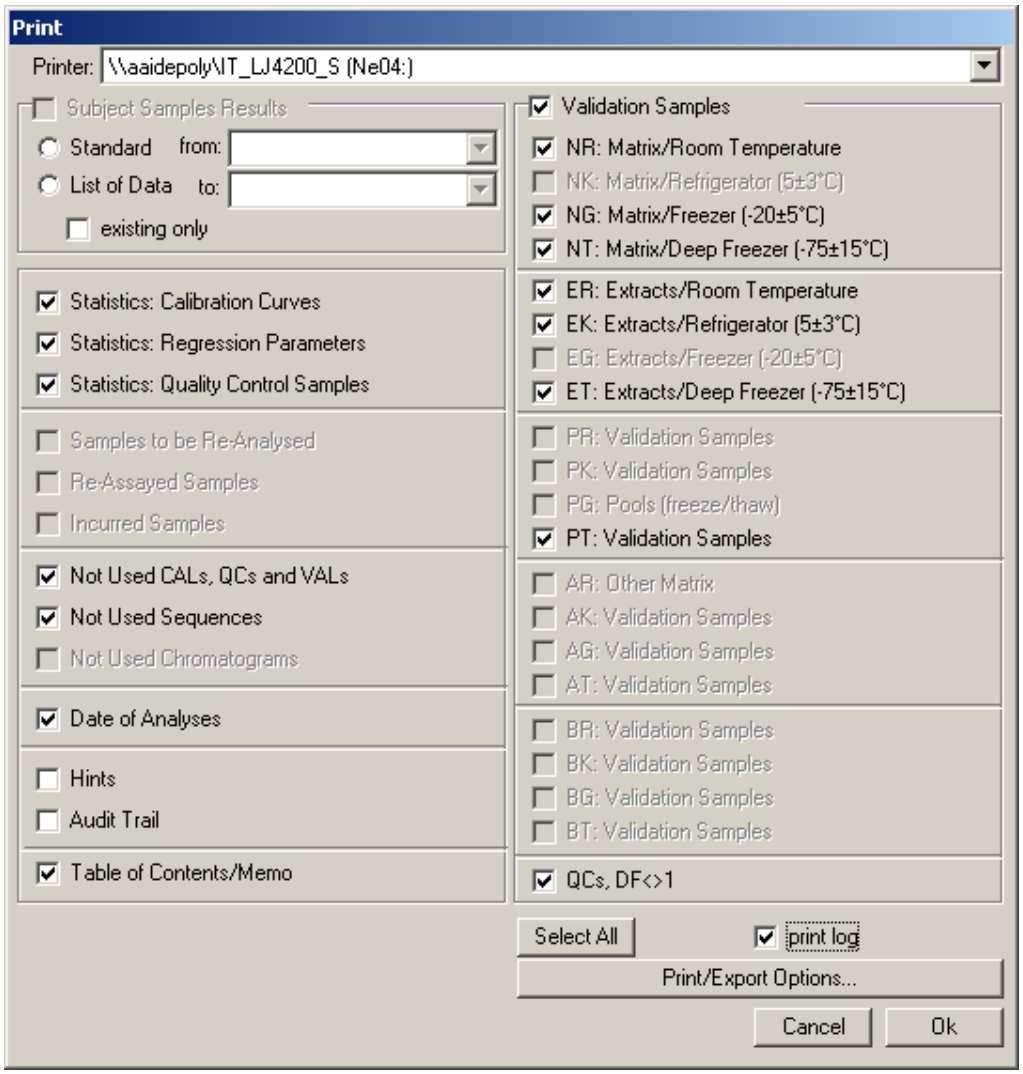
Audit Trail and Electronic Signature

The following user actions are recorded in the audit trail with date, time and name.
In some cases, the electronic signature is required and is also recorded in the audit trail.

Action	Electronic Signature **(ES)**
Defining a new project	
Editing project	**X**
Editing project permissions	**X**
Changing regression model, weighting, readings	
Changing acceptance criteria	**X**
Importing batch data	
Recalculating batch Checking acceptance criteria	
Changing batch status	**X** only if batch status changed from or to „excluded“
Changing unit or batch number	**X**
Changing batch start date	**X**
Changing sample names	**X** only if meanwhile batch status set
Changing a chromatogram flag	
Selecting final results of re-assays	
Changing project status	**X** only if project status reset to “started”
QC start and end QA end	**X** (when finishing QC)
Electronic signature entry	N/A

Print...

Project results can be printed out at any time. It is recommended to use only printouts from released studies for project documentation purposes.
If several analytes (in a chromatogram) were measured in the project the user has the choice to print the selected data only for the current analyte or simultaneously for all analytes (from a chromatogram).
The following points are common to all analytes if they were measured in a chromatogram:
- BATCH LIST
- SUBJECTS (ONLY IN STANDARD FORMAT, NOT IN LIST OF DATA FORMAT)
- SAMPLES TO BE RE-ANALYZED
- RE-ASSAYED SAMPLES
- INCURRED SAMPLES
- NOT USED CALs, QCs AND VALs
- NOT USED CHROMATOGRAMS
- NOT USED BATCHS
- DATE OF ANALYSES
- AUDIT TRAIL



Subjects are printed in the selected display format (Standard, List of Data, all or only measured samples).

Choosing ”Standard” as display format allows for printing the results for the individual subjects separately by entering the number of the first and the last subject.

Choose all Options with SELECT ALL. With Keeping CTRL key pressed while clicking on SELECT ALL button will deselect all options.

The appearance of the printout, e.g. font, font size, margins, shading etc., can be modified here in the Print dialog or via the menu PROJECT | OPTIONS | PRINT/EXPORT OPTIONS.

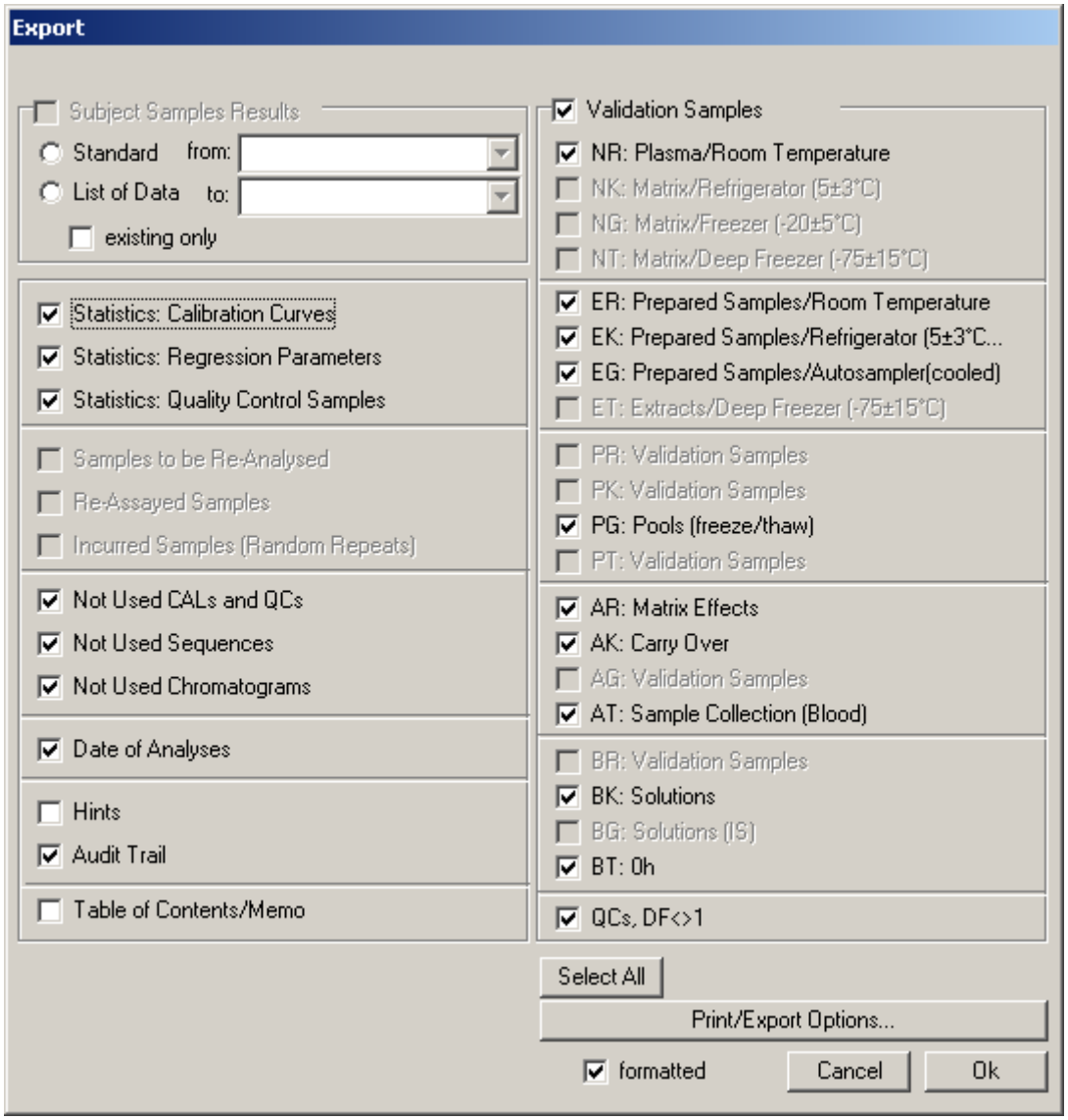
The current standard Windows printer is displayed and can be changed here.

Audit Trail details column is occasionally shortened to fit the page width. Use export to Word or Excel (windows clipboard) to print the whole details content.

Selecting PRINT LOG will finally print a summary of the whole print job.

Export...

A dialog very similar to the Print dialog is displayed. MS Word does not need to be started first since DBLABCAL starts Word automatically if required.



The data can be exported in a specified format, i.e. the tables are generated with margins, shading and correct column widths. The results should be exported into Word at the end of the document or, even better, into a separate document since font and font size for the Word document between the current cursor position and the end of the document may change during the export process according to the settings in DBLABCAL.

The format of the exported data, if a formatted export is desired, such as font, font size, margins, column widths, shading etc. can be modified here in the Export dialog or via the menu PROJECT | OPTIONS | PRINT/EXPORT OPTIONS.

Subjects are exported in the selected display format (Standard, Standard only measured Samples or List of Data).

It is also possible at any time to export all currently displayed data or only the marked data via the Windows clipboard (keys CTRL-C or CTRL-INSERT, or by clicking with the right mouse button for marked data) into other programs.

Changing Project Status

A project, or more precisely an analyte in a project, can have one of the following statuses:

Status	Comment	Is set...
Defined	project was created by the analyst or PI/study director, no data imported yet	automatically on creation of project
Started	Data have been imported for at least one analyte	automatically on importing the 1st batch
Finished	All chromatographic measurements are finished	by analyst (or PI/study director)
Data Released	All chromatograms and batches have been accepted and results to be reported are selected - all project data locked	by PI/study director
Archived	Similar to 'released', however, the projects cannot be reset (un-locked) by PI/study director	by administrator

By setting the project status to '**finished**' the **analyst** confirms that all batches of the project were imported and all chromatograms of the project (with the corresponding flag) have been accepted. The PI/study director can release and lock the project data only after the analyst has declared the project as 'finished'.

By setting the project status to '**released**' the **PI/study director** locks the database. The project data can then no longer be modified. Project results are once more checked during the release process. If, for instance, the user has not yet selected final values from re-assays, the release process will be aborted.

Also all batches are locked automatically!

Eventually, the DB administrator sets the project status to '**archived**' (under responsibility of the archivist). Read only access to data is still allowed for all in project involved user.

Changing the project status is an action with very far reaching consequences!

Documentation of the QC/QA review starts after the project was released (project status ='**released**'). There are following QC/QA status' of a released project:

Status	Comment	Set by…
…	QC not started yet	
QC in progress…	QC started by one of the authorized QC person	Automaticaly after first time saving the QC comments
QC-ed	QC process finished (ES)	By a QC autorized user
QA-ed	(ES) in dbLabCal just for documentation purposes. QA details are in the QM dept.	By user with „Reviewer" authorization (by default a user from the QM department)

Results for HoLaRo... / Results for BI...

This menu option is only displayed if unknown samples (SUB) were measured in the project, the project is released and the option has been enabled by the administrator. This option writes the results into a special ASCII file. First a dialog appears in which the data to the exported can be edited. A more detailed description is found in Appendix 1.

Results in ASCII File!

This menu option is only displayed if unknown samples (SUB) were measured in the project and the project is released. This option writes the results into (an) ASCII file(s) which, for instance, can be used for the biometric evaluations. The program names and assigns the files to the analytes, displays them after the export process and enters an audit trail entry. The file name is composed of project number, name of analyte and name of matrix (examples: HA107_ANALYT8_PLASMA.BIO, HA107_ANALYT8_PLASMA-02.BIO , RT001_SUBSTANCEX_SERUM.BIO, etc.). If required, an automatically incremented number is added to the file name if file with the same name already exists.

The files are written into a directory set as described on page 28.

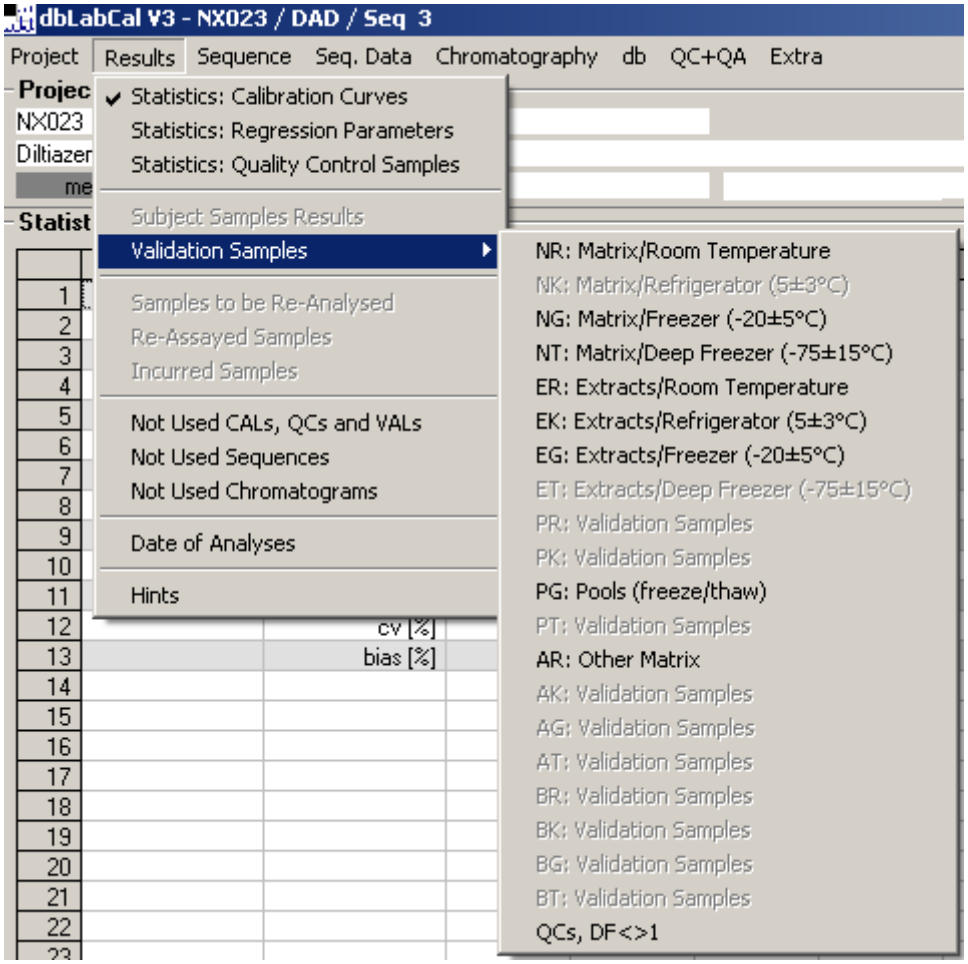
The ASCII file format is described in the dbLabCal Administration manual.

Exit

Selecting Exit closes the program. The user is asked whether the current data should be loaded automatically at the next program start.

Results Menu

Displays the results of the current project for the selected analyte and, if available, messages from the database, e.g. with regard to data discrepancies, threshold value violations in calibration, QC and/or validation samples, missing selections for values to the reported from repeat measurements etc...



When loading a project or an analyte attention should first be paid to the HINTS if generated by the database.

For technical reasons hints to validation samples can only be displayed after the user has reviewed the data at least once.

Statistics

... show the results of the statistical evaluations of calibration and quality control samples.

The following parameters are calculated: mean, standard deviation (sd), coefficient of variation (cv) and bias in percent.

$$mean = \frac{1}{n}\sum_{i=1}^{n} x_i$$

$$sd = \sqrt{\frac{\sum_{i=1}^{n}(x_i - \bar{x})^2}{n-1}} \quad ; \text{n>2}$$

$$range = |x1 - x2| \quad ; \text{n=2}$$

$$cv[\%] = 100\frac{sd}{mean} \quad ; \text{n>2}$$

cv[%]=n/a (range/mean) ; n=2

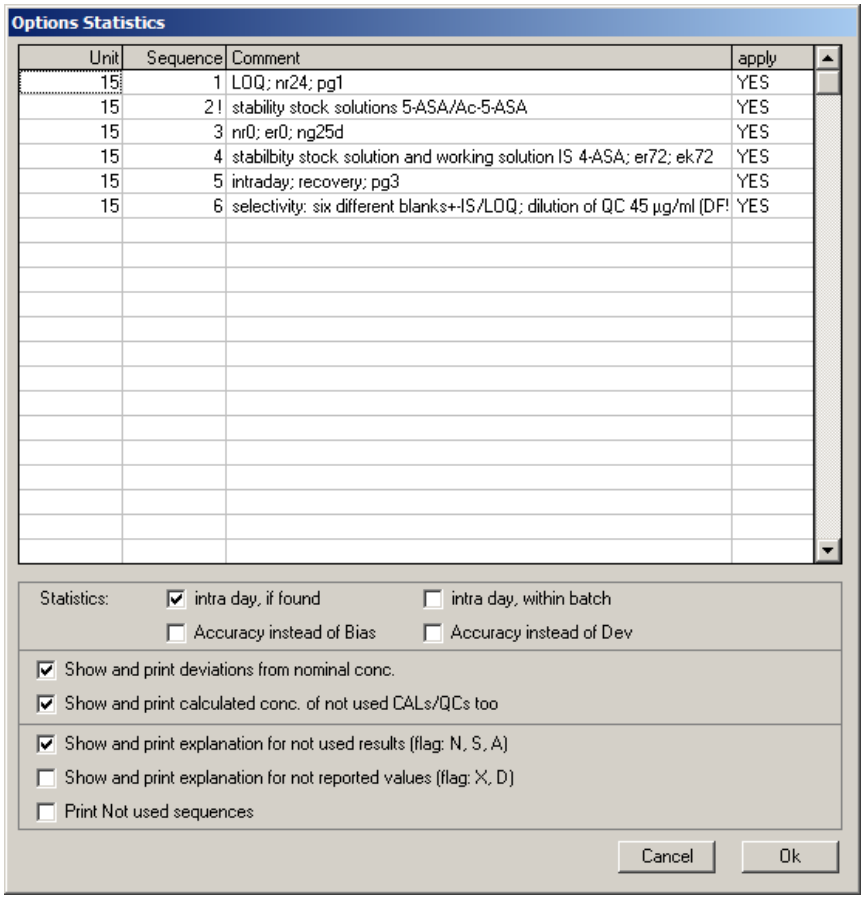
$$bias[\%] = 100\frac{calc.conc - nom.conc}{nom.conc}$$

If the program finds one (and only one) batch in which the number of QC samples is higher than in all other batches, the results of the 'intra-day' statistics for that batch are calculated and displayed in addition.

If there are some QC samples with E flag (excluded from statistics by user), dbLabCal automatically adds also the statistics including those values.

The user can take individual batches for the statistical calculations or exclude them from the statistics by clicking on the button >>> . Double-clicking or using buttons Y and N in the 'apply' columns toggles between Yes and No.
Using batches for statistics is independent of the batch status.

Only ACCEPTED batches are used for statistics by default. But it is possible to include also NOT ACCEPTED batches into the statistical evaluations.

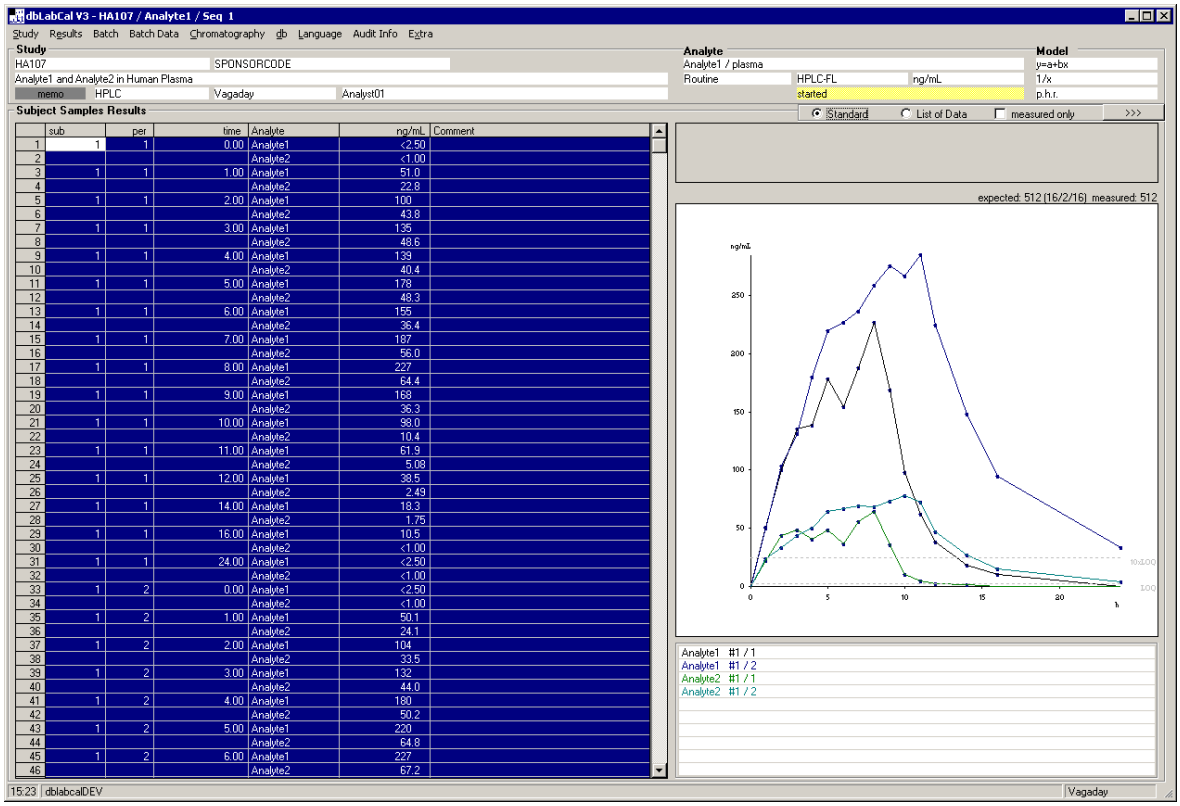


The user can hide parts of the statistical evaluation of the QC results and redisplay them or can initiate a printout of the respective chromatogram flag and the legend for the missing values (SHOW AND PRINT EXPLANATION FOR NOT...).
If SHOW AND PRINT DEVIATIONS... is selected the statistics obtained for calibration and QC samples include not only each individual result but also the corresponding percentage deviation from the nominal value.
Also, if SHOW AND PRINT CALCULATED.... is selected, the concentration for the Cals/QCs is displayed and printed with flags A or X in brackets. Of course, there is no calculated concentration for Cals/QCs with flags N or D.

If the project was measured at several units the user can also set the order of sorting (first by batch and then by unit number, or vice versa).

Subject Samples Results

The results from subjects can be displayed in four different ways (Standard, Standard/measured only, List of Data, List of Data/measured only). In the standard displays the results can also be displayed graphically. The axes are scaled automatically or the user selects fixed limits for the current analyte via the menu OPTIONS | GRAPHICS... or by double-click on the graphic.



The figure above shows the data from the marked rows. A subject should be selected by clicking on the upper left corner of the subject table. A list with all subjects in the project opens. After selection of a subject (or “all“ as the last entry) all results for the subject(s) are marked and the graphic is displayed. Then you can page through the subjects by using the keys PAGE↑ or PAGE↓, or through the subjects periods with CTRL - PAGE↑ or CTRL-PAGE↓.

The different dot colors have the following meaning:

blue	value Ok
purple	value Ok but should be repeated (R/C flag)
green	value is the result of repeat measurements
red	value is incorrect (further information in SAMPLES TO BE RE-ANALYZED and/or HINTS)

The individual periods are also identified by different line colors: black = 1st period, blue = 2nd period, green = 3rd period, magenta = 4th period, etc. The color assignments to the individual periods are shown under the graphic.

Pressing 1-9 keys (numeric pad) changes the point size and line thickness. Keeping CTRL key simultaneously with the numeric key changes also lines colors.

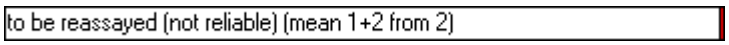
The concentration vs. time graph allows quick plausibility check of the results.

The number of expected and measured examples also helps in determining the correctness of the results obtained. (The program calculates the number of expected samples from all subjects, periods, and sampling times known so far.) If the analyst cannot explain difference between expected and measured samples it was likely due to incorrect naming of one or several subject samples. They can be found fairly quickly by ”paging” through the subjects as described above.

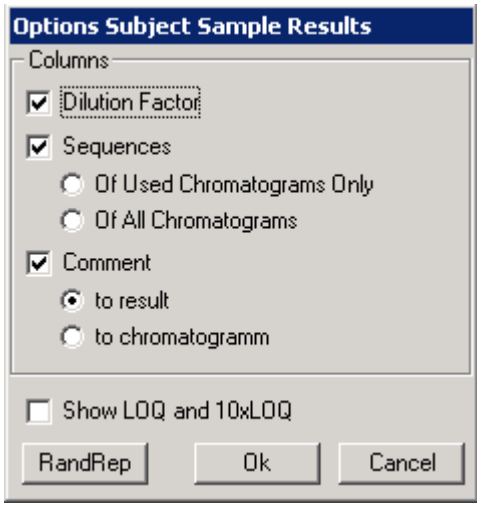
Missing samples and samples to which the analyst cannot report a value (or does not want to) are, if present, summarized and displayed in a small table. Subject samples with an ‘X’ flag are also shown as ‘missing’ if they were only measured once.

After double-click in the ‘comment’ column the user can enter a comment to each measured sample. This could include, for instance, additional information to the samples, such as coding of the sponsors.

In addition to the comment written by the analyst the program always shows the so-called ‘internal comment’ as well. The figure indicates, for instance: first sample was OK, the sample was measured twice and the average of both measurements was used as value to be reported. The user can accept or delete the ‘internal comment’. (It will nevertheless be displayed when the comment is opened again).



In addition to each subject result the dilution factor used and the batch number(s) in which the samples were measured can be displayed in the standard display via >>>
.



Dilution Factor
The dilution factor used is displayed in an additional column. Similarly, for repeatedly analyzed samples if all ‘re-assays’ were measured with the same dilution factor. No information is available if the ‘re-assays’ were measured with different dilution factors.

Batches of used chromatograms only
The batch number(s) in which the samples used for the final results were measured are shown in an additional column.

Batches of all chromatograms
Batch number(s) in which the unknown sample was measured are shown in an additional column even if the results were not used for the final result.

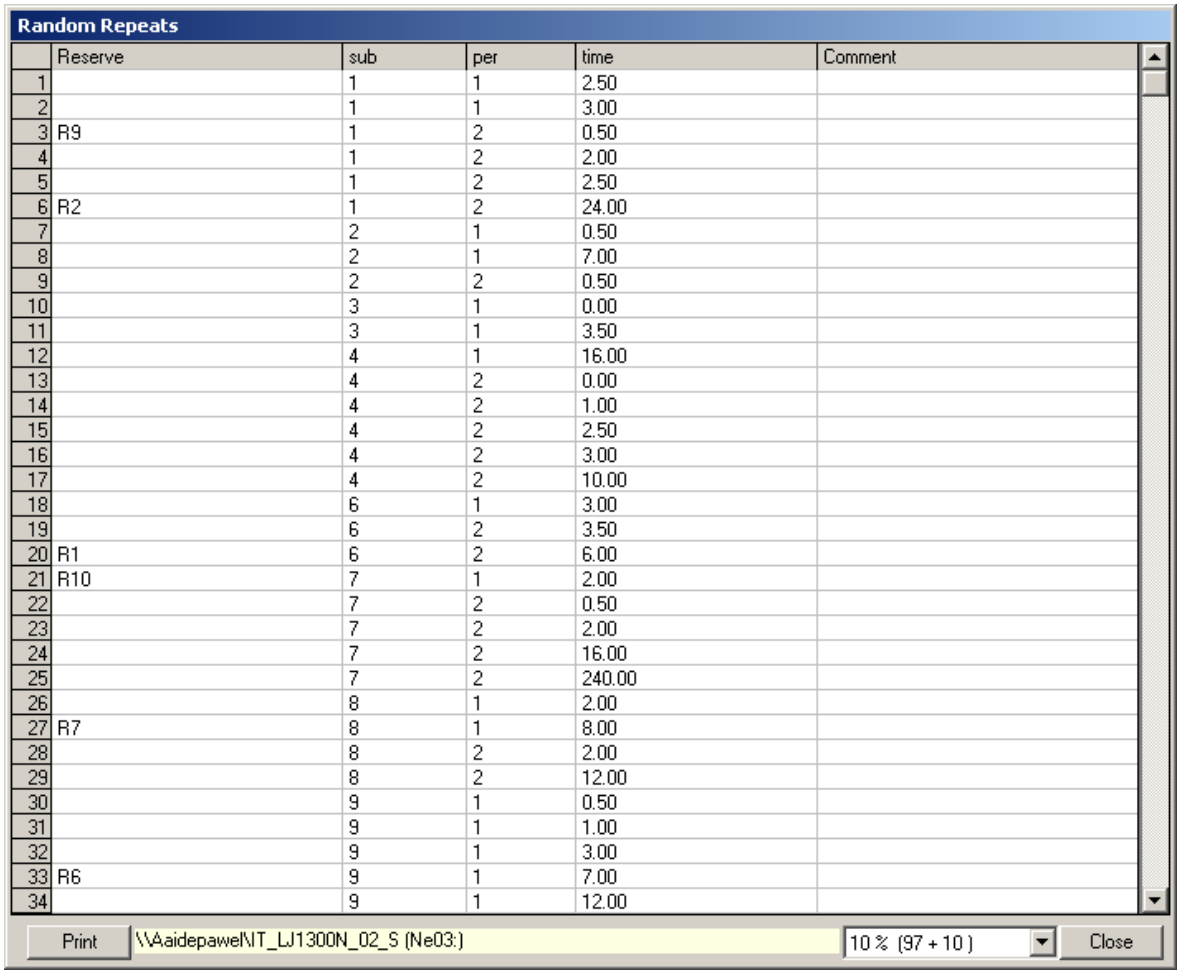
Comment
Comment column is shown or hidden.

Show LOQ and 10xLOQ
The results graphic display is shown with auxiliary lines for the quantification limit and the 10-fold value of the quantification limit.

The status line of the ‘List of Data’ display shows additional information to the sample under the table cursor.

RandRep

After click on RandRep button, the RandomRepeats dialog opens. Here it is possible to choose „Random Repeats“ or “Incurred Samples” from all until now analyzed AND selected subject samples. In addition, 10 „back-up“ samples are selected. They should be used in case that it was not possible to analyze the originally selected samples e.g. due to low sample volume.
This list can be printed.



	Reserve	sub	per	time	Comment
1		1	1	2.50	
2		1	1	3.00	
3	R9	1	2	0.50	
4		1	2	2.00	
5		1	2	2.50	
6	R2	1	2	24.00	
7		2	1	0.50	
8		2	1	7.00	
9		2	2	0.50	
10		3	1	0.00	
11		3	1	3.50	
12		4	1	16.00	
13		4	2	0.00	
14		4	2	1.00	
15		4	2	2.50	
16		4	2	3.00	
17		4	2	10.00	
18		6	1	3.00	
19		6	2	3.50	
20	R1	6	2	6.00	
21	R10	7	1	2.00	
22		7	2	0.50	
23		7	2	2.00	
24		7	2	16.00	
25		7	2	240.00	
26		8	1	2.00	
27	R7	8	1	8.00	
28		8	2	2.00	
29		8	2	12.00	
30		9	1	0.50	
31		9	1	1.00	
32		9	1	3.00	
33	R6	9	1	7.00	
34		9	1	12.00	

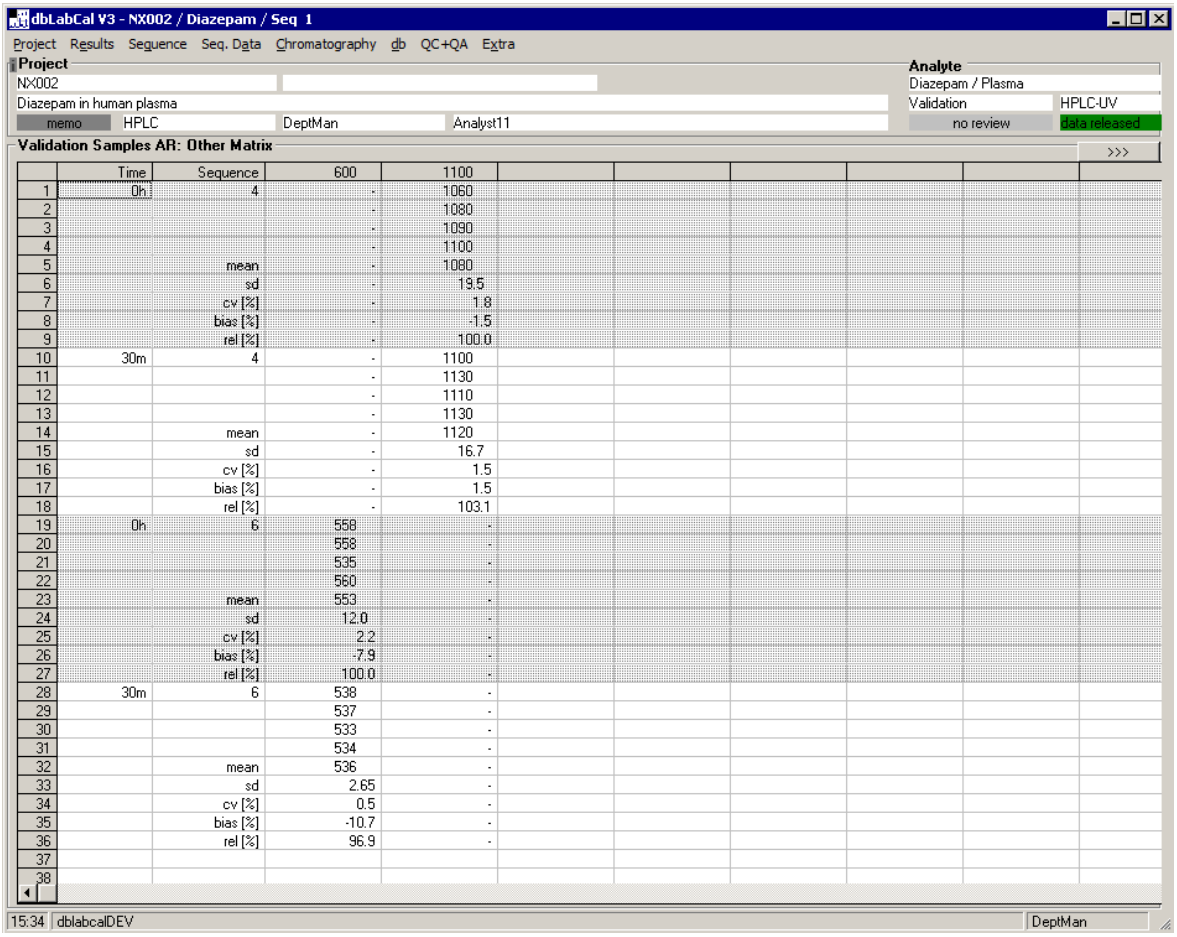
All „Random Repeats“ are marked yellow in RESULTS SUBJECT SAMPLE RESULTS, RE-ASSAYED SAMPLES and in the batch list.

Validation Samples

There are 20 “screens” available for the validation samples. These screens may be used freely for (stability) evaluations. The screens are defined by the character combinations NR, NK,…EK…PT…AG…BG, BT. Nominal concentration of the VAL sample determines the column and the time value determines the group of samples used for statistical calculations (mean, sd, cv).

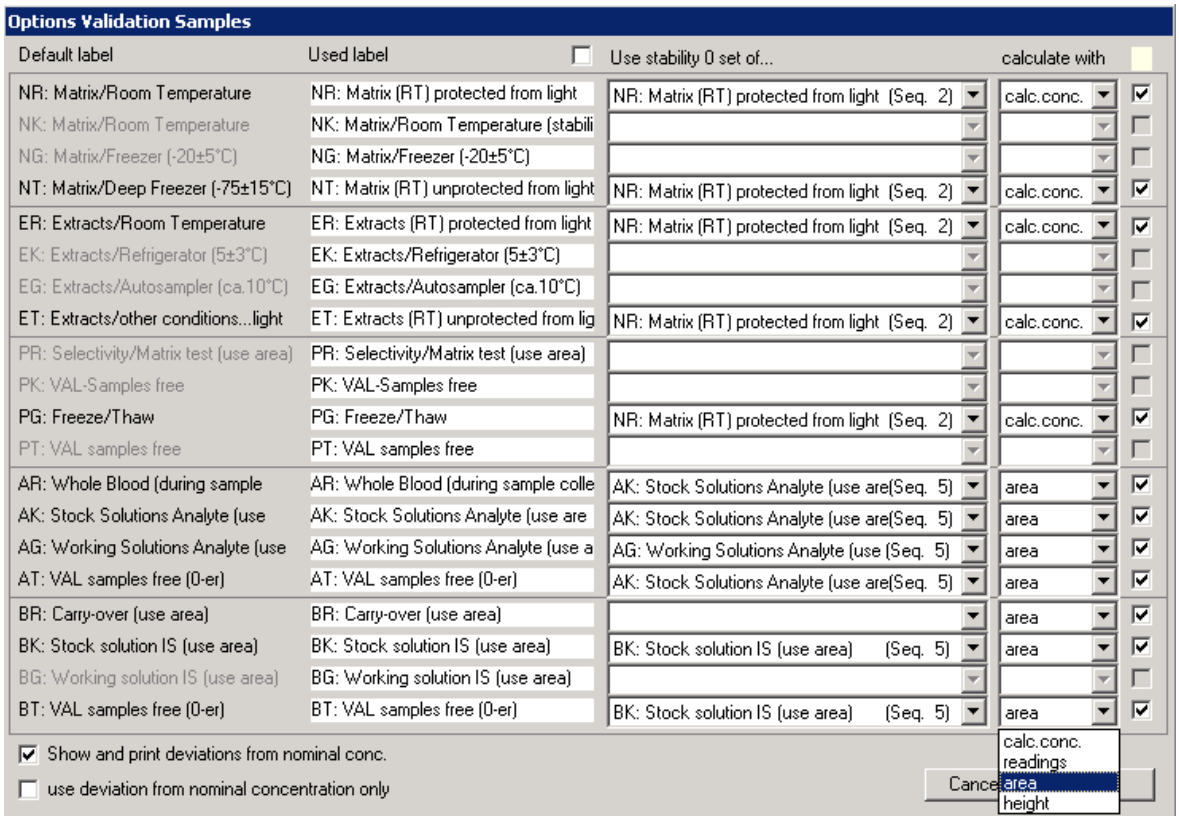
The 0 values are assigned to the individual types of stability samples as follows.

- If only one set of stability 0 values exists, it will automatically be assigned to all available “matrix/temperature“ combinations.
- If one or several sets of stability 0 values with the same combination of “matrix/temperature” exist for a given combination of “matrix/temperature”, they will be displayed together.



The “next” set of stability 0 values will automatically be set to 100% and the relative deviation of the stability values will be calculated in percent, based on this stability 0 set.

If no corresponding set of stability 0 values is available for a combination of "matrix/temperature" the analyst can manually assign the 0 values via the >>> button.



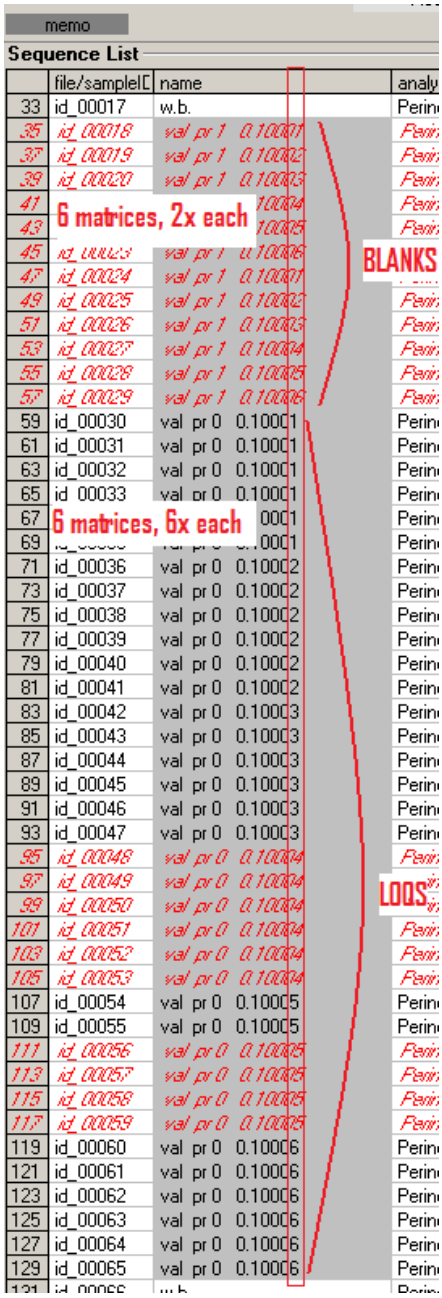
The description of the validation sample groups/types (used label) can be changed to better describe the stability data for other stability conditions and/or matrices than default. (e.g. „methanolic analyte solution at 5°C", „EDTA plasma at –80°C", „plasma with HCl at
-25°C", etc.).
Default label will be automatically used if „used label" is deleted

The user can also specify whether deviations from the nominal value will be displayed and/or the evaluation of the stability data will be done directly via the readings used for the analyte (p.h.r. or p.a.r.) , or with peak height or peak area.
If peak height or peak area is selected, dbLabCal shows automatically also internal standard results if available and possible.

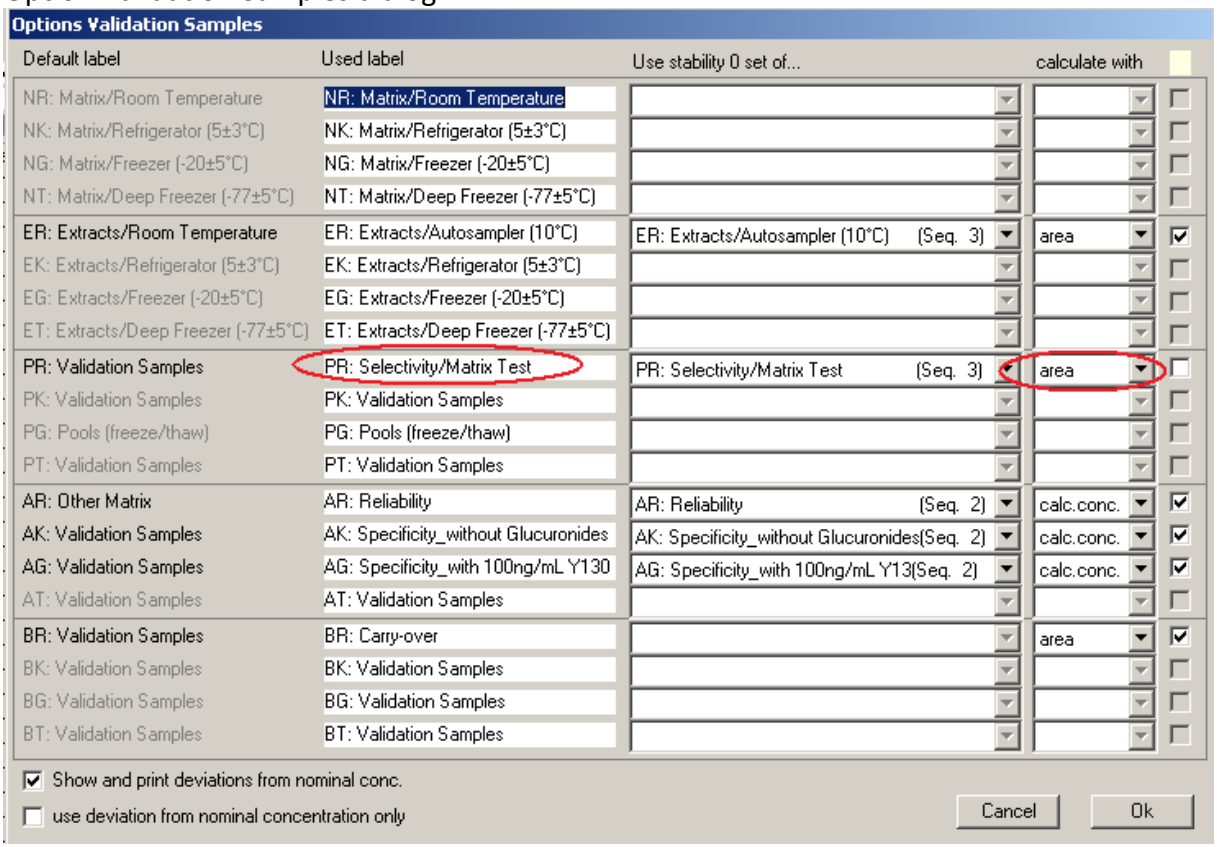
Validation Samples, special case „Matrix Test“

Following example shows matrix effect evaluation for 6 different matrix samples. Each matrix was evaluated by analysing a blank sample (2 injections) and matrix sample spiked with LOQ concentration (6 injections)

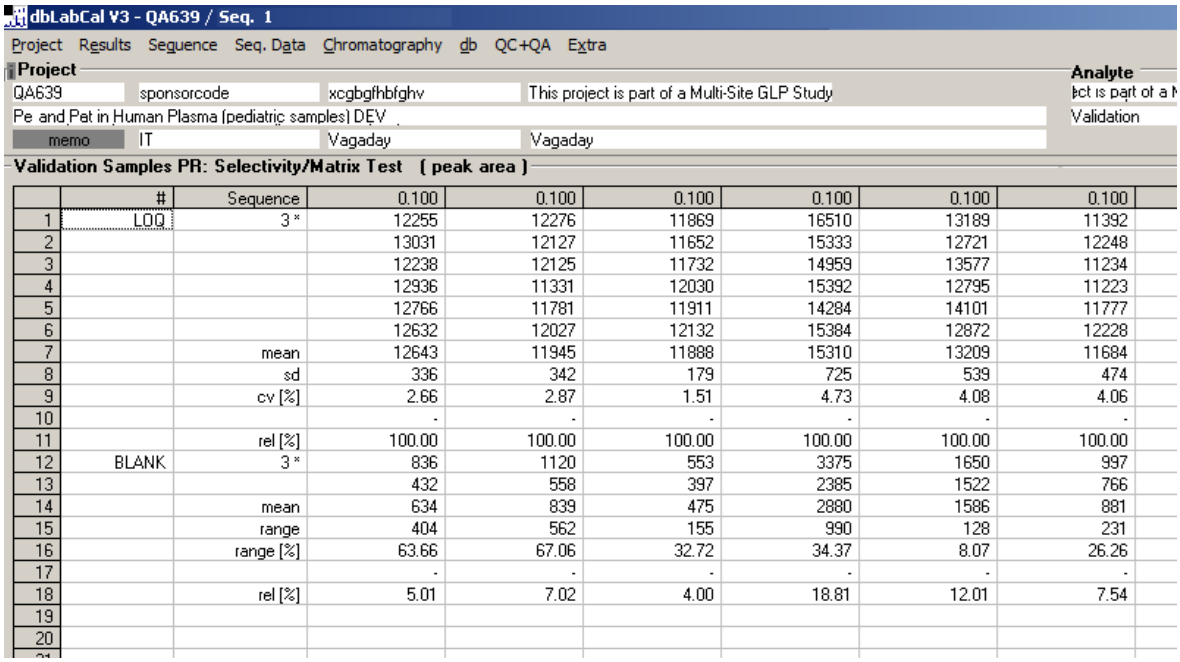
Step1: define the column position in the validation result evaluation table by adding the column position using the „hidden“ position oft he concentration value.



Step 2: enter the text „matrix“ in „Used label“ field and set „calculate with“ to „area“ in Option Validation Samples dialog.



Result:

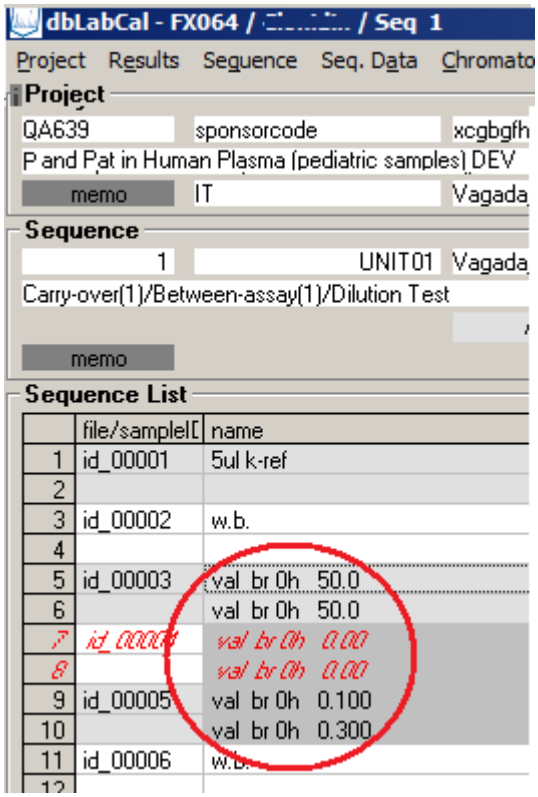


	#	Sequence	0.100	0.100	0.100	0.100	0.100	0.100
1	LOQ	3 *	12255	12276	11869	16510	13189	11392
2			13031	12127	11652	15333	12721	12248
3			12238	12125	11732	14959	13577	11234
4			12936	11331	12030	15392	12795	11223
5			12766	11781	11911	14284	14101	11777
6			12632	12027	12132	15384	12872	12228
7		mean	12643	11945	11888	15310	13209	11684
8		sd	336	342	179	725	539	474
9		cv [%]	2.66	2.87	1.51	4.73	4.08	4.06
10			-	-	-	-	-	-
11		rel [%]	100.00	100.00	100.00	100.00	100.00	100.00
12	BLANK	3 *	836	1120	553	3375	1650	997
13			432	558	397	2385	1522	766
14		mean	634	839	475	2880	1586	881
15		range	404	562	155	990	128	231
16		range [%]	63.66	67.06	32.72	34.37	8.07	26.26
17			-	-	-	-	-	-
18		rel [%]	5.01	7.02	4.00	18.81	12.01	7.54
19								
20								

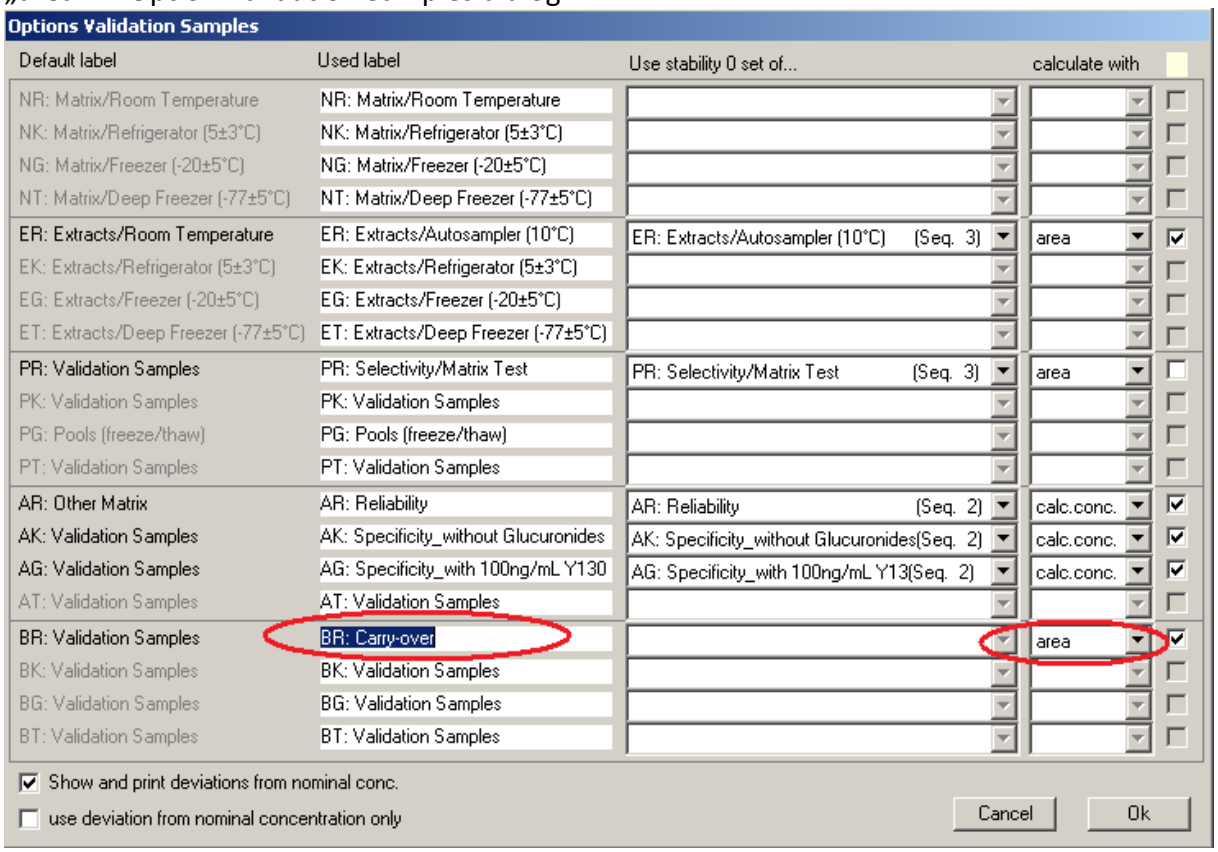
Validation Samples, special case „Carry-Over Test“

Following example shows how carry-over was evaluated in 6 different batches by injecting the samples in the sequence ULQ->BLANK->LOQ
It is also possible to inject more tha one BLANK sample e.g. ULQ->BLANK-> BLANK->LOQ…

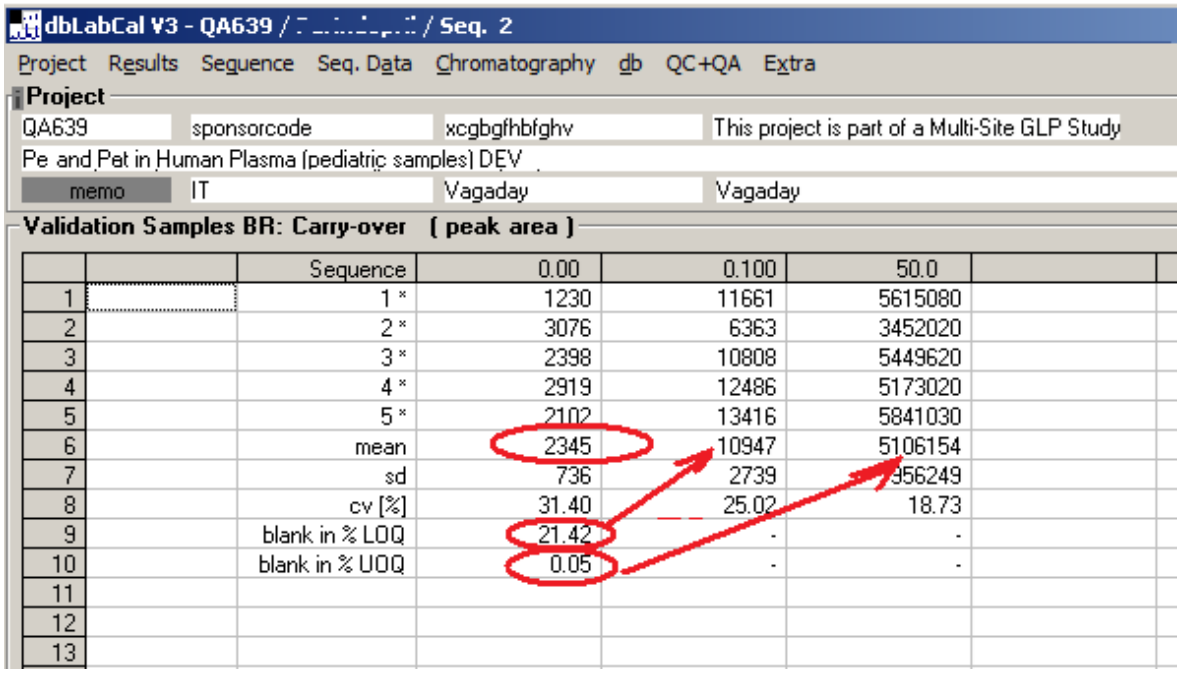
Step1:



Step 2: enter the text „carry“ and „over“ in „Used label“ field and set „calculate with“ to „area“ in Option Validation Samples dialog.



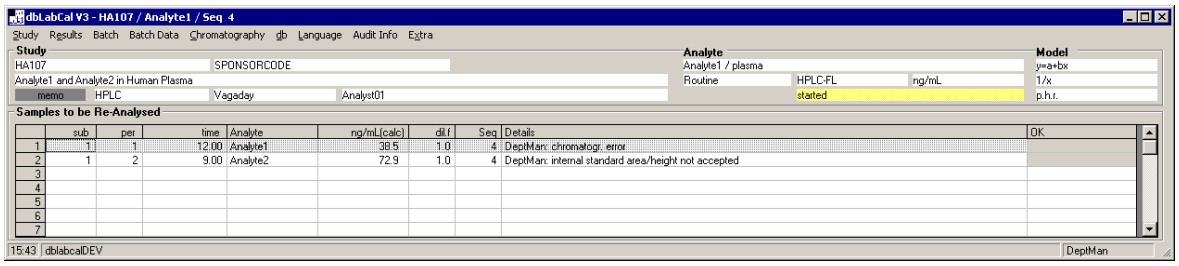
Result:



Re-Assays

Samples to be Re-analyzed

SAMPLES TO BE RE-ANALYZED shows all subject samples (chromatograms) with a flag 'N', 'R'; 'C', 'D' , 'V', '<', '>' or '+' which have not been re-analyzed yet. This list includes all chromatograms where the flag of any analyte in the chromatogram meets the above mentioned condition. Samples with the 'X' flag are ignored.



The column 'Details' shows the 'translation' of the respective chromatogram flag and the name of the analyst (for flags: 'N', 'R', 'C') or DBLABCAL (for flags: '<', '>', '+'). If a chromatogram flag was changed in VIEW | LIST the analyst should give a detailed reason in the 'comment' column. This comment to the chromatogram is also shown in here the 'Details' column.

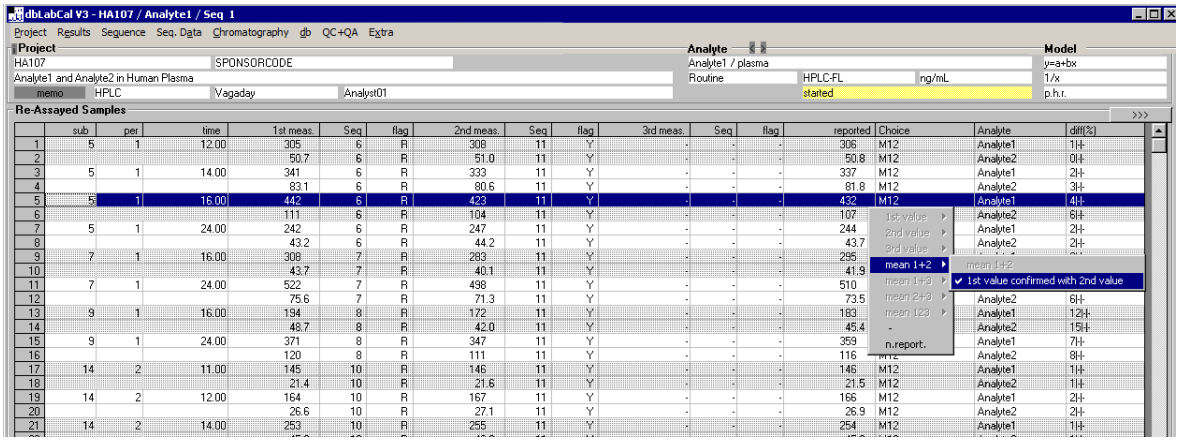
The analyst can accept the sample to be analyzed shown in the last column by double-click to confirm that the sample does not need to be re-analyzed. This, of course, is only possible if DBLABCAL has set the chromatogram flag and not the analyst.

Re-assayed Samples

RE-ASSAYED SAMPLES shows by default all standard re-assays without incurred samples.

Samples re-assayed for "standard reason" (flag N, R, D, >, <…) as well as for ISR are shown in both lists (RE-ASSAYED SAMPLES and INCURRED SAMPLES) with the respective back color (yellow or white).

Percent deviation of the re-assays is calculated and shown in the last column (sequence: 1.-2. | 2.-3. | 3.-1. measurement) and expressed in percent based on the respective mean. (See also OPTIONS RE-ASSAYS). If the individual values deviate from each other by more than specified in the dialog OPTIONS RE-ASSAYS the mean cannot be used for final result. *(but…remember the study director special wish key...)*



The analyst selects (right mouse button in the 'Choice' column) the value to be reported from re-assays. DBLABCAL shows only the allowed/accepted choices. E.g., if there is only one choice for value to be reported (e.g. 1st measurement=flag 'N', '>', '<', 'D' etc., 2. measurement=flag 'J/Y'), only this one is allowed. It is therefore recommended, and it saves several clicks, to let the reportable values be entered **automatically** first (see below).

There is also the option of not reporting any value. In this case a reason should be given in the 'comment' column in RESULTS | SUBJECT SAMPLES.

Incurred sample results are shown in a separate list/screen. Working with Incurred samples and the standard re-assay results is identical.

After the final results from re-assay was selected, the 'Choice column shows a code. The meanings of these codes are explained in the following table:

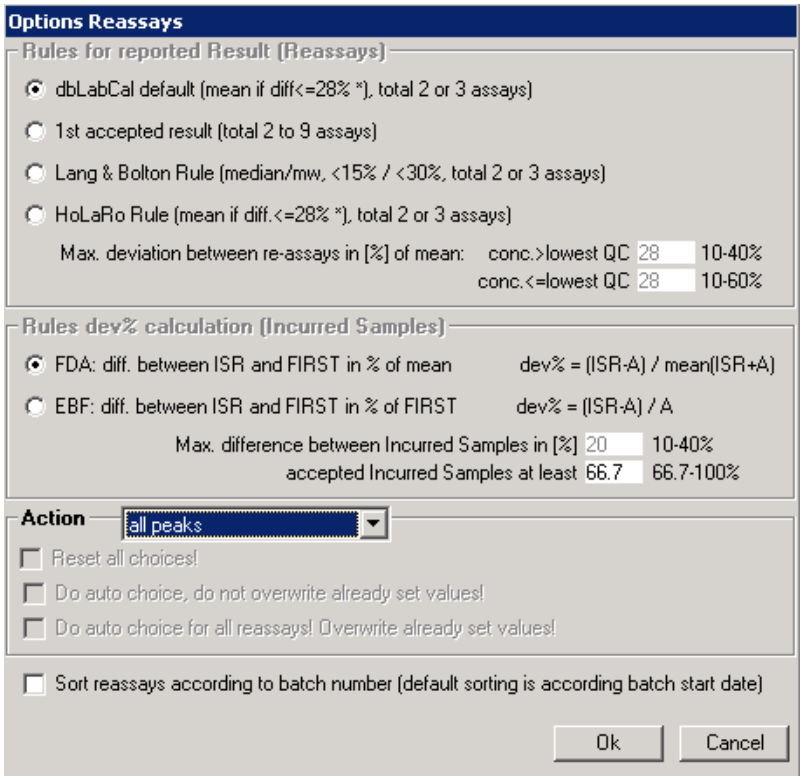
Short	Meaning
	The result of the first measurement is reported
1	- no correct second (or third) measurement
	The result of the second measurement is reported
2a	- no correct first (and third) measurement available
2b	- no reliable first measurement available
2c	- first measurement above the calibrated range
2d	- first measurement below the reduced calibrated range
	The result of the third – ninth measurement is reported
3	- no correct first and second measurements available
	The mean of two/three/four measurements is reported
M12	- first measurement confirmed by second measurement *)
M13	- first measurement confirmed by third measurement *)
M23	- second measurement confirmed by third measurement *)
M123	- first and second measurements confirmed by third measurement *)
M14	Etc.
M24	
M34	
M124	
M134	
M234	
M1234	

*) Difference of individual measurements is less than the value selected in the dialog OPTIONS | RE-ASSAYS.

After selecting the first submenu, or if this selection was done according to Lang&Bolton, the 'Choice' column does not show any of the above codes but only the information which result is reported (1st value, 2nd value, mean 1+2, mean123 etc.)

After click on >>> the Re-assay Option dialog is shown. In this dialog the PI/study director can chose the re-assay reporting rule, set the acceptance criteria for incurred samples as well as start automatic choice of final result.
Following reporting rules are possible:
- dbLabCal rule (confirmed mean, otherwise next assay is required …)
- first accepted result is reported
- according Lang/Bolton rule
  (J.R.Lang and S.Bolton, J.Pharm.Biomed.Anal. **9**, 357-361 (1991), see Att. 14)
- according HoLaRo rule, see Att. 15

PI/study director also define the accepted deviation [%] of the individual results from their mean. The user can define various acceptable deviations. If a result is less than or equal to the lowest QC the corresponding criterion is applied. Both criteria are set to 28% by default when defining a new project.



The automatic choice of final results is controlled in the **Action** part of the dialog.
Either the not yet set re-assays (2nd checkbox) can be set automatically or all „re-assays“ are set automatically (3rd checkbox). In that case dbLabCal will „overwrite“ already user set choice or even remove the currently set choice in case no distinct result exists.

If only one ”valid” result is available from the samples that were re-assayed, it will be automatically reported.

Criterion for selecting final result from two (or three) valid measurements (chromatogram flag: J, R/C) is the difference of the (two) values expressed in percent of their mean value. If the difference is less than the value selected in OPTIONS REASSAY the mean is calculated, otherwise no automatic selection occurs.

At first accepted result rule the first valid assay (Chromatogramm flag: J, 0, W/R) is reported.
Flow chart of the Lang&Bolton and HoLaRo rules are in attachments 14 and 15, respectively.

If more than maximally allowed measurements (3, 4 or max.9) were found (see HINTS) the analyst or the PI/study director must decide which three or four chromatograms are to be evaluated. The other chromatograms should be renamed (e.g. to DIV).

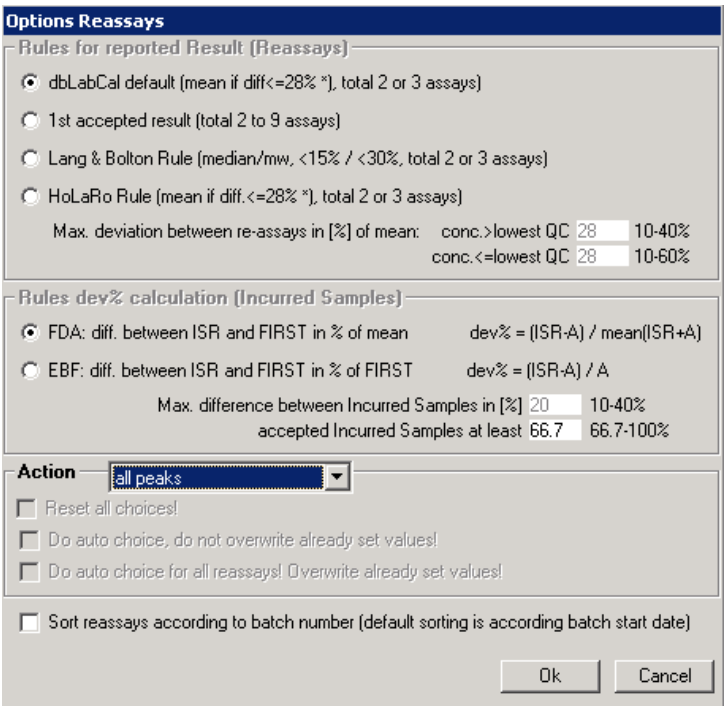
Multiple measurements where all concentrations were <LOQ are also shown here as an overview. If all LOQs (after taking the dilution factor into account) were identical, <LOQ is automatically taken as value to be reported and cannot be changed. If the LOQs, after taking the dilution factor into account, are different the analyst must decide which LOQ value will be reported.

It is not possible to choose final result, if the cell's back color is grey, It is the case if all concentrations were <LOQ or if another user with higher authorization have made the choice. The user name who have choosen the final result is shown automatically in the tooltips

Incurred Samples

In this list re-assays performed for ISR are shown.

Samples re-assayed for "standard reason" (flag N, R, D, >, <…) as well as for ISR are shown in both lists (RE-ASSAYED SAMPLES and INCURRED SAMPLES) with the respective back color (yellow or white).



Rules and acceptance criteria for Incurred Samples acceptance are defined in the middle part of the dialog.
Accepted deviation valid for incurred samples is in general different than the "standard re-assay" deviation (20%, 28% respectively).

Furthermore, dbLabCal checks if at least 2/3 of the Incurred Samples fulfilled the max. accepted deviation criterion

Excluded Values

This includes
- all NOT USED CALs, QCs and VALs,

i.e. calibration, QC or validation samples with flags 'N' or 'A/E',
- NOT USED BATCHES (status BATCH NOT ACCEPTED or EXCLUDED) and
- NOT USED CHROMATOGRAMS ('X' flag).

Date of Analyses

The menu option DATE OF ANALYSES shows the project performace. Extraction dates, start and end of batch measurements and the comments to each batch can be edited here. In addition, the unit and batch numbers can be directly modified.

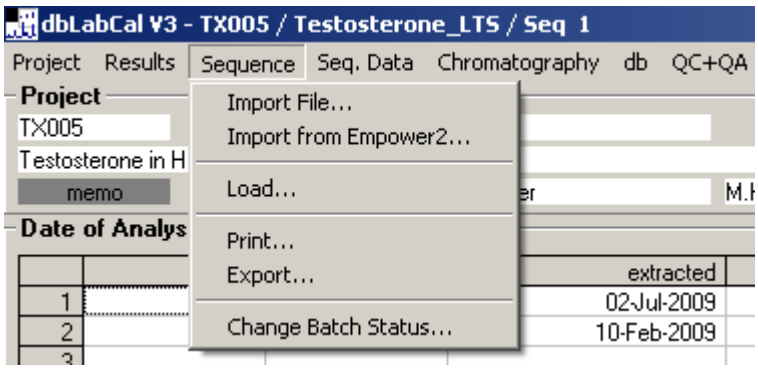
The comment should also include information to the samples measured in the batch, e.g. 'subjects 5 and 6', Cal/QC set numbers, 'stability 48h' etc., but not the batch number.

If the project was measured at several units the user can specify the sorting batch (first by batch number and then by unit number, or vice versa) by clicking on >>> .

DBLABCAL accept also date-related terms, such as "today, yesterday, day before yesterday, x days ago, Monday (or Mo), Tuesday (Tu) " etc. – like everywhere in the program where date-related information is required.

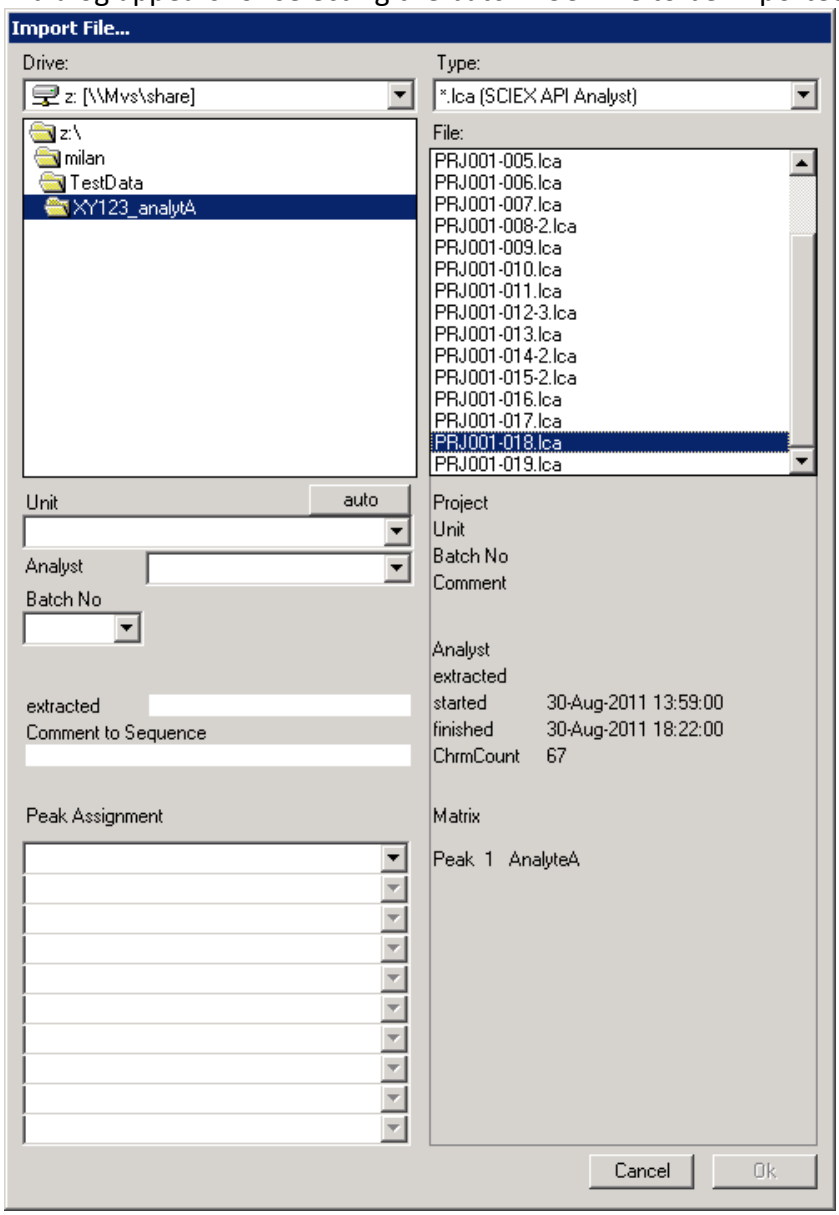
Batch Menu

Batches and batch data are managed via the Batch menu.

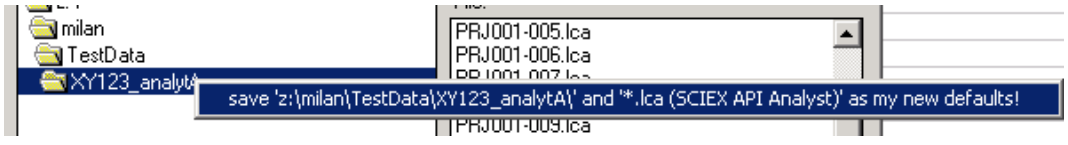


Import File...

A dialog appears for selecting the batch ASCII file to be imported.



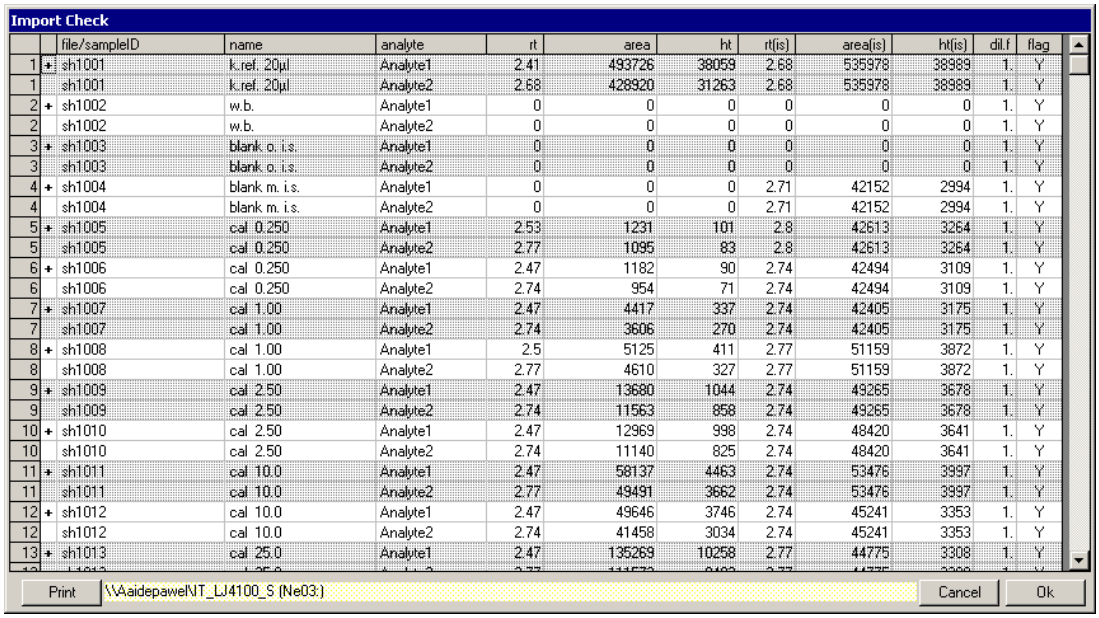
User can save currently selected data folder as start folder for next imports by right mouse click on the folder list:



Currently selected data folder is saved as start folder for next imports after successful import automatically.

All available information to the selected file is shown on the right side of the dialog.

Prior to importing an ASCII file a dialog with the content of the file to be imported is shown:



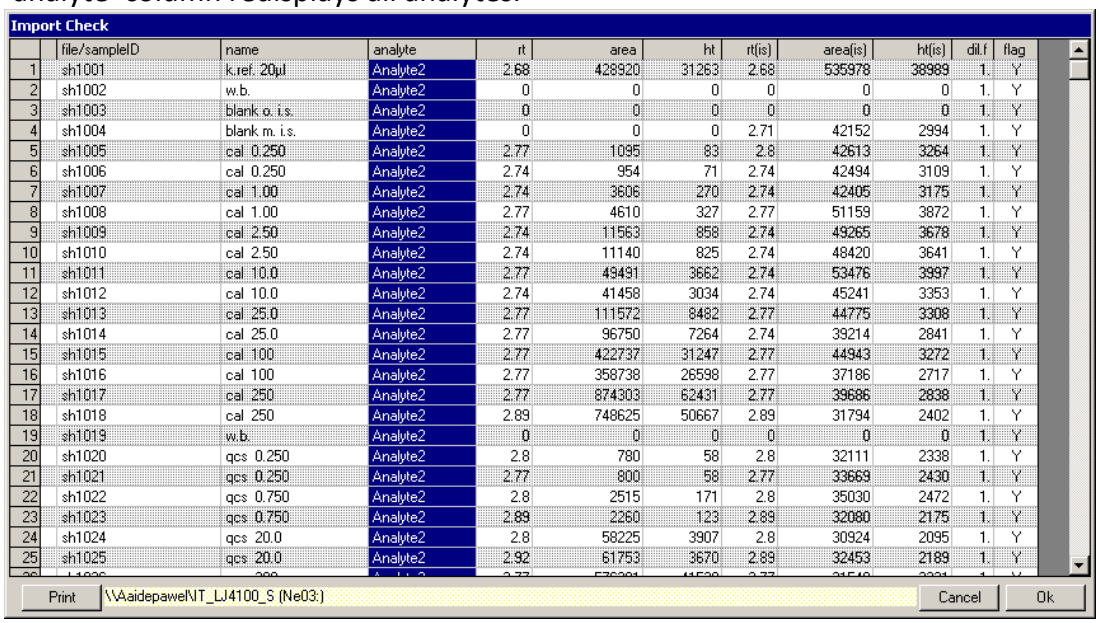
Import Check

		file/sampleID	name	analyte	rt	area	ht	rt(is)	area(is)	ht(is)	dil.f	flag
1	+	sh1001	k.ref. 20µl	Analyte1	2.41	493726	38059	2.68	535978	38989	1.	Y
1		sh1001	k.ref. 20µl	Analyte2	2.68	428920	31263	2.68	535978	38989	1.	Y
2	+	sh1002	w.b.	Analyte1	0	0	0	0	0	0	1.	Y
2		sh1002	w.b.	Analyte2	0	0	0	0	0	0	1.	Y
3	+	sh1003	blank o. i.s.	Analyte1	0	0	0	0	0	0	1.	Y
3		sh1003	blank o. i.s.	Analyte2	0	0	0	0	0	0	1.	Y
4	+	sh1004	blank m. i.s.	Analyte1	0	0	0	2.71	42152	2994	1.	Y
4		sh1004	blank m. i.s.	Analyte2	0	0	0	2.71	42152	2994	1.	Y
5	+	sh1005	cal 0.250	Analyte1	2.53	1231	101	2.8	42613	3264	1.	Y
5		sh1005	cal 0.250	Analyte2	2.77	1095	83	2.8	42613	3264	1.	Y
6	+	sh1006	cal 0.250	Analyte1	2.47	1182	90	2.74	42494	3109	1.	Y
6		sh1006	cal 0.250	Analyte2	2.74	954	71	2.74	42494	3109	1.	Y
7	+	sh1007	cal 1.00	Analyte1	2.47	4417	337	2.74	42405	3175	1.	Y
7		sh1007	cal 1.00	Analyte2	2.74	3606	270	2.74	42405	3175	1.	Y
8	+	sh1008	cal 1.00	Analyte1	2.5	5125	411	2.77	51159	3872	1.	Y
8		sh1008	cal 1.00	Analyte2	2.77	4610	327	2.77	51159	3872	1.	Y
9	+	sh1009	cal 2.50	Analyte1	2.47	13680	1044	2.74	49265	3678	1.	Y
9		sh1009	cal 2.50	Analyte2	2.74	11563	858	2.74	49265	3678	1.	Y
10	+	sh1010	cal 2.50	Analyte1	2.47	12969	998	2.74	48420	3641	1.	Y
10		sh1010	cal 2.50	Analyte2	2.74	11140	825	2.74	48420	3641	1.	Y
11	+	sh1011	cal 10.0	Analyte1	2.47	58137	4463	2.74	53476	3997	1.	Y
11		sh1011	cal 10.0	Analyte2	2.77	49491	3662	2.74	53476	3997	1.	Y
12	+	sh1012	cal 10.0	Analyte1	2.47	49646	3746	2.74	45241	3353	1.	Y
12		sh1012	cal 10.0	Analyte2	2.74	41458	3034	2.74	45241	3353	1.	Y
13	+	sh1013	cal 25.0	Analyte1	2.47	135269	10258	2.77	44775	3308	1.	Y

Print | \\Aaidepawel\NT_LJ4100_S (Ne03:) | Cancel | Ok

In this dialog, it is possible to include / exclude single chromatograms from import by clicking on + sign in the first column (include: **+**, exclude: **-**).

If more than one analyte were measured in a chromatogram double-clicking in the 'analyte' column reduces the display to only one analyte. A second double-click in the 'analyte' column redisplays all analytes.



Import Check

	file/sampleID	name	analyte	rt	area	ht	rt(is)	area(is)	ht(is)	dil.f	flag
1	sh1001	k.ref. 20µl	Analyte2	2.68	428920	31263	2.68	535978	38989	1.	Y
2	sh1002	w.b.	Analyte2	0	0	0	0	0	0	1.	Y
3	sh1003	blank o. i.s.	Analyte2	0	0	0	0	0	0	1.	Y
4	sh1004	blank m. i.s.	Analyte2	0	0	0	2.71	42152	2994	1.	Y
5	sh1005	cal 0.250	Analyte2	2.77	1095	83	2.8	42613	3264	1.	Y
6	sh1006	cal 0.250	Analyte2	2.74	954	71	2.74	42494	3109	1.	Y
7	sh1007	cal 1.00	Analyte2	2.74	3606	270	2.74	42405	3175	1.	Y
8	sh1008	cal 1.00	Analyte2	2.77	4610	327	2.77	51159	3872	1.	Y
9	sh1009	cal 2.50	Analyte2	2.74	11563	858	2.74	49265	3678	1.	Y
10	sh1010	cal 2.50	Analyte2	2.74	11140	825	2.74	48420	3641	1.	Y
11	sh1011	cal 10.0	Analyte2	2.77	49491	3662	2.74	53476	3997	1.	Y
12	sh1012	cal 10.0	Analyte2	2.74	41458	3034	2.74	45241	3353	1.	Y
13	sh1013	cal 25.0	Analyte2	2.77	111572	8482	2.77	44775	3308	1.	Y
14	sh1014	cal 25.0	Analyte2	2.77	96750	7264	2.74	39214	2841	1.	Y
15	sh1015	cal 100	Analyte2	2.77	422737	31247	2.77	44943	3272	1.	Y
16	sh1016	cal 100	Analyte2	2.77	358738	26598	2.77	37186	2717	1.	Y
17	sh1017	cal 250	Analyte2	2.77	874303	62431	2.77	39686	2838	1.	Y
18	sh1018	cal 250	Analyte2	2.89	748625	50667	2.89	31794	2402	1.	Y
19	sh1019	w.b.	Analyte2	0	0	0	0	0	0	1.	Y
20	sh1020	qcs 0.250	Analyte2	2.8	780	58	2.8	32111	2338	1.	Y
21	sh1021	qcs 0.250	Analyte2	2.77	800	58	2.77	33669	2430	1.	Y
22	sh1022	qcs 0.750	Analyte2	2.8	2515	171	2.8	35030	2472	1.	Y
23	sh1023	qcs 0.750	Analyte2	2.89	2260	123	2.89	32080	2175	1.	Y
24	sh1024	qcs 20.0	Analyte2	2.8	58225	3907	2.8	30924	2095	1.	Y
25	sh1025	qcs 20.0	Analyte2	2.92	61753	3670	2.89	32453	2189	1.	Y

Print | \\Aaidepawel\NT_LJ4100_S (Ne03:) | Cancel | Ok

After click on AUTO button, DBLABCAL suggests the required batch data like batch number, unit, analyst name as well as the peaks assignments as good as possible.
The user has to check the proposed values and enter the missing data. DBLABCAL supports the user in that OK button is allowed only if the batch data are complete and reasonable.

It is important that all files for analytes analyzed in one chromatogram be imported TOGETHER at the first batch import. This way, the information, how many and which analytes belongs together (were analyzed in one run) is saved in dbLabCal!

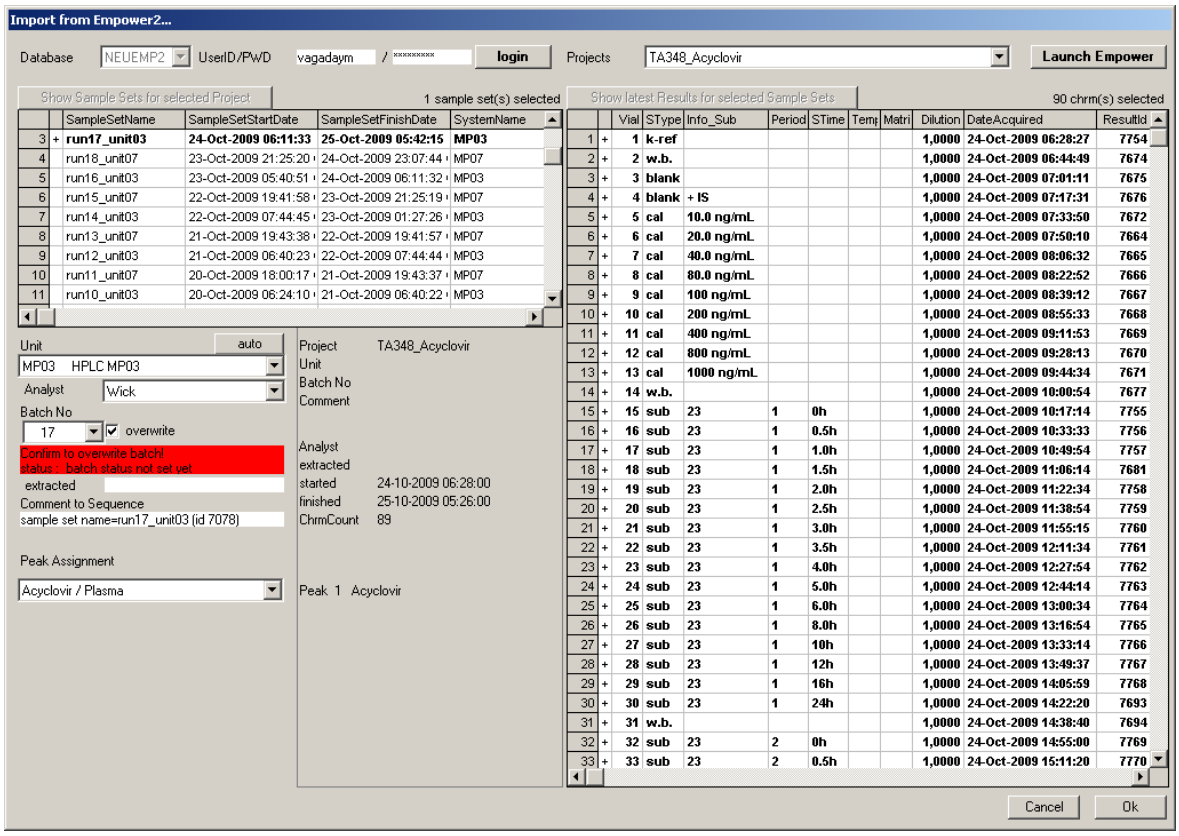
DBLABCAL allows import (OK button) at next batch imports only if the analyte count in the file fits to the database known analyte count.

It is almost impossible to import an file into an 'wrong' project.

Import from Empower2...

It may be possible to import data from Empower2 into dbLabCal directly, if Empower2 and dbLabCal are installed on a PC, and if the administrator has allowed this function.

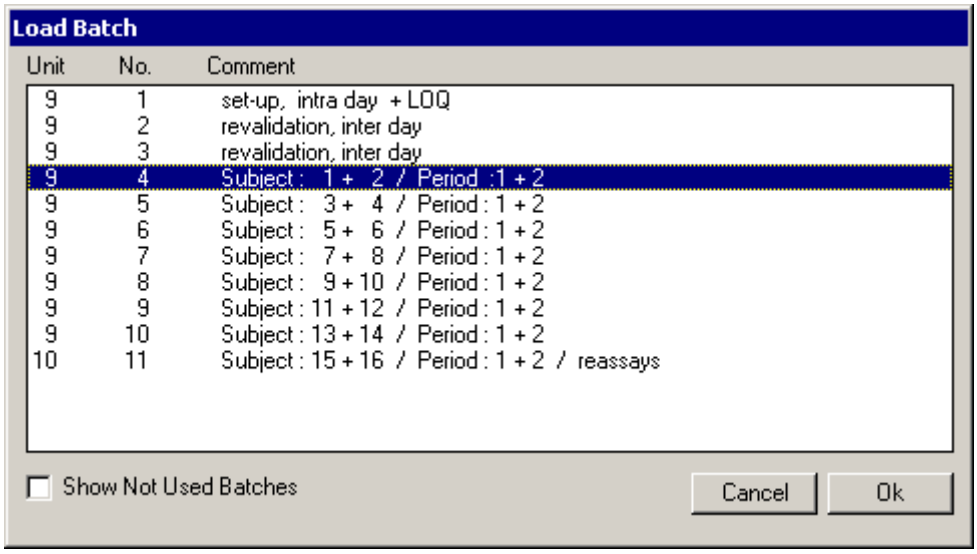
The user has to log-in with his Empower2 account into Empower2 in this dialog. He loads a Project, one or more Sample Sets and finally the Results. After completion the missing data entry (button AUTO) the selected Results (**+**) areimported into dbLabCal.



To open the current Empower2 Project click LAUNCH EMPOWER button.

Load...

A list of all batches in the current project (and for the current analyte) is displayed.



Batches are sorted by unit number and batch number.

The batch number is (sometimes) followed by a character which indicates the batch status:

* status undetermined
batch accepted
N batch not accepted
X batch excluded
D batch marked as deleted (overwritten)
L batch was locked by PI
or project was released and then project status reset to "started" since dbLabCal locks all batches when status is set to released automatically

The meaning of batch status is described further below.

An exclamation mark (!) after the batch number indicates that (at least) one analyte did not meet the acceptance criteria applicable to the current project.

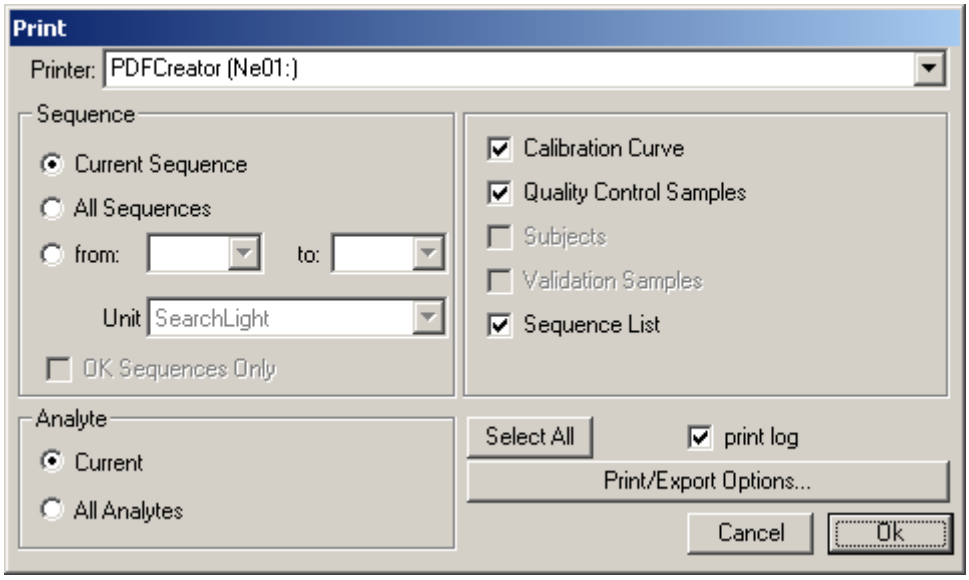
The display of overwritten and excluded batchs can be activated via the option SHOW NOT USED BATCHES.

Quick access: double-clicking anywhere within the screen section 'batch'.

The next or the previous batch can also be loaded directly via "paging" (keys CTRL – + or CTRL –; PLUS/MINUS keys on the numerical key pad - in a batch view) without first opening the dialog LOAD BATCH...

Print...

Data from the current batch or from all other batches can be printed irrespective of their status. However, for documentation purposes, only printouts of batchs with a project status **‚released'** should be used. If several analytes in a chromatogram were measured in a project the user can print the selected data either for the current analyte only or simultaneously for all analytes that were measured together with the current analyte in a chromatogram.



Printouts from calibration and quality control samples and the complete batch list are sufficient for documentation of the batch data. Data to subject or validation samples are documented on the printouts of the project results..

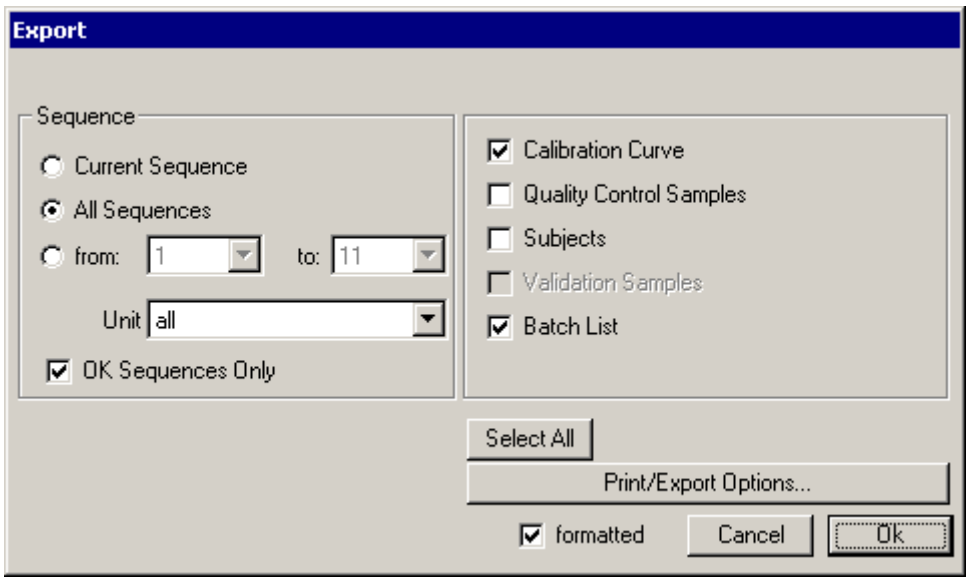
Select all options with SELECT ALL, or de-select all options with CTRL- SELECT ALL.

The appearance of the printout, e.g. font, font size, margins, shading etc., can be modified here in the Print dialog or via the menu PROJECT | OPTIONS | PRINT/EXPORT OPTIONS.

The current standard Windows printer is displayed and can be changed here as well.

Export...

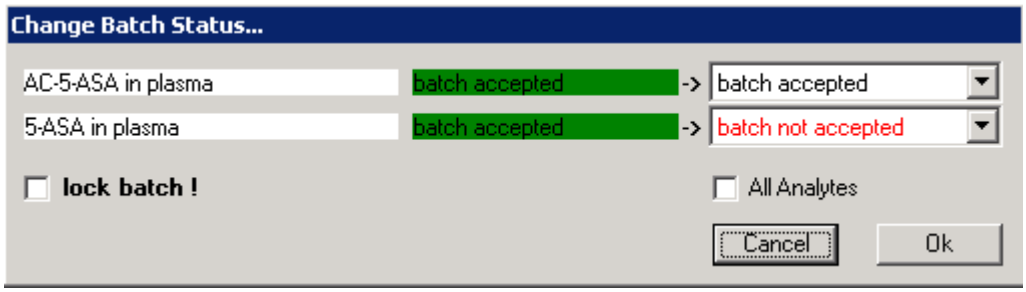
Same procedure as described for BATCH | PRINT. Only data for the current analyte can be exported.



Furthermore, the current data can be exported at any time via the Windows clipboard (keys CTRL-C or CTRL-INSERT or with the right mouse click (for selected data) into other programs.

Change Batch Status...

Batch status can be changed for each analyte individually. It means, that it is possible to accept batch data for one analyte, while rejecting the data for another analyte (due to not fulfilled acceptance criteria) of the same batch.
Batch status from/to BATCH EXCLUDED is always performed for all analytes of one chromatogram.



	Text	Comment	Is set...
*	Status undetermined!	After import each batch is automatically set to status '*'	automatically
(Y)	Batch accepted	Can be set by analyst if the batch met the **acceptance criteria**. Can (theoretically) be set by PI/study director even where the acceptance criteria have not been met.	by analyst or PI/study director
N	Batch not accepted	Is set whenever the batch does not meet the valid **acceptance criteria**. The subject samples measured in this batch are shown in SAMPLES TO BE RE-ANALYZED.	by analyst or PI/study director
X	Batch excluded	Example:"system set-up" batch or a batch that was not evaluated for other reasons... This batch is ignored in the evaluation.	by analyst or PI/study director
D	Batch deleted	A new batch (with the same batch number) was imported. This batch is ignored in the evaluation.	Automatically
L	Batch locked	Project was released and then project status reset to "started" since dbLabCal keeps batch status "locked" even if project status was reset. PI/study director have to remove batch lock explicitly if needed	Automatically or PI/study director

Changing the batch status is an action with far reaching consequences!
(At least for the analyst...)

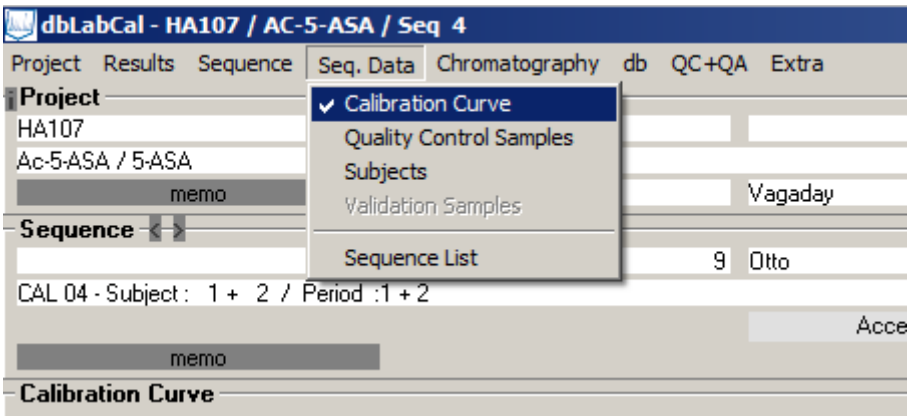
If the batch is set to status BATCH ACCEPTED, DBLABCAL checks whether the calibration curve, QC samples and r^2 met the current acceptance criteria.
If the acceptance criteria were not met the batch release is aborted. Only the PI/study director has authority to set such a batch to status BATCH ACCEPTED.

Quick access: right mouse button over status....

Batch Data Menu

shows several views of the current batch data.

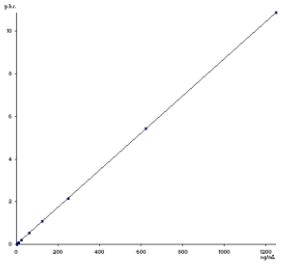
Standars, QCs, Subjects and Validation Samples...



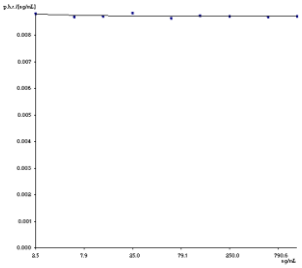
The user can view the calibration curve or quality control samples of the current batch with graphics. Red dots indicate that the deviation from the nominal concentration is higher than specified in the menu PROJECT | OPTIONS | ACCEPTANCE CRITERIA.

By holding down the CTRL key and clicking on the figure the calibration curve is sequentially shown in three different ways:

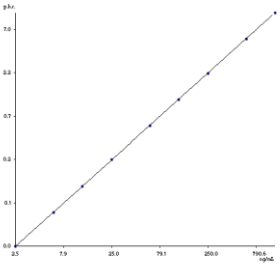
x: concentration
y: readings



x: concentration, logarithmic
y: readings/concentration



x: concentration, logarithmic
y: readings, logarithmic



The subject samples and validation samples measured in the current batch can also be viewed.

There is a difference between subject samples and validation samples shown here and those from the RESULTS menu. The menu RESULTS (of the project) summarizes the values to be reported (re-assays evaluated, flag 'Y' etc...) whereas the menu VIEW (of batch data) shows only the values measured in the current batch, irrespective of re-assays or flags and samples that were measured in other batches.

In subject view, as in RESULTS | SUBJECT SAMPLES the values can also be displayed graphically. Red colored dots indicate only that the flag is not 'Y'.

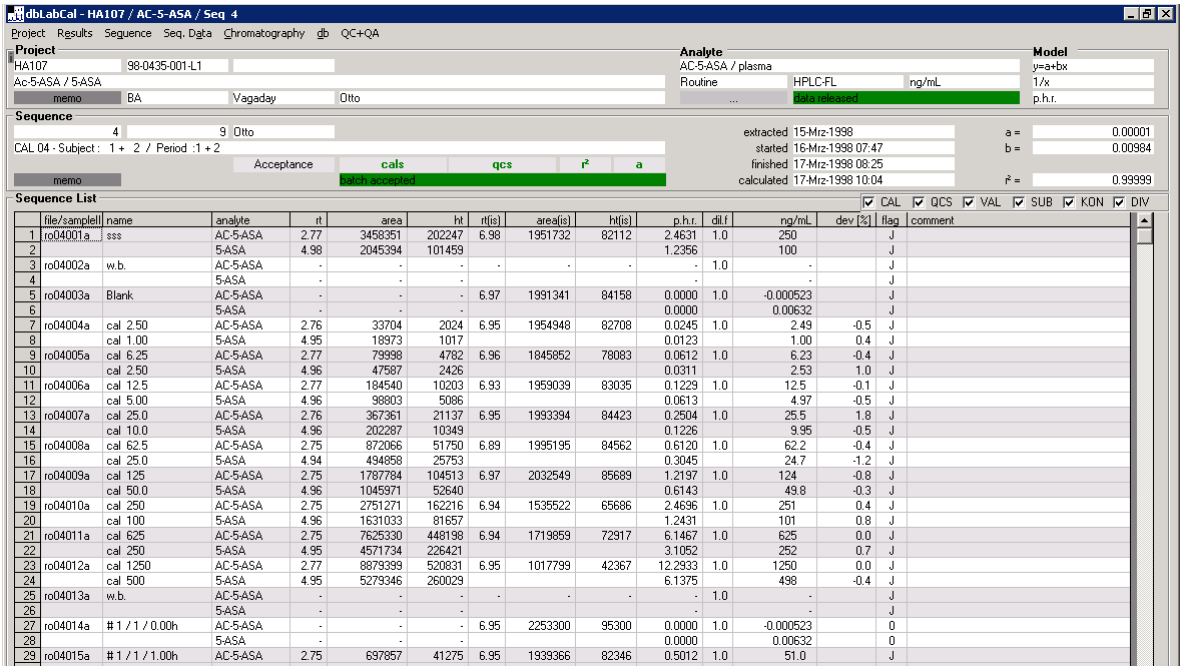
The subject results display of a batch can be used to view the results after importing the batch, for instance, in order to immediately recognize 'not plausible results' and set the 'R' flags.

The user can edit unit number, batch number, comment, extraction date as well as date and time of start and end of the current batch In menu RESULTS | DATE OF ANALYSES. Information to the start of the batch is very important since a subsequent validation defines the set of 0 values for the stability studies and the order of re-assays for subject results.

Furthermore, by pressing the right mouse button over the first (gray) table row in BATCH DATA view the number of decimal digits for the display of values in the respective column can be quickly changed. The number of significant digits can only be changed via the menu PROJECT | OPTIONS | NUMBER FORMAT.

Batch List

A complete list of the chromatography data of the current batch for all analytes measured in a chromatogram is displayed in the order in which they were measured. Sample name and chromatogram flags can be modified by the analyst as long as the batch status is ‘not set yet’.



dbLabCal - HA107 / AC-5-ASA / Seq 4

Project Results Sequence Seq. Data Chromatography db QC+QA

Project: HA107 | 98-0435-001-L1 | Ac-5-ASA / 5-ASA | memo | BA | Vagaday | Otto

Analyte: AC-5-ASA / plasma | Routine | HPLC-FL | ng/mL | ... | data released

Model: y=a+bx | 1/x | p.h.r.

Sequence: 4 | 9 | Otto | CAL 04 - Subject : 1 + 2 / Period :1 + 2 | Acceptance | cals | qcs | r² | a | memo | batch accepted

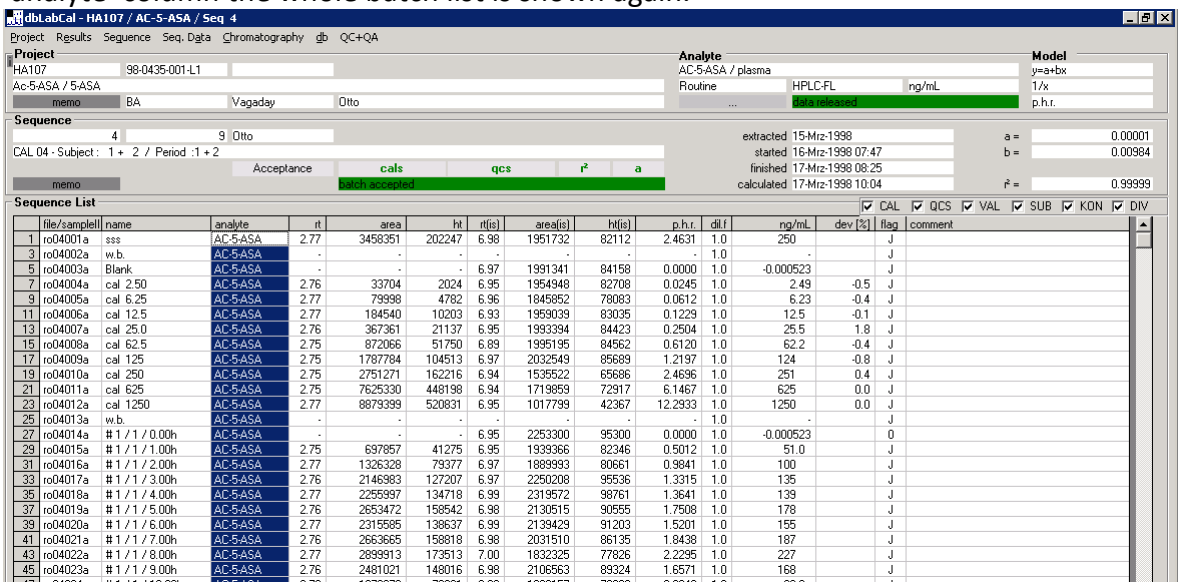
extracted 15-Mrz-1998 | started 16-Mrz-1998 07:47 | finished 17-Mrz-1998 08:25 | calculated 17-Mrz-1998 10:04

a = 0.00001 | b = 0.00984 | r² = 0.99999

Sequence List — CAL QCS VAL SUB KON DIV

	file/sampleID	name	analyte	rt	area	ht	rt(is)	area(is)	ht(is)	p.h.r.	dil.f	ng/mL	dev [%]	flag	comment
1	ro04001a	sss	AC-5-ASA	2.77	3458351	202247	6.98	1951732	82112	2.4631	1.0	250		J	
2			5-ASA	4.98	2045394	101459				1.2356		100		J	
3	ro04002a	w.b.	AC-5-ASA	-	-	-	-	-	-	-	1.0	-		J	
4			5-ASA	-	-	-				-		-		J	
5	ro04003a	Blank	AC-5-ASA	-	-	-	6.97	1991341	84158	0.0000	1.0	-0.000523		J	
6			5-ASA	-	-	-				0.0000		0.00632		J	
7	ro04004a	cal 2.50	AC-5-ASA	2.76	33704	2024	6.95	1954948	82708	0.0245	1.0	2.49	-0.5	J	
8		cal 1.00	5-ASA	4.95	18973	1017				0.0123		1.00	0.4	J	
9	ro04005a	cal 6.25	AC-5-ASA	2.77	79998	4782	6.96	1845852	78083	0.0612	1.0	6.23	-0.4	J	
10		cal 2.50	5-ASA	4.96	47587	2426				0.0311		2.53	1.0	J	
11	ro04006a	cal 12.5	AC-5-ASA	2.77	184540	10203	6.93	1959039	83035	0.1229	1.0	12.5	-0.1	J	
12		cal 5.00	5-ASA	4.96	98803	5086				0.0613		4.97	-0.5	J	
13	ro04007a	cal 25.0	AC-5-ASA	2.76	367361	21137	6.95	1993394	84423	0.2504	1.0	25.5	1.8	J	
14		cal 10.0	5-ASA	4.96	202287	10349				0.1226		9.95	-0.5	J	
15	ro04008a	cal 62.5	AC-5-ASA	2.75	872066	51750	6.89	1995195	84562	0.6120	1.0	62.2	-0.4	J	
16		cal 25.0	5-ASA	4.94	494858	25753				0.3045		24.7	-1.2	J	
17	ro04009a	cal 125	AC-5-ASA	2.75	1787784	104513	6.97	2032549	85689	1.2197	1.0	124	-0.8	J	
18		cal 50.0	5-ASA	4.96	1045971	52640				0.6143		49.8	-0.3	J	
19	ro04010a	cal 250	AC-5-ASA	2.75	2751271	162216	6.94	1535522	65686	2.4696	1.0	251	0.4	J	
20		cal 100	5-ASA	4.96	1631033	81657				1.2431		101	0.8	J	
21	ro04011a	cal 625	AC-5-ASA	2.75	7625330	448198	6.94	1719859	72917	6.1467	1.0	625	0.0	J	
22		cal 250	5-ASA	4.95	4571734	226421				3.1052		252	0.7	J	
23	ro04012a	cal 1250	AC-5-ASA	2.77	8879399	520831	6.95	1017799	42367	12.2933	1.0	1250	0.0	J	
24		cal 500	5-ASA	4.95	5279346	260029				6.1375		498	-0.4	J	
25	ro04013a	w.b.	AC-5-ASA	-	-	-	-	-	-	-	1.0	-		J	
26			5-ASA	-	-	-				-		-		J	
27	ro04014a	# 1 / 1 / 0.00h	AC-5-ASA	-	-	-	6.95	2253300	95300	0.0000	1.0	-0.000523		0	
28			5-ASA	-	-	-				0.0000		0.00632		0	
29	ro04015a	# 1 / 1 / 1.00h	AC-5-ASA	2.75	697857	41275	6.95	1939366	82346	0.5012	1.0	51.0		J	

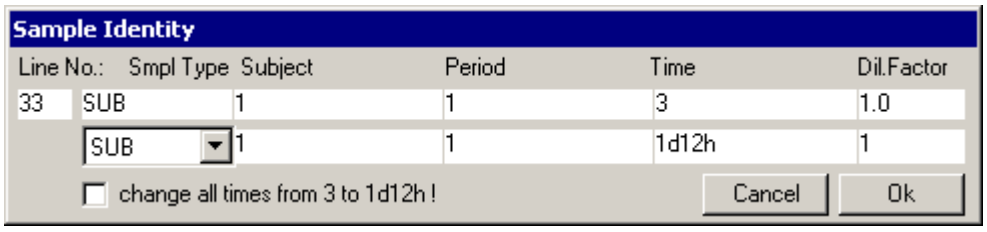
The list can be reduced to one analyte by double-clicking in the ‘analyte’ column if more than 1 analyte were measured in one chromatogram. After second double-click in the ‘analyte’ column the whole batch list is shown again.



	file/sample	name	analyte	rt	area	ht	rt(is)	area(is)	ht(is)	p.h.r.	dil.f	ng/mL	dev [%]	flag	comment
1	ro04001a	sss	AC-5-ASA	2.77	3458351	202247	6.98	1951732	82112	2.4631	1.0	250		J	
3	ro04002a	w.b.	AC-5-ASA	-	-	-	-	-	-	-	1.0	-		J	
5	ro04003a	Blank	AC-5-ASA	-	-	-	6.97	1991341	84158	0.0000	1.0	-0.000523		J	
7	ro04004a	cal 2.50	AC-5-ASA	2.76	33704	2024	6.95	1954948	82708	0.0245	1.0	2.49	-0.5	J	
9	ro04005a	cal 6.25	AC-5-ASA	2.77	79998	4782	6.96	1845852	78083	0.0612	1.0	6.23	-0.4	J	
11	ro04006a	cal 12.5	AC-5-ASA	2.77	184540	10203	6.93	1959039	83035	0.1229	1.0	12.5	-0.1	J	
13	ro04007a	cal 25.0	AC-5-ASA	2.76	367361	21137	6.95	1993394	84423	0.2504	1.0	25.5	1.8	J	
15	ro04008a	cal 62.5	AC-5-ASA	2.75	872066	51750	6.89	1995195	84562	0.6120	1.0	62.2	-0.4	J	
17	ro04009a	cal 125	AC-5-ASA	2.75	1787784	104513	6.97	2032549	85689	1.2197	1.0	124	-0.8	J	
19	ro04010a	cal 250	AC-5-ASA	2.75	2751271	162216	6.94	1535522	65686	2.4696	1.0	251	0.4	J	
21	ro04011a	cal 625	AC-5-ASA	2.75	7625330	448198	6.94	1719859	72917	6.1467	1.0	625	0.0	J	
23	ro04012a	cal 1250	AC-5-ASA	2.77	8879399	520831	6.95	1017799	42367	12.2933	1.0	1250	0.0	J	
25	ro04013a	w.b.	AC-5-ASA	-	-	-	-	-	-	-	1.0	-		J	
27	ro04014a	# 1 / 1 / 0.00h	AC-5-ASA	-	-	-	6.95	2253300	95300	0.0000	1.0	-0.000523		0	
29	ro04015a	# 1 / 1 / 1.00h	AC-5-ASA	2.75	697857	41275	6.95	1939366	82346	0.5012	1.0	51.0		J	
31	ro04016a	# 1 / 1 / 2.00h	AC-5-ASA	2.77	1326328	79377	6.97	1889993	80661	0.9841	1.0	100		J	
33	ro04017a	# 1 / 1 / 3.00h	AC-5-ASA	2.76	2146983	127207	6.97	2250208	95536	1.3315	1.0	135		J	
35	ro04018a	# 1 / 1 / 4.00h	AC-5-ASA	2.77	2255997	134718	6.99	2319572	98761	1.3641	1.0	139		J	
37	ro04019a	# 1 / 1 / 5.00h	AC-5-ASA	2.76	2653472	158542	6.98	2130515	90555	1.7508	1.0	178		J	
39	ro04020a	# 1 / 1 / 6.00h	AC-5-ASA	2.77	2315585	138637	6.99	2139429	91203	1.5201	1.0	155		J	
41	ro04021a	# 1 / 1 / 7.00h	AC-5-ASA	2.76	2663665	158818	6.98	2031510	86135	1.8438	1.0	187		J	
43	ro04022a	# 1 / 1 / 8.00h	AC-5-ASA	2.77	2898913	173513	7.00	1832325	77826	2.2295	1.0	227		J	
45	ro04023a	# 1 / 1 / 9.00h	AC-5-ASA	2.76	2481021	148016	6.98	2106563	89324	1.6571	1.0	168		J	

Editing Sample Names

After double-clicking (or ENTER) in the ‘name’ column a dialog appears for entering the new sample name. Times are given in the format ”__d__h__m”. Expressions such as 2w, 1d2h30m, 5d10m, 20m, 1d etc. are valid. If a number is not followed by a letter the system automatically assumes a h.
Choosing CHANGE ALL TIMES FROM... changes all time information for all SUB samples to the new value. The example below shows that all SUB samples for the current analyte in the project which up to now have the time of 3h will be assigned the new time of 1d12h.



The key combination CTRL-first letter of sample type offers a quick way to change the sample type. CTRL-C changes sample type to CAL, CTRL-Q to QC, CTRL-V to VAL, CTRL-S to SUB etc.

Editing Chromatogram Flags

Die Chromatogram flags indicate acceptance of the results for a specific analyte in a chromatogram. They can be directly entered into the column via the keyboard (only entries valid for the current sample type will be accepted), or the user can 'page' through the possible flags by double-clicking, or the flags are set via the context menu (right mouse button). If several analytes were measured in a chromatogram the flags can be changed for all analytes of the respective chromatogram at the same time by keeping the CTRL key pressed while changing the flag. If the new or old flag is 'D', it will be set for all analytes of the respective chromatogram anyway (of course!).

Analysts-Flags

Flag	CAL/QCS	VAL	SUB	Explanation
Y	+	+	+	everything OK
N	+	+	+	chromatography error (e.g. peak interferences...), instrument error **must be re-assayed** (for SUB)
S	+	+	+	chromatographically Ok internal standard not accepted (peak to small/too large) **must be re-assayed** (for SUB)
X	+	+	+	chromatogram will be ignored in results
D	+	+	+	sample destroyed during work-up **must be re-assayed (only SUB)**
E	+	+		chromatographically Ok will not be used for statistic as outside the acceptance limits
R			+	chromatographically Ok, but value not plausible, therefore , marked to re-assay **should be re-assayed**
C			+	chromatographically Ok, but selected by client for re-assay **must be re-assayed**
V			+	A "dummy" SUB sample is marked with V (Volume) to report that sample was received but assay/reassay is not possible due to lack of sample material (empty tube) **should be re-assayed if in the next sample shipment**
I			+	A "dummy" SUB sample is marked with I (Ignore) to report the sample as "Sample received, but not analyzed (NOA) **must not be re-assayed**

DBLABCAL sets its own chromatogram flags for chromatograms from unknown samples (SUB) that were accepted by the analyst (with flag Y), and only for these:

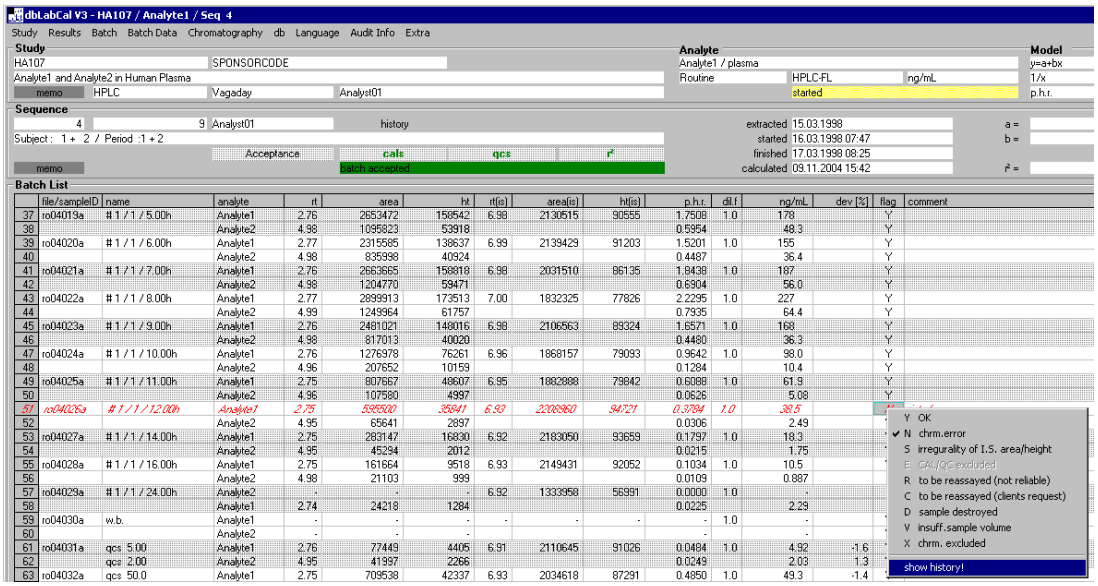
Databases-Flags

Flag	Explanation
0	chromatographically Ok, calculated concentration <LOQ
<	calculated concentration less than the lowest CAL value in the current batch, but higher than the project LOQ (can happen when the lowest CAL value is not used)
>	calculated concentration higher than the highest CAL values in the current batch
+	calculated concentration higher than the LOQ found in a pre-dose sample (SUB sample with time<=0)
#	double assays acceptance criterion (CV value of the double assays) nut fulfilled (only at regression model „double assays)

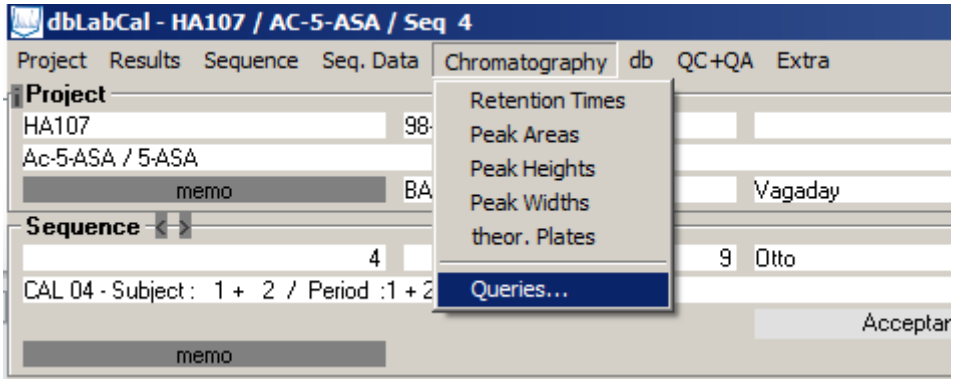
All chromatograms with flags N, S, D, R, C, <, >, + and # are automatically listed under SAMPLES TO BE RE-ANALYZED.

The analyst must not set a flag to (for instance) 'N' or 'R' just because the concentration in a pre-dose sample was <LOQ, >ULQ or >LOQ...

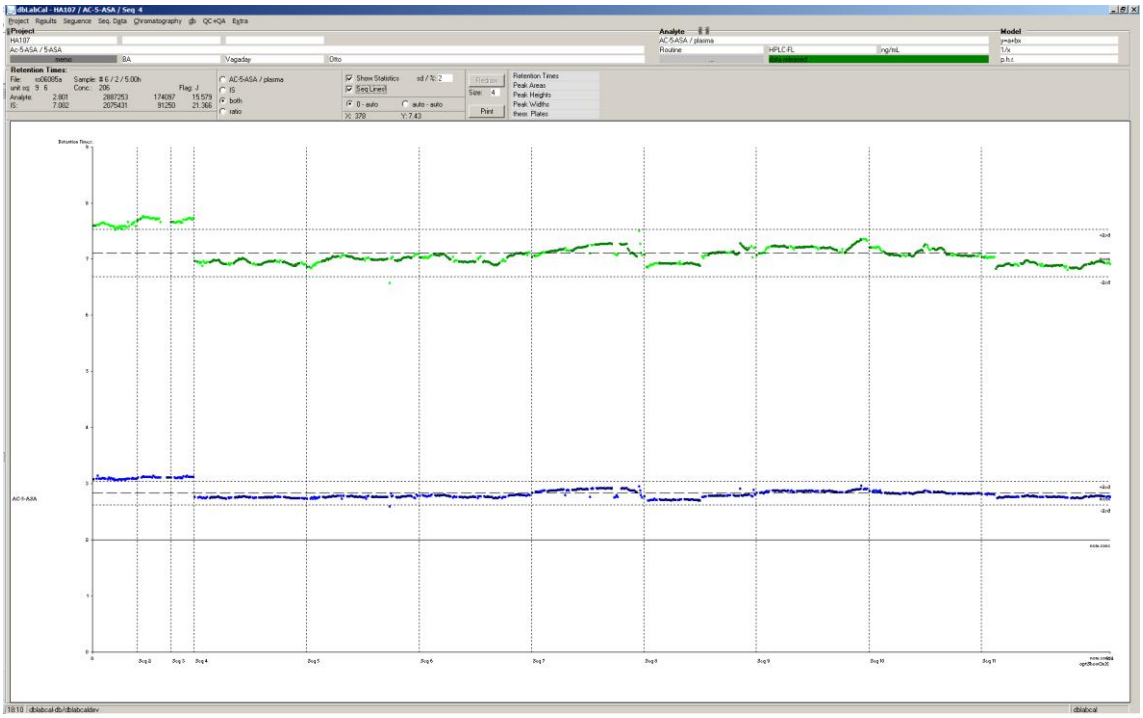
The respective table's cell back color is gray to indicate that sample name or chromatogram flag were changed by the user (at least once).
It is possible, with SHOW HISTORY (right mouse button) to view the Audit Trail for the chosen changes.



Chromatography Menu



The user can view retention times, peak areas, peak heights, peak widths and number of theoretical plates for the current analyte and the internal standard (if used).
These evaluations primarily allow for a quick review and check whether the integration software has correctly assigned peaks (retention time, relative retention time) and correctly positioned the baseline (peak width, theoretical plates).

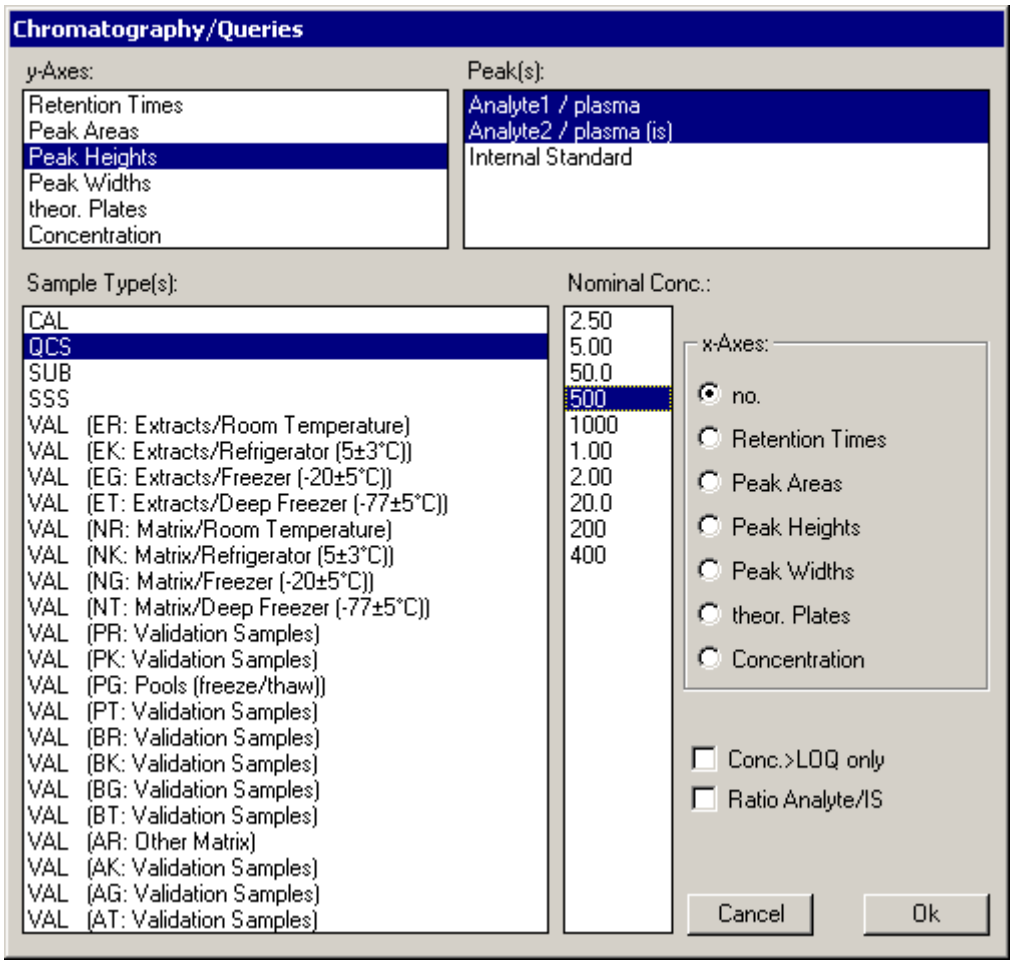


Moving the mouse across the graph automatically displays sample information under the current mouse cursor position in the following order: retention time, peak area, peak height, and peak width.

User may „jump“ to the underlying chromatogram with CTRL-double click.

Queries...

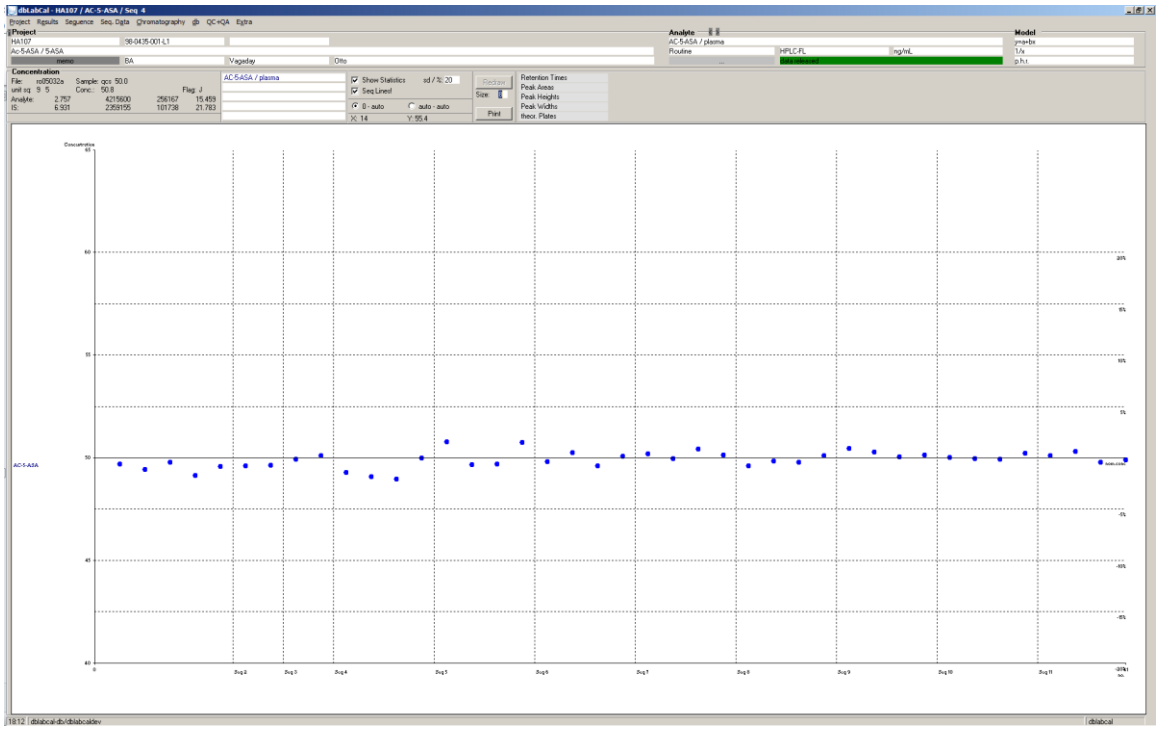
This offers the chance to select only specific samples types and/or concentrations for the chromatographic evaluation; to view data for all peaks of the chromatogram (instead of only the current analyte) etc...



For viewing data to several peaks only the running chromatogram number (no.) is allowed for the x-axis.

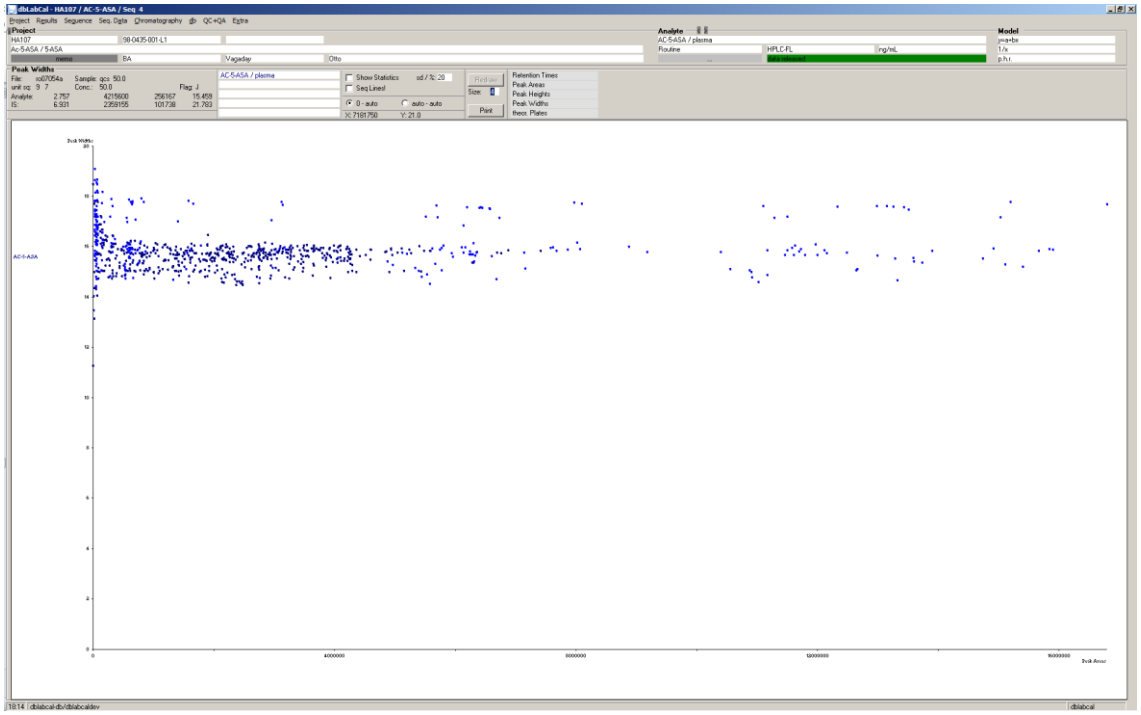
Choosing Conc.>LOQ only displays only data from chromatograms with a calculated concentration that is higher than LOQ. Choosing Ratio Analyte/IS calculates and displays the size of the y-axis relative to that of the internal standard. Peak area changes to p.a.r. and peak height to p.h.r...

Quality Control Chart data presentation is also possible:
Nominal concentration (instead of MEAN) and %-deviation lines (instead of SD) are displayed if the number for SD / % is set to >=5.



It is often useful to view peak width as a function of peak height or peak area.

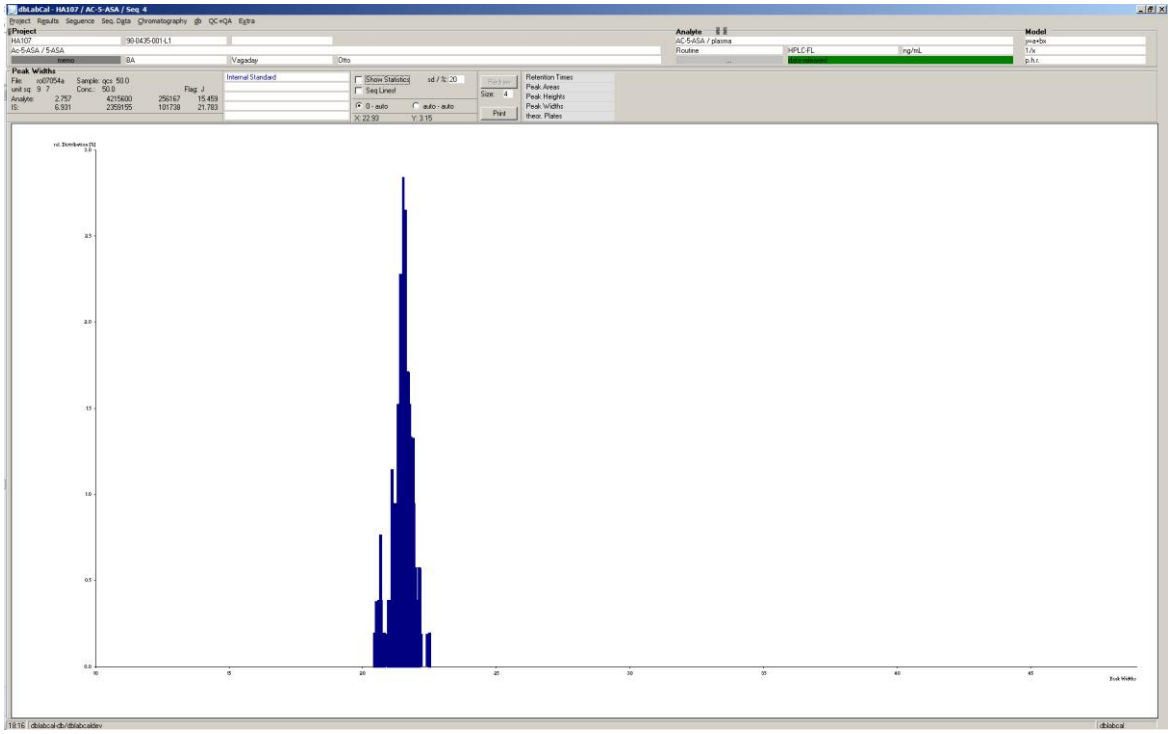
If, for instance, the following figure would show a peak width of 18 for a peak with a height of 300,000, the respective chromatogram should be closely examined. A peak width of 18 would be acceptable for small peaks.



The data on which the graphic display is based can also be exported. This offers a way to export these 'special data' from the data base as well.

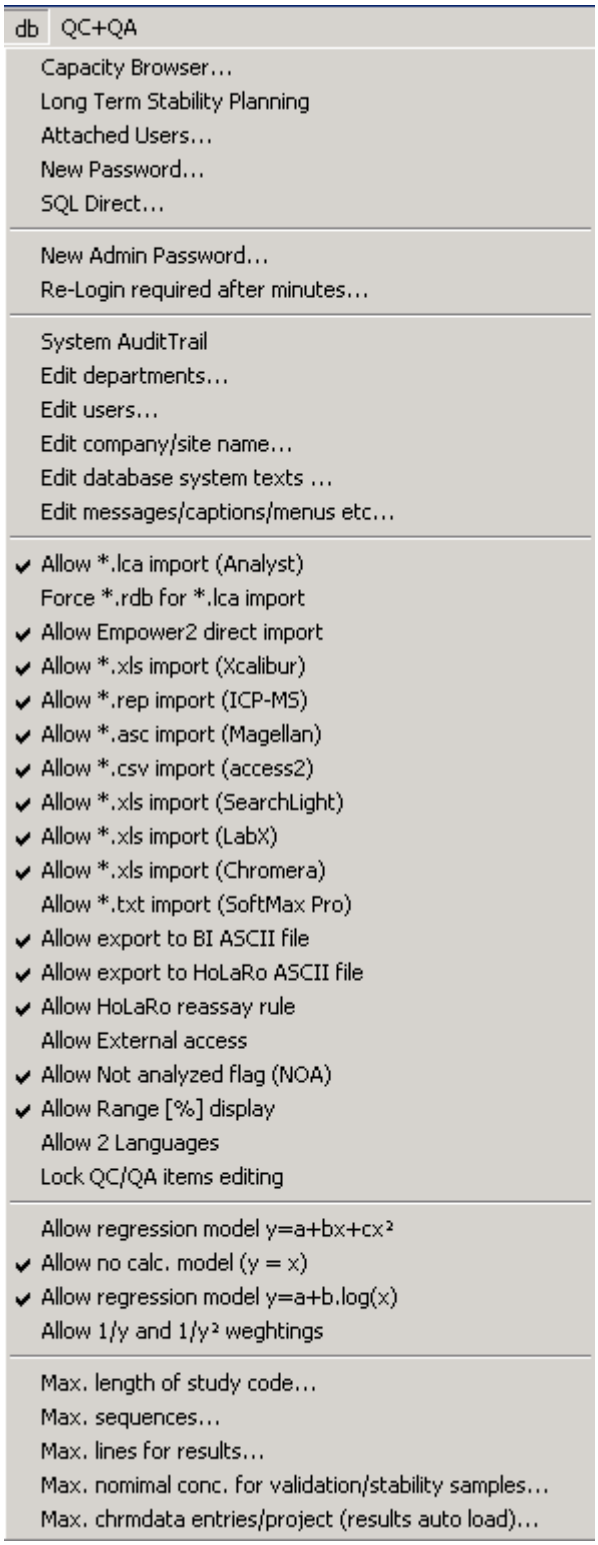
It is also possible to display, print and export various and often very interesting correlations (e.g. between peak width and concentration, or peak height and peak area etc.).

If the same parameters are chosen for the x- and y-axis the percentage distribution density of the data can be viewed.



All graphics as well as the data can be copied at any time into windows clipboard. (CTRL-INS or CTRL-C)

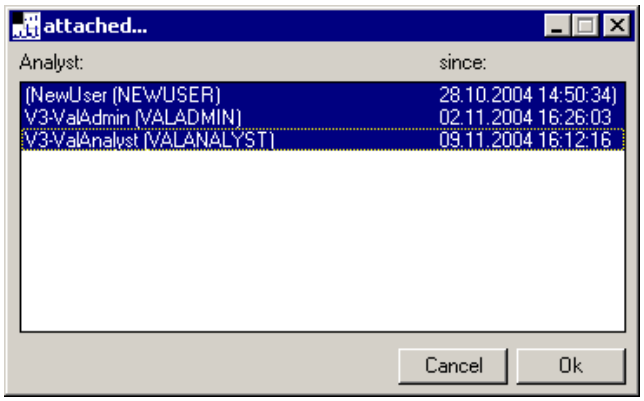
db Menu



Most entries (starting with the first line) are only accessible to the dbLabCal administrator.

Attached users...

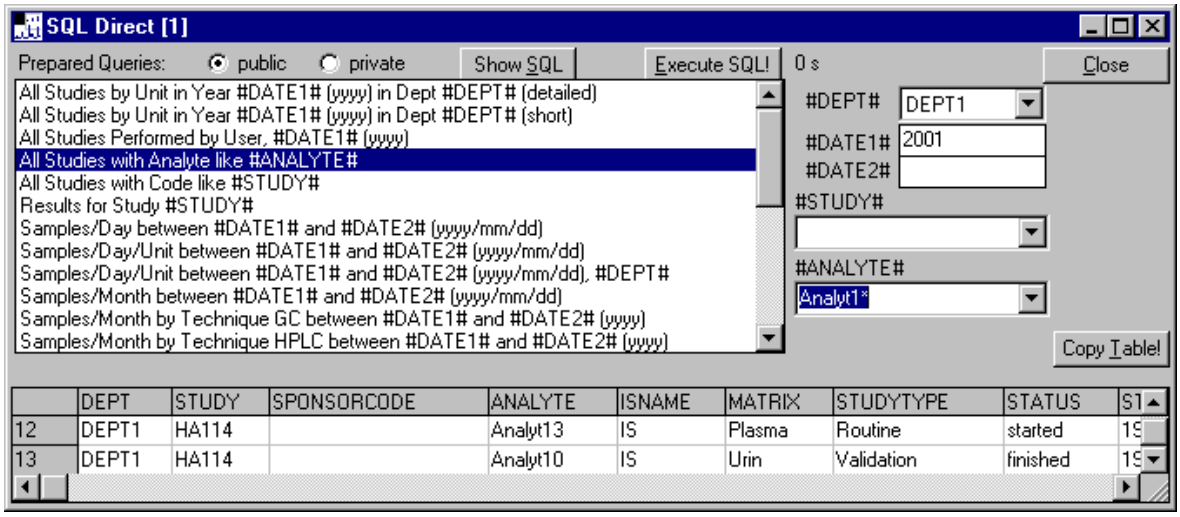
This menu item is displayed for department managers and higher authorities. Through this menu the department manager can log off users (by 'clicking away' the name) who, because of incorrectly exiting the program, are still logged into the database and may therefore block the editing of project data by other users.



SQL Direct...

This menu allows for extracting additional information from the database. Examples: status of all studies in the database, number of samples measured within a specific period of time, with a specific analytical method etc. As the paragraph title indicates this process involves ad-hoc SQL queries of the database. Even though only SELECT queries are allowed they still can keep the database busy for a while, especially if the sql statement was incorrect.
In order to be able create own SQL queries the authorized users must be familiar with both SQL and the structure of the DBLABCAL database.

Some SQL queries are already predefined after installation.



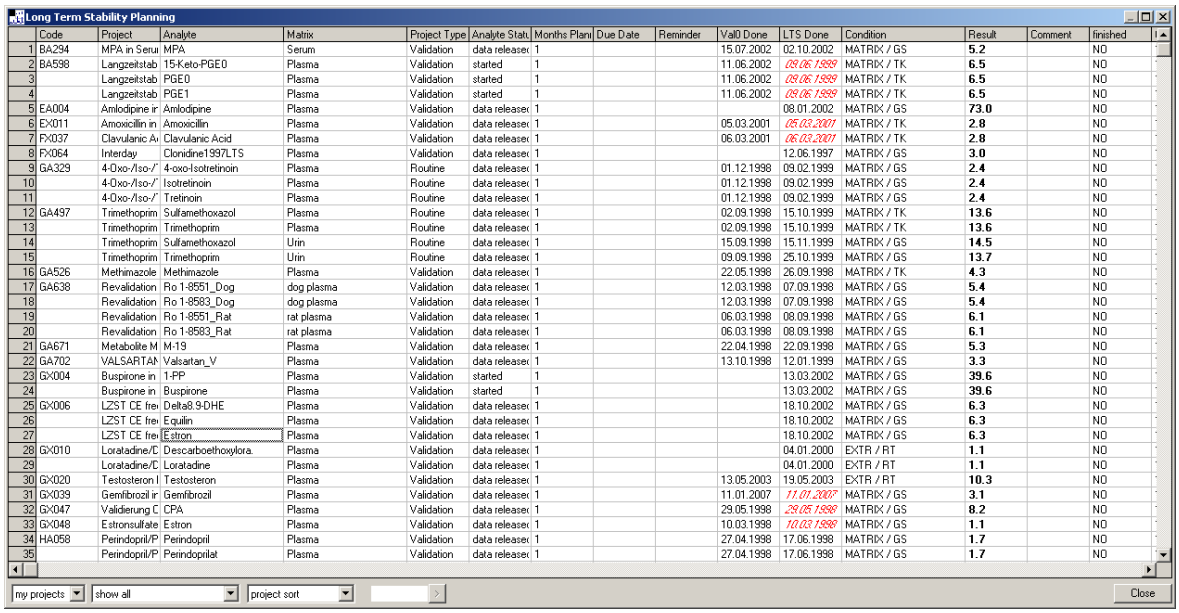
Up to four SQL Direct dialogs can be opened simultaneously.

Capacity Browser

Der berechtigte Benutzer hat hier einen Überblick über die Ausnutzung der einzelnen Messplätze (Kapazitätsauslastung) und über die Anzahl der gemessenen Proben pro Tag oder pro Monat

Long Term Stability Planning

This dialog is useful to plan long term stability experiments.
It shows also all stability data results. All results are maintained automatically by dbLabCal. It means, dbLabCal adds the result into this list immediately after respective VAL samples were imported or renamed.



Language

Here, the user can toggle at any time between the two pre-defined languages. In such a switch the data of the current project are reloaded and redisplayed in the newly selected language.

New Password...

The user can change his/her Oracle password at any time through this menu.

The following menu options are only accessible to the DBLABCAL administrator

New Admin Password...

The administrator can change the Oracle admin password at any time through this menu.

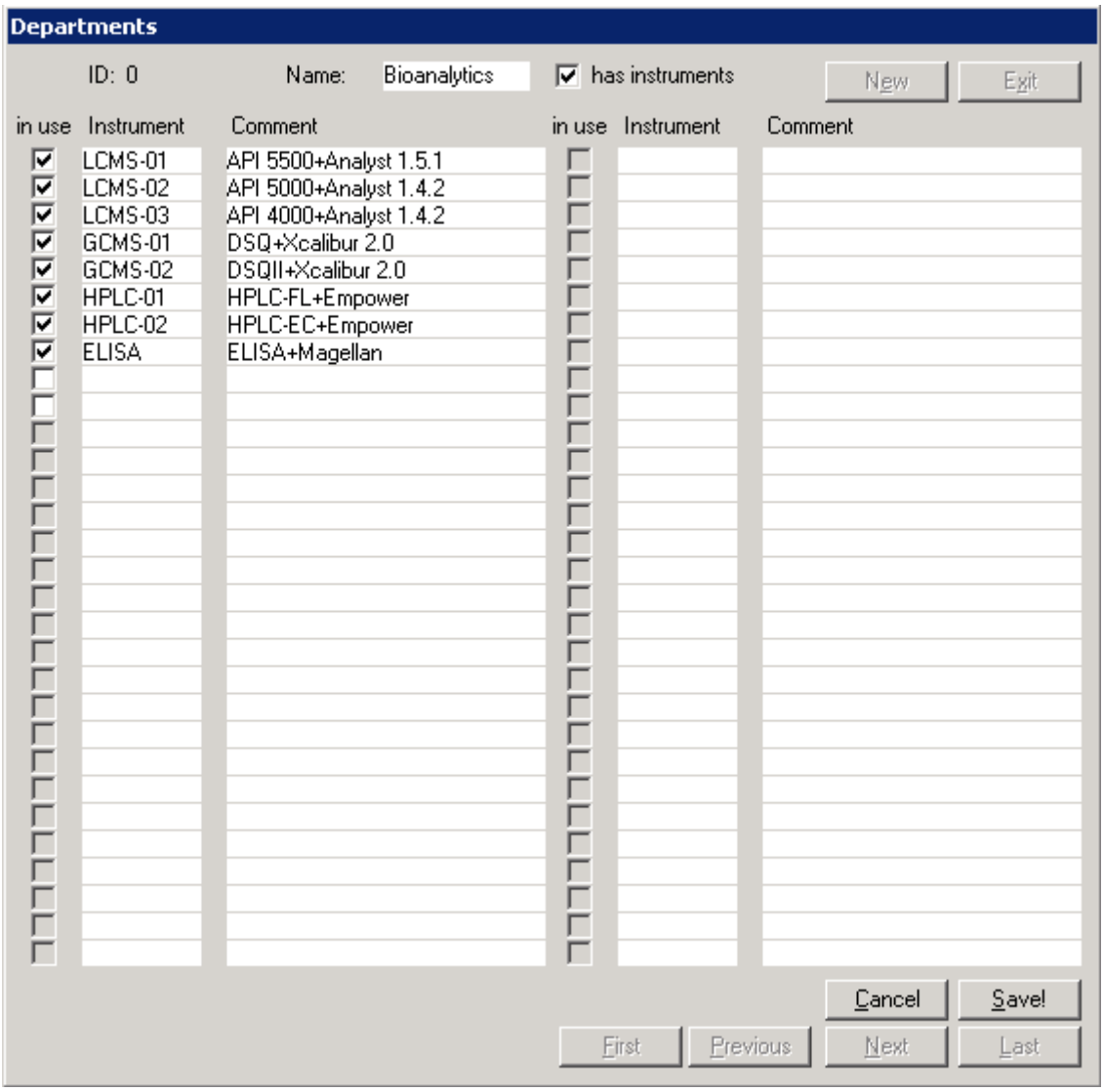
Re-Login required after minutes...

If the user logged into DBLABCAL is different from that logged into the PC/network and if over the period of time specified in this option no activity is registered, the user logged into DBLABCAL will automatically be logged off for security reasons.

Edit company/site name...

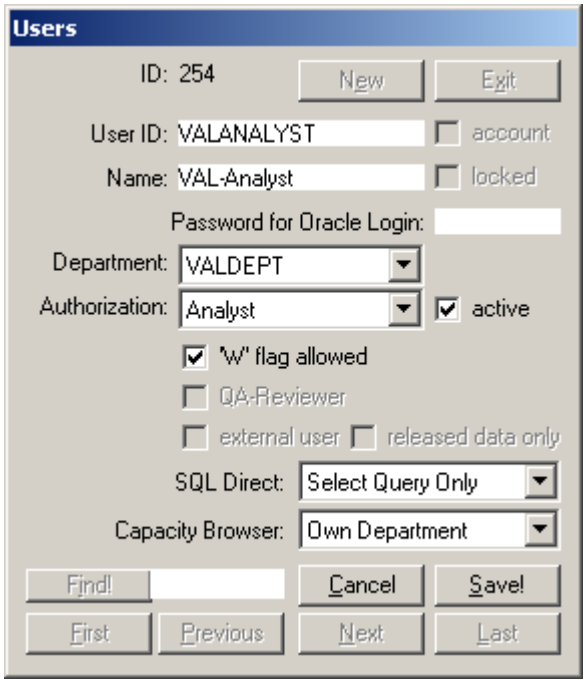
The name of the company and/or site as it should appear on the DBLABCAL printouts is entered through this option.

Edit departments...



The department names are entered through this dialog. If the respective department belongs to QM, for instance, and therefore it is not an analytical department, the check box
HAS INSTRUMENTS will be deactivated.

Edit users...



ACTIVE is activated if the user is an analyst. This ensures that this analyst is displayed in the lists of analysts during the editing of a project or the import of batchs. DBLABCAL does not delete any users (and also no departments). If a user does not work with DBLABCAL, only ACTIVE will be reset and/or the Oracle user locked in Oracle database.

UserID is the user name with which the user logs into the network. The name appears in dbLabCal in the lists of analysts and also in the status line. Permission levels are: ReadOnly, Analyst, PI/Study Director, Dept. Manager and Administrator. SQL Direct is used for specifying whether a specific user sees the SQL Direct menu at all and whether he/she can write SQL queries. "'R' flag allowed" is always enabled for users with access authority of PI/study director and higher.

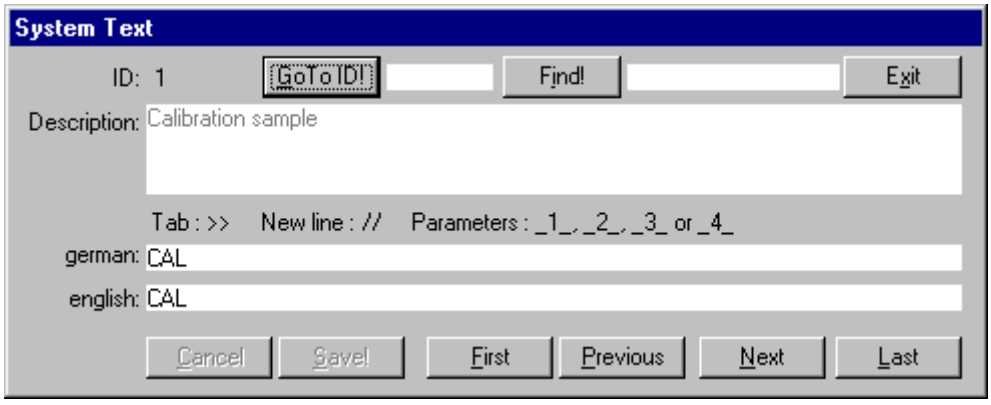
„QA-Reviewer" is a ReadOnly user with the additional permission to edit the QC/QA dialog.

Check boxes ACCOUNT and LOCKED show current Oracle status of the user. Does user exist in Oracle DB? Is user locked by Oracle DB?

Edit messages/captions/menus etc...

In this dialog all program texts, annotations etc. can be changed/edited. Any changes are immediately visible to the administrator, all other users will see them only after DBLABCAL is restarted.

Edit database system texts...



This dialog allows for defining the sample type (CAL, QCS, SUB, etc.), codes for matrix and temperature (EXTR, RT, GS, etc.), codes for chromatogram flags, codes for batch status, project type, batch type, readings, audit/trail texts etc.
Any changes are shown after restarting DBLABCAL.

Allow...

This dialog allows for specifying which menu options are visible and thereby defines the overall user functionality of DBLABCAL.

Max...

If desired, this item allows for extending the database limits.

Menü Extra

This menu is visible if set-up by the administrator. It allows to start any other program including extensions of DBLABCAL. Purpose and use of such extra programs must be described separately.

Tips and Tricks

The change in the mode of working with analytical data when going from a 'paper' office to an 'Excel' office using the database is reiterated. The major points are as follows:

Naming of samples:
This must be well thought out since the results are 'tightly connected' to the sample names. It is possible to change the samples names later in the database (batch status, audit trail), but this is an elaborate, time-consuming process involving each time a complete recalculation of batch data and update of the project results.

Setting of chromatogram flags, batch status and project status
Chromatogram flags, batch status and project status are at least as important as the analytical values and have well defined meanings and conbatchs.

If sample names and/or chromatogram flags are changed in the database later on, the user must not forget to make the same changes on the chromatograms as well.

The data received from he database is still as correct or as incorrect as the data written into the database. The easier the 'not quite correct' data are passed on the more important it is that the raw data imported into the database are 100% checked.

The data path from unit to report is as follows:

1) Generation of chromatograms (**raw data**) at the unit
   ANALYST, EMPOWER2...

2) Summarizing the chromatographic results of a batch in an ASCII file
   EXPORT-OPTION DER CHROMATOGRAPHIE-SOFTWARE, QUANCAL, MANCAL

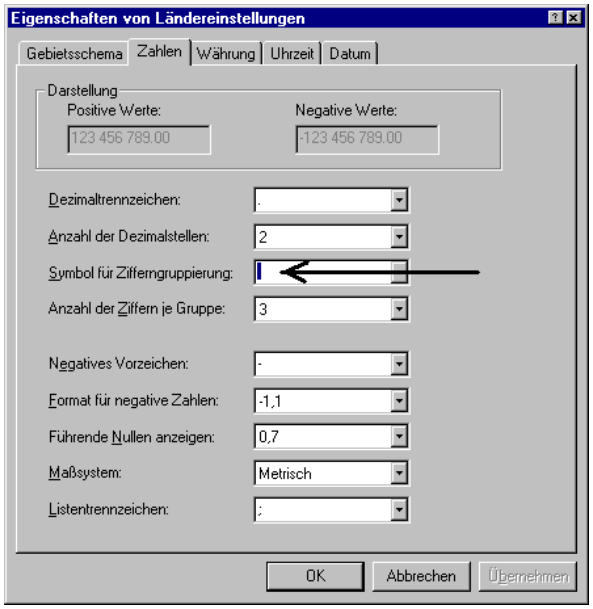
3) If required (when units are not connected to network) transferring the ASCII file generated by copying the file onto data server

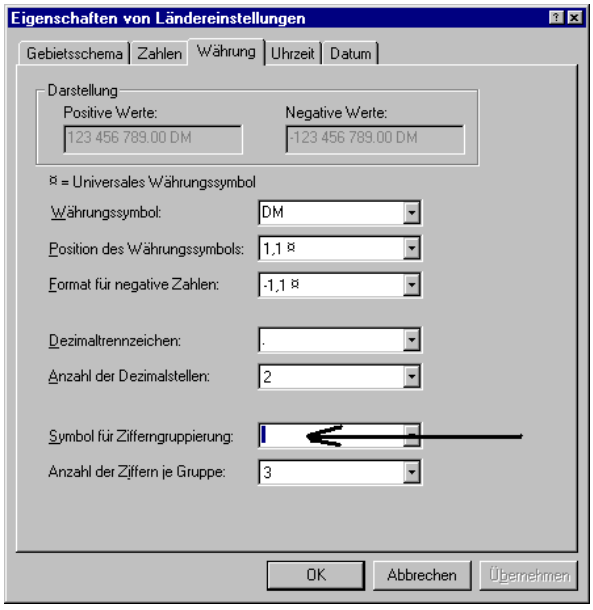
4) **Importing** the ASCII file into the database
   From here on ASCII files are not needed. Changes to or deletion of the files have no impact whatsoever on the data in the database.

5) Exporting the data from the database into the report
   DBLABCAL, WORD, EXCEL

The number are „unrealistic high“

dbLabCal works at best with windows international setting (numbers,currency) set to US. It can have problems with the representation of numbers if both decimal separators (period and comma) are selected in the number/currency format.
Solution: check settings in workplace – control panel – country settings/currency format. The separator for groups of numbers should be set to blank.





A chromatogram imported into the database must be reintegrated

Since the data are imported batch-wise into the data base any modification in the data of a chromatogram necessitates a full ”import” process, that is:

If the user notices in the database (?!) that the integration software generated incorrect peak assignments or baselines, the following actions are required:

1) (Manually) re-integrate the chromatogram with the integration software
2) Ensure that the new results can be further processed with QUANCAL, MANCAL (i.e. perform “save as ASCII” if required)
3) Import the new file into the database
   If the original batch still shows the ‘not set yet’ status, this is no problem;
   if the original batch shows the ‘batch accepted’ status it must be set to ‘excluded’ beforehand since an ‘accepted’ batch must not be overwritten

The program incorrectly generates the message: ”locked by XYZ”

XYZ could not log off the database because a malfunction terminated the program.
XYZ should load the respective project and re-exit it by selecting another project or terminating the program.
The PI/study director can also manually log off the user (DB | ATTACHED USERS...).

Changing readings or weightings in a routine project

Readings or weightings can only be changed in a validation project. Therefore the project type must first be changed to validation. Then a new selection can be made via the menus PROJECT | WEIGHTING or PROJECT | READINGS. All data for all analytes that were measured in a chromatogram will be recalculated based on the new settings. Don't forget afterwards to reset the project type back to routine.

Subject samples must be measured twice (e.g. measuring protein binding)

In order that the program does not output the twice-measured samples as re-assays they must not carry the same name. This is best achieved by changing the period, e.g.:

subject 1	period 1	4.00 h	plasma
subject 1	period 2	4.00 h	plasma
subject 1	period 3	4.00 h	actually period 1, buffer
subject 1	period 4	4.00 h	actually period 2, buffer

User wants to print batches, but not nothing prints

This is possible with batches still having the ‚not set yet' status and the user forgot to deselect the option ONLY 'OK' BATCHES.

Printing figures with subject concentration curves

DBLABCAL does not make provisions for printing subject concentration curves. However, the figure can be exported into another program and printed from within there.

1) Press CTRL-INSERT (or CTRL-C), select GRAPHIC, or right mouse over the picture
2) Change into the target program
3) In the Edit menu of the target program select PASTE or a similar expression, or press SHIFT-INSERT (or CTRL-V).

You also can generate your own presentation of the concentration curve by exporting the (selected) data from DBLABCAL into, for instance, Excel.

Saving data in an ASCII file

An ASCII file with TABs is best be generated with Windows Notepad as follows:

1) Export data into Notepad - either with CTRL-INSERT (or CTRL-C), or right mouse button at marked data
2) Select PASTE in the Edit menu of Notepad, or press SHIFT-INSERT (or CTRL-V)
3) Save file

In subjects, some time values shown twice, with 'missing' or with value...

This happens if some (one is already enough!) samples were assigned only slightly different times. Example: A sample was named SUBxxDGxxTP 0.17h, and later perhaps SUBxxDGxxTP 10m. Since 0.17h is basically 10.2min DBLABCAL differentiates between the two times even though (rounded) each time 10m (or 0.17h) is shown. Change in this case for one SUB sample with time 0.17h the time to 10m and select ALL TIMES FROM... in the dialog SAMPLE NAME (see page 67)

After selecting the validation samples results the following message displays: "No validation 0 values found..., check sample names and/or dates...

This exactly means what it says. In most cases the database lacks information about the date "start of batch". Best course of action is to enter the missing date in RESULTS | DATE OF ANALYSES. If the database does contain all dates to the start of batch the reason may be found in missing information about matrix and/or temperature in the sample names for the validation 0 results. You should load the corresponding batch(s) and check for correct sample names.

In a project (the same) analytes are defined in different matrices. Samples with different matrices were simultaneously measured in a batch. However, DBLABCAL only allows a sequential import into one specific analyte/matrix pair defined for a project

The file to be imported contains the information about the analyte(s) measured in the batch and the (one) matrix. During the import, DBLABCAL checks this information and compares it with that in the current project. If DBLABCAL finds a match, the batch data will be imported into the database.
In such case, the ASCII file has to be imported twice:
then imports the file and manually assigns the first analyte/matrix pair, and then re-imports the same file and manually assigns into the next analyte/matrix pair, etc. The chromatogram flags of the chromatograms with the 'other' matrix will then be set in the database to 'X' – or will be renamed (DIV).

Describing this situation is much more complicated than actually doing it. Therefore an example:
The following are defined in the project: - analyte1 in rat plasma
- analyte1 in dog plasma

The following were measured in the batch: - calibration curve (analyte1 in whatever)
- 50 samples of analyte1 in rat plasma
- 10 samples of analyte1 in dog plasma

In generating the batch file (see the respective program) analyte1 will be defined in matrix 'XXX'

- During import DBLABCAL does not recognize analyte1 in matrix 'XXX' and prompts for a manual peak assignment.
- The user selects 'analyte1 in rat plasma'
- After the batch has been imported the user sets the chromatogram flags of the 10 chromatograms of analyte1 in dog plasma to 'X' – or renames them into DIV.
- The batch file is re-imported. DBLABCAL again prompts for a manual peak assignment.
- This time the user selects 'analyte1 in dog plasma'
- The chromatogram flags of the 50 chromatograms of analyte1 in rat plasma are now set to 'X' - or they are renamed into DIV.
- Finished

Program limits

The program limits are chosen such that the vast majority of studies can be processed without undue demands on the PC's resources.
The program limits are set in a table of the database and can only be modified by the administrator. If during the processing of a project the program limits are exceeded, an appropriate message will display.

Errors and Error Messages

Apart from the case mentioned above and a number of other questions, notes and security queries, there are three different kinds of error messages:

1) The message clearly states what happened where.
   Example: ”Error when drawing the dots...”, or ”Problems with OLE“. Action aborted...”. This type of error is not really critical even though ”something” is wrong with the data.

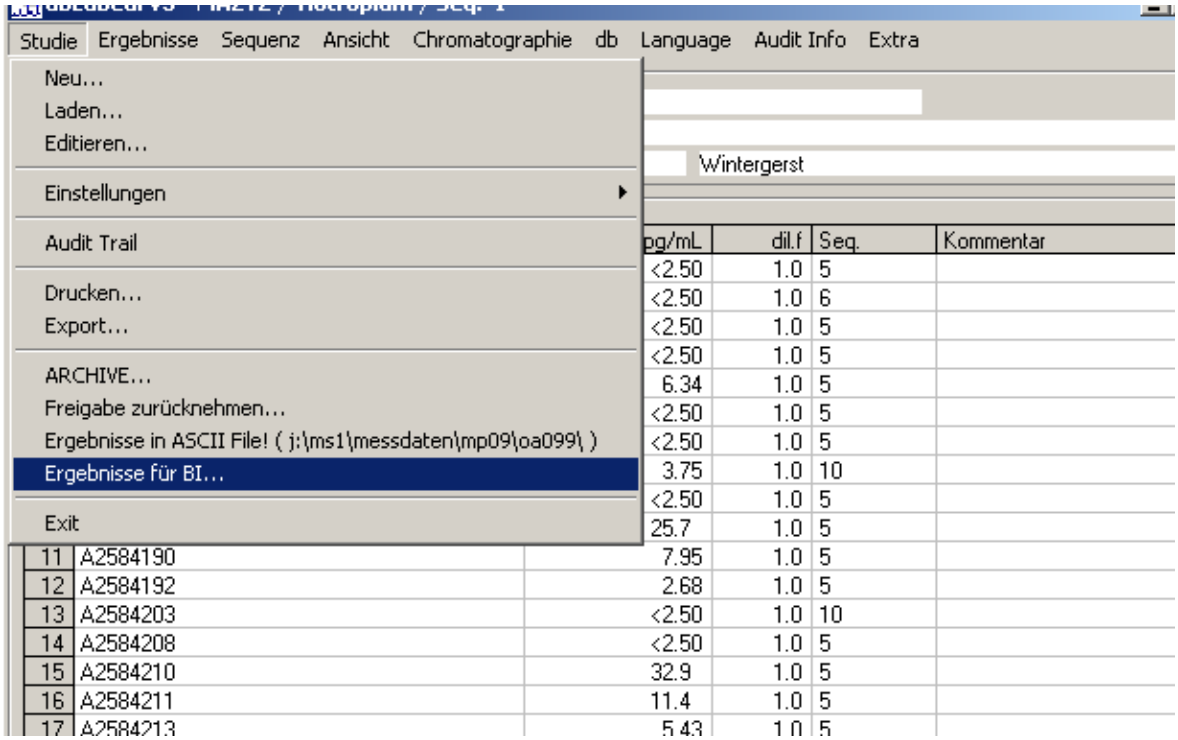
2) The message starts with ”Unexpected error...”.
   This is more critical. Even though the program is still stable it is not sure for how long. All ”Unexpected errors” are logged in the database so that the administrator can retrieve all required information. The administrator should be informed about any occurrences of such an error.

3) Short error message.
   This means that right after clicking on OK the program is gone! Probably due to serious problems with computer HW or SW. Re-boot the PC and try again.
   In case the error message can be reproduced make sure to note all of the following information and pass it on to the programmer:
   Project, analyte, batch, and last action performed.
   Since it is highly unlikely that the reason for such a situation is a bug :-) the user should always first check whether the server may have been unavailable for a short period of time or whether the computer may be defect...

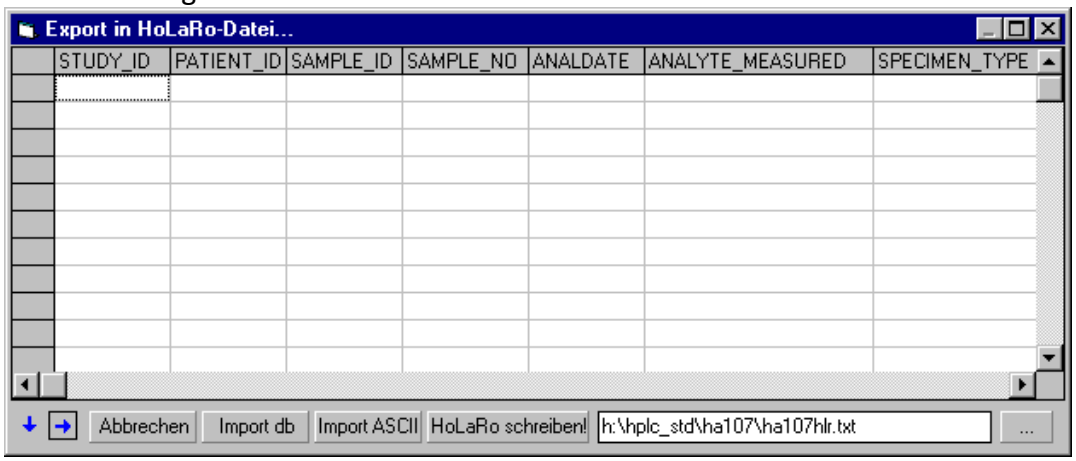
Appendix 1: HoLaRo- and. BI- ASCII-Files

This menu option is only visible if enabled by the administrator and if the project has been released.
HoLaRo ASCII is a well-defined ASCII format from Hoffman-LaRoche Company for transferring analytical results. Similarly, Boehringer-Ingelheim Co. has defined an own ASCII format. Data with this ASCII format can be generated via the following dialogs.

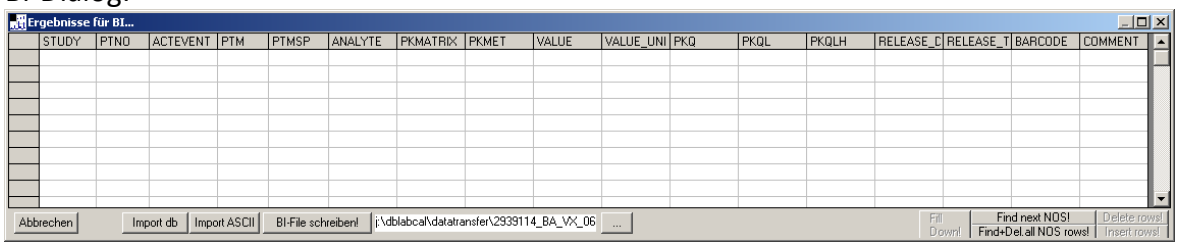
Project load, Project Menu -> Results for BI...



HoLaRo-Dialog:

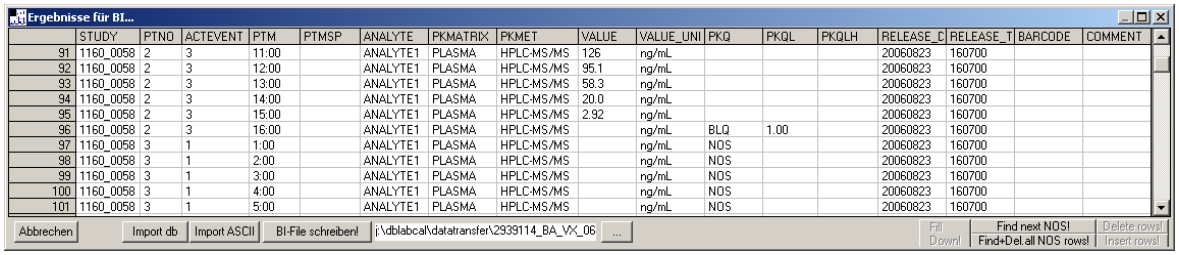


BI-Dialog:



IMPORT DB allows for first loading the data contained in DBLABCAL into the table. It is also possible to load data from an ASCII file (text with TAB separators) with IMPORT ASCII. The data can be edited in the above dialog (or in Excel). The data can be exchanged at any time via the clipboard (or an ASCII file) between Excel and DBLABCAL for editing. Name and path of the file(s) can be entered directly or via '...'.

dbLabCal loads „as good as possible" the data from the database into the dialog



„as good as possible" means:

BI:

dbLabCal	*BI-ASCII-File-Column*
Subject	*PTNO*
Period	*ACTEVENT*
Time	*PTM und PTMSP*

HoLaRo:

dbLabCal	*HoLaRo-ASCII-File- Column*
subPATIENT_ID_SAMPLE_ID_SAMPLENO	*PATIENT_ID*
subPATIENT_ID	
subPATIENT_IDdg1tpSAMPLENO	
Period: N/A	*SAMPLE_ID*
Time : N/A	*SAMPLENO*

In this dialog all data could be modified (in this dialog ONLY, not in the database).

The dialog data need very likely to be edited according to the DTA (data transmission agreement)
i.e.. „TIOTROPIUM“ to „BA 679“ or „LC-MS/MS“ to „HPLC-MS/MS“ etc...

That’s simple and fast with following keys or key combinations:

Edit a CELL

Double click or ENTER in cell	->	opens cell for editing
ENTER in opened cell	->	closes cell with new content
ESCAPE in opened cell	->	closes cell with original content

SEARCH&REPLACE

CTRL-D in opened cell	->	fills cells below current cell with current cell content
SHIFT-CTRL-D in opened cell	->	fills EMPTY cells below current cell with current cell content
CTRL-R in opened cell	->	replaces all cells below current cell with same content as the current cells original content with the current (visible) content

Edit ROW

DEL / INS (cell closed)	->	row will be deleted / empty row inserted

CTRL-C / CTRL -INS / right mouse + Copy with selected cells

	->	copy into clipboard
CTRL-V oder SHIFT-INS	->	copy from clipboard

It is possible to exchange the data between this dialogs and e.g. Excel at any time wia windows clipboard.

Choose file name according toDTA

Lastly, the file is generated in ASCII format with WRITE TO HOLARO or WRITE TO BI!

IMPORTANT! : All exported data in the ASCII file must be checked with DBLABCALS data!

Appendix 2: PE SCIEX LC-MS (Analyst)

Data are exported from the PE SCIEX Software ANALYST (V 1.1 – 1.5.2 were tested) as follows.
In ANALYST start the QUANTITATION WIZARD, select QUANTITATE.
After selecting the batch file (*.wiff) and the chromatograms in the wizard the RESULTS TABLE will be displayed.
The following columns **must** be defined in this RESULTS TABLE (if not yet done...).

Sample Name	Analyte Peak Name	Analyte Concentration	…
…	Analyte Retention Time	Analyte Peak Area	Analyte Peak Height
…	IS Retention Time	IS Peak Area	IS Peak Height
…	Acquisition Date	Sample ID	Dilution Factor

The **first column must** be SAMPLE NAME -it will be shown in Analyst by default as first column.

The order of the other columns is arbitrary. Additional columns may be defined in the RESULT TABLE.

The RESULT TABLE must be sorted according to chromatograms – e.g. in the measurement sequence.

After selecting EXPORT... in the FILE... menu the system prompts for a name for the ASCII file to be exported. The user should enter a name that contains any two letters and not more than three numbers (=batch number). File name extension should be *.LCA. This 'tells' DBLABCAL that the file is a ASCII file generated by Analyst. (Example: sq01.lca, we7.lca, ab115.lca...)

If there is no Sample ID found in the Result Table, dbLabCal creates a „file name/Sample ID" from first 5 characters of the lca file and the vial position.

The *.lca ASCII file is imported into dbLabCal via menu BATCH IMPORT...

Appendix 3: Empower2

In order to export data, it is required that following custom fields are defined . These user-defined custom fields are defined in Empower2:

SType: type of sample, see table below
Info_Sub: subject number for SUB, concentration for CAL, QC or VAL samples
Period: period number
STime: subject sampling time or storage duration for validation/stability samples
Matrix: matrix group used in validation/stability samples
Temp: temperature group for validation/stability samples

Empower2 naming convention

SType	**Info_Sub**	**Period**	**STime**	**Matrix**	**Temp**
cal	nom. concentration *)				
qc	nom. concentration				
sub	number or name	Period	sampling time in h or _d_h_m		
eqc	number or name				
val	nom. Concentration		Dauer in h oder _d_h_m	E Extracts N Matrix P freeze/thaw A A group B B group	R (RT) K (KS) G (GS) T (TK)
blank	e.g. with or without ISor batch number, etc				
diverse	Name				
sss					
w.b.					

*) first dbLabCal „tries“ to get nom. concentration for CAL from the Amount value in Empower2. If Amount was not used in Empower2, dbLabCal extracts the nominal concentration from the Info_Sub field.

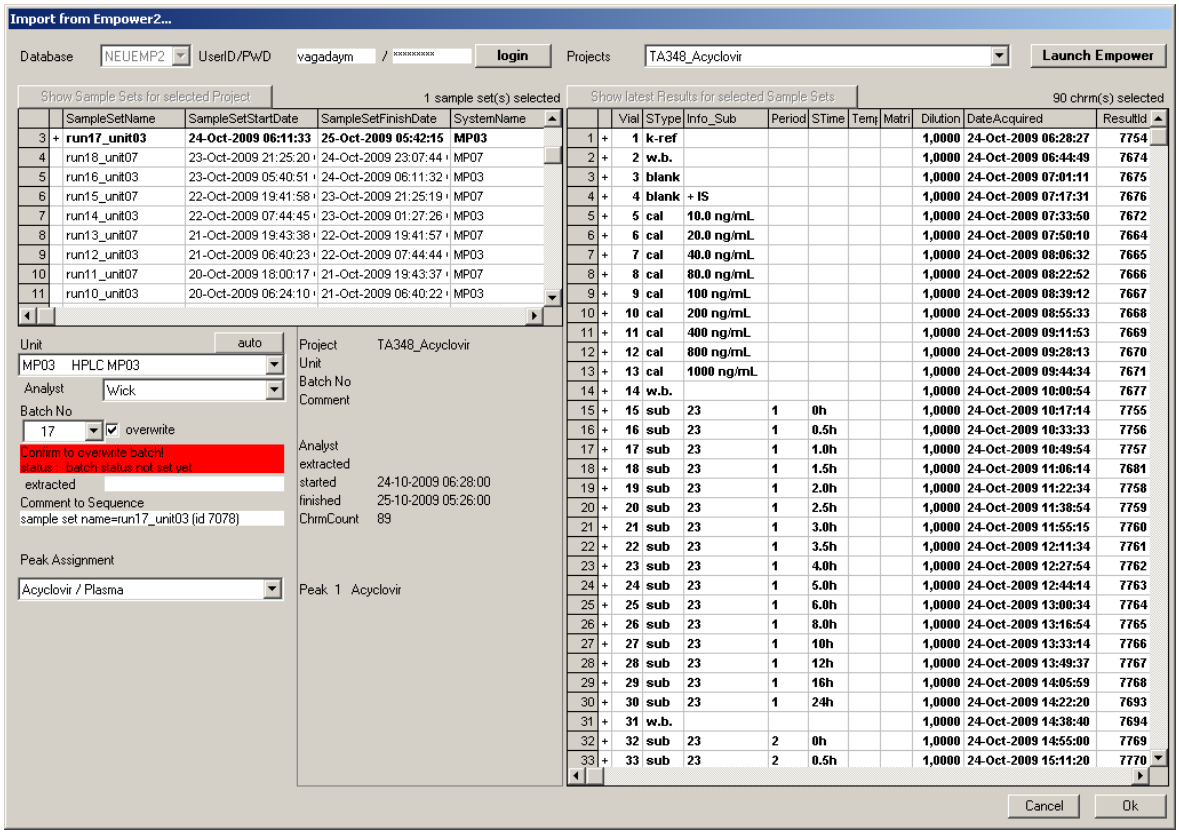
Two possibilities for combining the fields Info_Sub, Period and STime for SUB samples exist.

Either
Info_Sub and Period are entered as **numbers** and STime in hours or as _d_h_m, then dbLabCal interprets the entries as “subject/period/time“
or
if even one entry is **not a number** (or _d_h_m for STime) dbLabCal interprets the entries as “subject” with the fields Info_Sub, Period and STime being connected by an underscore.

Apart from the sample name field and the custom fields the following data must be exported as well: vial, dilution, and (of course) retention times, peak areas and peak heights.

Data from Empower2 are imported directly without using any ASCII file with a special dbLabCal's dialog „Import from Empower2…".

User has to login into Empower2 entering Empower2 userID and password. Current project is selected in the drop down box if found in Empower2.
User selects SampleSet (or SampleSets), then chromatograms to be imported. Selected data are imported after click on **Ok** button.



Appendix 4: Xcalibur

Start QUANBROWSER in Xcalibur (Version 1.4 was tested). Load the sequence file (*.sld) into QUANBROWSER from the data folder (e.g.: c:\Xcalibur\data\PROJECT\BATCH\ )

Choose EXPORT DATA TO EXCEL in FILE menu of QuanBrowser, then choose EXPORT LONG EXCEL REPORT.
The file name should be a combination of 2 characters and maximally 3 numbers (for the batch number). File extention is always *.xls.

The *.xls file is imported into dbLabCal via menu BATCH IMPORT...

Appendix 5: SoftMax Pro

Create the export file (*.txt, plain ASCII with TABs) as described in SoftMax Pro.
File structure should be as in the following example:

COL	1	2	3	4	5	6	7	8	9	10	11
ROW											
1	##BLOCKS= 4										
2	Group:	DONT	1								
3	Sample	Wells	Sample#	Values	MeanValue						
4	SSS01	A3	1	0.327	0.328						
5		A4		0.328							
6											
7	~End										
8	Group:	SUB	1								
9	Sample	Wells	Sample#	Values	MeanVa	BackCal	Mean Conc.				
10	SUB01DGITP1	D1	1	0.108	0.112	5.78	5.42				
11		D2		0.117			6.14				
12	SUB01DGITP2	D4	2	0.146	0.146	8.45	8.44				
13		E3		0.146			8.46				
14	SUB01DGITP3	D5	3	0.12	0.121	6.45	6.43				
15		D6		0.121			6.47				
16	SUB01DGITP4	D7	4	0.089	0.089	3.96	3.95				
17		D8		0.09			3.97				
18	SUB01DGITP5	D9	5	0.049	0.049	0.71	0.71				
19		D10		0.049			0.71				
20											
21	~End										
22	Group:	QCS	1								
23	Sample	Wells	Concent	Values	MeanVa	BackCal	% Bias	Mean			
24	QCS 15	C1	15	0.225	0.223	14.81	-1.3	14.7			
25		C2		0.222		14.6	-2.6				
26		C7		0.22		14.43	-3.8				
27		C8		0.226		14.89	-0.7				
28	QCS 45	C3	45	0.588	0.585	44.83	-0.4	44.6			
29		C4		0.587		44.76	-0.5				
30		C9		0.573		43.55	-3.2				
31		C10		0.591		45.11	0.3				
32	QCS 80	C5	80	0.961	0.972	77.69	-2.9	78.6			
33		C6		0.982		80.45	0.6				
34		C11		0.97		78.51	-1.9				
35		C12		0.963		77.84	-2.7				
36											
37	~End										
38	Group:	CAL	1								
39	Sample	Wells	Mean Cc	Concent	BackCal	Mean Cc	Values	Mean'	Std.D	CV%	% bias
40	Cal 5	B1	5.02	5	5.07	5.02	0.103	0.1	0	0.8	1.4
41		B2			4.98		0.102				-0.4
42	Cal 10	B3	9.9	10	9.92	9.9	0.164	0.16	0	0.3	-0.8
43		B4			9.88		0.164				-1.2
44	Cal 25	B5	25.22	25	25.31	25.22	0.354	0.35	0	0.4	1.2
45		B6			25.13		0.352				0.5
46	Cal 50	B7	49.7	50	50.17	49.7	0.65	0.64	0.01	1.2	0.3
47		B8			49.23		0.639				-1.5
48	Cal 75	B9	75.25	75	75.75	75.25	0.94	0.93	0.01	0.8	1
49		B10			74.76		0.929				-0.3
50	cal 100	B11	99.94	100	99.37	99.94	1.195	1.2	0.01	0.7	-0.6
51		B12			100.5		1.207				0.5
52											
53	Smallest standard value: 0.103										
54											
55	Largest standard value: 1.201										
56											
57	~End										

- use dbLabCals naming conventions for the Group name
  (CAL, QCS, SUB, VAL, SSS, DIV) if you want import data of that group
  (if you don't want to import data from a group, just name the group with some text unknown to dbLabCal)
- use dbLabCals naming conventions for the sample name
  (CAL, QCS, SUB, VAL, SSS, DIV)
  it is sufficient to name the samples only once, if the following row has data of the same sample, as shown above

- define the data columns for each sample type in the softmaxpro.col file in the dbLabCals working folder

softmaxpro.col file – example:

```
[default]
DataColCAL=5
DataColQCS=6
DataColSUB=7
DataColSUBDILF=-1
DataColVAL=6
DataColKON=6
DataColDIV=5
```

- sample name is in the first column for all sample types

The *.txt file is imported into dbLabCal via menu BATCH IMPORT...

All individual data (not only the mean values!) will be imported.
It means:

- there is NO regression calculation in dbLabCal, and therefore, NO concentration calculation for QCS, SUB, VAL and SSS samples
- the user will have to make choice on final SUB results for ALL samples since for ALL SUB samples at least two individual results were imported.

Appendix 6: Magellan (ELISA Reader)

Magellan data (Magellan V 3.11) with extension "asc" are saved automatically in pre-defined folder on the file server.

The *.asc file is imported into dbLabCal via menu BATCH IMPORT...

Important: asc file import is possible only if current project uses regression model NO CALC.(DOUBLE ASSAYS)

asc File Example:

Definition: 96 rows
Column 1 Position
Column 2 sample name (or „empty" if sample position not used)
Columns 3,4 not used
Columns 5-9 Data

A1	CAL 0.00			0.067	<Min	<Min		
B1	CAL 0.00			0.069	<Min			
C1	CAL 0.313			0.109	<Min	0.3331		6.4218
D1	CAL 0.313			0.121	0.3331			
E1	CAL 0.625			0.223	0.65434	0.62479	6.6885	-0.033407
F1	CAL 0.625			0.203	0.59524			
G1	CAL 1.25			0.449	1.271	1.2499	2.38	-0.0050019
H1	CAL 1.25			0.433	1.2289			
A2	CAL 2.50			0.958	2.474	2.5001	1.4778	0.0048336
B2	CAL 2.50			0.979	2.5262			
C2	CAL 5.00			1.663	5.0925	5.0005	2.6038	0.0094718
D2	CAL 5.00			1.625	4.9084			
E2	CAL 10.0			2.361	10.039	10	0.54452	0.0014085
F2	CAL 10.0			2.354	9.9616			
G2	CAL 20.0			2.759	>Max	18.827		-5.8664
H2	CAL 20.0			2.732	18.827			
A3	QCS 0.750			0.247	0.72357	0.71499	1.6976	-4.668
B3	QCS 0.750			0.241	0.70641			
C3	QCS 7.50			2.273	9.1401	8.6304	8.3535	15.071
D3	QCS 7.50			2.155	8.1206			
E3	QCS 15.0			2.683	16.26	16.599	2.8895	10.662
F3	QCS 15.0			2.699	16.938			
G3	empty							
H3	empty							
A4	QCS 0.750			0.234	0.68627	0.71771	6.1966	-4.3049
B4	QCS 0.750			0.256	0.74916			
C4	QCS 7.50			2.11	7.7737	8.3231	9.3361	10.975
D4	QCS 7.50			2.244	8.8726			
E4	QCS 15.0			2.688	16.461	16.942	4.0176	12.95
F4	QCS 15.0			2.709	17.424			
G4	empty							
H4	empty							
A5	QCS 0.750			0.255	0.74633	0.75622	1.8507	0.82971
B5	QCS 0.750			0.262	0.76612			
C5	QCS 7.50			2.113	7.7962	8.3798	9.8497	11.731
D5	QCS 7.50			2.254	8.9635			
E5	QCS 15.0			2.811	>Max	>Max		>Max
F5	QCS 15.0			2.821	>Max			

Appendix 7: Access2

Acces2 results are copied (pcAnywhere) from the Access2 system into pre-defined folder on the file server.

The *.csv file is imported into dbLabCal via menu BATCH IMPORT...

Important: csv file import is possible only if current project uses regression model NO CALC.(DOUBLE ASSAYS)

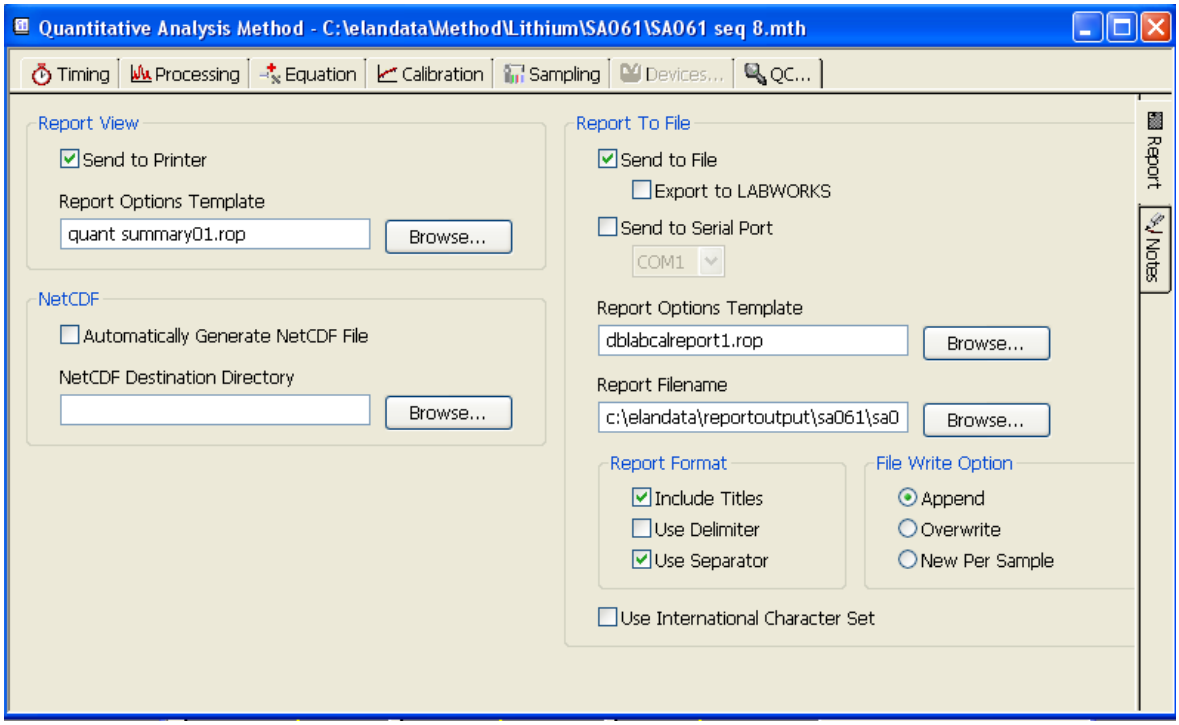
Appendix 8: ISE

The *.xls file is imported into dbLabCal via menu BATCH IMPORT...

Important: xls file import is possible only if current project uses regression model LOG.REGRESSION

Appendix 9: ICP-MS Elan

Define Method (Icon „Method“).
Define the export rep file with „Report Filename“.



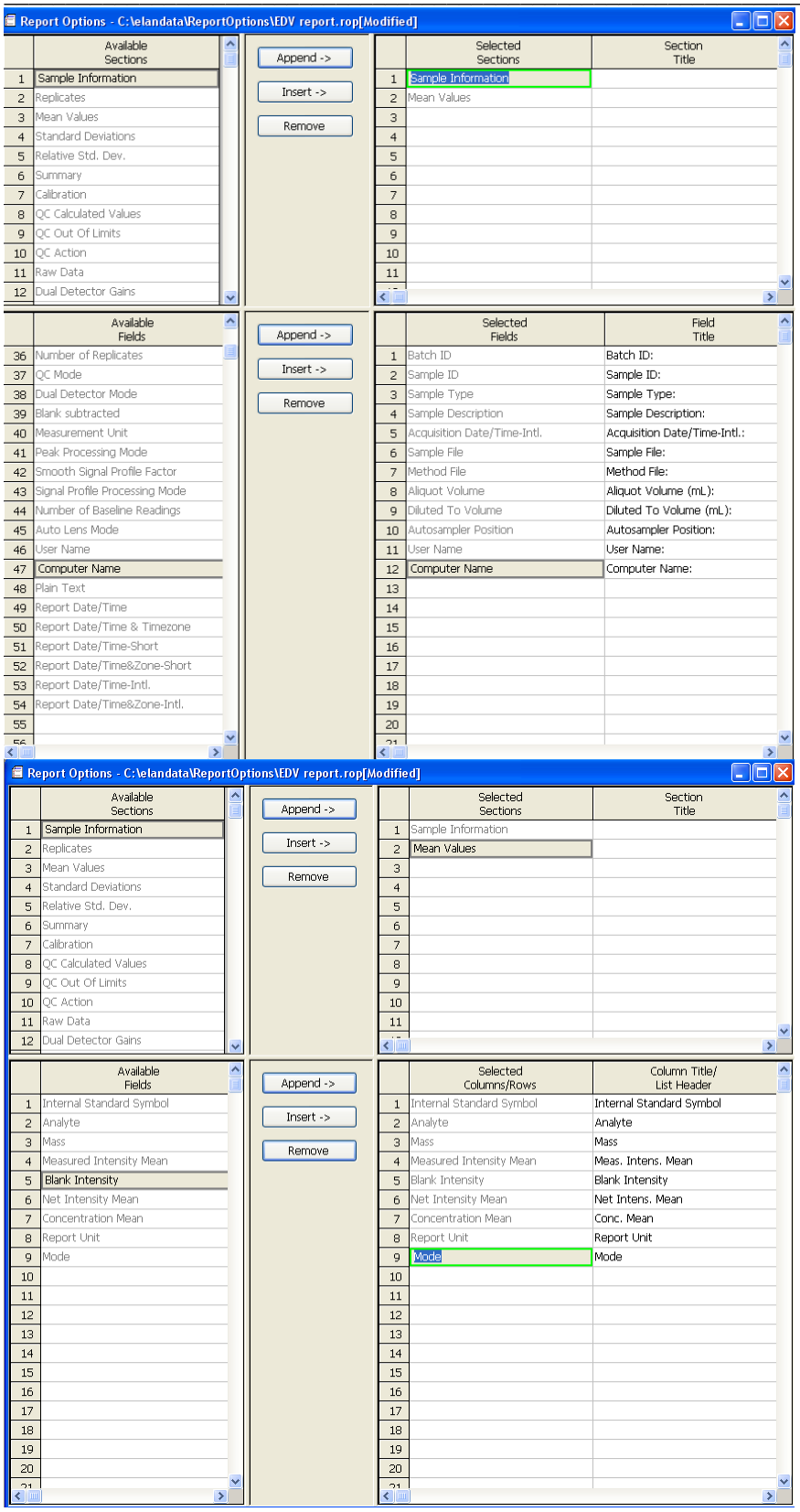
Define export settings in „Report Option Template“. The rop file saves the export settings.

Select following sections in the rop file „Report Option“:

- Sample Information
- Mean Values

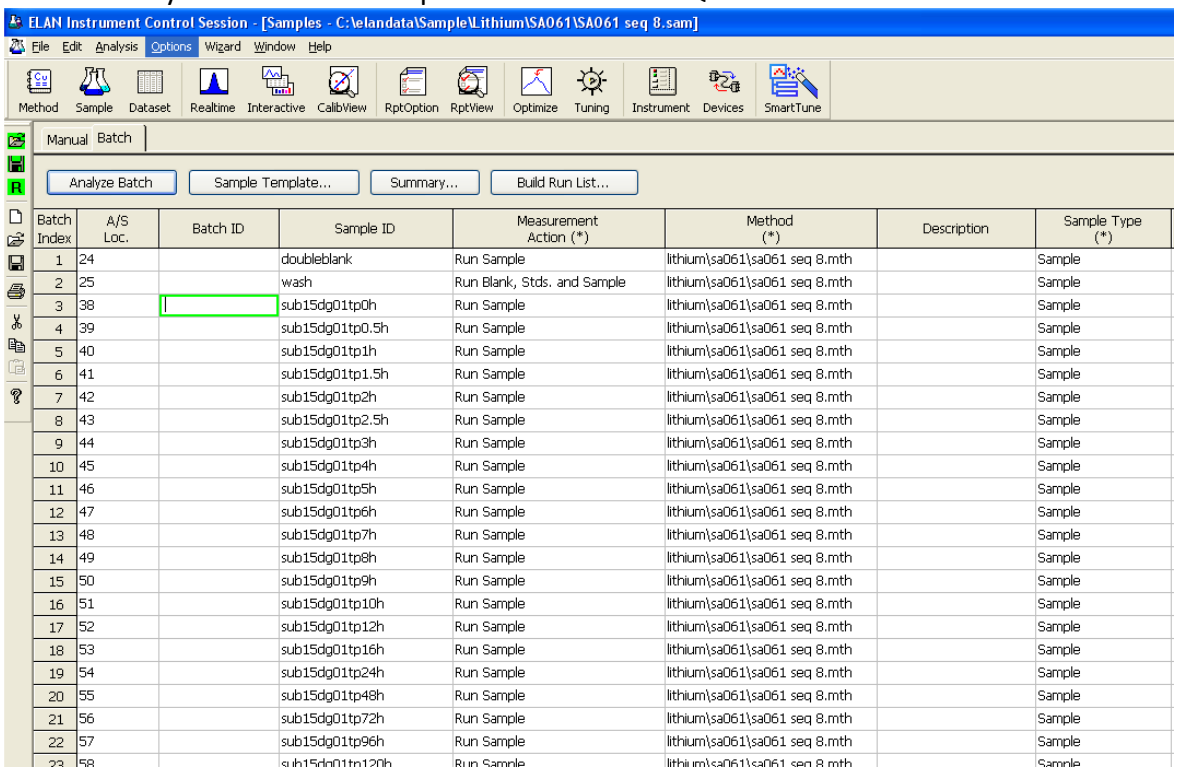
Save report method e.g. as dblabcalreport.rop (Report Template)

See following screen shots for details:


Report Options - C:\elandata\ReportOptions\EDV report.rop[Modified]
Available Sections
Append ->
Insert ->
Remove
Selected Sections
Section Title
1 Sample Information
2 Replicates
3 Mean Values
4 Standard Deviations
5 Relative Std. Dev.
6 Summary
7 Calibration
8 QC Calculated Values
9 QC Out Of Limits
10 QC Action
11 Raw Data
12 Dual Detector Gains
1 Sample Information
2 Mean Values
Available Fields
Append ->
Insert ->
Remove
Selected Fields
Field Title
36 Number of Replicates
37 QC Mode
38 Dual Detector Mode
39 Blank subtracted
40 Measurement Unit
41 Peak Processing Mode
42 Smooth Signal Profile Factor
43 Signal Profile Processing Mode
44 Number of Baseline Readings
45 Auto Lens Mode
46 User Name
47 Computer Name
48 Plain Text
49 Report Date/Time
50 Report Date/Time & Timezone
51 Report Date/Time-Short
52 Report Date/Time&Zone-Short
53 Report Date/Time-Intl.
54 Report Date/Time&Zone-Intl.
55
1 Batch ID
2 Sample ID
3 Sample Type
4 Sample Description
5 Acquisition Date/Time-Intl.
6 Sample File
7 Method File
8 Aliquot Volume
9 Diluted To Volume
10 Autosampler Position
11 User Name
12 Computer Name
Batch ID:
Sample ID:
Sample Type:
Sample Description:
Acquisition Date/Time-Intl.:
Sample File:
Method File:
Aliquot Volume (mL):
Diluted To Volume (mL):
Autosampler Position:
User Name:
Computer Name:
Report Options - C:\elandata\ReportOptions\EDV report.rop[Modified]
Available Sections
Append ->
Insert ->
Remove
Selected Sections
Section Title
1 Sample Information
2 Replicates
3 Mean Values
4 Standard Deviations
5 Relative Std. Dev.
6 Summary
7 Calibration
8 QC Calculated Values
9 QC Out Of Limits
10 QC Action
11 Raw Data
12 Dual Detector Gains
1 Sample Information
2 Mean Values
Available Fields
Append ->
Insert ->
Remove
Selected Columns/Rows
Column Title/ List Header
1 Internal Standard Symbol
2 Analyte
3 Mass
4 Measured Intensity Mean
5 Blank Intensity
6 Net Intensity Mean
7 Concentration Mean
8 Report Unit
9 Mode
1 Internal Standard Symbol
2 Analyte
3 Mass
4 Measured Intensity Mean
5 Blank Intensity
6 Net Intensity Mean
7 Concentration Mean
8 Report Unit
9 Mode
Internal Standard Symbol
Analyte
Mass
Meas. Intens. Mean
Blank Intensity
Net Intens. Mean
Conc. Mean
Report Unit
Mode

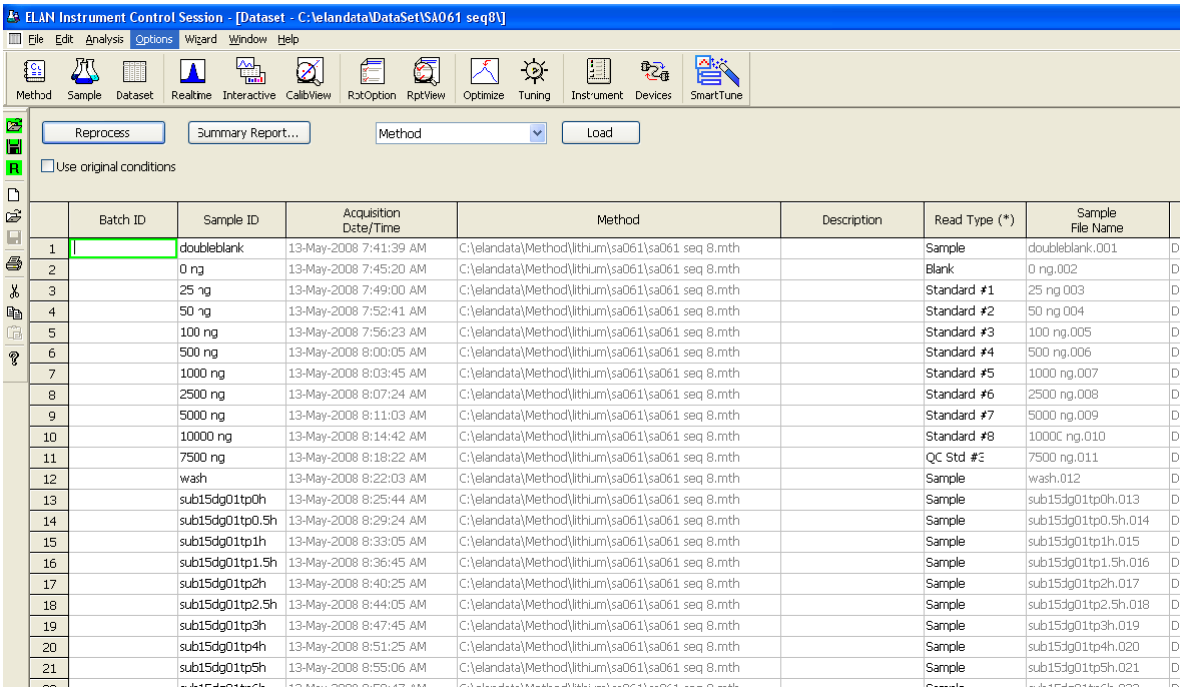
Write Sample list (Icon „Sample“).

Here are only the unknown samples. Standards and QCs are defined in the method.



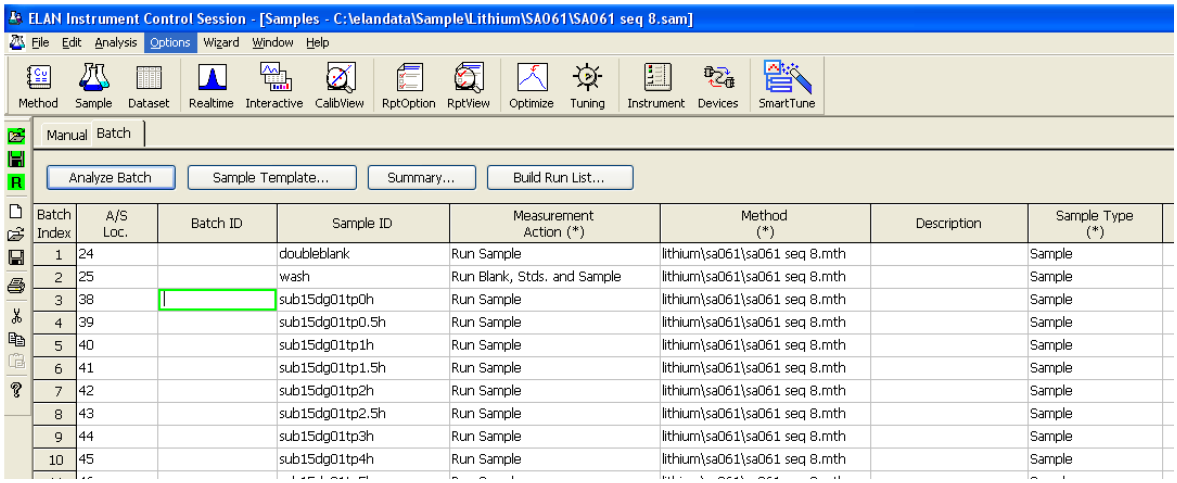
Batch Index	A/S Loc.	Batch ID	Sample ID	Measurement Action (*)	Method (*)	Description	Sample Type (*)
1	24		doubleblank	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
2	25		wash	Run Blank, Stds. and Sample	lithium\sa061\sa061 seq 8.mth		Sample
3	38		sub15dg01tp0h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
4	39		sub15dg01tp0.5h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
5	40		sub15dg01tp1h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
6	41		sub15dg01tp1.5h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
7	42		sub15dg01tp2h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
8	43		sub15dg01tp2.5h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
9	44		sub15dg01tp3h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
10	45		sub15dg01tp4h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
11	46		sub15dg01tp5h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
12	47		sub15dg01tp6h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
13	48		sub15dg01tp7h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
14	49		sub15dg01tp8h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
15	50		sub15dg01tp9h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
16	51		sub15dg01tp10h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
17	52		sub15dg01tp12h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
18	53		sub15dg01tp16h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
19	54		sub15dg01tp24h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
20	55		sub15dg01tp48h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
21	56		sub15dg01tp72h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
22	57		sub15dg01tp96h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
23	58		sub15dg01tp120h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample

Define the result file „Dataset“ (Icon „Dataset“)



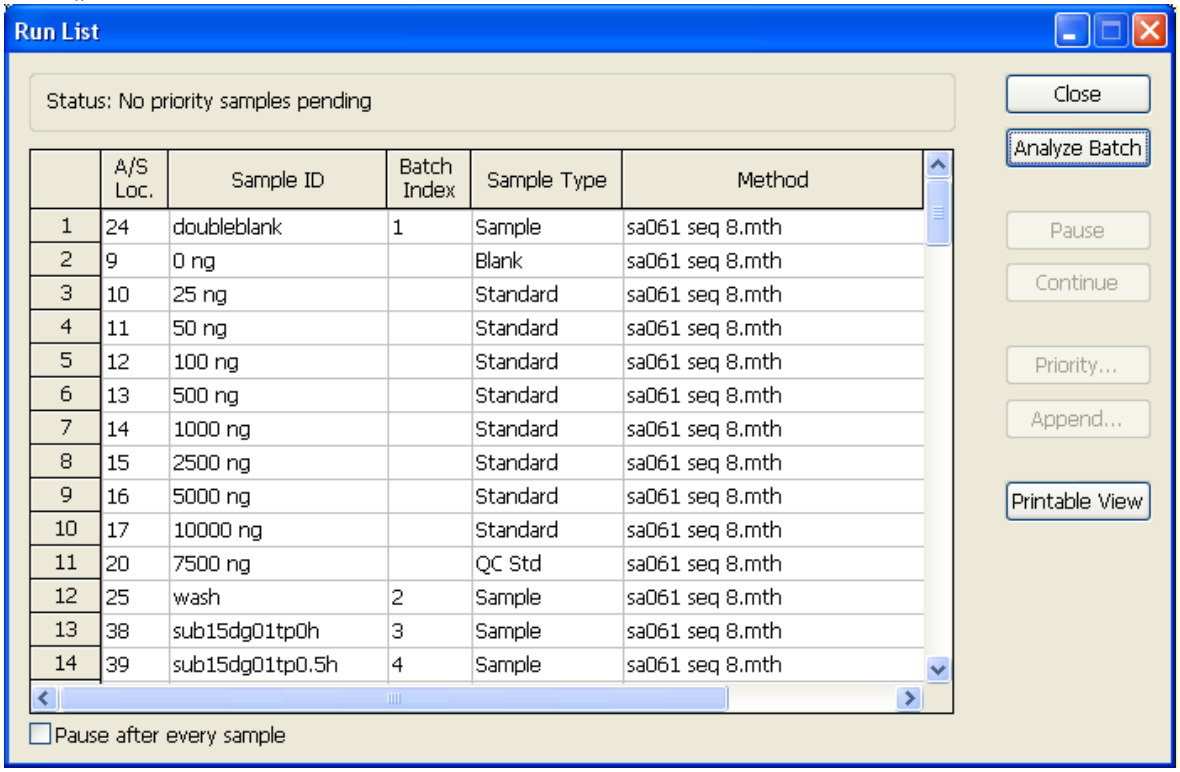
	Batch ID	Sample ID	Acquisition Date/Time	Method	Description	Read Type (*)	Sample File Name
1		doubleblank	13-May-2008 7:41:39 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	doubleblank.001
2		0 ng	13-May-2008 7:45:20 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Blank	0 ng.002
3		25 ng	13-May-2008 7:49:00 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Standard #1	25 ng.003
4		50 ng	13-May-2008 7:52:41 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Standard #2	50 ng.004
5		100 ng	13-May-2008 7:56:23 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Standard #3	100 ng.005
6		500 ng	13-May-2008 8:00:05 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Standard #4	500 ng.006
7		1000 ng	13-May-2008 8:03:45 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Standard #5	1000 ng.007
8		2500 ng	13-May-2008 8:07:24 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Standard #6	2500 ng.008
9		5000 ng	13-May-2008 8:11:03 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Standard #7	5000 ng.009
10		10000 ng	13-May-2008 8:14:42 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Standard #8	10000 ng.010
11		7500 ng	13-May-2008 8:18:22 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		QC Std #3	7500 ng.011
12		wash	13-May-2008 8:22:03 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	wash.012
13		sub15dg01tp0h	13-May-2008 8:25:44 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	sub15dg01tp0h.013
14		sub15dg01tp0.5h	13-May-2008 8:29:24 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	sub15dg01tp0.5h.014
15		sub15dg01tp1h	13-May-2008 8:33:05 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	sub15dg01tp1h.015
16		sub15dg01tp1.5h	13-May-2008 8:36:45 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	sub15dg01tp1.5h.016
17		sub15dg01tp2h	13-May-2008 8:40:25 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	sub15dg01tp2h.017
18		sub15dg01tp2.5h	13-May-2008 8:44:05 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	sub15dg01tp2.5h.018
19		sub15dg01tp3h	13-May-2008 8:47:45 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	sub15dg01tp3h.019
20		sub15dg01tp4h	13-May-2008 8:51:25 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	sub15dg01tp4h.020
21		sub15dg01tp5h	13-May-2008 8:55:06 AM	C:\elandata\Method\lithium\sa061\sa061 seq 8.mth		Sample	sub15dg01tp5h.021

Select „Sample“ icon again, select all and click „.**Build Run List**“ button



Batch Index	A/S Loc.	Batch ID	Sample ID	Measurement Action (*)	Method (*)	Description	Sample Type (*)
1	24		doubleblank	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
2	25		wash	Run Blank, Stds. and Sample	lithium\sa061\sa061 seq 8.mth		Sample
3	38		sub15dg01tp0h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
4	39		sub15dg01tp0.5h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
5	40		sub15dg01tp1h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
6	41		sub15dg01tp1.5h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
7	42		sub15dg01tp2h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
8	43		sub15dg01tp2.5h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
9	44		sub15dg01tp3h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample
10	45		sub15dg01tp4h	Run Sample	lithium\sa061\sa061 seq 8.mth		Sample

Print „Run List“



	A/S Loc.	Sample ID	Batch Index	Sample Type	Method
1	24	doubleblank	1	Sample	sa061 seq 8.mth
2	9	0 ng		Blank	sa061 seq 8.mth
3	10	25 ng		Standard	sa061 seq 8.mth
4	11	50 ng		Standard	sa061 seq 8.mth
5	12	100 ng		Standard	sa061 seq 8.mth
6	13	500 ng		Standard	sa061 seq 8.mth
7	14	1000 ng		Standard	sa061 seq 8.mth
8	15	2500 ng		Standard	sa061 seq 8.mth
9	16	5000 ng		Standard	sa061 seq 8.mth
10	17	10000 ng		Standard	sa061 seq 8.mth
11	20	7500 ng		QC Std	sa061 seq 8.mth
12	25	wash	2	Sample	sa061 seq 8.mth
13	38	sub15dg01tp0h	3	Sample	sa061 seq 8.mth
14	39	sub15dg01tp0.5h	4	Sample	sa061 seq 8.mth

Click „Analyze Batch“button. **Analysis is running**…
All data are in the rep file after the analysis is finished.

The *.rep file is imported into dbLabCal via menu BATCH IMPORT...

All data including the "MEAS. INTENS. MEAN" values as well as the "NET INTENS. MEAN" values are in a rep file after the measurement was finished.

dbLabCal imports either "MEAS. INTENS. MEAN" or "NET INTENS. MEAN" depending on the column position (the most left column data are imported) which can be defined while creating the rep file.

Appendix 10: ICP-HPLC-MS Chromera

Designed for ONLY 1 Analyte plus 1 Internal Standard

In Excel „Search&Replace „ISName“ mit “ IS “+„ISName“

dbLabCal identifies internal standard (one of the 2 allowed entries) if the element name starts with “IS “ characters vor

Sample Name	Sample Description	Injection Number	Vial Number	Sample Type	Standard Name	Group
QCs 150 ng		1	1	Sample		UA290

Channel	Ret. Time	Component Name	Area	Height
Gd 160	17.14168111		129811.6075	1507.66624
IS Lu 175	19.32693663	Lutetium	1370701.828	10672.56676

QCs 1500 ng		1	2	Sample		UA290

Channel	Ret. Time	Component Name	Area	Height
Gd 160	17.03649412		1236305.684	14069.79958
IS Lu 175	19.3152	Lutetium	1415110.746	10364.69024

QCs 4000 ng		1	3	Sample		UA290

Channel	Ret. Time	Component Name	Area	Height
Gd 160	17.09205576		3432714.392	39252.48262
IS Lu 175	19.3431267	Lutetium	1515799.547	10645.02664

wash		1	4	Sample		UA290

Channel	Ret. Time	Component Name	Area	Height
Gd 160	17.01013632		28490.2845	331.671417
IS Lu 175	19.17466486	Lutetium	6196.9763	61.08675937

wash		1	5	Sample		UA290

Channel	Ret. Time	Component Name	Area	Height
Gd 160	17.12721705		12902.0261	157.6733076
IS Lu 175	19.45235138	Lutetium	3814.75719	33.17419784

wash		1	6	Sample		UA290

usw...

Appendix 11: FACS

Export results (program FlowCytomix Pro 2.3, view EVALUATION RESULTS) into a csv-file.

The *.csv file is imported into dbLabCal via menu BATCH IMPORT...

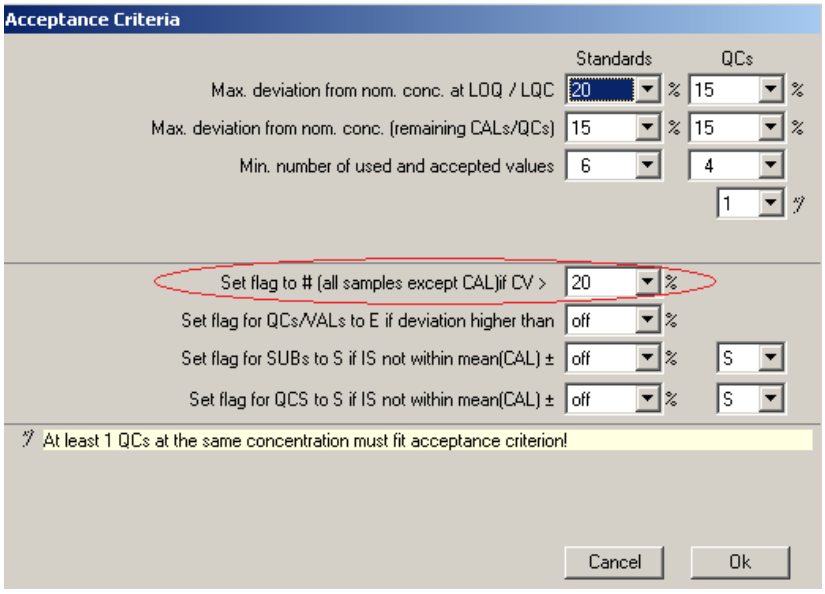
Important:
dbLabCal imports only calculated results. Therefore, xls file import is possible only if current project uses regression model NO CALC.

Appendix 12: SearchLight

SearchLight software creates results in a xls file. xls file has also a special sheet adapted for dbLabCal import called PG-ML DATA2.

dbLabCal imports data from PG-ML DATA2 sheet automatically when selecting the xls file via dbLabCal's BATCH IMPORT... menu

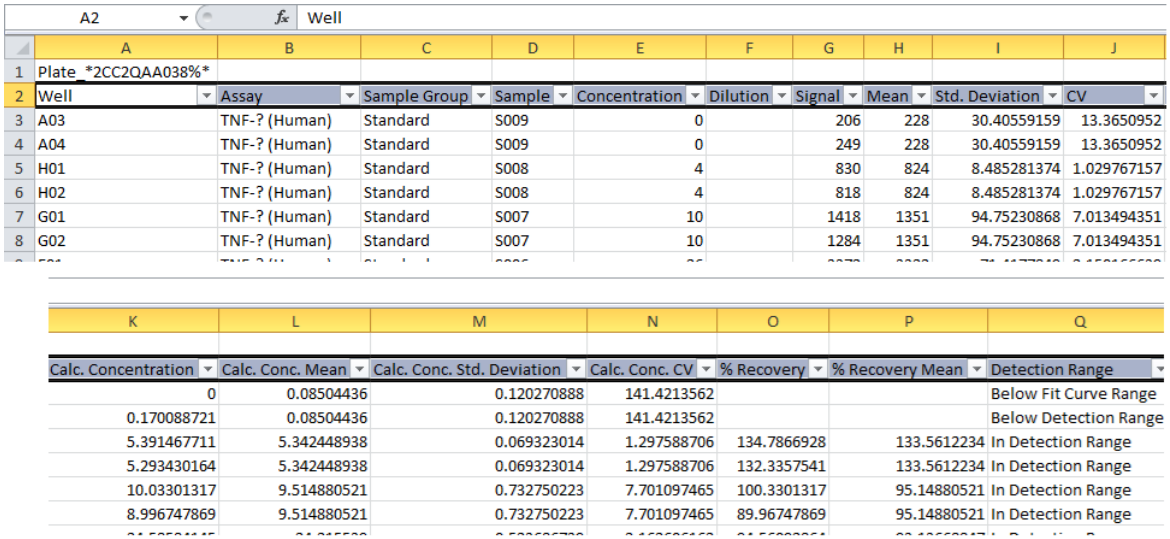
dbLabCal checks also automatically double assay CV acceptance criterion if activated – see below- and set # flag if necessary.



Important: xls file import is possible only if current project uses regression model NO CALC.(DOUBLE ASSAYS)

Appendix 13: Mesoscale (MSD)

Die MSD Discovery Bench Software creates one CSV file containing all results of all analytes. Analyte names are defined in the second column („Assay“). See following screen shot for an example of a MSD export file.



A2 | Well

	A	B	C	D	E	F	G	H	I	J
1	Plate_*2CC2QAA038%*									
2	Well	Assay	Sample Group	Sample	Concentration	Dilution	Signal	Mean	Std. Deviation	CV
3	A03	TNF-? (Human)	Standard	S009	0		206	228	30.40559159	13.3650952
4	A04	TNF-? (Human)	Standard	S009	0		249	228	30.40559159	13.3650952
5	H01	TNF-? (Human)	Standard	S008	4		830	824	8.485281374	1.029767157
6	H02	TNF-? (Human)	Standard	S008	4		818	824	8.485281374	1.029767157
7	G01	TNF-? (Human)	Standard	S007	10		1418	1351	94.75230868	7.013494351
8	G02	TNF-? (Human)	Standard	S007	10		1284	1351	94.75230868	7.013494351

K	L	M	N	O	P	Q
Calc. Concentration	Calc. Conc. Mean	Calc. Conc. Std. Deviation	Calc. Conc. CV	% Recovery	% Recovery Mean	Detection Range
0	0.08504436	0.120270888	141.4213562			Below Fit Curve Range
0.170088721	0.08504436	0.120270888	141.4213562			Below Detection Range
5.391467711	5.342448938	0.069323014	1.297588706	134.7866928	133.5612234	In Detection Range
5.293430164	5.342448938	0.069323014	1.297588706	132.3357541	133.5612234	In Detection Range
10.03301317	9.514880521	0.732750223	7.701097465	100.3301317	95.14880521	In Detection Range
8.996747869	9.514880521	0.732750223	7.701097465	89.96747869	95.14880521	In Detection Range

dbLabCal creates individual batch for every imported analyte.
This is the difference to the standard behaviour of dbLabCal: dbLabCal creates one batch containing all analytes analysed in one batch.

Appendix 14: Calculation of weighted linear regression

$$y = a + b \cdot x$$

Weighting:

none:	$w_i = 1$		
1/X:	$w_i = \frac{1}{x_i}$	1/Y:	$w_i = \frac{1}{y_i}$
1/X^2:	$w_i = \frac{1}{x_i^2}$	1/Y^2:	$w_i = \frac{1}{y_i^2}$

$$S_w = \sum_{i=1}^{n} w_i$$

$$S_x = \sum_{i=1}^{n} w_i \cdot x_i$$

$$S_y = \sum_{i=1}^{n} w_i \cdot y_i$$

$$S_{xy} = \sum_{i=1}^{n} w_i \cdot x_i \cdot y_i$$

$$S_{x2} = \sum_{i=1}^{n} w_i \cdot x_i^2$$

$$S_{y2} = \sum_{i=1}^{n} w_i \cdot y_i^2$$

Intercept:

$$a = \frac{S_y \cdot S_{x2} - S_x \cdot S_{xy}}{S_w \cdot S_{x2} - S_x^2}$$

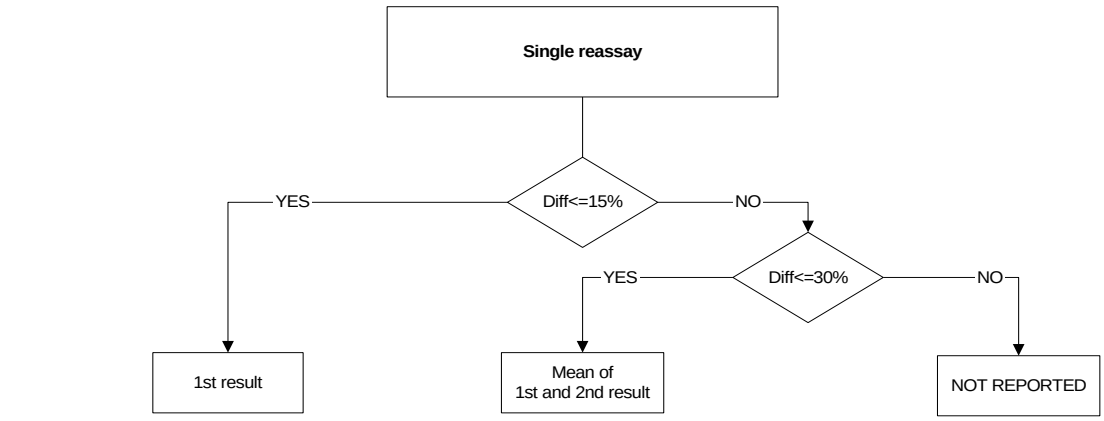
Slope:

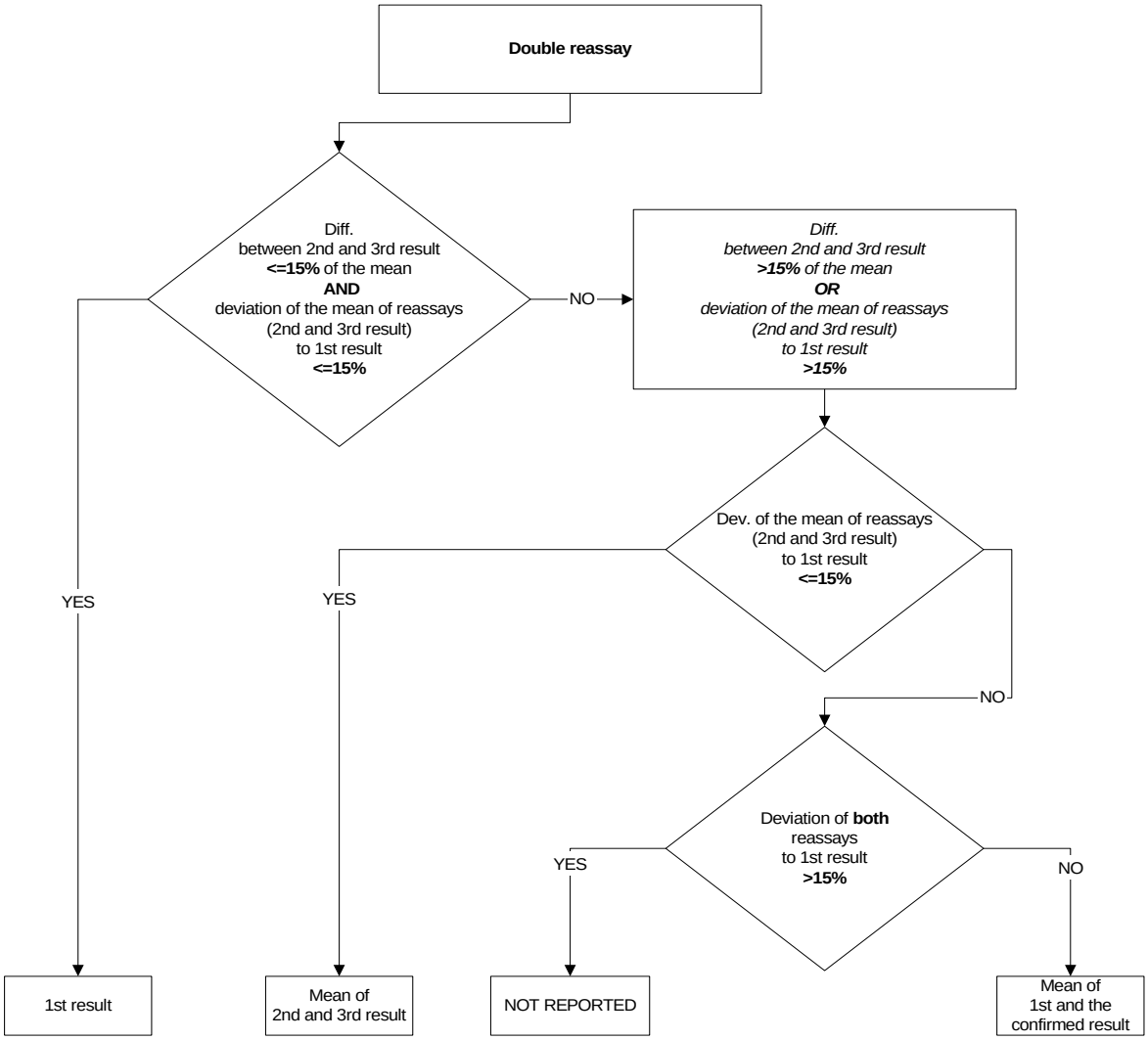
$$b = \frac{S_w \cdot S_{xy} - S_x \cdot S_y}{S_w \cdot S_{x2} - S_x^2}$$

Determination Coefficient:

$$r^2 = \frac{\left(S_w \cdot S_{xy} - S_x \cdot S_y\right)}{\left(S_w \cdot S_{x2} - S_x^2\right) \cdot \left(S_w \cdot S_{y2} - S_y^2\right)}$$

Appendix 15: Flowchart: Reporting Final Results (Lang&Bolton)





Appendix 16: Flowchart: Reporting Final Results (HoLaRo)