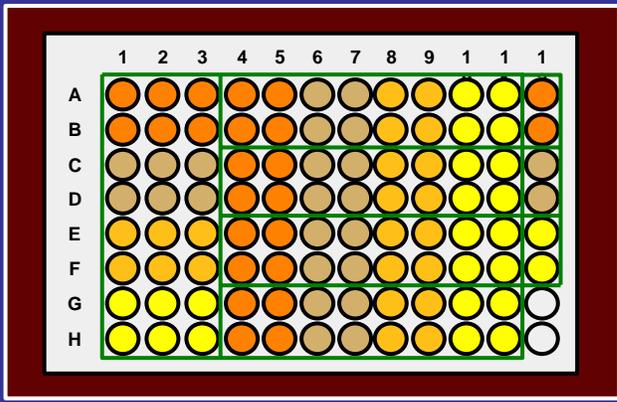


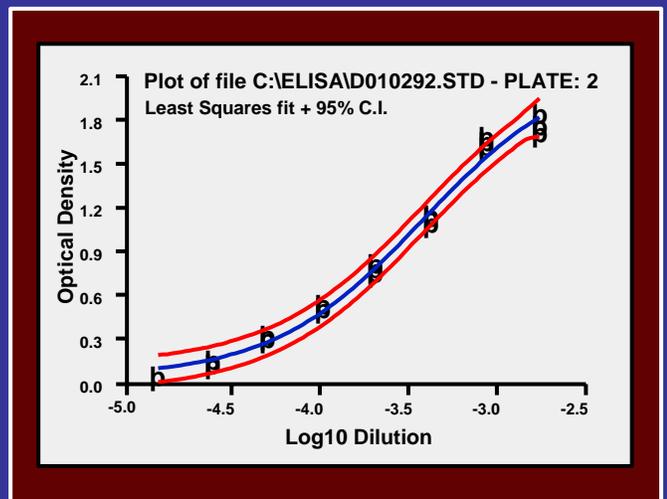
# ELISA

## *for Windows*



# User's Manual

- Customized ELISA plate formats
- Robust regression
- Iteratively reweighted least squares
- Outlier detection
- Antibody quantitation



U.S. DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service  
Centers for Disease Control and Prevention  
National Center for Infectious Diseases  
Division of Bacterial and Mycotic Diseases  
Atlanta, GA 30333 USA



# Program **ELISA** *for Windows*

**Version 2.00**

## User's Manual

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# INTRODUCTION

**ELISA** *for Windows* is a collection of public domain programs prepared for general release to those individuals who typically perform bioassays using a 96-well ELISA plate. This program is flexible and applicable to a wide body of researchers and analysis protocols.

We are pleased to distribute the routines to anyone who requests them with the proviso that each investigator will need to spend some time learning the functions of each module to benefit from the whole collection of programs. The authors also request that they be cited as the source for this work when these techniques are incorporated into new or existing software or used in the preparation of published reports. A suggested citation for **ELISA** *for Windows* appears at the bottom of the title page of this manual.

The programs are complex and contain many checks to monitor for user errors when responding to screen prompts. However, it is not feasible to make these error checks exhaustive, and it is possible to lock up the program by entering illogical responses to screen prompts or by selecting various options in an incorrect order. Users may guard against these eventualities by exercising care in forming their analysis strategies and responses to various inquiries.

This documentation was prepared as carefully as possible and, hopefully, is complete to the extent that most users will be able to install and use **ELISA** *for Windows* with minimal complications. We would appreciate being notified of any additions or modifications which could be made to this manual to clarify the program's operation.

This documentation was intentionally written to be verbose and, at times, somewhat repetitive. We have attempted to anticipate all problems and questions involved with running the programs. The repetitive nature of this document is meant to facilitate running the different modules without having to leaf back and forth through the manual looking for pertinent information related to the task at hand. It should be noted that we are not able to test every possible combination of options and prompts which the program offers. We also cannot foresee all possible computer configurations, hard disk subdirectory structures, etc. which may cause **ELISA** *for Windows* to perform errati-

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cally. If any inconsistencies do occur, we would appreciate being notified so that we may be able to rectify any problems. In the long run, we believe that in its present implementation, **ELISA for Windows** is extremely stable. We would not distribute it otherwise.

Questions related to program execution should be directed to one of the members of the Respiratory Diseases Immunology Section, Respiratory Diseases Branch, DBMD/NCID/CDC. Questions regarding the theoretical background of the techniques involved (e.g., the iteratively reweighted robust/least squares fit) as well as program 'bugs' should be directed to Brian D. Plikaytis, Biostatistics and Information Management Branch/DBMD/NCID/CDC.

**ELISA for Windows** has been formally validated. The software and all accompanying documentation may be downloaded from the web site <http://www.cdc.gov/ncidod/dbmd/bimb/elisa.htm>. In addition to this manual the web site also offers several additional documents for downloading. An Installation Qualification Protocol is available with instructions for downloading and installation of the software. An Operational Qualification Protocol guides users through every module and offers comparison data files so users may check to see if they are operating the software correctly. A Process Qualification Report provides the theoretical background for the analytical methods implemented in the software. The Validation Protocol details the steps taken to validate the software and the Validation Report details the results of the validation process.

## Getting Started

---

### Installation

**ELISA for Windows** is a 32-bit application and will run under current Windows operating systems.

The software and accompanying documentation may be downloaded from the web site <http://www.cdc.gov/ncidod/dbmd/bimb/elisa.htm>. Installation instructions are contained in the Installation Qualification Protocol. To confirm the software is installed correctly, an Operational Qualification Protocol may be downloaded. This protocol guides users through every module. Comparison files are included so users may check each processing step.

### Standard Curve Formation

**ELISA for Windows** uses several techniques for estimating standard or calibration curve parameters. Users may employ a parametric model, the four-parameter logistic-log function to form standard curves. In this case, the user may exercise several fitting options when forming standard curves. An iteratively unweighted least squares method and a robust iteratively reweighted least squares technique may be employed. Users may also select between two estimation algorithms, Taylor series-linearization, and Marquardt's Compromise. These options are described in much more detail in the parameter estimation section of this documentation. Alternatively, a spline fit may be used for those instances where the parametric curves cannot adequately describe the standards. The spline may be selected in the standard curve plotting module or the antibody concentration calculation module. The standard curve line described by the spline fit is programmed to pass through the median value of the replicate optical densities at each dilution along the curve.

## Module Output

Numeric output from the various modules is formatted as concisely as possible while retaining the maximum degree of information. In almost all cases, procedure output is designed to span a fixed 80 column line so that results may be viewed on-screen as well as directed to a printer. While designing the output format for each of the modules, we endeavored to allocate enough spaces for numeric results which would accommodate most any data processed by the program. If numeric results exceed available space unpredictable results may occur (e.g., 0's reported instead of real results). This should not be an issue with normal data sets. If it does prove to be a problem, please inform us. Module output is directed to a windowing screen with both vertical and horizontal scroll bars along the right and bottom edges, respectively, of the window. Users may scroll through the output using these scroll bars. Additionally, some windows permit users to position the cursor anywhere within the frame and enter comments from the keyboard. These functions will be described more fully in the pertinent sections of this documentation.

All output may be directed to a file for later retrieval and printing using any word processing program. The output is stored in standard ASCII text format.

## Dialog Windows

Dialog windows are used throughout *ELISA for Windows* and serve as a mechanism for users to input various parameters and select options for module execution. In general, dialog windows are composed of three basic constructs for user input, check boxes, option buttons, and text boxes and appear as:

[X]	Check box
(°)	Option button
[ ]	Text box

Check boxes are used to turn any number of user options on [X] and off [ ]. By clicking on the check box with the left mouse button, users are able to select/deselect check box items.

Option buttons are arranged in groups and are mutually exclusive. That is, a user may select only one option from a group of options. Also, one option button in a group must be selected. Option buttons are activated (°) by clicking on them with the left mouse button.

Text boxes are used for free-field text entry (e.g., titles for reports) or to enter numbers which are used in subsequent calculations (e.g., initial parameter estimates for standard curve estimation). When numbers are required, **ELISA for Windows** will restrict text entry to just numeric data, beeping if a letter or other nonnumeric character is entered. Text boxes are accessed by clicking anywhere between the square brackets. Data or text are then entered from the keyboard.

**ELISA for Windows** will restrict the selection of some options based on previous user input. An example of this feature may be found in the standard curve plotting module where users may choose from three possible fitting techniques (robust, unweighted least squares, and spline fits). In this circumstance, **ELISA for Windows** will only allow users to select the spline fit or any other fit chosen in the parameter estimation module for the given standards data file. That is, if the user selected just the robust fit during parameter estimation, he/she will only have access to the spline and robust fit options in the plotting module. The unweighted least squares option will be suppressed.

---

## File Structures

---

### Raw Data

**ELISA for Windows** is not a program intended to interface with an ELISA reader. **ELISA for Windows** will process files captured from an ELISA reader using the reader's or some third-party software. Pre-processing filters are implemented in the 'Process ELISA Reader Data' module to translate output captured from a variety of readers to a uniform format which the remaining modules of the program may access.

If the user employs an ELISA reader for which a filter does not exist, **ELISA for Windows** may still analyze the data as long as the raw data conform to the uniform format which **ELISA for Windows** expects to process. ? outlines the format for the raw data (.DAT) file required by **ELISA for Windows**.

Raw data files are named with a .DAT extension such as *file*.DAT, where *file* is the root name assigned by the user. The .DAT extension is not required for program execution but will facilitate certain operations in different program modules. It is strongly recommended that users adhere to this convention. One or more comment lines may be placed at the beginning of each plate in the manner displayed in ?. These comment lines are optional. If they are included, the word **COMMENT** must be capitalized, start in column 1 and be followed by a colon (:). **ELISA for Windows** detects the end of the comment lines and the beginning of the data by the absence of

```

COMMENT:This is comment line 1
COMMENT:This is comment line 2
 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
repeat for second plate.
repeat for third plate.
.
. Include as many plates as desired.
.

```

Figure 1. Uniform format for .DAT file required by program **ELISA** for Windows.

the character string **COMMENT**. The data portion is arranged in the standard 8 row, 12 column ELISA plate format. Additional plates may be chained together so that a .DAT file may contain data from several plates. Comment lines are not required as **ELISA** for Windows simply counts each 8 rows of numbers as one plate. If comment lines are present then the third module, Abstract Data, will place these in a .LBL file. This file will later be used to annotate output from module 4, Parameter Estimation and module 6, Calculate Concentrations.

When **ELISA** for Windows creates .DAT files using the unprocessed data directly captured from any ELISA reader, the program translates all negative and 0.0 optical density measurements to 0.001. When users create the .DAT files, all absorbance values must be greater than or equal to 0.001. This is a requirement for the successful execution of many of the subsequent modules in the program.

## File and Subdirectory Naming Conventions

**ELISA** for Windows creates several files some of which are transitory in nature. This is to say they are rewritten with new information each time the program is executed. Some of these files are meant for internal use by the program and are of little interest to the user other than to recognize their existence. Other files contain some forms of output which are generated automatically each time certain modules within **ELISA** for Windows are executed.

A second form of file with defined extensions is created during the data processing and analysis stages of **ELISA** for Windows. In this situation, the user is prompted for a root file name (name without an extension), and the program will automatically generate the necessary formatted file with a defined extension. Figure 2

outlines these different types of files. Each file or file type will be discussed in the appropriate section of this documentation.

Each of the different data file types, *file.DAT*, *file.STD*, *file.UNK*, *file.QC*, *file.LBL*, and *file.CFT*, where *file* is a joint file name created by the user and **ELISA for Windows**, **must** reside in the same subdirectory of the local hard disk drive or on the same diskette. These files are used in a linked fashion during data processing and analysis and are treated as a unified group. If the file group is split into two or more subdirectories, **ELISA for Windows** will not be able to locate all of them and the program will continue with unpredictable results.

Data and program files should not be stored in subdirectory with names that include an extension. The period (.) in a subdirectory name that includes an extension will adversely affect the parts of the program that automatically add predefined extensions to root file names. This will ultimately lead to a program execution error.

## File Types

All files created by **ELISA for Windows** are ASCII text files which may be viewed using any DOS or Windows text editor. These files may additionally be used as data for input into other programs. The one exception to this is the coefficient files with the .CFT extension. The coefficient files are so-called 'random-access' files and are stored in a compressed or packed format. These files may only be read reliably by **ELISA for Windows**.

## Archiving Files

.DAT	Raw data file.
.STD	Standards data file.
.UNK	Unknowns data file.
.QC	Quality control samples file.
.LBL	Plate label file with comments from the .DAT file (If there are any).
.CFT	Coefficient file generated from Module 4 -Parameter Estimation.
.TPL	Template file details abstraction protocol for standards, unknowns and quality control samples.
.FIT	Report file from Module 4 - Parameter Estimation.
.RPT	Expanded report file from module 6 - Calculate Concentrations.
.SUM	Summary report file from Module 6 - Calculate Concentrations.
TEMPFILE	Scratch file used in the parameter estimation and concentration calculation modules.

Figure 2. File types used by program **ELISA for Windows**.

Outdated files should be archived periodically. When a particular file is archived, **all** files with the same root name should be archived as well. This will keep the linked files together in one group. That is, if it is desired to archive a series of .DAT files, the associated .STD, .UNK, .QC, .LBL, and .CFT files should be archived as well to keep the file groups intact. **ELISA for Windows** will not operate correctly unless the entire group of files are contained in the same subdirectory.

---

## Program Execution

---

**ELISA for Windows** is initiated by double-clicking the ELISA Windows icon. The opening menu, as shown in Figure 3, will appear. The version number and date may differ from that in the figure.

The opening menu consists of a list of options corresponding to program modules. Single clicking each program module option will display the descriptive text in the box to the right. Double clicking the module option will select it and execute the program module. The remainder of this documentation will deal with each of these modules in detail.

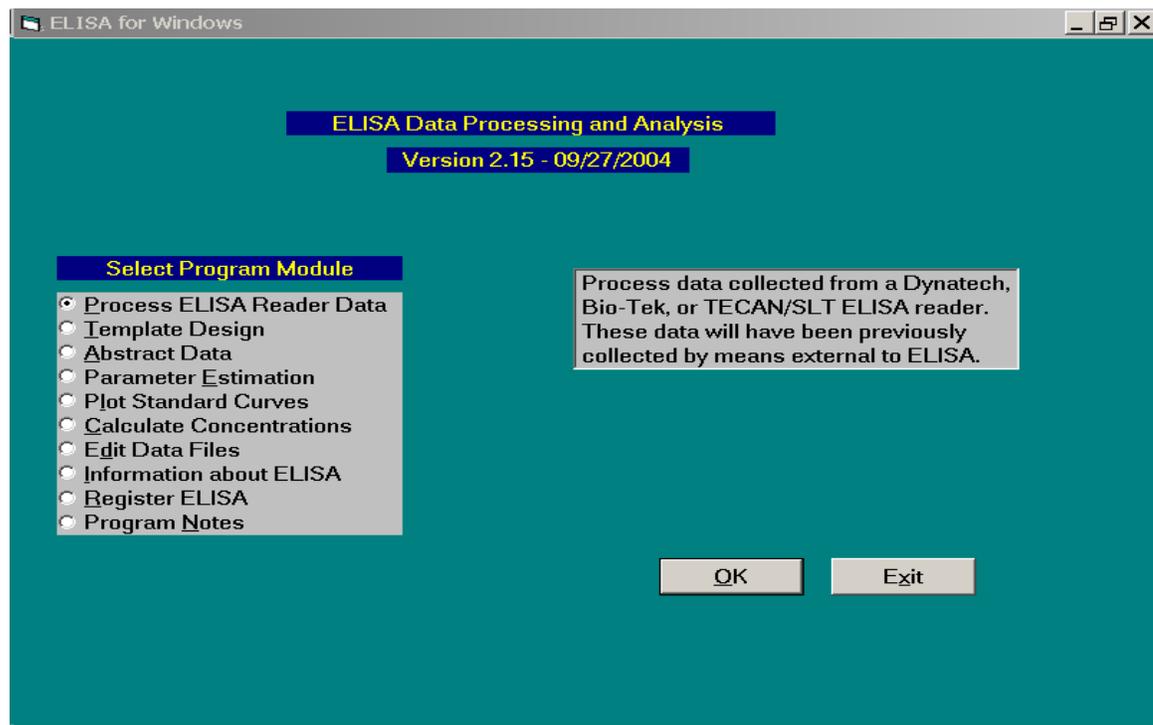


Figure 3. **ELISA for Windows** opening menu screen.

# MODULE 1

## PROCESS ELISA READER DATA

This first module processes data collected from a variety of different ELISA readers and writes these data to *file.DAT* where *file* is specified by the user in response to a file selection dialog window. It is understood that these data have already been captured from the instrument. **ELISA for Windows** will not interface with an ELISA reader to collect raw data from these instruments. The filters in this module strip off extraneous text to produce a data file as shown in ?. If it is desired to use this software with ELISA readers not included in the list in Figure 4, **ELISA for Windows** may still be used to process data files if they are edited to match the format displayed in ?.

This module is entered from the main menu (Figure 3). **ELISA for Windows** responds with the dialog window shown in Figure 4. Unfortunately, current ELISA readers offer great flexibility in formatting files exported with the plate data. Consequently, even if a user owns an ELISA reader represented in the list in Figure 4, the filter may not operate correctly. The Operations Qualification Protocol contains sample raw data files for each of the filters in Figure 4 which may be used as references for how each raw data file is constructed. Two examples of raw data files are shown in Figure 5 and Figure 6.

Figure 5 outlines the format produced by the Dynatech MR5000 reader. The

Select ELISA reader data file format.

- Dynatech (MR5000/MR600/MR700)
- Bio-Tek EL309/EL310 - FDA
- Bio-Tek EL900 - FDA
- Bio-Tek EL309 - U. of Rochester
- TECAN/SLT Absorbance data
- TECAN/SLT Abs. data from Spectrafluor
- TECAN/SLT Fluorescence data
- Multiskan Plus MK II
- Dynex - AVRP - NHP antibody detrm.
- Dynex - AVRP - Human antibody determ.
- Bio-Tek Powerwave x340 - FDA
- THERMOmax - Bioport Corp.

Enter the date which may be associated with the subsequent ELISA data filename. Only used for the Dynatech reader option:

Date (mm/dd/yy)

Ok

Exit

Figure 4. Dialog window for Module 1 - Process ELISA Reader Data.

values in the header records may differ depending on the application and instrument settings used for a particular assay. The first few lines of the file outlined in Figure 5 are comment lines entered by the operator. **ELISA for Windows** abstracts these comment lines and writes them to the .DAT file. The MR5000 ELISA reader's actual raw data begin with the MODE REF SAM line.

Figure 6 displays the data format as collected from the Dynatech MR700 reader. The reader software allows the user to enter one comment line which is the third line of the header records. **ELISA for Windows** will abstract this one line and place it in the processed .DAT file. Any additional comment lines entered by the user during data capture will be ignored.

It is possible for **ELISA for Windows** to correctly abstract data from other models of Dynatech readers. If the data conform to one of the two formats outlined in Figure 5 or Figure 6, the program should abstract the data without difficulty. As an example, the older Dynatech MR600 readers transmit data in the same format as the MR5000 so readings from this older instrument may also be processed by **ELISA for Windows**.

The file selection dialog window appears after selecting the data conversion option.

Clients using the Dynatech readers adopted a particular file naming convention which must be adhered to if the Dynatech option is selected. Raw data files captured from the ELISA readers are given two letter or digit names without an extension. These files may contain one or more plates of observations. All files two characters in length without an extension will appear in the file list box if the Dynatech option is

```

comment line 1
comment line 2
.
.
.
  MODE REF SAM
  DUAL 5 1
  THRESHLD= 0.00
  CAL=      1.00
  DATE:_____
  OPER:_____
  1 A      1.234
  1 B      1.234
  1 C      1.234
.
.
.
12 H     1.234

Repeat as many plates as desired.
```

selected. The user is required to enter the date for the Dynatech option only - the date information will be ignored for the remaining filters. The date is appended to the two-character file name when creating the .DAT file.

The second through fourth options, dealing with the Bio-Tek readers, assume the user has completely specified the filename with a .EIA extension. These files may also contain one or more plates. All files with a .EIA extension will appear in the file list box upon selecting one of these two options.

Figure 5. Raw data format - Dynatech MR5000 ELISA reader.

```

Date(/m/d/y): 5/25/91
Plate number: 1
Comment: This is a comment line
Time: 3:36 PM
Template name: alk phos
Procedure name: alk phos
Instrument: MR700
Mode: Dual
Test Filter: 1
Reference filter: 1
DATA:
1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234 1.234
Template:
      1   2   3   4   5   6   7   8   9   10  11  12
A    T1  T9  T17 T25 T33 T41 T49 T57 T65 T73 T81 T89
B    .   .   .   .   .   .   .   .   .   .   .   .
C    .   .   .   .   .   .   .   .   .   .   .   .
D
E
F
G
H    T8  T16 T24 T32 T40 T48 T56 T64 T72 T80 T88 T96
Labels:
T 1:
T 2:
.
.
.
T95:
T96:

Repeat as many plates as desired.

```

Figure 6. Raw data format - Dynatech MR700 ELISA reader.

As an example, if the Dynatech option is chosen, the file ML selected, and the date entered in the format specified (month/day/year). The program will append the date to the two-character raw data file name to create an eight character file name with a .DAT extension. Thus, if ML was entered as the two-letter raw data file name, and 08/12/04 was entered as the date of data collection, **ELISA for Windows** would create the file name ML081204.DAT as the destination for the processed data.

For the remaining filters, the file name is assumed to be fully specified by the user during data capture and the date information is not used.

Since a raw data file may contain several plates, **ELISA for Windows** will echo the plate number within the raw data file as it is processed:

```
Processing plate number 1
Processing plate number 2
.
.   Continues for all plates
.
```

After all plates have been processed, a message detailing the file name and number of plates contained within the file is displayed (this example for the two-character raw data file BP and date 11/08/96):



Clicking on OK will return the user to the main menu (Figure 3).

# MODULE 2

## TEMPLATE DESIGN

This option abstracts three types of data from a 96-well ELISA plate: standards, unknowns, and quality control samples. This option gives the user a wide degree of latitude in creating template formats for this data abstraction. The main restriction involved with this operation is that samples must be arranged in rectangular arrays and like samples (replicates) must be contiguous.

The template file selection dialog window appears after selecting this module for processing from the main menu (Figure 3). All files with a .TPL extension will appear in the file list box. Select the file for processing and the template will be loaded for viewing and editing.

To create a new template, move the cursor to the File Name box in the template file selection dialog window. Erase all characters in this box and enter the word 'NEW' (without the quotes) and then click on OK. *ELISA for Windows* will respond with the default dialog window shown in Figure 7.

A schematic diagram for a blank plate is displayed along with several boxes to select options and input data. Through the use of these options a template may be designed from scratch or an existing template edited to produce a new template.

The 'Project ID' field allows users to assign a code to the template and may be used to group unknown samples under one study or project identification heading. This field is optional.

In the 'Block Info' box, the user may select one of three types of blocks, standard (Std), unknown (Unk), or quality control (QC). Additionally, the user may edit an existing block or delete a block. The Block ID is another optional mechanism used to assign a unique code to a particular block. As an example, this may be used to code unknowns within a particular project. All subsequent output dealing with the unknown specimens will be annotated with these unique identification codes.

To define a block, position the cursor within the brackets of the upper left cell and click with the left mouse button. An 'X' will appear within the brackets. Repeat this procedure for the lower right cell. Two 'X's will now indicate the opposing corners of the block. Select the type of block just outlined by clicking on 'Std', 'Unk', or 'QC' in the Block Info box. If desired, enter a Block ID. In the 'Dilution Information' box enter the starting dilution (Start) and the magnitude of change between the dilutions in the series (Factor). *ELISA for Windows* deals with reciprocal dilutions. Thus, if a series begins with a 1:600 dilution, 600 would be entered in the Start field. If the series follows a twofold dilution then '2' would be entered in the Factor field. If the series proceeds in an ascending fashion (i.e., 1:600, 1:1200, 1:2400, etc), then select the 'low to high' option. If the series progresses in a descending order (i.e., 1:600, 1:300, 1:150, etc.), then select the 'high to low' option. This may seem backwards at first. The way to conceptualize these prompts is to think of the reciprocal dilution

numbers. If there are three dilutions, 600 is less than 2400 so low to high means start at 600 and proceed through 2400. High to low is just the opposite: start with 600 and step down to 150.

In the 'Replicate Information' box the number of replicates and their orientation are selected. **ELISA** for Windows will check to make sure these responses are consistent with the block defined by the user. For example, a block defined as A1 - H3 contains eight rows and three columns. This allows for a replicate series running three across (horizontally) or eight down (vertically). Any other responses in these fields will be flagged as an error and the program will ask the user to reenter the required information.

Once all the information necessary to define a block is entered, clicking on the 'Record' command button will save the block definition for later recall and/or editing. The 'Boundary' field in the Block Info box will contain the coordinates for the upper left and lower right corner cells of the newly defined block. **ELISA** for Windows allows only one standards block per plate. After the standards block has been defined, the standards option button in the Block Info box will be inactivated. If an existing standards block is deleted, this option button will be reactivated.

Once a block's information is recorded, the cells are filled in to indicate they are no longer free to be included in succeeding blocks. The cells within a standards block

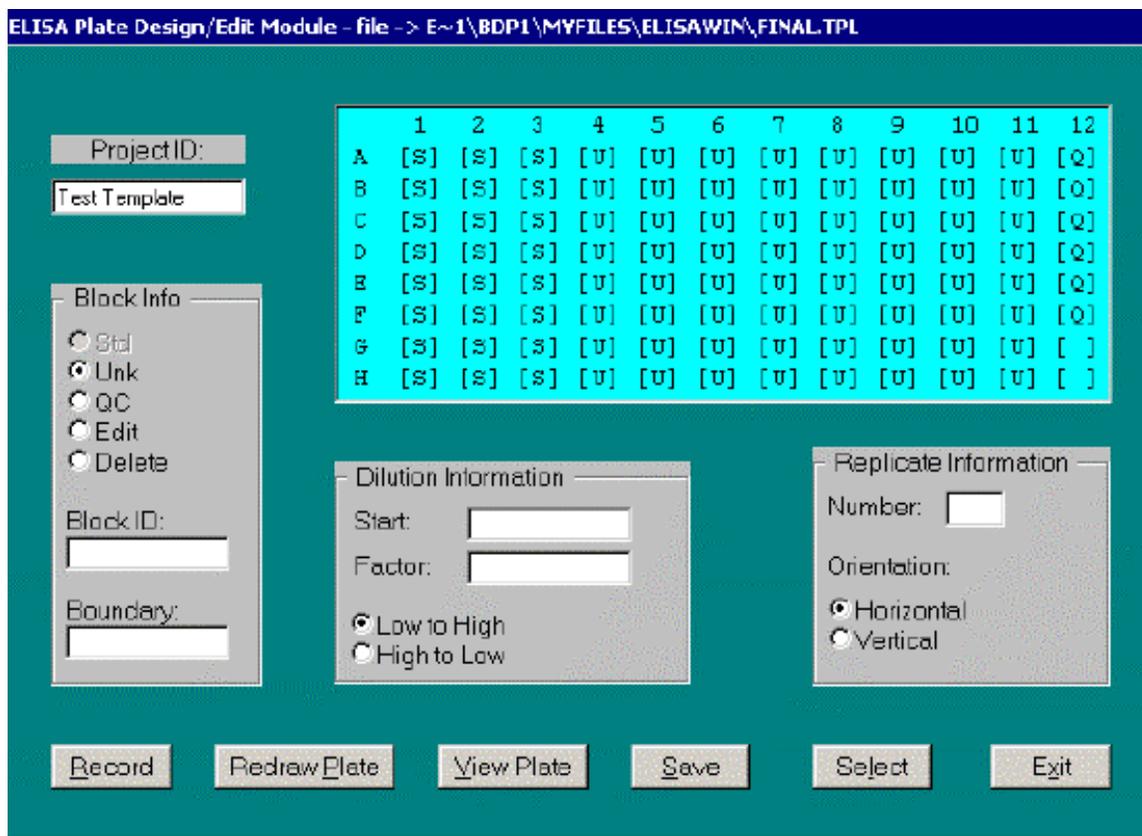


Figure 7. Dialog window for Module 2 - Template Design.

are indicated with an 'S'; unknowns with a 'U'; and quality control samples with a 'Q'. If any block is subsequently deleted, the letters in the corresponding cells will be blanked out indicating the availability of the cells for future block definitions.

To delete a block, click on any cell within the block with the left mouse button. An 'X' will appear in the cell. Select the 'Delete' option in the Block Info box and click on the 'Record' command button. The cells in the block will be blanked out indicating the block has been deleted.

To recall a block's defining parameters, click on any cell within the block with the left mouse button. An 'X' will appear in the cell. Click on the 'Redraw Plate' command button and the information previously entered for that block will be inserted into the appropriate entry fields. Once this information is retrieved, any part of it may be altered. Once the information has been edited, again, click on any cell within the block (confirmed with the placement of the 'X' in the cell) and select the 'Edit' option in the Block Info box. Finally click on the 'Record' button to register the change. To reset or blank out the data entry fields, click on the 'Redraw Plate' command button without first marking a cell in an existing block.

This technique may also be used to copy the contents of one block to another block. This is useful if several unknowns with identical defining parameters are being added to a plate. Once one unknown is established, its information may be recalled and used for any subsequent block's definition. Once the information is inserted in the data entry fields, a new block may be defined by clicking on the opposing corner cells in the plate schematic diagram. Clicking on the 'Record' command button will then establish the new block using all the parameters from the block which was previously recalled. When applying this technique care must be taken to change the Block ID or this information will also be copied over to the new block. This is only necessary if each unknown requires a unique block identifier.

Clicking on the 'View Plate' command button will present an expanded view of the plate with each well defined with its dilution and block designation. Unknowns and quality control samples are numbered in the order in which they are defined. A sample display is shown in Figure 8. If the window is not large enough to contain the entire plate diagram, the scroll bars may be used to pan horizontally and vertically through the display. The block identifiers are listed under the plate diagram and may be viewed using the vertical scroll bar.

It is possible to create a block with a single point dilution. In this case, the user would block off the desired cells and enter the single dilution value in the 'Start' data entry field. Enter 1 in the 'Factor' data entry field. Finally, enter the necessary data in the Replicate Information box. If there are no replicates (a single point determination in a single well) then enter 1 for the number of replicates and ignore the orientation.

There is no limit to the number of blocks which may be assigned to any one plate with the proviso that there be only one block of standards.

When all blocks of information have been defined, clicking on the 'Save' command button will lead to the template file selection dialog box. The user will be

prompted for a filename for the newly created template. A new file name may be specified or the old template file may be over-written and replaced. Retain the .TPL extension to insure the file name will appear in subsequent file name lists when this module is entered in the future. The program will return to the main menu (Figure 3) and the name of the template will appear in the descriptive box to the right of the option group on the opening menu screen when the template design option is selected.

This completes the template creation description. Once the template module is entered from the main menu, all template files will be listed in the file list box in the template file selection dialog window and the user may select the desired template for data processing. Once the selection is made, the formatted template will appear on screen in the context of the dialog window shown in Figure 7.

The 'Select' command button will choose the given template for subsequent processing in the data abstraction module. 'View Plate' allows the user to examine the chosen template checking the dilution settings within each block of standards, unknowns, and quality control samples. The various options in the Block Info box may be selected to add new blocks to existing templates, delete blocks from templates and change various parameters for any block. In this manner *ELISA for Windows* allows users to easily alter existing templates. These editing functions facilitate the creation of new templates that are only slightly different from existing ones without starting from

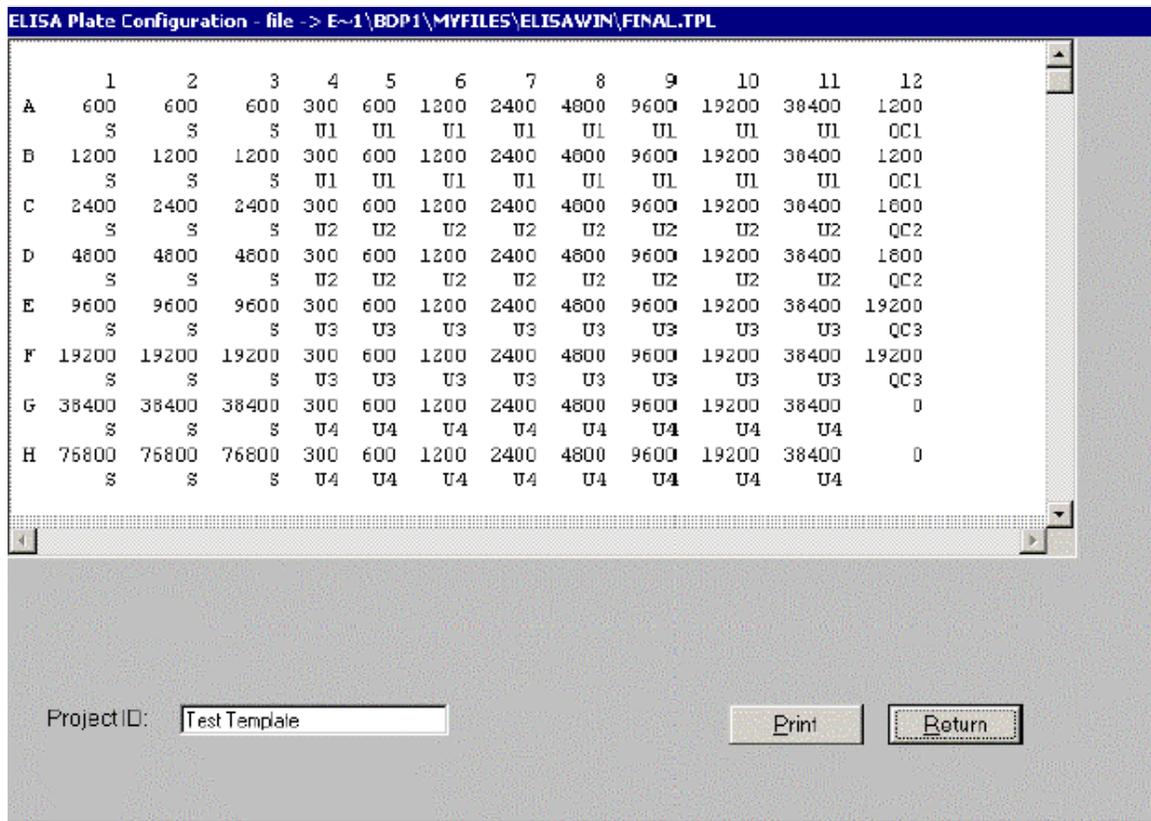


Figure 8. Display of sample template design.

the beginning with a blank template. These editing functions may also be used during the creation of templates to correct entry errors. If a user misspecifies one of the parameters within a block of standards, unknowns or quality control samples, the block may be edited or deleted and recreated. When a template is edited, the user will be given the opportunity to name the new template at the end of the procedure. A template file selection window appears with the original name of the template located in the file name box. Clicking on OK will store the changes in the original template file. The file name may be edited. If the user does not wish to overwrite the existing template file.

If the user is unsure which template to use, the plate may be queried using the 'View Plate' command button. If it is determined that the template is not the one truly desired, exiting the dialog menu screen with the 'Exit' command button, will return the user to the main menu where the Template module may be reentered and a new template selected.

Never assign a dilution  $\leq 0.0$  to any well, for standards, unknowns, or quality control samples. This will result in a fatal error when the concentration calculation module is entered. If dilutions  $\leq 0.0$  exist, **ELISA** *for Windows* will end with unpredictable results when calculating concentrations from optical densities associated with the dilutions.

Be careful to click on the 'Record' command button after each operation (defining or editing a block, etc.) to ensure that the action is recorded in the template file. The 'View Plate' option may be used to check the accuracy of each operation.

In conclusion, each template is not required to contain blocks of wells representing all three data types. Users are free to create templates with any combination of standards, patient unknowns and quality control samples. The only restriction is that there may be only one block of standards per template.

The Operational Qualification Protocol contains several examples illustrating the different options in this module.

Refer to Appendix B for a description of the template (.TPL) file format.

# MODULE 3

## ABSTRACT DATA

This module applies a template protocol to abstract the three different data types: standards, unknowns, and quality control samples, from 96-well ELISA plates stored in plate data files with a .DAT extension. Before executing this option, Module 2 may be used to pick a template, with the 'Select' command button. Refer to the Template Design section for further details.

The present module begins by displaying a data file selection dialog window used to choose a plate data file for processing. All files with a .DAT extension will appear in the file list box.

If a template was not selected prior to entering this module, the user will be presented with a template file selection dialog window where a template file may then be chosen.

Once the plate and template data files have been selected, a dialog window appears as is shown in Figure 9. The dialog window displays the name of the plate data file as well as listing the number of plates contained in that file. Also listed is the cur-

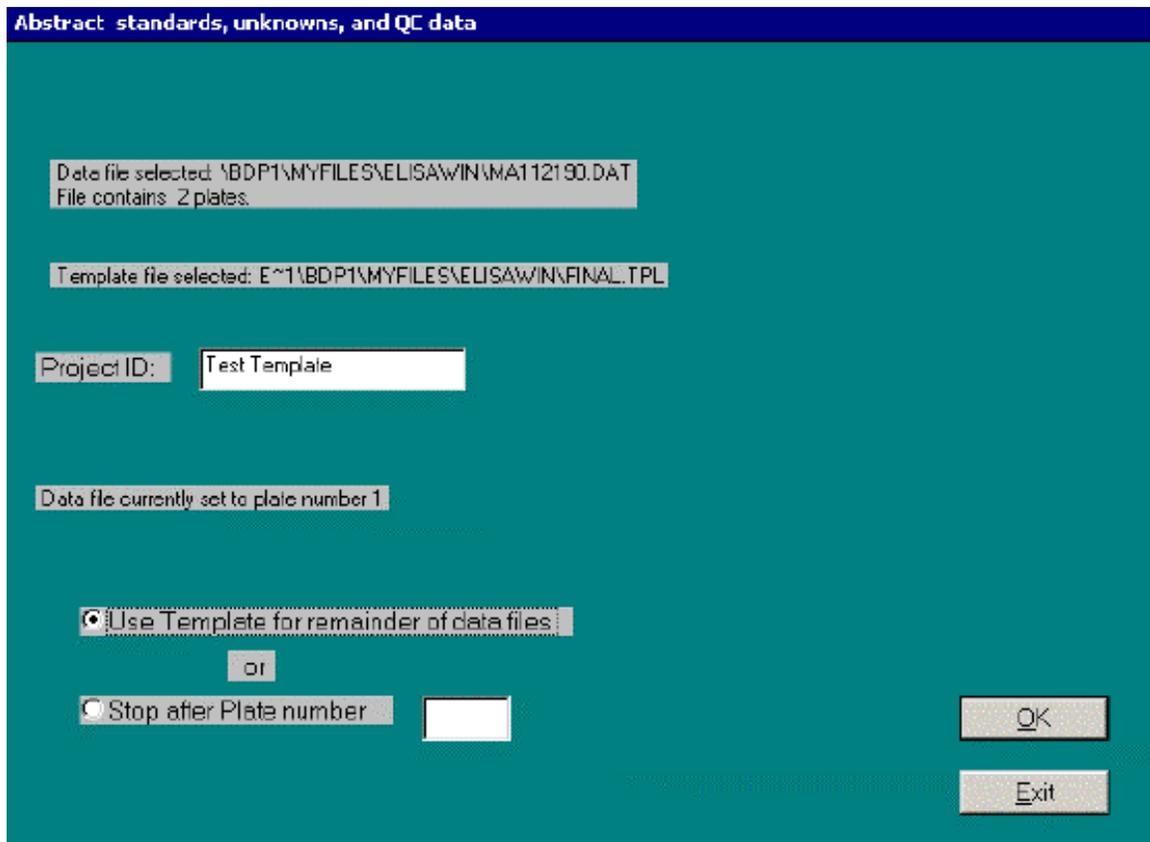


Figure 9. Dialog window for Module 3 - Abstract Data.

rent template chosen for plate data abstraction. Additionally, the dialog window informs the user of the plate number where processing will begin.

As mentioned in the data file structure section in the Introduction, several plates may be stacked or concatenated in one .DAT file. However, it is not necessary for all of these plates to be analyzed with the same template protocol. Conceivably, the placement of standards, unknowns, and quality control samples may be the same from plate to plate, but the dilution series may differ for some of the plates. Conversely, the different plates within one plate data file may have entirely different configurations. A new template is required each time the dilutions or the plate configuration change. The dialog window in Figure 9 permits the user to abstract the data from each .DAT file using one or more template protocols. If the default option, 'Use template for remainder of file', is selected, each of the three file types will be extracted using the selected template starting with the plate number listed in the dialog window. If the 'Stop after plate number' option is selected, the user will need to enter that plate number in the text box to the right of the option label. If this second option is chosen, the current template protocol will be used to extract the data starting with the plate number the file is currently set to (listed in the dialog window) through plate  $n$  where  $n$  is the number entered in the text box previously described. Note that the user must first select the 'Stop after plate number' option before actually entering the plate number itself. That is, the program will restrict plate number entry in the text box until the appropriate option has been selected. **ELISA for Windows** abstracts the data and then returns to the template file selection dialog window where a new template is chosen. The dialog window in Figure 9 reappears and includes the updated plate pointer: 'Data file currently set to plate number  $n+1$ '. The user now may choose to apply the new template to the remainder of the file or to stop after another plate number,  $m$ , where  $m > n$ .

To begin, assume the first option is selected where one template will be used for all plates. Once the plate data file has been specified, **ELISA for Windows** abstracts the three data types, standards, unknowns, and quality control samples. The abstracted data will scroll up the computer screen. The first column of the screen listing is the dilution in decimal form (e.g., 600 entered in the template module is converted to 0.001666667), the second column is the optical density, and the third column is STD, UNK, or QC for each of the three data types. These three data types will be written to three separate files named using the root file name of the plate data file selected above and the appropriate extension. Thus the standards are written to *file*.STD, the unknowns to *file*.UNK, and the quality control samples to *file*.QC, where *file* is the root file name of the plate data file previously selected. Any comment lines in the .DAT file will be abstracted and written to *file*.LBL. These four files will be written to the same subdirectory as the plate data file. An informational message detailing this will appear as shown in Figure 10.

Clicking on OK will return the user to the main menu (Figure 3).

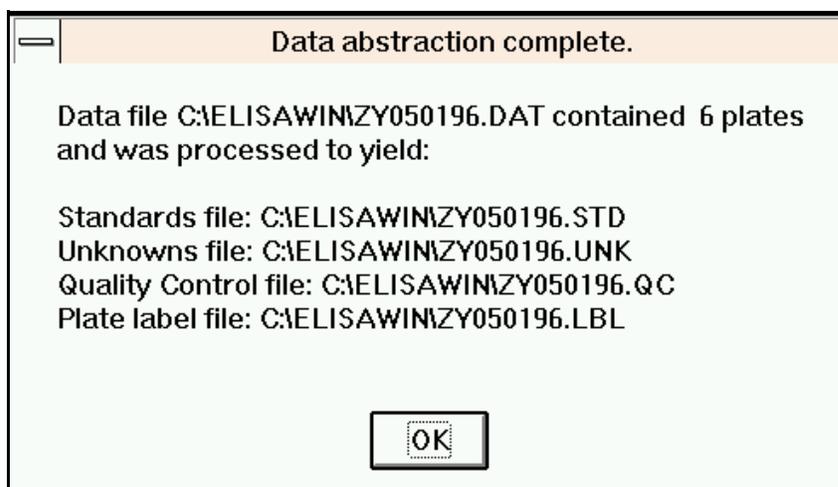


Figure 10. Concluding message for Module 3 - Abstract Data.

The user selects the second option in the dialog window (Figure 9) to apply more than one template to a group of plates in a .DAT file.

As an example, consider a plate data file with six plates. It is desired that three separate templates be used to process plates 1-3, 4, and 5-6, respectively. The dialog window (Figure 9) initially reports that the file is set to plate 1; select the second option and type 3 in the text box to indicate the current template will process plates 1 through 3. When these plates are processed, the template file selection dialog window will reappear and a new template may be chosen. The dialog window (Figure 9) will then appear stating that the plate data file is now set to plate 4. Select the second option again and type 4 in the text box. After plate 4 is processed, another template is selected and the dialog window reappears. Now the window indicates the plate data file is set to plate 5. choose the first option to process the rest of the plate data file (plates 5 and 6), or select the second option and type 6 in the text window to indicate processing should stop after plate 6. The module will conclude either way with the informational message shown in Figure 10.

If the template employed for abstracting the plate data does not contain one or more of these three data types or if there are no comment lines in the .DAT file, the associated files will still be created. They will, however, be empty. Also, if this module is exited using one of the earlier prompts, these files will also be created and, in this case, each of them will be incomplete. If an empty file is created, do not delete it because, in some cases, its presence may be required by succeeding modules in the data analysis modules of **ELISA** for Windows.

# MODULE 4

## PARAMETER ESTIMATION

This module uses a four parameter logistic-log function to describe standards data and form calibration curves. Standard curves may be formed using two fitting techniques, iteratively unweighted least squares and robust iteratively reweighted least squares. Users may also elect one of two estimation algorithms, Taylor series-linearization or Marquardt's Compromise, to estimate the four parameters. It is beyond the scope of this document to describe these two techniques in detail. Briefly, the unweighted least squares method estimates the parameters without taking into account the possible differences in the variability of optical density measurements as one moves from dilution to dilution. Recognizing that this fit may be unduly influenced by aberrant observations (outliers), the robust fitting technique weights each observation individually and inversely proportionally to the residual difference between the observed and predicted values for each point. In this way, outliers are assigned low weights and exert little influence in the overall fit of the curve to the data.

Interested readers may refer to references 4 and 7 (listed at the end of this section) and to the Process Qualification Report for a further discussion of the theoretical details. Note that in their article, Tiede and Pagano refer to the four parameter function as a 'modified hyperbola.' In fact, it is algebraically equivalent to the logistic-log model. References 5 and 6 provide additional articles of interest. Our philosophy governing the use of these models in assay methodology is described in reference 1. For a discussion of the Taylor series-linearization and Marquardt's Compromise estimation algorithm, readers are referred to Chapter 24, an Introduction to Nonlinear Estimation, in reference 2. Reference 3 describes the Marquardt's Compromise technique in detail.

Users should be aware of the following broad generalizations when deciding which fitting algorithm to use. The Marquardt's Compromise algorithm may, at times, expend more calculations, take more CPU time to arrive at a final set of estimates, and involve more iterations than does the Taylor series-linearization technique. The iterative steps tend to be smaller, especially as the converging process nears an end. However, this algorithm is more elaborate and is not as sensitive to poor starting values as the Taylor series technique. Marquardt's Compromise is usually used when the Taylor series-linearization process fails to converge to a solution.

Since the model describing the standards data is the four parameter logistic-log function, a minimum of five data points is required for parameter estimation. Note that this does not mean there need be a minimum of five separate dilutions, just five data points spread out over some number of dilutions. Of course, if the data do not adhere to some semblance of a sigmoidal, S-shaped curve, this procedure will fail. It is the responsibility of the user to select a dilution schedule that will insure that there is

enough information for **ELISA for Windows** to successfully estimate the four parameters.

A third fitting technique, the cubic spline, is also implemented in **ELISA for Windows**. This method is accessed directly in the 'Plot Standard Curves' (Module 5) and 'Calculate Concentrations' (Module 6) segments of the program and is discussed in further detail in those sections of this documentation. The spline fit is a useful technique in those cases where the parametric logistic-log function will not converge to a solution. This is often the case when the standards do not fully describe a sigmoidal-shaped curve. It is inherently difficult to arrive at reliable parameter estimates for the logistic-log function without a clear indication of the minimum and maximum optical densities associated with the assay. That is, if it is difficult to discern both lower and upper asymptotes for the sigmoidal-shaped curve (areas where the curve flattens out), then the logistic-log function fitting techniques may not converge to a solution. In this case, the spline fit may be used to interpolate antibody concentrations for unknown patient samples in Module 6.

## Standards File Selection

This module is entered from the main menu (Figure 3) and begins by displaying a standards data file selection dialog window. If the user enters this module directly after abstracting the data from a .DAT file (Module 3), **ELISA for Windows** will insert a file name in the file name box which corresponds to the .DAT file just processed. This is offered as a convenience to the user in an attempt to eliminate repetitive entry of file names. This file is selected by clicking on OK. The user may also select a different file from the file list box.

Once the standards data file has been selected, **ELISA for Windows** responds with the dialog window shown in Figure 11.

The default selections in this dialog window include using the Marquardt's compromise estimation algorithm with the robust fitting technique. All output will be directed towards the printer. The entire standards data file will be processed without interruption with each step using up to 100 iterations. The starting values for the iterative estimation process will be calculated by the program.

Users may alter these default settings to best handle their data sets. The estimation techniques are options and, as such, only one may be selected. The destination of the results are also options and users may select either the printer, computer screen, or file. If the screen is selected then the results of each plate are displayed on screen. Users then have the option of exiting to the next plate or printing the contents of the screen. If 'file' is selected, the user will be prompted for the name of a file to save the results. **ELISA for Windows** will suggest *file.FIT*, where *file* is the root file name of the standards data file. If the user selects the printer or file, the standards data will be processed without interruption with all output directed towards the printer or the designated file. The type of least squares fit are marked with check

boxes. As such, robust, unweighted least squares, or both may be selected. If the user inadvertently neglects to select a type of fit, the robust fit is used as the default.

## Coefficient Update

Users have the opportunity to enter the proportion for coefficient update. Note that this parameter is only valid when the Taylor series estimation algorithm is selected. If the Marquardt's Compromise algorithm is chosen then this option is suppressed, as the Marquardt technique calculates the update factor automatically. This number must be greater than 0.0 and less than or equal to 1.0. We have found that the value 0.4 works well for our applications and is the default value which appears in the text box in the dialog window when the Taylor series estimation technique is selected. If desired, the user may alter this value. The program may occasionally fail to converge to a solution with some data sets. Outliers will severely affect the outcome of the algorithm used to calculate initial starting values for the iterative fitting procedure. In this case, coefficients from a previously successful run with similar data may be substituted for the calculated starting values and the iterative

Four Parameter Logistic Log Estimation - Standard Curves.

Estimation Technique

Marquardt's Compromise

Taylor series-linearization

Standards file is \BDF1\MYFILES\EUSAWIN\MA112190.STD

Type of Least Squares Fit

Robust LS

Unweighted LS

Maximum number of iterations: 100

Proportion for coefficient update (must be >0.0 and <= 1.0):

Pause after each iteration

Enter starting values for parameter estimation:

A B

C D

Send Results To:

Printer

Screen

File

OK

Exit

Figure 11. Dialog window for Module 4 - Parameter Estimation.

process retried. Alternatively, the proportion for the coefficient vector update can be modified. This is seen more clearly if one examines the weighted least squares equation:

$$\mathbf{O}_{j+1} = \mathbf{O}_j + (\mathbf{A}_j^T \mathbf{W}_j \mathbf{A}_j)^{-1} \mathbf{A}_j^T \mathbf{W}_j \mathbf{R}_j$$

and re-expresses it as:

$$\mathbf{O}_{j+1} = \mathbf{O}_j + \mathbf{B}_j$$

where  $\mathbf{B}_j = (\mathbf{A}_j^T \mathbf{W}_j \mathbf{A}_j)^{-1} \mathbf{A}_j^T \mathbf{W}_j \mathbf{R}_j$

The most recent estimate for the parameter vector  $\mathbf{O} = \mathbf{O}_{j+1}$  is equal to the last estimate,  $\mathbf{O}_j$ , plus an amount equal to  $\mathbf{B}_j$ . If  $\mathbf{B}_j$  is very large the solution may circle around some value without actually converging, or it may rapidly expand and diverge to the point of causing a numeric overflow in the program. To avoid this, the magnitude of  $\mathbf{B}_j$  may be decreased by altering the proportion for the coefficient vector update. If the user enters 1.0 then the result is the standard equations listed above. If the solution does not converge or if it diverges to numeric overflow, a smaller proportion, e.g. 0.4, may be used. This would modify the second equation, above, to:

$$\mathbf{O}_{j+1} = \mathbf{O}_j + (0.4)\mathbf{B}_j$$

The proportion may be altered at will to compute smaller and smaller increments of change for the  $\mathbf{O}_j$  vector. *ELISA for Windows* suggests a starting value of 0.4 and uses this as its default entry. The user is free to experiment with this value. Numbers close to 1.0 will result in larger steps between iterations and may lead to faster convergence (it may also lead to faster *divergence* as well). Numbers close to 0.0 will lead to smaller steps between iterations and lead to a slower convergence. This may be necessary for difficult data sets.

## Number of Iterations

If the coefficient for vector update is small (less than 0.4), then the iterative increments tend to be smaller, requiring more steps to reach a stable set of coefficients. The default number of iterations is 100 and this may be increased to accommodate these situations. This is particularly true for those instances where the standards data do not fully describe a sigmoidal-shaped curve causing the iterative steps to proceed slowly to a final solution.

Note that the default setting for the number of iterations is set to 100. If the program is left unattended and loops around a solution, it will print out the results of

the 100th iteration as though this were the final answer. Take care to examine the output. If the number of iterations is listed as 100 or 101, or, if the number is listed as that which was entered by the user, then the solution may be suspect. If this occurs, the user should examine the standards data as well as the fitted calibration curve using Module 5 - 'Plotting Standard Curves'.

## Pause after Iteration

The user may elect to view the results of each iteration by checking the 'Pause after each iteration' box. Coefficients with the resulting sum of squares of residuals and correlation coefficient are displayed on screen after each step of the fitting procedure. A general guideline as to whether or not a revised set of coefficients is performing better than the previous set is the sum of squares of the residuals which should decrease with each successive iteration. If the number steadily increases, this is an indication that the solution is starting to diverge. The program may still converge at a later stage or it may continue to diverge until a numeric overflow occurs. If it decreases then increases and starts to decrease again in a cyclic fashion, this is an indication that the program is circling around a solution without actually being able to achieve convergence.

It is important to note that there are two sums of squares of residuals returned for the approximate least squares fit and the robust fit. The regular sum of squares is simply the sum of the squared residuals. When fitting a simple linear model to a data set, this is the quantity that is minimized when solutions for the coefficients are found. In the case where a nonlinear function such as the four parameter logistic-log model is being fit using the Taylor series expansion method, an approximation to this quantity (the approximate sum of squares) is actually minimized when the coefficients are solved. As the solution converges, notice that these two quantities approach each other in magnitude. They should be fairly close to each other if the process concludes successfully. Interested users are referred to Chapter 24 of reference 2 - pages 508-511 for further details. In particular, equation 24.1.9 details the regular sum of squares of the residuals and equation 24.2.7 the approximation to this quantity resulting from the Taylor series expansion. Note the four coefficients change with smaller and smaller increments as they also converge to their final estimated values.

At the end of each iteration, **ELISA** for *Windows* will pause and display information as shown in Figure 12. If this particular iteration is satisfactory, and the user wishes to end the process, selecting 'No' will conclude the estimation process for the current plate, record the coefficients as detailed on screen, and proceed to the next plate. Selecting 'Yes' will initiate another iteration step. This process cycles until **ELISA** for *Windows* iterates to its own solution or the user stops the process by selecting 'No'.

## Estimation Starting Values

Good starting values are essential for the success of any nonlinear iterative fitting process. We have incorporated an algorithm which computes starting values for the iterative process used by **ELISA** for *Windows* to estimate the four parameters of the logistic-log function (see reference 4). Occasionally, these values will not lead to a solution, that is, the process will diverge away from a solution or circle around a solution without actually settling in on one set of values which may be used for parameter estimates. This is especially true if there are outliers in the data or if there are a small number of data points. **ELISA** for *Windows* gives the user the option of overriding the automatically calculated starting values so that a set of possibly more accurate values from a previously run standards file may be used in their place.

If the user elects to input starting values, the box for this option must be checked, otherwise, coefficient data entry will be suppressed. One or more starting values for coefficient estimation may then be entered. **ELISA** for *Windows* will insert the automatically calculated starting values in those instances where the user did not manually enter them. As an example, one may manually enter starting values for the first two coefficients (A and B) and leave the remaining coefficients (C and D) blank. The program will access the user inputted values for A and B and internally calculate values for C and D.

```

COMPUTING ROBUST AND LEAST SQUARES LOGISTIC CURVE COEFFICIENTS
(Taylor Series-Linearization algorithm)
Processing file: C:\ELISA\BD010292.STD Plate: 1
Results stored to file: C:\ELISA\BD010292.FIT
Robust Fit
Coefficient vector update: .4
=====
+-|          Continue coefficient estimation?          |-+
|
|  Yes -> continue with another estimation iteration.
|  No  -> exit and save current estimates of coefficients.
|
|          +=====+ +-----+
|          || Yes  || |   No   |
|          +=====+ +-----+
|-----+

```

Iteration	A	B	C	D
2	11.22451	-11.22593	0.00204	1.01412
Regular and Adjusted sum of squares of the residuals				
	4.75814D-03	4.27754D-03		
Approximate multiple R <sup>2</sup> = 0.9991				

Figure 12. Module 4 - 'Pause after each iteration' screen.

At the conclusion of this module **ELISA for Windows** informs the user of the creation of the coefficient file, as shown in Figure 13.

Clicking on OK will return the user to the main menu (Figure 3).

## Solution Nonconvergence

**ELISA for Windows**, will complete process a standards data file even when one or more plates within the file contain data where coefficients may not be estimated. In those instances the output will be annotated with the message ‘Solution did not converge’ on the right side of the listing (described below). In this fashion the program will not end midstream while analyzing a standards file containing many plates. **ELISA for Windows** will keep track of those plates where convergence was not achieved. In succeeding modules, these situations are addressed by offering the spline fit as the only option for plotting standard curves or calculating antibody concentrations.

## Analysis Strategies

Through the various options just outlined, an analysis strategy could proceed as follows: Select the Taylor series estimation technique with 0.4 for the proportion for the coefficient vector update. Choose the desired type of fit. The program will proceed through the selected type of fit for each set of standards in the .STD file.

There are a variety of strategies to employ if the program does not converge to a solution. If the starting values generated from **ELISA for Windows**’s internal algorithm are distant enough from the true solution, the fitting procedure may not converge to a final set of values. Users should try the Marquardt’s Compromise algorithm if the Taylor series technique fails.

When the program fails to converge, the investigator should first try to select coefficients from a previously successful run with similar data and substitute them for

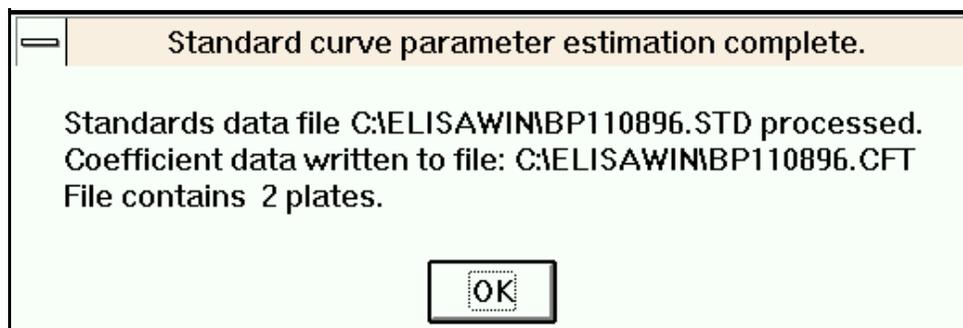


Figure 13. Concluding message for Module 4 - Parameter Estimation.

the calculated starting values through the manual entry of starting values detailed previously. If such values are unavailable, the investigator should rerun the program choosing a smaller proportion for the coefficient vector update - say 0.3 or 0.2. As the program proceeds, the user should inspect the coefficients and the sum of squares of the residuals. The coefficients should stabilize and the sum of squares decrease.

If the solution does not converge but circles around a solution without actually converging, again, examine the sum of squares of the residuals that is returned after each iteration. The coefficients that return the smallest sum of squares can be used as starting values for another attempt at finding a solution. When re-executing the program, manually enter these coefficients and select a smaller proportion for the coefficient vector update than was used previously, and monitor the iterative process.

If the solution continues to circle around a set of values without actually converging, select those values which return the smallest sum of squares of the residuals and test them examining the goodness of fit statistics. If the error rates are acceptable, these coefficients may be used to form the standard curve. These results may also be examined graphically using Module 5, which produces a logistic-log plot.

## Output Interpretation

Figure 14 contains an abbreviated listing of output generated from this module (Refer to page 52 for a sample of a complete listing). A complete listing for a sample data file is included in Appendix A. The logistic model used in **ELISA for Windows** is parameterized as:

$$y_i = a + \frac{b}{1 + c(x_i^d)}$$

Where **a** = the upper asymptote of the sigmoidal curve, **a + b** = the lower asymptote, **c** is related to the dilution at the midpoint of the assay, and **d** is a curvature parameter, related to the slope of the curve; **y<sub>i</sub>** = the **i**th optical density and **x<sub>i</sub>** = the **i**th relative dilution (individual sample dilution / maximum dilution in the series) multiplied by 100.0.

The output will list the file name of the standards file and the plate position within the file along with the type of fit, least squares or robust. Recall that a standards (.STD) file may include several plates of standards. Next the output will list the number of iterations required to reach a solution. Again, if this number is at the maximum set by the user, the results are suspect. **ELISA for Windows** simply stopped the iterative process after the maximum possible iterations and chose the last set of coefficients as the final set. The starting values for the coefficients used in the iterative process are listed next.

A table of values follows for each of the standards. The first column is the sample dilution. The second column is the relative dilution calculated as:

$$((\text{sample dilution}/\text{maximum dilution}) \times 100).$$

The measured or known optical density occupies the third column followed by the predicted optical density from the fitted curve. The residual is calculated as:  
the known OD - predicted OD.

The % error equals the absolute value of:

$$(\text{residual} / \text{known OD}) \times 100.0.$$

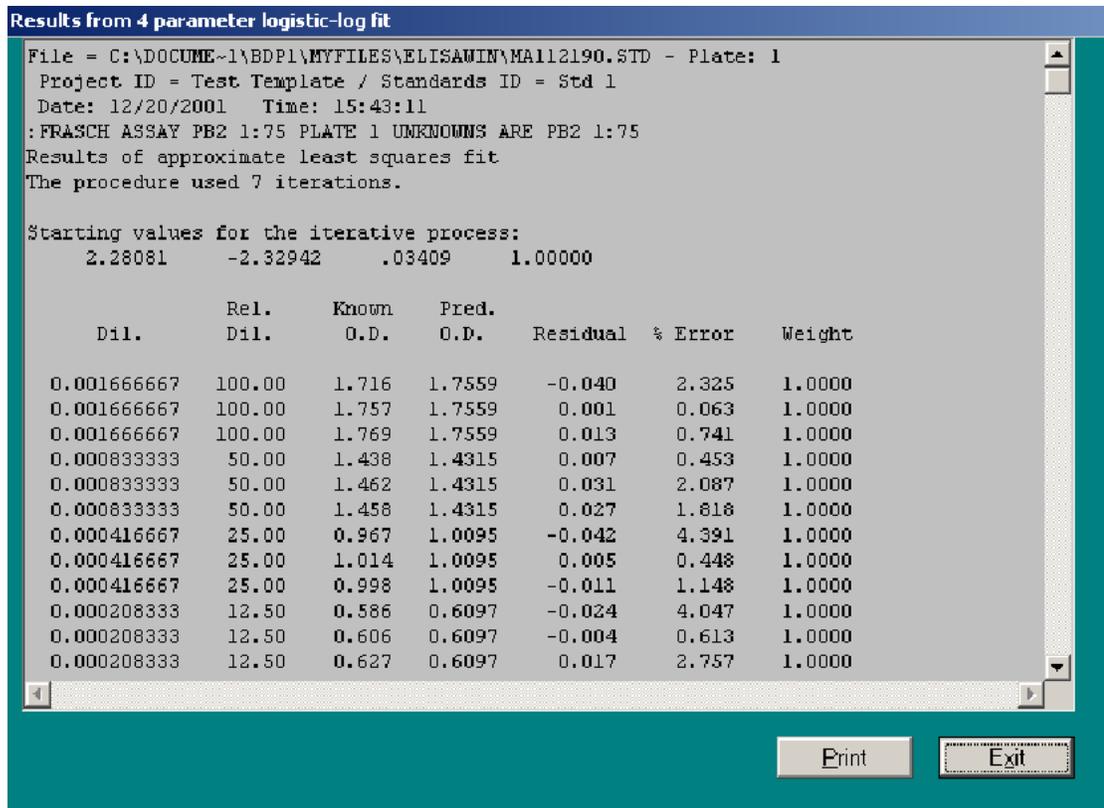


Figure 14. Sample output from Module 4 - Parameter Estimation.

Note that the % error may not precisely equal this quantity when performed on a hand-held calculator. This is due to roundoff error since **ELISA for Windows** performs most of these calculations in double precision and retains many more significant digits than are displayed in the output window. The weight column lists the individual weights used for the observation in the final fit of the logistic-log model to the data. For the least squares fit this weight will be set at 1.00 for all observations, indicating that each data point exerted equal influence in the final fit of the model to the data. This essentially is the result of an unweighted fit. For the robust fit, these weights will range from 0.0 to 1.0. The closer the weight is to 0.0, the less influence that point will exert on the fit. The points with weights closer to 1.0 will exert much more influence in the final fit than points with weights close to 0.0. Points with low weights may be considered potential outliers.

The final estimates for the four coefficients follow in order of **a**, **b**, **c**, and **d** (refer to listing in Appendix A). The regular and adjusted sums of squares, as well as the approximate multiple  $R^2$  follow. For the least squares fit, the variances of the four coefficients are reported.

Typically, the window used to display the results will not be large enough to frame the entire listing. There are horizontal and vertical scroll bars on the bottom and right side of the window, respectively. Clicking the left mouse key on the down arrow of the vertical scroll bar will advance the listing one line. Clicking just above the arrow key will advance the listing by one screen. The horizontal scroll bar is used in the same manner to shift the listing left and right.

It should be noted that users may edit the contents of the output window. Comments may be added to further annotate the output. Several rudimentary Microsoft Word operations will work in these windows. For example, text may be marked by clicking the left mouse key and dragging the cursor through the target text or pressing the shift key while moving the cursor through the text with the cursor control keys. Once text is marked it may be deleted, moved, etc.

After reviewing the contents of the output window, clicking on 'Exit' will erase the screen and proceed to the next round of estimation with a new plate or additional type of fit. Clicking on 'Print' will send the contents of the output window to the printer. If edits were made in the output window, these changes will be reflected in the printed outputs. They will not be saved once the user clicks on 'Exit'.

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- (4) B. D. Plikaytis, G. M. Carlone, P. Edmonds, and L. W. Mayer, Robust estimation of standard curves for protein molecular weight and linear-duplex DNA base-pair number after gel electrophoresis, (1986) *Anal. Biochem.*, **152**:346-364. Erratum **154**: 702 (1986).
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- (7) J. J. Tiede and M. Pagano, The application of robust calibration to radioimmunoassay, (1979) *Biometrics* **35**:567-574.

# MODULE 5

## PLOT STANDARD CURVES

This module forms a fully annotated plot of the points contained in a standards data file along with the fitted standard curve. This module will access the coefficient data file to determine which fitting techniques were chosen during parameter estimation and only offer these for plotting. Thus, if only the robust fit was selected in Module 4, the user would not have the option of selecting unweighted least squares for plotting.

A nonparametric fit, the three point cubic spline, is also offered as an additional option which is always available for selection. The standard curve line described by the spline fit is programmed to pass through the median value of the replicate optical densities at each dilution along the curve. The user may enter this module prior to parameter estimation if it is desired to view the shape of the data in the standards data file before an attempt is made to fit the logistic-log function. In this case, the spline fit will be the only option available. In addition, if there were any plates in a standards data file where the solution did not converge to a stable set of parameter estimates after processing the data with Module 4, then the spline fit, again, will be the only option available for these plates.

These standard curve plots may be directed to the screen and any printer addressed through the Windows interface. The user may direct a single plot or an entire file of standard curve plots to the printer.

This module is entered from the main menu (Figure 3) and begins by displaying a standards data file selection dialog window. If the user enters this module directly after abstracting the data from a .DAT file (Module 3), or estimating the logistic-log parameters (Module 4), **ELISA for Windows** will insert a file name in the file name box which corresponds to the .DAT or .STD file just processed. This is offered as a convenience to the user in an attempt to eliminate repetitive entry of file names. This file is selected by clicking on OK. The user may also select a different file from the file list box.

After a standards data file has been chosen, the dialog window in Figure 15 appears. The window lists the name of the file and the number of plates contained in the file. The user should enter the desired plate in the appropriate text box. When the plate number field is exited, **ELISA for Windows** will interrogate the coefficient file associated with the standards data file and determine which types of fit should be made available for selection for that particular plate. Fits which were not used during parameter estimation will be suppressed as options here. If a coefficient file does not exist then the spline fit will be the only available option. As stated earlier, when a coefficient file does exist, the spline fit is the only method allowed for those plates where the solution did not converge during parameter estimation.

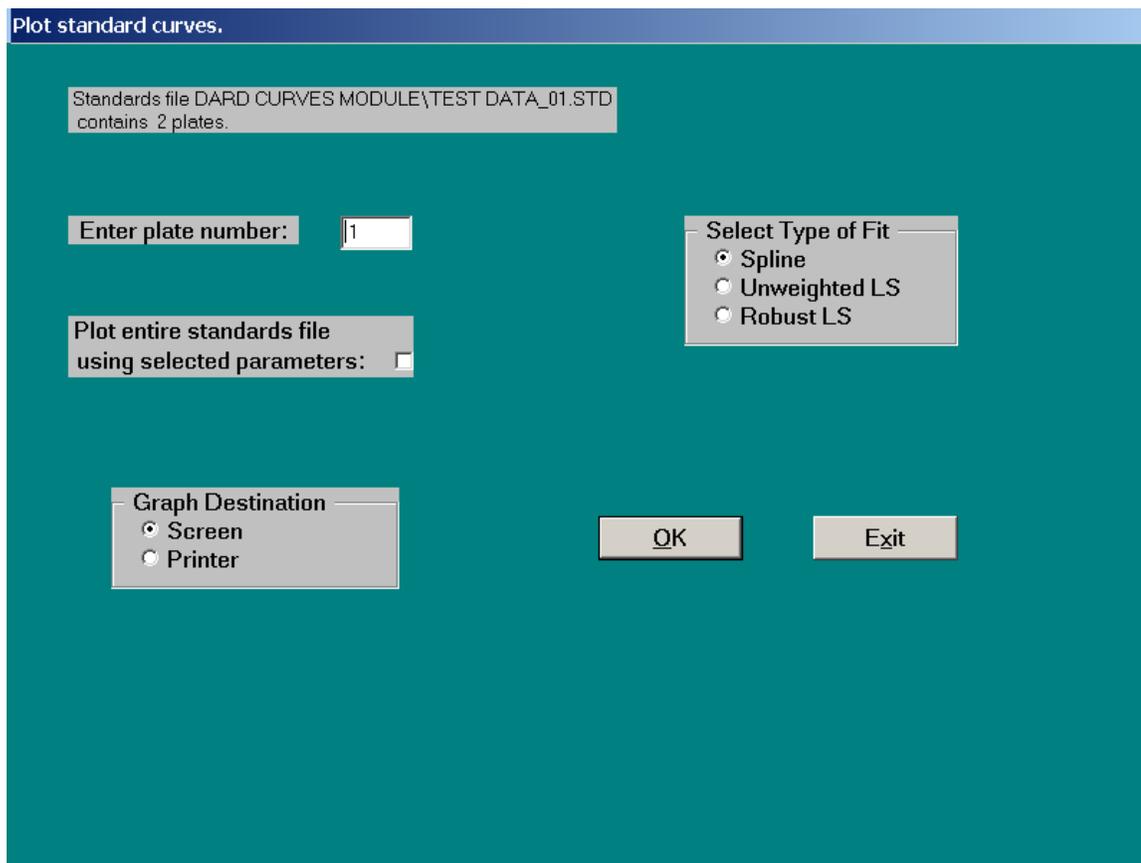


Figure 15. Dialog window for Module 5 - Plot Standard Curves.

If the user selected the printer as the graph destinations, *ELISA for Windows* will display the plot onscreen and then automatically send the screen image to the printer without user intervention. If the entire file is selected for processing, the printer is the only allowed destination. The user will be presented with all options for type of fit. If the program was unable to estimate coefficients for the standard curve for one or more of the plates in the file, the spline fit will automatically be chosen for these when they are displayed to the screen and sent to the printer.

If the screen is selected as the destination for the graph, a plot will follow with the type of fit and standards file name appearing at the top of the screen. A typical plot will appear as shown in Figure 16. The 95% confidence intervals are included with the unweighted least squares fit. The user may scroll through the other standards series in the file by clicking on the Next and Previous buttons. Each plot may be directed to the printer at this stage. If the user elected to plot the entire file, each one will be transmitted to the printer automatically, without user intervention.

The user may choose another plate for standard curve plotting or exit to the main menu (Figure 3).

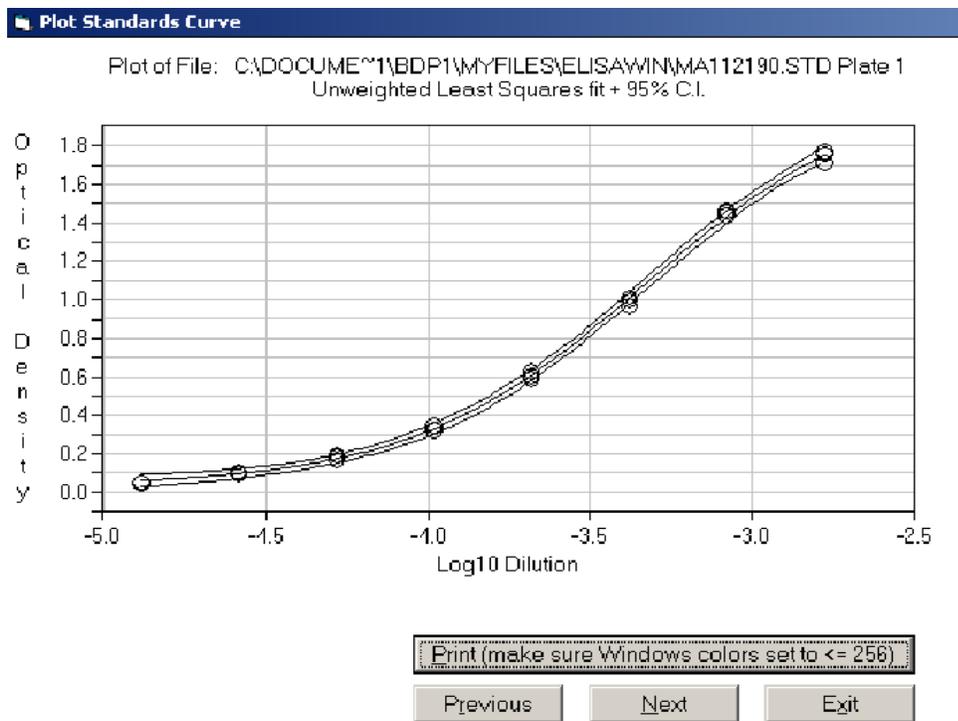


Figure 16. Typical plot of standards data overlaid with fitted standard curve.

# MODULE 6

## CALCULATE CONCENTRATIONS

### Introduction

This module facilitates calculating antibody concentrations from patient serum samples and quality control samples. These concentrations may be arbitrarily assigned units (e.g., antibody units/ml), or mass values (e.g.,  $\mu\text{g/ml}$ ). A diagram used to illustrate the concentration calculations is shown in Figure 17. In this diagram, the absorbance is plotted on the logit-log scale to simplify the example. **ELISA for Windows** performs the actual calculations using the results of the more accurate four parameter logistic-log fit.

Figure 17 displays a rather idealized standard curve bracketed by two twofold serially diluted patient serum samples or unknown curves. For the purposes of this example, assume the antibody concentration of the standard reference serum (the

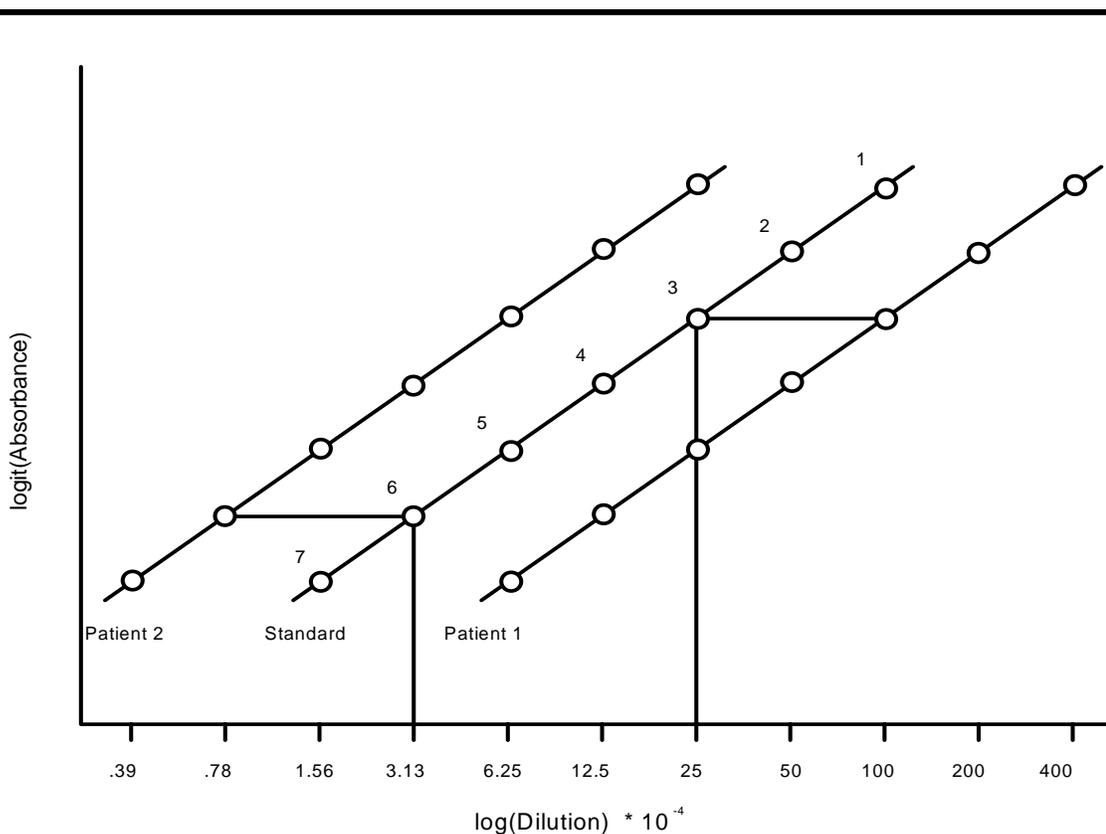


Figure 17. Diagram illustrating antibody concentration calculation for patient unknowns.

calibration factor) is 135.8 micrograms/ml ( $\mu\text{g}/\text{ml}$ ), and that the standard was initially diluted 1/100 with six subsequent twofold serial dilutions. This would lead to standard point 1 containing 1.358  $\mu\text{g}/\text{ml}$ , point 2 containing 0.679  $\mu\text{g}/\text{ml}$ , etc. The sample from Patient 1 was initially diluted 1/400 and that from Patient 2 was initially diluted at 1/25.

**ELISA for Windows** uses the following formula to calculate antibody concentration:

$$\text{concentration} = \frac{\text{interpolated dilution from standard curve}}{\text{actual dilution of sample}} \times \text{calibration factor}$$

The calculated concentration for Patient 1, using the third point on the patient curve would be:

$$33.95 \mu\text{g}/\text{ml} = \frac{0.0025}{0.01} \times 135.8$$

Alternatively, the calculated antibody concentration for patient 2, using the sixth point on the patient curve would be:

$$543.20 \mu\text{g}/\text{ml} = \frac{0.0003125}{0.000078125} \times 135.8$$

The optical densities and dilutions corresponding to patient and quality control samples are located in the *file.UNK* (patient serum samples or unknowns), and *file.QC* (quality control samples), where *file* is the root file name associated with the collection of samples.

The user **must** perform parameter estimation (Module 4) prior to entering this module. This module will access the coefficient data file to determine which fitting techniques were chosen during parameter estimation and only offer these for antibody concentration calculations. Thus, if only the robust fit were selected in Module 4, the user would not have the option of selecting unweighted least squares for calculation purposes. **ELISA for Windows**, also offers a nonparametric fit, the three point cubic spline, as an additional option which is always available for selection. If there were any plates in a standards data file where the solution did not converge to a stable set of

parameter estimates after processing the data with Module 4, then the spline fit, again, will be the only option available for these plates.

## Opening Menu Dialog

This module is entered from the main menu (Figure 3) and begins by displaying a standards data file selection dialog window. If the user enters this module directly after estimating the logistic-log parameters (Module 4), **ELISA for Windows** will insert a file name in the file name box which corresponds to the .DAT or .STD file just processed. This is offered as a convenience to the user in an attempt to eliminate repetitive entry of file names. This file is selected by clicking on OK. The user may also select a different file from the file list box.

After a standards data file has been chosen, the dialog window in Figure 18 appears.

The window displays the standards data file name along with the number of plates contained in the file. Initially, the window is set to plate 1, unknown 1. The number of unknowns within each plate is also listed. Users may then select the plate and unknown for antibody concentration calculations. When a new plate number is entered in the plate number field, **ELISA for Windows** will interrogate the unknowns data file to determine how many unknowns are contained on that plate and display this in the dialog window. This information is updated when the plate number field is exited.

When the user exits the plate number field, **ELISA for Windows** also interrogates the coefficient file associated with the standards data file and determines which types of fit should be made available for selection. Fits which were not used during parameter estimation (Module 4) will be suppressed as options in the type of fit option box. As mentioned earlier, the spline fit will be the only choice allowed for those plates where the solution did not converge during parameter estimation.

Users may analyze an entire plate of serum samples or an entire file of plates without returning to the dialog window. In these cases, the parameters set initially (type of fit, calibration factor, etc) will apply for the entire plate or file. By default, when either of these two options are selected, the program will save the results to a report file and not display them on screen.

The construction of the report is designed using the choices in the 'Select computation parameters' box. Serum samples and quality control samples may be estimated alone or together depending on which boxes are checked. If a particular plate does not contain serum samples or quality control samples, these check boxes will be suppressed. If both boxes are checked, the QC samples will follow the serum samples in the output file described later. Next, the calibration factor **must** be entered - **ELISA for Windows** will not exit this dialog window without a number specified for this quantity. If a calibration factor is not needed, enter 1 in this box.

The user may elect to save the results of the subsequent calculations to a report file by checking the 'Save report to file (.RPT)' box. This output file will remain in effect and open throughout the procedure, that is, until the user exits the module and returns to the main menu. **ELISA for Windows** will annotate the output with the comment lines contained in the *file.LBL* file. An additional title for the report may be entered in the dialog window.

The user also has the option of storing a distilled version of the output to a summary file which has an assigned .SUM extension. The summary file is an abridged version of the report file. This file abstracts pertinent information about each plate, unknown, and QC sample, eliminating much of the detail included in the report file. This file contains the overall mean for each unknown, excluding the dilution-specific information. However, dilution means are recorded for quality control samples. The report file is cumulative in nature. Each result is appended to the end of this file. The summary file is updated in that information is revised as users censor optical densities and recalculate results.

If the user selected the option to save the results to a report file, an output file selection dialog window will now appear. **ELISA for Windows** will suggest *file.RPT*, where *file* is the root name of the standards data file. If this file already exists, it will be

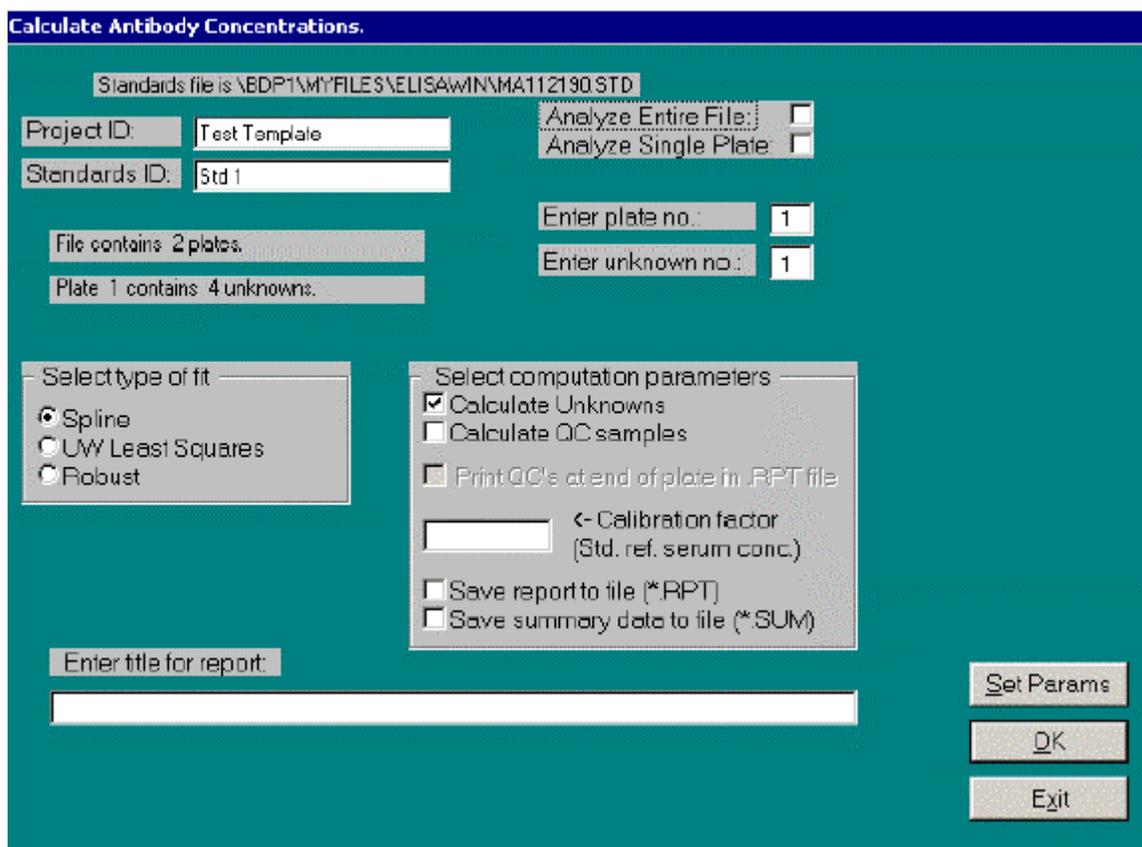


Figure 18. Dialog window for Module 6 - Calculate Concentrations.

appended with information from the current session. If the user elects to analyze an entire plate or file of plates, the output will be stored in this file. If the user selects one serum sample, the results will be displayed on screen where they may be stored to file by clicking on the 'Save report to file' option button. If a single plate or an entire file is selected for processing, the opening dialog window for this module will reappear after the current round of processing has finished.

If the user selected the option to save the results to a summary file, an output file selection dialog window will appear next. **ELISA for Windows** will suggest *file*.SUM, where *file* is the root name of the standards data file. If this file already exists, it will be *updated* with information from the current session. Recording summary results is automatic—it is not necessary to click on a save-to-file button as is the case with the report file. If the user elected to analyze an entire plate or file of plates, the output will be stored in this file. If the user selected one unknown, the results will be displayed on screen and recorded in the summary file. If optical densities are subsequently censored and the unknown recalculated, the summary file will be automatically updated to reflect the revised mean, standard deviation and CV.

## Calculation Parameters

**ELISA for Windows** contains a feature that allows users to pre-screen optical densities which are included in mean, standard deviation, and CV calculations. This gives an investigator a wide degree of latitude in eliminating observations that would normally be excluded from these calculations without examining each unknown in detail. This is meant as a time-saving device which will facilitate analysis of large numbers of plates in high-volume laboratories. Trying different options and different combinations of options will enable the user to arrive at optimized settings for a given experimental design.

Clicking on the 'SetParams' button will open a new window offering these different options. This window is diagramed in Figure 19.

The 'Set Calculation Parameters' screen offers a number of choices for censoring optical densities. Users may select as many options as desired. A particular optical density will be eliminated from subsequent calculations if it is excluded by any one condition. Essentially, all selected conditions are chained with 'OR' logic.

The first block allows users to enter minimum and maximum OD filters. In this instance, all optical densities below the minimum or above the maximum OD filter settings will be censored.

The next option is a check box which will censor all optical densities which fall outside the range of the standard's optical densities which is listed within parentheses.

The next box allows the user to enter a CV filter. This will effectively exclude from overall mean calculations all ODs for a particular dilution where the within

dilution CV is above this selected setting. Enter the number as a percentage, i.e., a number between 1 and 100.

The following box allows users to screen optical densities based on the asymptotes of the fitted standard curve. If the spline fit was selected on the previous screen, this box will be disabled. ODs will be censored if they fall below the lower or above the upper asymptote settings. For reference, the asymptotes are listed in the section title. When a percentage is entered, upon tabbing out of the box or clicking on another option, the program will calculate what the OD filter setting will be and echos this out in the gray area in the right side of the box. For example, if the upper asymptote for the standard curve is 3.5 and the user wishes to include only those unknown ODs that fall within 95% of the upper asymptote of the standard curve fit, then 5.0 would be entered in the 'Include values \_\_\_ % below the upper asymptote' box. This would set the upper asymptote OD filter at  $3.5 - (3.5 \times 0.05) = 3.325$  and all unknown ODs greater than this value will be censored. If the user wishes to use the values of the asymptotes themselves then enter 0.0 in both the lower and upper asymptote text boxes. This is unnecessary, however, as it is impossible to calculate concentrations for

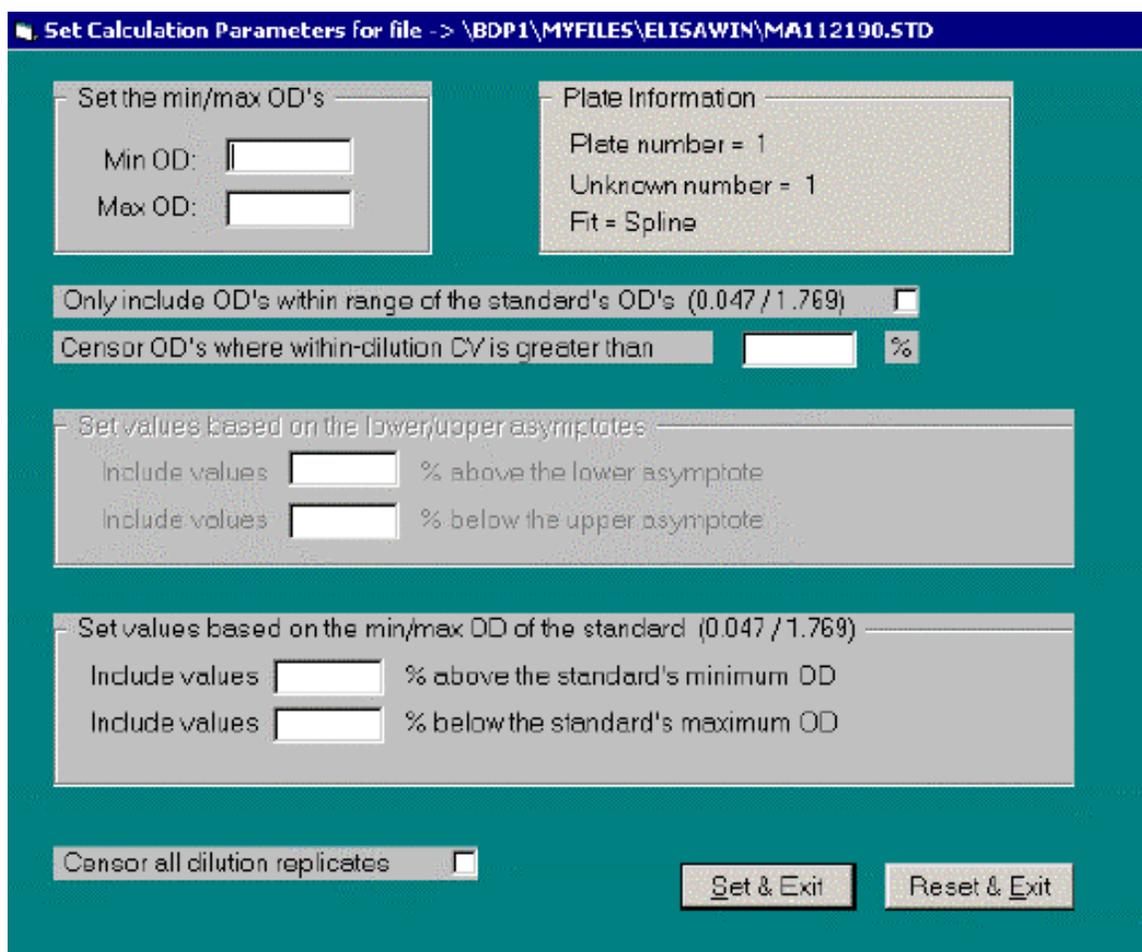


Figure 19. Dialog window for optical density filter settings.

ODs that fall outside the range of the asymptotes. The program will flag these situations automatically as non calculable (N/C - see below).

The next box works in the same way as the asymptotes box using the range of the standard optical densities in place of the bracketing asymptotes. As with the asymptotes, the values for the minimum and maximum standard OD are listed in the box title. When a percentage is entered, the newly defined filter is calculated and listed in the gray area in the right side of the box. All OD's below the minimum filter or above the maximum filter will be censored.

The final censoring criteria is a check box which instructs the program to exclude *all* optical densities within a specific dilution if any one of them is censored using any one of the other options.

Click on 'Set and Exit' to save the filter settings and apply them to subsequent analyses. They will stay in place until the module is exited to the main menu or they may be erased by clicking on the 'Reset and Exit' button.

## Results Window

Figure 20 displays a typical screen displaying the results from this module. A complete listing is provided in Appendix A.

The header comments record the one line title statement if entered by the user in the opening dialog window (Figure 18). Also included are: the file name, the date and time the report was generated, the type of fit, and the four coefficients from the four parameter logistic-log function (which, of course, are missing if the spline fit was chosen in the dialog window, Figure 18). Note that the present parameterization of the logistic-log function determines the lower asymptote of the sigmoidal curve be defined as the **sum** of the first two coefficients. The upper asymptote is equal to the first coefficient. This is all to say that it is impossible to calculate concentrations for optical densities from patient unknowns or quality control samples which fall below the lower asymptote or above the upper asymptote as seen in Figure 21. The range of calculable values is listed in the report just under the coefficients. The report also lists the range of the dilutions for the standard reference serum. Next, the calibration factor is listed. If any optical density filters were set to automatically exclude ODs based on predetermined criteria. They will be detailed next. Each criteria will be followed by a letter in parentheses which is used to annotate the line listing for the report.

The body of the report begins with listing the plate and serum sample number selected by the user. It includes a listing of the sample number, and the optical densities which are grouped into blocks of serum samples as specified by the template used to abstract the original data. The dilutions corresponding to the optical densities are also detailed. The average optical density and concentration are given for each group of replicate samples in the serum sample series. **ELISA for Windows** considers all samples with the same dilution as members of a replicate series. If the serum sample

did not contain a replicate sample, these averages would simply amount to the single OD and concentration. The report also lists the standard deviation and the coefficient of variation (CV) for the replicates. The CV is defined as:

$$(\text{std.dev./average concentration}) \times 100.0.$$

If the serum sample does not contain a replicate sample the standard deviation and coefficient of variation are set equal to 0.0.

Referring to Figure 20, the 'N/C' designation in the right margin beside the second sample stands for **Non Calculable**. The optical densities for line number 2 is outside the range of permissible ODs as detailed in the header comments to the report. The descriptive statistics for the dilution containing this sample has been adjusted to

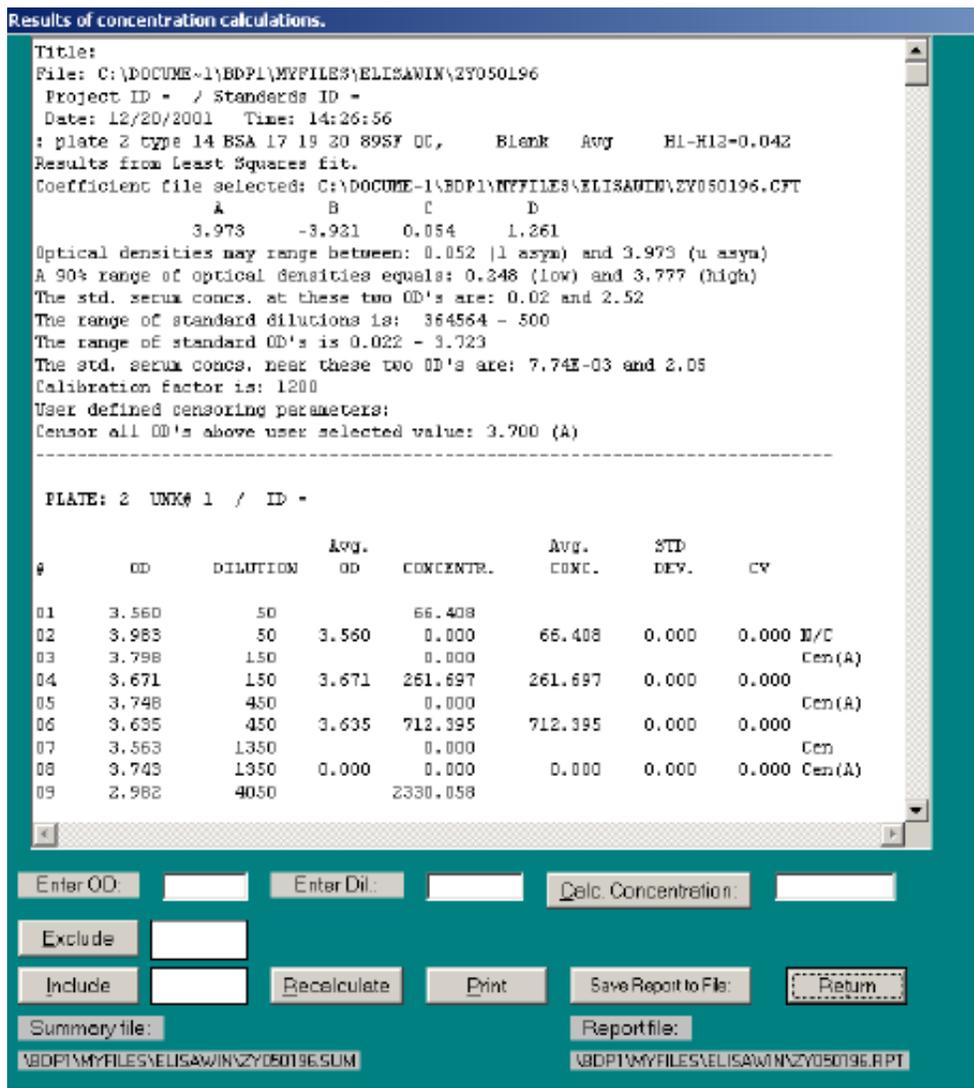


Figure 20. Sample output from Module 6 - Calculate Concentrations.

reflect the absence of one calculated concentration value. If a plate is formatted that includes several replicates and only one or two ODs fell out of the range of permissible values, these statistics would still be calculated, using the subset of acceptable optical densities. The two entries for dilution 50 illustrate this, where line number 2 was excluded from the calculations. The average concentration for the pair is simply the value for the remaining line number in the replicate series. Figure 21 illustrates the primary cause for N/C conditions - the observed optical densities fall above or below the upper or lower, respectively, asymptotes for the standard curve.

Line numbers 3, 5, and 8 are excluded from the summary calculations due to a user defined filtering criteria—their optical densities fell above the preset level of 3.700. The last line lists the grand average concentration, standard deviation, and CV over all calculable samples within the unknown series. Refer to page 53 for a sample of a complete listing.

Typically, the window used to display the results will not be large enough to frame the entire listing. There are horizontal and vertical scroll bars on the bottom and right side of the window, respectively.

It should be noted that users may edit the contents of the output window. Comments may be added to further annotate the output. Several rudimentary Microsoft Word operations will work in these windows. For example, text may be marked by clicking the left mouse key and dragging the cursor through the target text or pressing the shift key while moving the cursor through the text with the cursor control keys. Once text is marked it may be deleted, moved, etc.

The options available to the user at this stage appear at the bottom of the output window, beneath the horizontal scroll bar. If the user elected to save the results to a file, the option to save the results will be active and the output file name will be listed underneath the option button. Results will not be saved unless the 'Save

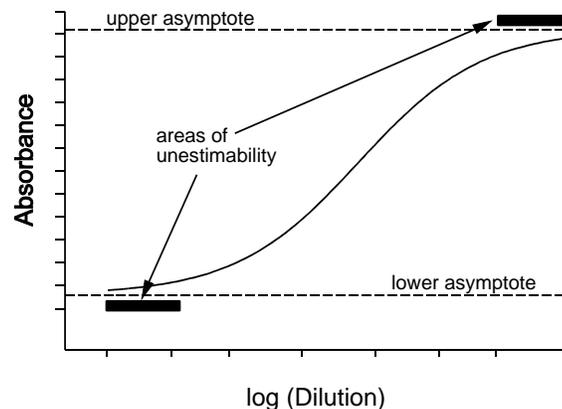


Figure 21. Logistic-log plot showing areas of antibody concentration unestimability.

Results to File' button is clicked. This allows the user to censor optical densities at will, using many steps and examining intervening results before deciding which set to actually save to the results file. If the user did not select the save file option in the opening dialog window for this module, the 'Save Report to File' option in the output screen will be suppressed. The user may also send the contents of the output window directly to the printer. In either case, all additional comments added to the output window will be included during the save and print operations. If the user elects to create a summary file, this will be indicated on the results screen. Results will be recorded automatically when the program returns to the previous screen (clicking the Return button). In this case the last round of calculations represents the results which will be recorded. If the summary file already contains an entry for the particular plate and unknown, it will be over-written by the present results. This is contrary to the results file where all results are appended to the end of an existing file. Previous results are never over-written.

The first line of options under the results window provides the flexibility of manually calculating antibody concentrations for optical densities not included in the unknowns file. After the optical density and dilution are entered in their respective boxes, clicking the Calc Concentration button will yield the concentration. Dilutions may be entered as the actual decimal number or the reciprocal equivalent (e.g., 0.00333333, 3.333E-3, or 300).

Another option gives the user the ability to include and/or exclude one or more data points and recalculate replicate and overall means, standard deviations, and CVs. This option is displayed as:

<Exclude:> [                    ]  
 <Include:> [                    ]

The user may enter a single line number, several line numbers or a range of line numbers within the total range of line for the serum sample series (in the present example, this would be 1-14, listed in the first column of the output window). Single line numbers must be separated with a comma (,); a range of line numbers is indicated by using a hyphen (-); spaces are optional. Thus

1, 5, 7, 9 - 11, 15

would indicate the operation involves samples 1, 5, 7, 9, 10, 11, and 15.

Once a series of line numbers has been entered, clicking on Exclude or Include will mark those sample numbers for exclusion or inclusion from subsequent calculations. 'Ex' and 'In' will appear between the line number and the optical density to remind the user which sample numbers are to be excluded and included, respectively, from the next round of calculations. This operation may be repeated until just the desired samples are finally included in the summary statistics. To effect these final

calculations, click the left mouse button on the Recalculate button. This will revise the output window, excluding/ including all previously marked samples. The notation 'Cen' will appear in the extreme right margin, indicating all samples that have been censured. Excluded samples may be re-included using the Include box. Note that the 'Ex' and 'In' markers will appear temporarily, that is, they disappear after recalculation. Lastly, if the user attempts to include samples that have been automatically censured because they are out of range of permissible optical densities (N/C samples), **ELISA for Windows** will ignore these and continue to exclude them. In this case, the 'N/C' notation will remain in the right margin. Optical densities that were censured due to preset filters may be re-included with the Include function. They will re-enter the summary statistics after clicking on Recalculate.

Additional user comments added to the output window will be lost after recalculation.

Figure 20 displays the result of censoring line number 7. Again, this technique works in a toggle fashion. That is, the user may experiment with deleting and re-entering specimens to observe the effect on the calculations of the descriptive statistics. If the user desired to reclaim sample number 7, simply entering 7 in the Include box, clicking on Include and then Recalculate would include the sample back into the calculations of means, standard deviations and CVs upon recalculation. Samples 3, 5, and 8 were censured due to preset filtering criteria—their optical densities fell above 3.700. They may also be re-included in the summary calculations using the Include function.

Users must experiment with these different features to achieve the final desired results. Once the selected line numbers have been censured, the user may record the results by saving them to a file or printing them. In this fashion, users may record their results at any point in the analysis stage. Alternatively, users may record results at the start of the process to retain a record of the unknown before any data were censured, and then record the output again after all relevant points have been deleted from statistics calculations.

If, in the opening dialog window, the user selects both serum sample and quality control samples to be included in the report, they will both appear in the output window with the QC report following the unknown listing (see page 53 for a sample listing). In this case, each will have its own set of descriptive statistics. While the preset filters will operate on both types of samples, the user will only be allowed to include/exclude line numbers from the serum sample series using the Recalculate function in the Report window. It will not be possible to manually censor samples in the QC part of the report. If it is necessary to exclude one or more samples from the QC block, then select only the QC option for the type of calculations in the opening dialog window (Figure 18).

Clicking on Exit will return the program to the initial dialog window (Figure 18).

A sample summary file is displayed in Figure 22. This file is mainly intended for export into other statistical analysis programs. However, it also serves as a useful compressed listing of results for each unknown and quality control sample in a file containing many plates. This file is grouped by plate and contains information pertinent to each plate. Plates are numbered sequentially. The header or comment lines which precede each plate are prefixed with a period (.) In column 1, followed by the plate number. This will help programmers extract these lines from the following data to facilitate data analysis. Each serum sample is represented by one line which contains the overall summary statistics. Each quality control sample contains as many lines as there are unique dilutions for each sample. The dilution is listed for the QC samples and is indicated as combined for the unknowns as their results are summarized over all dilutions.

Upon exiting this module **ELISA** for *Windows* returns to the main menu (Figure 3).

```

. 1
. 1 C:\ELISAWIN\ZY050196 11/18/96 18:25:07
. 1 Plate 1 : Title :
. 1 Lbl Comment : plate 1 type 4 BSA 17 19 20 89SF QC, Blank Avg
. 1
. 1 Plt # Type ID Dil. Concent. S.D. CV.
. 1
1 1 U Unk 1 Combined 178.2268 49.196 27.603
1 2 U Unk 2 Combined 838.2361 89.733 10.705
1 3 U Unk 3 Combined 547.4713 95.769 17.493
1 4 U Unk 4 Combined 80.7430 10.877 13.471
1 4 Q 2nd qc 1500 2.4182 0.106 4.399
1 6 Q 2nd qc 4500 2.2931 0.073 3.189
1 8 Q 2nd qc 13500 2.1469 0.024 1.120
1 10 Q 2nd qc 40500 1.9941 0.045 2.233
1 12 Q 2nd qc 121500 1.7661 0.016 0.910
1 14 Q 2nd qc 364500 1.3786 0.387 28.072

```

Figure 22. Sample summary (.SUM) file.

# MODULE 7

## EDIT DATA FILES

This module allows users to edit data files associated with their ELISA plates. These include raw data (.DAT files), standards data (.STD files), unknowns data (.UNK files), quality control sample data (.QC files), and label files (.LBL). Files up to 64K may be edited in this module. If an attempt is made to edit a file greater than 64K an error will result and the user will be exited from the module. Users may not edit coefficient data (.CFT files) in this module. If, while estimating the coefficients for a logistic-log standard curve, it is determined that one or more of the standards data points are outliers, this module may be used to remove those points and the estimation procedure re-executed. Data may also be altered to suit the needs of individual investigators. This may occur with raw data files (.DAT files), where small negative optical densities have been recorded. As explained in the raw data section of the Introduction, negative optical densities will adversely effect parameter estimation and must be converted to non 0 positive numbers. The simple editing capabilities of the present module may be used to change these values.

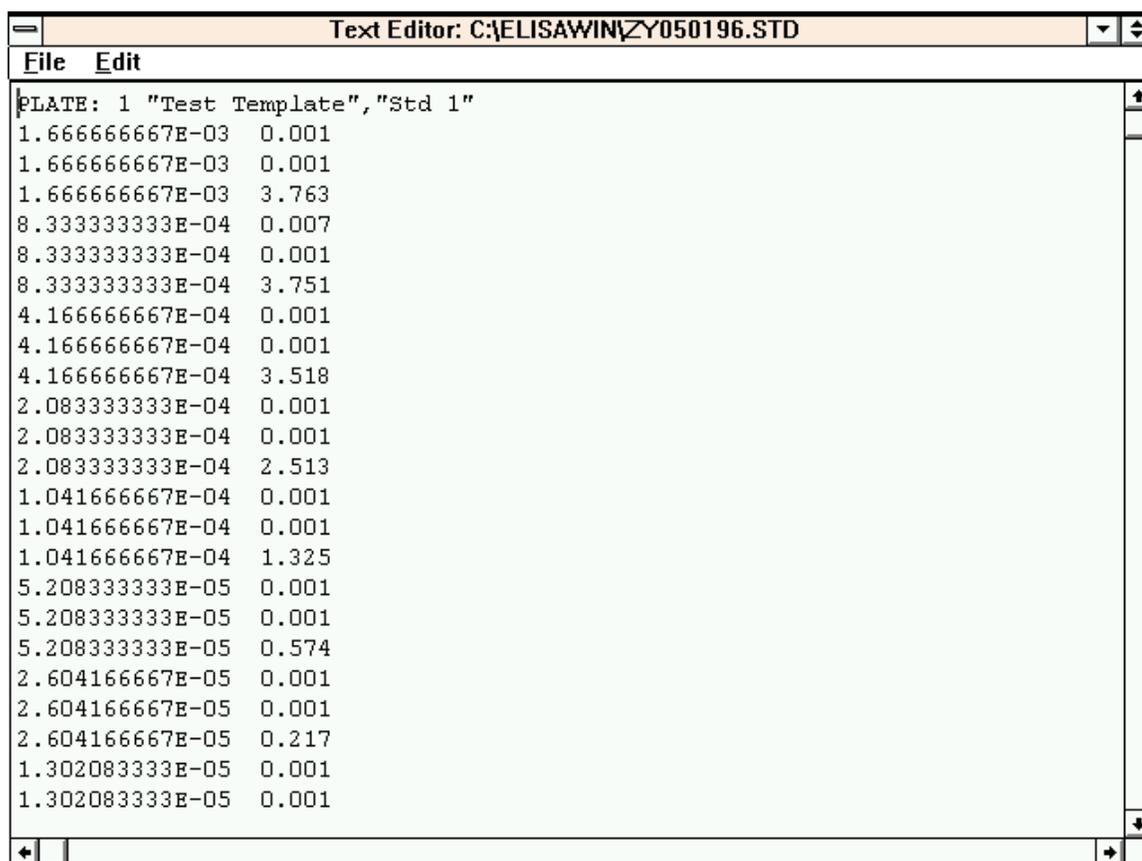
This module is entered from the main menu (Figure 3) and begins by displaying a data file selection dialog window. Once a file has been selected, it will be placed in a text editing window as shown in Figure 23. The cursor may be moved through the window using a mouse or the cursor control keys.

Users must be careful not to create extra lines by accidentally pressing the ENTER key. Also, standards data (.STD), unknowns data (.UNK), and quality control data (.QC) must be separated by '99999'.

The file may be printed to obtain a hard-copy listing of the file. The window may also be exited without saving and edits, permitting the user to back out of the procedure without changing any data. Finally, the user may save the changes made to the selected data file.

If the user desires to save the changed file, a file selection dialog window will reappear. The current file name will be placed in the file name box. Users may change this file name if they wish to save the changes to a different file.

Upon exiting this module, **ELISA for Windows** returns to the main menu (Figure 3).



The image shows a text editor window titled "Text Editor: C:\ELISAWIN\ZY050196.STD". The window contains a list of data entries, each consisting of a scientific notation value followed by a decimal value. The data is as follows:

Value 1	Value 2
PLATE: 1 "Test Template", "Std 1"	
1.666666667E-03	0.001
1.666666667E-03	0.001
1.666666667E-03	3.763
8.333333333E-04	0.007
8.333333333E-04	0.001
8.333333333E-04	3.751
4.166666667E-04	0.001
4.166666667E-04	0.001
4.166666667E-04	3.518
2.083333333E-04	0.001
2.083333333E-04	0.001
2.083333333E-04	2.513
1.041666667E-04	0.001
1.041666667E-04	0.001
1.041666667E-04	1.325
5.208333333E-05	0.001
5.208333333E-05	0.001
5.208333333E-05	0.574
2.604166667E-05	0.001
2.604166667E-05	0.001
2.604166667E-05	0.217
1.302083333E-05	0.001
1.302083333E-05	0.001

Figure 23. Edit window from Module 7 - Edit Data Files.

# APPENDIX A

## Sample Data and Output

A collection of sample data files and program output is included on the distribution diskette. These files may be used to test the program and check results after selecting various options in the different modules. The sample data file is MA112190.DAT and appears as:

```
COMMENT:FRASCH ASSAY PB2 1:75 PLATE 1 UNKNOWNNS ARE PB2 1:75
 1.716  1.757  1.769  1.840  1.462  0.960  0.562  0.313  0.171  0.090  0.041  1.440
 1.438  1.462  1.458  1.800  1.493  1.013  0.590  0.346  0.173  0.092  0.044  1.409
 0.967  1.014  0.998  1.790  1.484  0.984  0.589  0.334  0.175  0.096  0.047  1.255
 0.586  0.606  0.627  1.801  1.472  0.970  0.588  0.322  0.169  0.085  0.043  1.239
 0.319  0.347  0.346  1.794  1.445  0.958  0.587  0.312  0.175  0.086  0.045  0.233
 0.167  0.186  0.190  1.746  1.424  0.948  0.573  0.312  0.168  0.090  0.046  0.255
 0.094  0.103  0.099  1.791  1.531  0.955  0.584  0.325  0.170  0.091  0.040  0.001
 0.047  0.051  0.051  1.822  1.478  0.906  0.536  0.305  0.158  0.082  0.040  0.001
COMMENT:FRASCH ASSAY PB2 1:75 PLATE 2 UNKNOWNNS PB2 1:75
 1.830  1.843  1.914  1.898  1.637  1.045  0.620  0.341  0.178  0.091  0.046  1.446
 1.655  1.681  1.690  1.884  1.628  1.077  0.630  0.350  0.184  0.091  0.047  1.461
 1.078  1.103  1.059  1.896  1.652  1.094  0.641  0.343  0.182  0.099  0.050  1.207
 0.655  0.658  0.635  1.898  1.644  1.091  0.623  0.348  0.173  0.095  0.048  1.203
 0.363  0.361  0.353  1.884  1.653  1.054  0.626  0.352  0.186  0.099  0.050  0.223
 0.193  0.198  0.188  1.914  1.652  1.084  0.624  0.338  0.175  0.090  0.043  0.225
 0.091  0.095  0.094  1.841  1.612  1.079  0.624  0.349  0.172  0.068  0.046  0.001
 0.048  0.047  0.045  1.769  1.603  1.053  0.643  0.326  0.179  0.093  0.046  0.001
```

The template used to abstract the data is located in file FINAL.TPL. Module 2 may be used to examine the template format and the dilution schedules (refer to Module 2 and Appendix B). Users may run the data abstraction module (Module 3) to produce the .STD, .UNK, .QC, and .LBL files. These are also included on the distribution diskette: MA112190.STD, MA112190.UNK, MA112190.QC, and MA112190.LBL.

Modules 4 may then be used to estimate the four parameters of the logistic-log fit. A sample file of standard curve fitting information is MA112190.FIT contains these results. A portion of that file is reproduced here:

```
File = C:\ELISAWIN\DOWNLOAD\MA112190.STD- Plate: 1
Project ID = Test Template / Standards ID = Std 1
Date: 11/19/96 Time: 11:22:53
:FRASCH ASSAY PB2 1:75 PLATE 1 UNKNOWNNS ARE PB2 1:75
Results of approximate least squares fit
The procedure used 7 iterations.
```

```
Starting values for the iterative process:
2.28081 -2.32942 .03409 1.00000
```

Dil.	Rel. Dil.	Known O.D.	Pred. O.D.	Residual	% Error	Weight
0.001666667	100.00	1.716	1.7559	-0.040	2.325	1.0000
0.001666667	100.00	1.757	1.7559	0.001	0.063	1.0000
0.001666667	100.00	1.769	1.7559	0.013	0.741	1.0000
0.000833333	50.00	1.438	1.4315	0.007	0.453	1.0000
0.000833333	50.00	1.462	1.4315	0.031	2.087	1.0000
0.000833333	50.00	1.458	1.4315	0.027	1.818	1.0000
0.000416667	25.00	0.967	1.0095	-0.042	4.391	1.0000
0.000416667	25.00	1.014	1.0095	0.005	0.448	1.0000
0.000416667	25.00	0.998	1.0095	-0.011	1.148	1.0000
0.000208333	12.50	0.586	0.6097	-0.024	4.047	1.0000
0.000208333	12.50	0.606	0.6097	-0.004	0.613	1.0000
0.000208333	12.50	0.627	0.6097	0.017	2.757	1.0000
0.000104167	6.25	0.319	0.3300	-0.011	3.458	1.0000
0.000104167	6.25	0.347	0.3300	0.017	4.890	1.0000
0.000104167	6.25	0.346	0.3300	0.016	4.615	1.0000
0.000052083	3.12	0.167	0.1732	-0.006	3.697	1.0000
0.000052083	3.12	0.186	0.1732	0.013	6.896	1.0000
0.000052083	3.12	0.190	0.1732	0.017	8.856	1.0000
0.000026042	1.56	0.094	0.0959	-0.002	2.049	1.0000
0.000026042	1.56	0.103	0.0959	0.007	6.868	1.0000
0.000026042	1.56	0.099	0.0959	0.003	3.105	1.0000
0.000013021	0.78	0.047	0.0603	-0.013	28.335	1.0000
0.000013021	0.78	0.051	0.0603	-0.009	18.270	1.0000
0.000013021	0.78	0.051	0.0603	-0.009	18.270	1.0000

```
The final coefficients (a, b, c, d) are:
2.13195 -2.10001 0.01841 1.19810
```

```
Variances of coefficients = 0.00245 0.00328 0.00000 0.00211
```

```
Regular and adjusted sums of squares = 0.007834 0.007834
```

```
Approximate multiple R^2 = 0.9991
```

Logistic-log and spline fit plots may be viewed using Module 5.

Module 6 may then be entered to calculate patient serum sample or unknown antibody concentrations. In this sample data set a calibration factor of 1500 was chosen. A complete listing of these results using the unweighted least squares fit is included in file MA112190.RPT. A sample of the report file is reproduced here:

Title:  
 File: C:\ELISAWIN\DOWNLOAD\MA112190  
 Project ID = Test Template / Standards ID = Std 1  
 Date: 11/19/96 Time: 11:23:32  
 :FRASCH ASSAY PB2 1:75 PLATE 1 UNKNOWNS ARE PB2 1:75  
 Results from Least Squares fit.  
 Coefficient file selected: C:\ELISAWIN\DOWNLOAD\MA112190.CFT  
 A B C D  
 2.132 -2.100 0.018 1.198  
 Optical densities may range between: 0.032 (l asym) and 2.132 (u asym)  
 The range of standard dilutions is: 76800 - 600  
 The range of standard OD's is 0.047 - 1.769  
 Calibration factor is: 1500

-----  
 PLATE: 1 UNK# 1 / ID = Unk 1

#	OD	DILUTION	Avg. OD	CONCENTR.	Avg. CONC.	STD DEV.	CV
01	1.840	300		964.043			
02	1.800	300	1.820	850.047	907.045	80.607	8.887
03	1.462	600		792.541			
04	1.493	600	1.477	839.400	815.970	33.134	4.061
05	0.960	1200		692.807			
06	1.013	1200	0.987	754.256	723.532	43.451	6.005
07	0.562	2400		680.189			
08	0.590	2400	0.576	720.796	700.493	28.713	4.099
09	0.313	4800		708.477			
10	0.346	4800	0.329	789.232	748.855	57.102	7.625
11	0.171	9600		739.668			
12	0.173	9600	0.172	749.174	744.421	6.722	0.903
13	0.090	19200		689.887			
14	0.092	19200	0.091	710.248	700.068	14.398	2.057
15	0.041	38400		286.910			
16	0.044	38400	0.043	364.736	325.823	55.031	16.890
Mean (Excludes N/C & Cen):				708.276		166.979	23.575

PLATE: 1 QUALITY CONTROL

#	OD	DILUTION	Avg. OD	CONCENTR.	Avg. CONC.	STD DEV.	CV
01	1.440	1200		1523.070			
02	1.409	1200	1.424	1441.331	1482.200	57.798	3.899
03	1.255	1800		1666.735			
04	1.239	1800	1.247	1623.825	1645.280	30.342	1.844
05	0.233	19200		2067.105			
06	0.255	19200	0.244	2276.285	2171.695	147.913	6.811
Mean (Excludes N/C & Cen):				1766.392		330.317	18.700

# APPENDIX B

## Template File Format

The FINAL.TPL file which describes a sample template and is distributed with other sample data files along with the program **ELISA** for *Windows* contains the following information:

```
8,"Test Template"  
"S","1","1","8","3","600","2","L","3","H","Std 1"  
"U","1","4","2","11","300","2","L","2","V","Unk 1"  
"U","3","4","4","11","300","2","L","2","V","Unk 2"  
"U","5","4","6","11","300","2","L","2","V","Unk 3"  
"U","7","4","8","11","300","2","L","2","V","Unk 4"  
"Q","1","12","2","12","1200","2","L","2","V","QC1"  
"Q","3","12","4","12","1800","2","L","2","V","QC2"  
"Q","5","12","6","12","19200","2","L","2","V","QC3"
```

From Module 2, the format for the 96-well ELISA plate which corresponds to the above file appears as in Figure 24.

Using this illustration, the FINAL.TPL file may be interpreted as follows: The first record contains a single integer which details how many lines follow in the rest of the file. The text to the right of this integer is the Project ID. There are eight lines of information, each of which defines one block of standards, unknowns or QC's.

Each line describes one block and contains 11 fields. These fields are:

- 1) Block category where S=standards; Q=quality control samples; and U=unknowns.
- 2) The row number for the top left well in the block.
- 3) The column number for the top left well in the block.
- 4) The row number for the bottom right well in the block.
- 5) The column number for the bottom right well in the block.
- 6) The starting dilution in the series.
- 7) The fold change or dilution factor.
- 8) Indicator for dilution increase or decrease where L=low to high and H=high to low.
- 9) The number of replicates in the block.
- 10) "H" for horizontal or "V" for vertical. This details the orientation of the replicates in the block.
- 11) The block ID.

As an example, the second line of file FINAL.TPL (the first line to follow the number 8) is information pertaining to a standard. The block of wells defining the standard range from row 1, column 1 to row 8, column 3. The initial dilution is 600; the dilution series is 2 fold and the dilutions proceed from low to high. There are three replicates per dilution which run horizontally. The block ID is 'Std 1'.

**ELISA Plate Configuration - file -> C:\ELISAWIN\FINAL.TPL**

	1	2	3	4	5	6	7	8	9	10	11	12
A	600	600	600	300	600	1200	2400	4800	9600	19200	38400	1200
	S	S	S	U1	U1	U1	U1	U1	U1	U1	U1	QC1
B	1200	1200	1200	300	600	1200	2400	4800	9600	19200	38400	1200
	S	S	S	U1	U1	U1	U1	U1	U1	U1	U1	QC1
C	2400	2400	2400	300	600	1200	2400	4800	9600	19200	38400	1800
	S	S	S	U2	U2	U2	U2	U2	U2	U2	U2	QC2
D	4800	4800	4800	300	600	1200	2400	4800	9600	19200	38400	1800
	S	S	S	U2	U2	U2	U2	U2	U2	U2	U2	QC2
E	9600	9600	9600	300	600	1200	2400	4800	9600	19200	38400	19200
	S	S	S	U3	U3	U3	U3	U3	U3	U3	U3	QC3
F	19200	19200	19200	300	600	1200	2400	4800	9600	19200	38400	19200
	S	S	S	U3	U3	U3	U3	U3	U3	U3	U3	QC3
G	38400	38400	38400	300	600	1200	2400	4800	9600	19200	38400	0
	S	S	S	U4	U4	U4	U4	U4	U4	U4	U4	0
H	76800	76800	76800	300	600	1200	2400	4800	9600	19200	38400	0
	S	S	S	U4	U4	U4	U4	U4	U4	U4	U4	0

Project ID:

Figure 24. Display of sample template design.