



## HellabioScan Software v.03 Film Analysis Quick Guide

### Protein electrophoresis film analysis

#### Scan Films

HellabioScan analyzes images that are stored at any picture format (\*.jpg, \*.pif, \*.tif, \*.bmp etc) in your computer. The user can use any peripheral device in order to obtain these images (such as Scanner, Digital Cameras etc.) and store them to his computer.

Recommended analysis for a typical Electrophoresis film is **100 dpi** by 256 gray level color depth (it combines a very good final result with a small image size in computer's hard disk). At this point we must refer that the basic scanning parameters such as dpi analysis or color depth have small effect to the final results of HellabioScan software.

#### Saving Images

After scanning completion HellabioScan program asks the user to save the image. Recommended storage file → Follow the path **C: →program files (X86)→evresis→HellabioScan(SQL) → Images**. Alternatively the user can save the archives to a folder of his choice.

After saving completion HellabioScan captures automatically the scanned image and presents it on the Application's Desktop (default position is on the right side of desktop). **Figure 1** shows HellabioScan desktop after a typical electrophoresis film scanning.

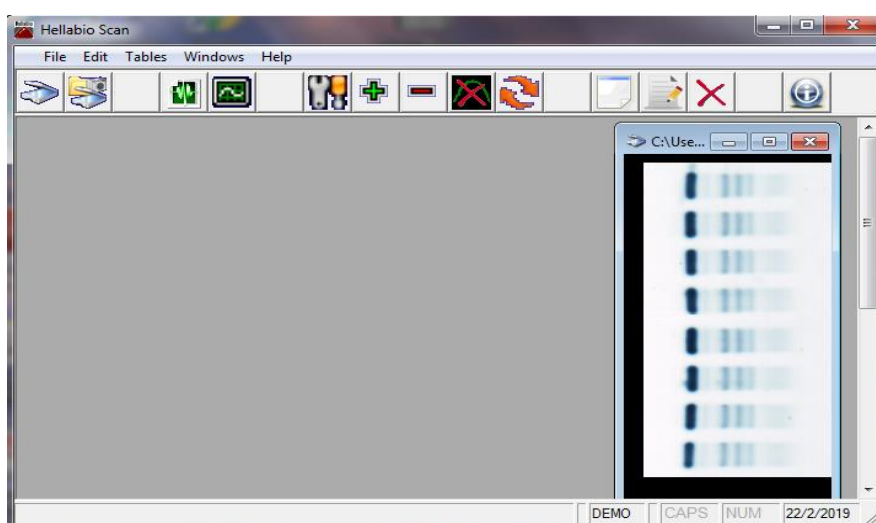



Fig. 1

Additionally the user can load a saved image at any time, using the Open Image selection in File submenu (Ctrl + O) or by click on Toolbar's Open Image  Icon.

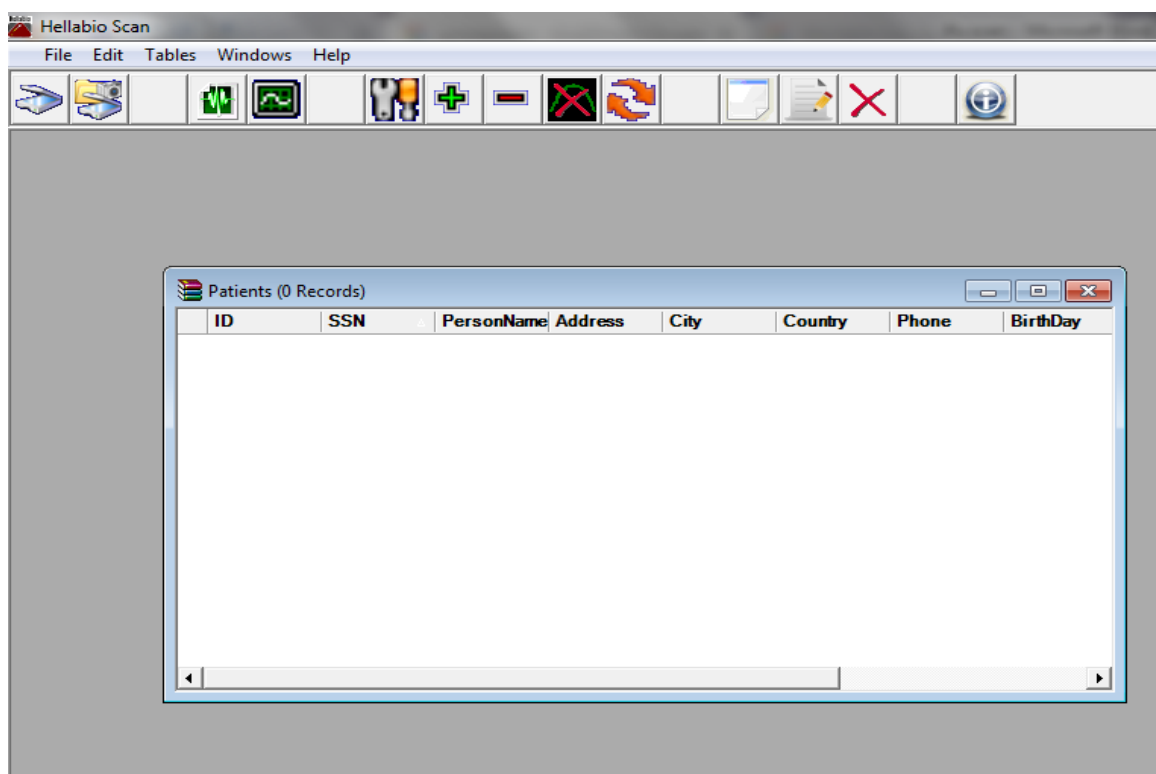
### **Importing patient data**

After scanning and saving completion, the user should enter the patient's personal data. HellabioScan software uses a database for patient registration. Using the option **tables** (above the toolbar), select the **Patients** option (**Fig. 2**)



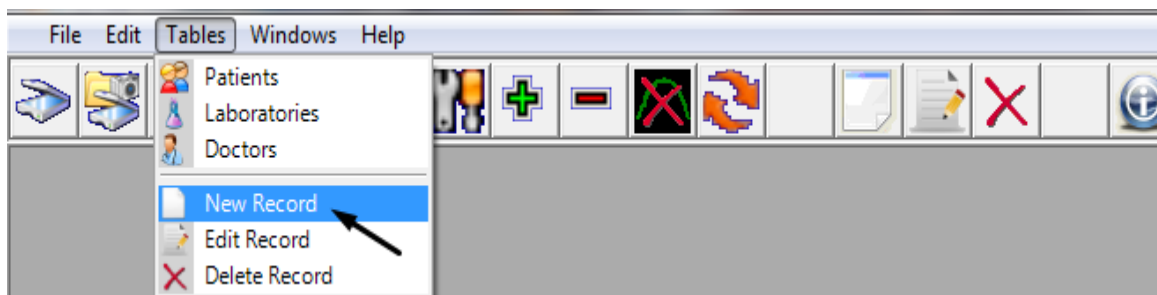
**Fig. 2**

The database table will appear (**Fig. 3**).



**Fig. 3**

Using the option **Tables** again, select the **New Record** option, from the Tables submenu (**Fig. 4**)



**Fig. 4**

The program displays a submission form. The user should fill in all details, for each patient. **Figure 5** shows the submission form. Click on the option **Save**, to register the new patient.

A screenshot of a 'Patients' submission form. The form has a title bar with a person icon and the text 'Patients'. It contains several input fields: 'SSN', 'PersonName', 'Address', 'City', 'Country', 'Phone', 'Date of Birth' (with a dropdown menu showing '1/1/1990'), 'Doctor's Name', 'Laboratory', and 'Comments'. There are also two buttons: 'Protocols' (with a small icon) and 'Save' (with a floppy disk icon). At the bottom right, there is a 'Cancel' button (with a red X icon). The form is set against a light gray background.

**Fig. 5**

## Selecting Lanes

In general occasion Electrophoresis films contains more than one lane. The user can select for analyzing one or more lanes by drawing a rectangle using the computer's mouse. Just click on upper left corner and drag the mouse to the bottom right corner, drawing a rectangle that contains the lanes you want to analyze (**Fig. 6, 7, 8**).

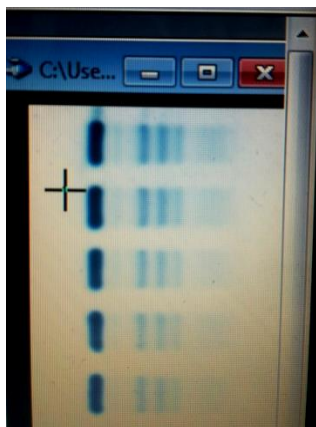


Fig. 6

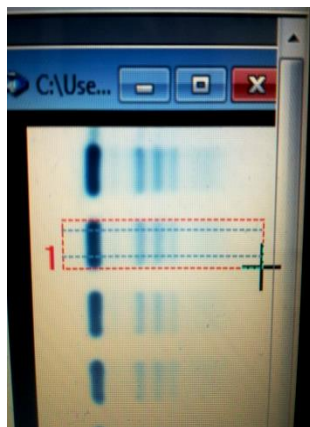


Fig. 7

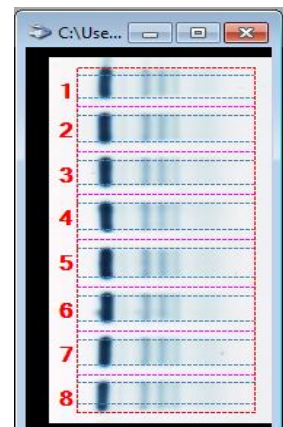



Fig. 8

After the lane selection the user can analyze the selected lanes using the Analyze button  on Toolbar or choosing **Analyze** in File submenu (**Fig. 9**).

The program asks about the type of Electrophoresis film. Select **Protein** Electrophoresis Type (**Fig. 10**).

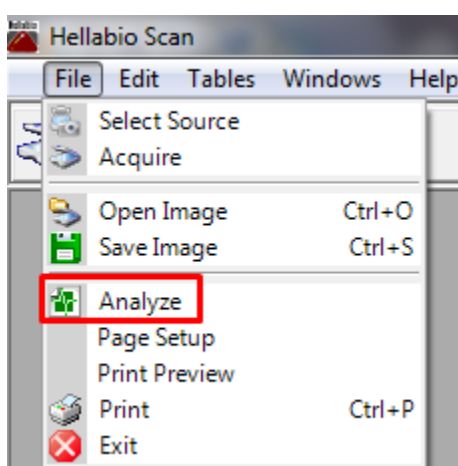


Fig. 9

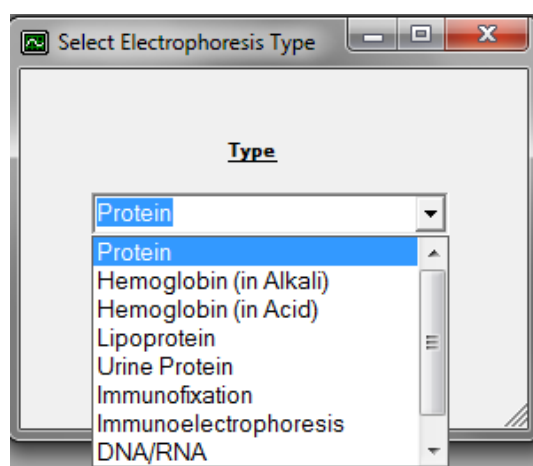


Fig. 10

After the type selection the program automatically appears as many Calculation Windows as the selected lanes of the film. Figure 11 shows the HellabioScan Desktop after a 4-lanes selection of a **serum sample**.

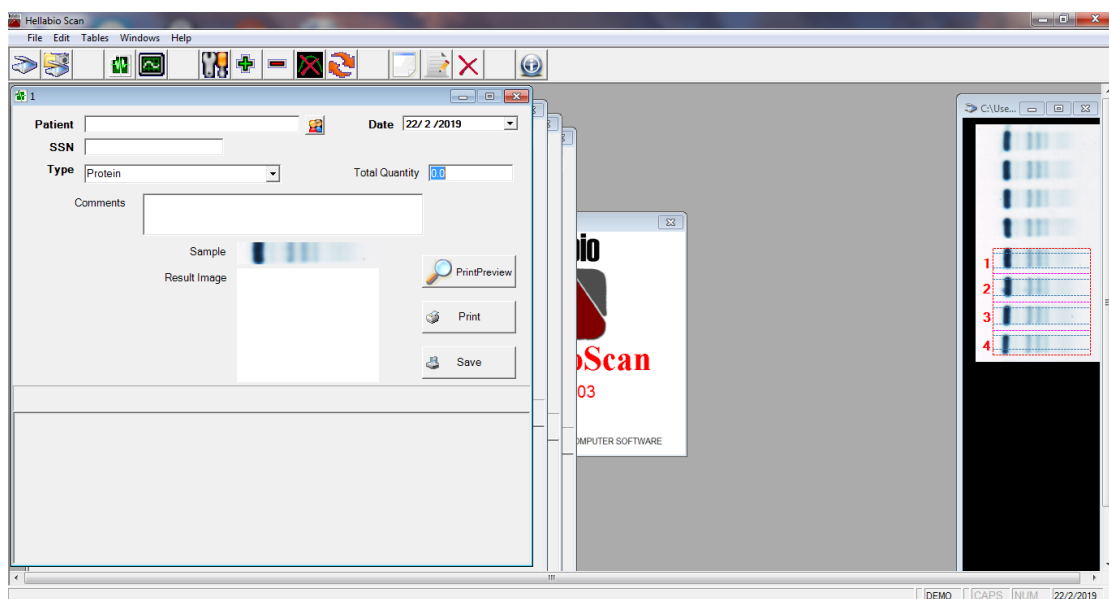



Fig. 11

Every Calculation window is an independent object. User can minimize, move or close any of the windows. Every Calculation window is labeled by a number according to the number of the lane in the film. In a Calculation Window the user can input several data about the examined sample. The **Patient** field must contain information about the examined sample (e.g. *the patient's name*) because it will be the filename of the specific examination. This is the name that the user must search in the future, if he wants to retrieve data about this examination.

Using the button  the user can enter the patient's name (Fig. 12).

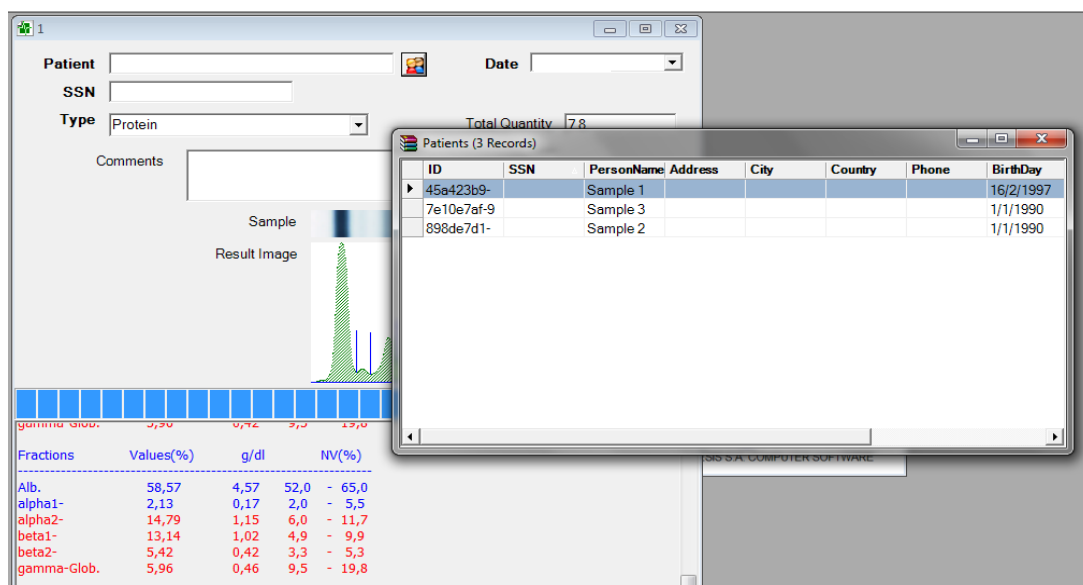
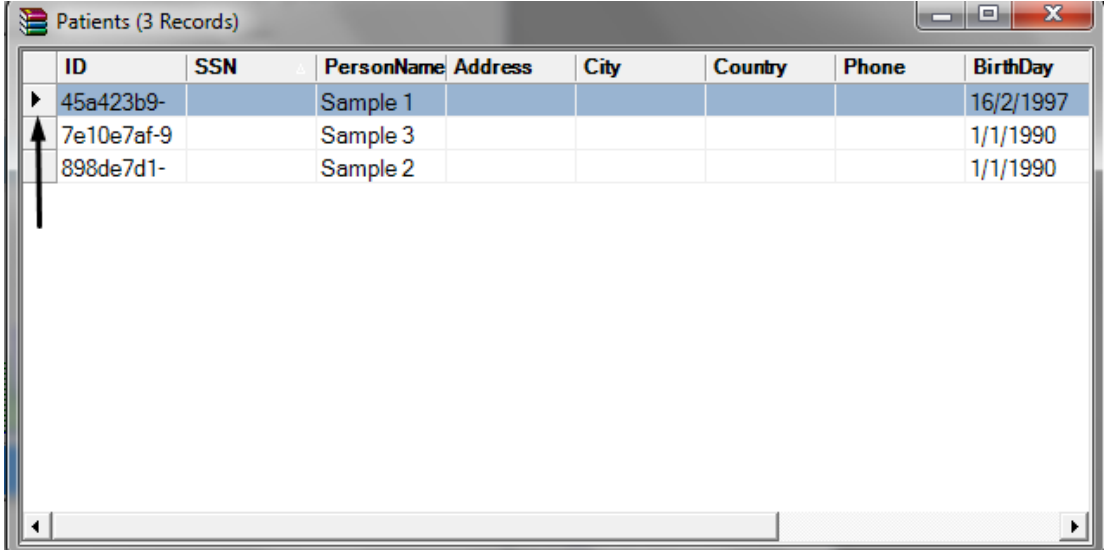



Fig. 12

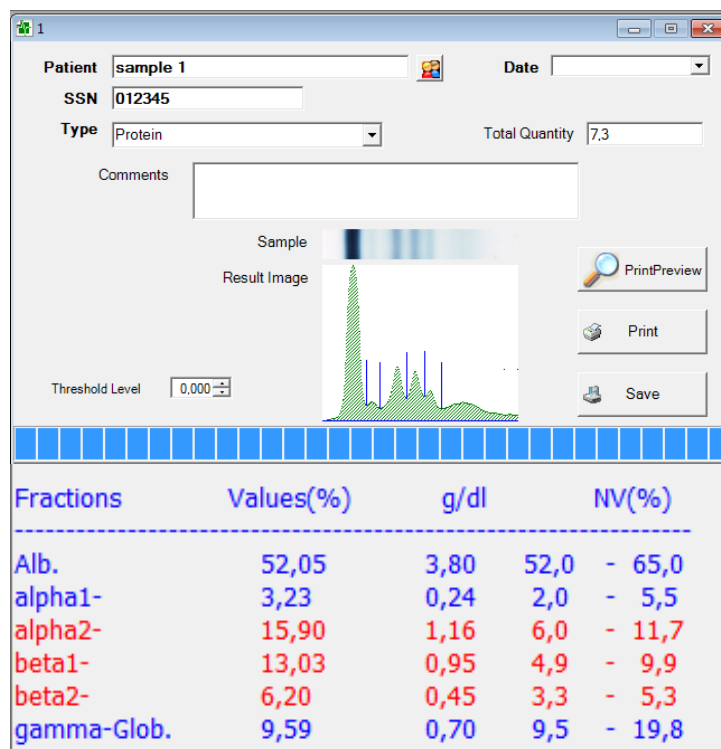
Select the patient by double-clicking on the arrow that appears on the left side of the table (**Fig. 13**).



ID	SSN	PersonName	Address	City	Country	Phone	BirthDay
45a423b9-		Sample 1					16/2/1997
7e10e7af-9		Sample 3					1/1/1990
898de7d1-		Sample 2					1/1/1990

**Fig. 13**

Using the Calculate button  on Toolbar the program executes an image processing algorithm that automatically defines the fractions of the image and calculates the density of each area. The results are presented at the down white part of the calculation window (**Fig. 14**).



**Fig. 14**

The user can enter various data information's (e.g. total quantity of proteins, comments concerning the diagnosis) (**Fig. 15**).

The screenshot shows a software window titled '1'. It contains several input fields: 'Patient' with the value 'sample 1', 'SSN' with '012345', 'Date' with a dropdown arrow, and 'Type' with a dropdown menu showing 'Protein'. A 'Total Quantity' field is highlighted with a red box and contains the value '7,3'. Below this, a 'Comments' text area is also highlighted with a red box and contains the text 'No abnormal proteinemia is observed'. In the center, there is a 'Sample Result Image' showing an electropherogram with a green shaded area and several vertical blue lines. To the left of the image is a 'Threshold Level' field with a value of '0,000'. To the right of the image are three buttons: 'PrintPreview' (with a magnifying glass icon), 'Print' (with a printer icon), and 'Save' (with a floppy disk icon). The bottom of the window features a blue progress bar.

Fig. 15

After the electropherogram analysis, the user can **Save** and **Print** the protocol (**Fig. 16**).

This screenshot is identical to the one in Fig. 15, showing the same patient data and electropherogram. However, the 'Save' button, located at the bottom right of the interface next to the 'Print' button, is now highlighted with a red box. The 'Total Quantity' field still shows '7,3' and the 'Comments' field still contains 'No abnormal proteinemia is observed'.

Fig. 16

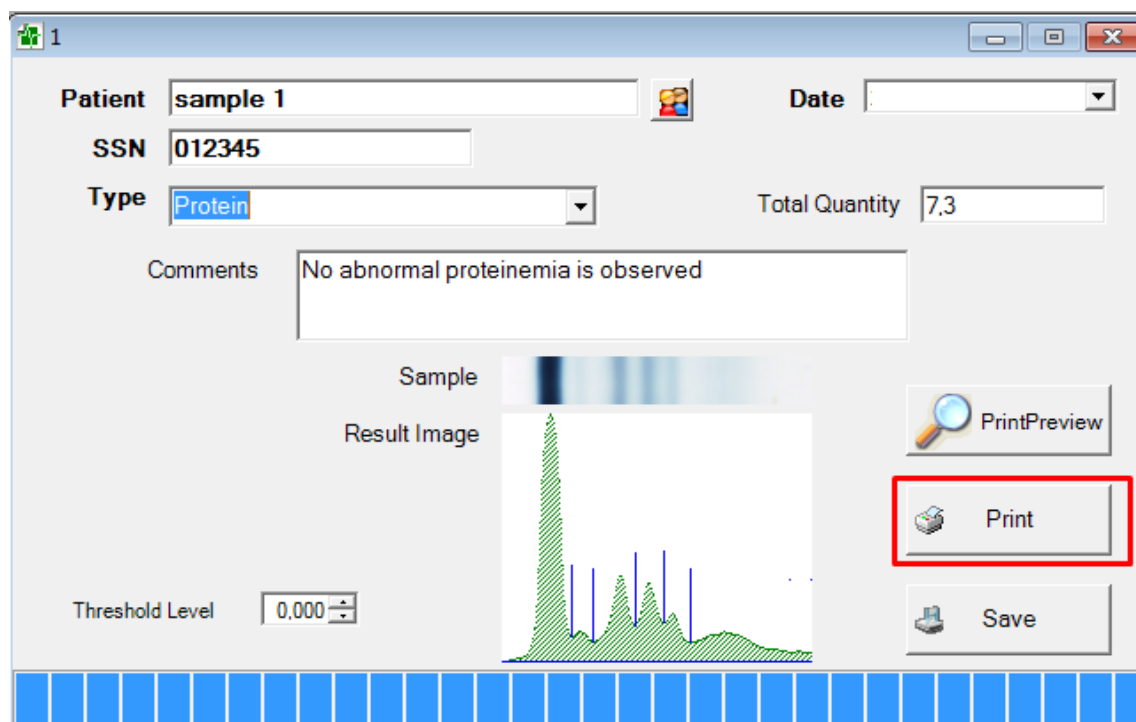


Fig. 16

### Adding an image to the protocol

Before printing, the user has the ability to preview the protocol (**Fig. 17**). HellabioScan software is automatically inserting the image of the electropherogram into the protocol. The user can choose whether or not to display the image in the protocol (**Fig. 18, 19**).

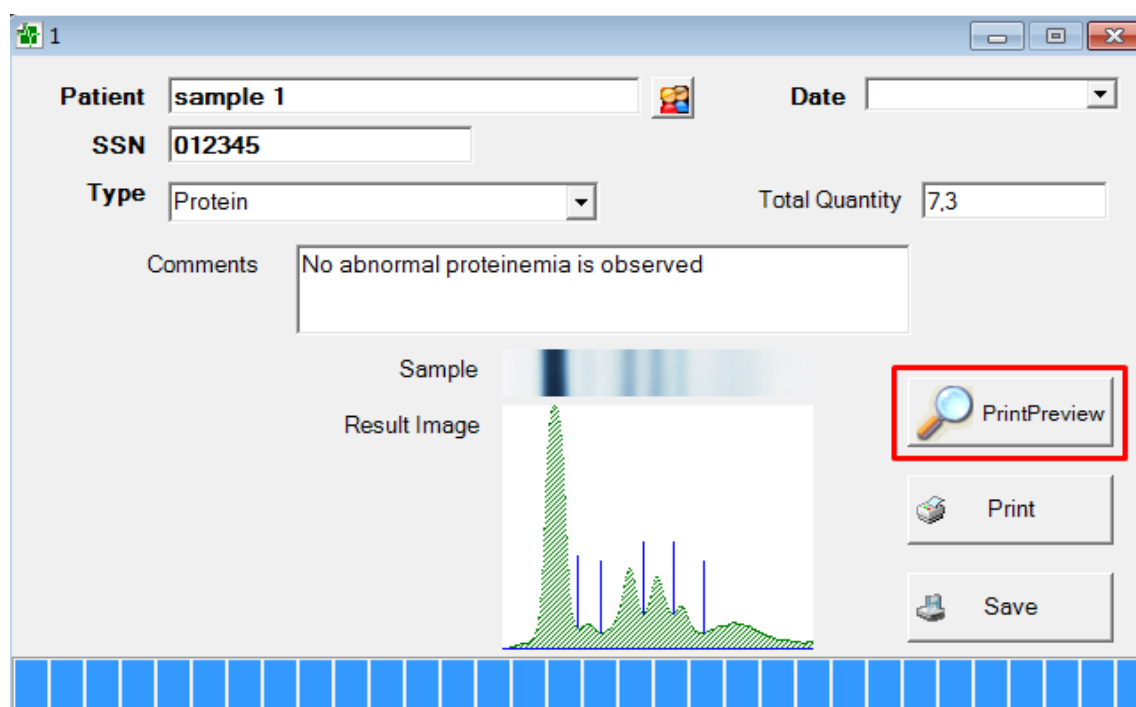


Fig. 17



**Labels & Normal Values**

Band Label	Normal Values	
Alb.	52,0	65,0
alpha1-	2,0	5,5
alpha2-	6,0	11,7
beta1-	4,9	9,9
beta2-	3,3	5,3
gamma-Glob.	9,5	19,8

Header Image

Secondary Image

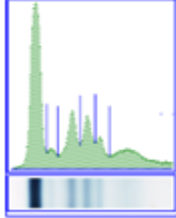
Ok Cancel

Fig. 18 The scanned film will appear in the protocol.

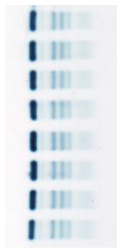
## Protein Electrophoresis

Patient : **sample 1**  
SSN : **012345**  
Date :

Examined Sample



Fractions	Values(%)	g/dL	NV(%)
Alb.	60,75	4,43	52,0 - 65,0
alpha1-	1,72	0,13	2,0 - 5,5
alpha2-	15,29	1,12	6,0 - 11,7
beta1-	13,24	0,97	4,9 - 9,9
beta2-	4,86	0,35	3,3 - 5,3
gamma-Glob.	4,13	0,30	9,5 - 19,8
<b>TOTAL</b>		<b>7,30</b>	<b>A/G: 1,55</b>



Comments: No abnormal proteinemia is observed

The Doctor

Copyright 2008-2015 EVRESIS S.A. Computer Software

Protein electrophoresis protocol

Labels & Normal Values

Band Label	Normal Values	
Alb.	52,0	65,0
alpha1-	2,0	5,5
alpha2-	6,0	11,7
beta1-	4,9	9,9
beta2-	3,3	5,3
gamma-Glob.	9,5	19,8

Header Image

Secondary Image

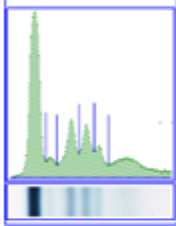
Ok Cancel

Fig. 19 Blank window. The scanned image will not appear in the protocol.

## Protein Electrophoresis

Patient : **sample 1**  
SSN : **012345**  
Date :

Examined Sample



Fractions	Values(%)	g/dL	NV(%)
Alb.	60,75	4,43	52,0 - 65,0
alpha1-	1,72	0,13	2,0 - 5,5
alpha2-	15,29	1,12	6,0 - 11,7
beta1-	13,24	0,97	4,9 - 9,9
beta2-	4,86	0,35	3,3 - 5,3
gamma-Glob.	4,13	0,30	9,5 - 19,8
<b>TOTAL</b>		<b>7,30</b>	<b>A/G: 1,55</b>

Comments: No abnormal proteinemia is observed

The Doctor

Copyright 2008-2015 EVRESIS S.A. Computer Software

Protein electrophoresis protocol

## Manual correction

In some cases the software may not define the fractions properly. This may be due to technical errors (improper sample application, gel injury, insufficient staining-destaining). In this case the software allows the user to correct the errors manually.

## Toolbar

In the toolbar, the user has the following options:



Manual correction



Noise cleaning



Add a fraction separator

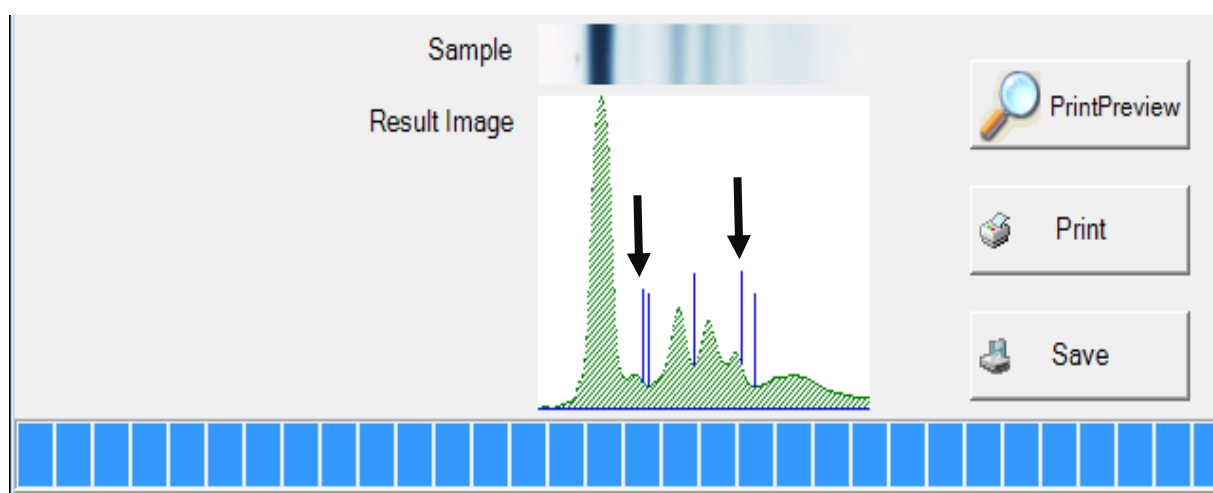


Undo last operation




Delete a fraction separator

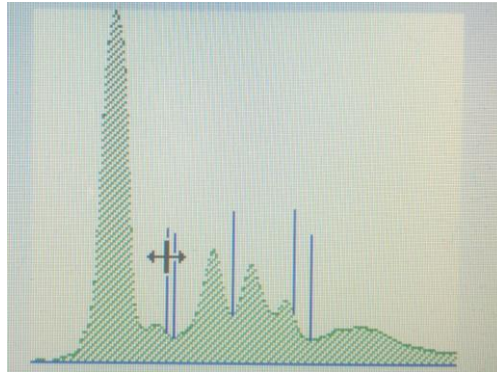
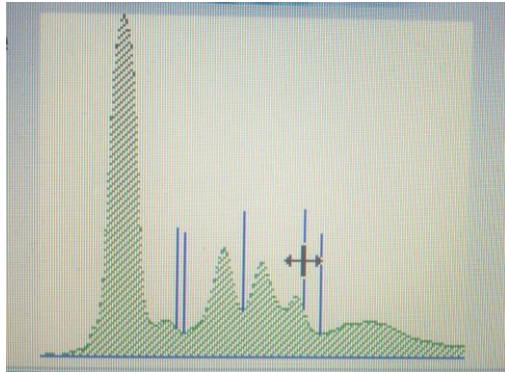
## Example 1



Displaced position of separators

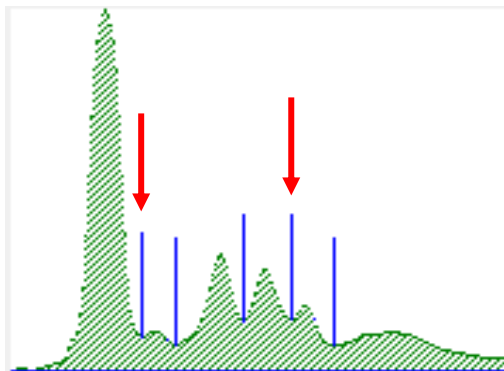
For manually correction, the user must follow the following steps:

- I. Click on the option 
- II. Move the mouse to the displaced separator. A cross will appear on the separator (**Fig. 1.1**).



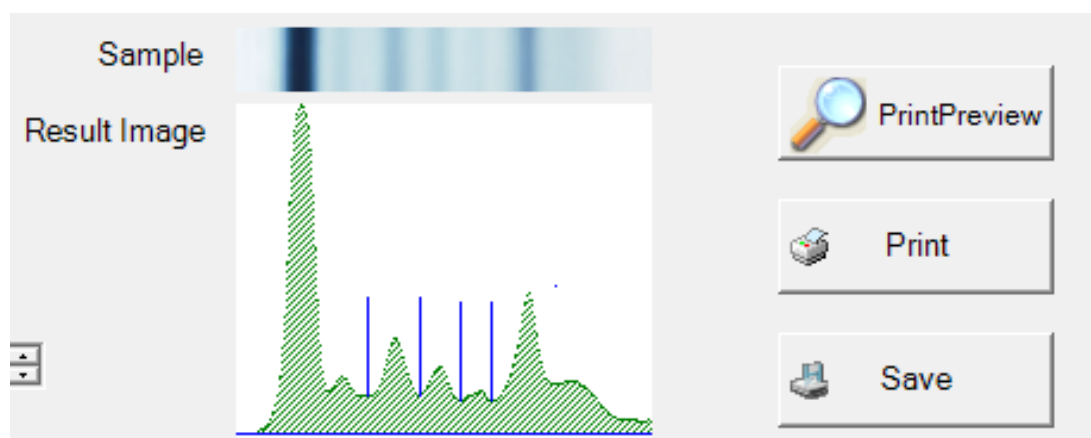
**Fig. 1.1**

- III. Move the separators (**Fig. 1.2**)




**Fig. 1.2**

### **Example 2**



A separator is missing

For manually correction, the user must follow the following steps:

- I. Click on the option 
- II. Move the mouse between the two peaks (**Fig. 2.1**).
- III. Right-clicking will display the following table (**Fig 2.2**)
- IV. Click on the option **Yes**.

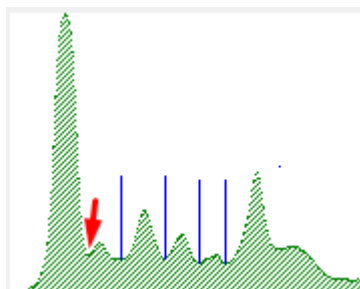


Fig. 2.1

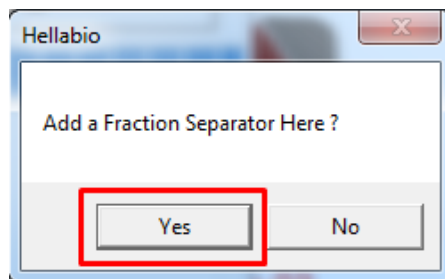


Fig. 2.2

- V. The separator will appear on the histogram (**Fig 2.3**).

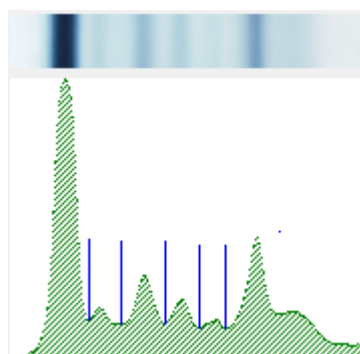
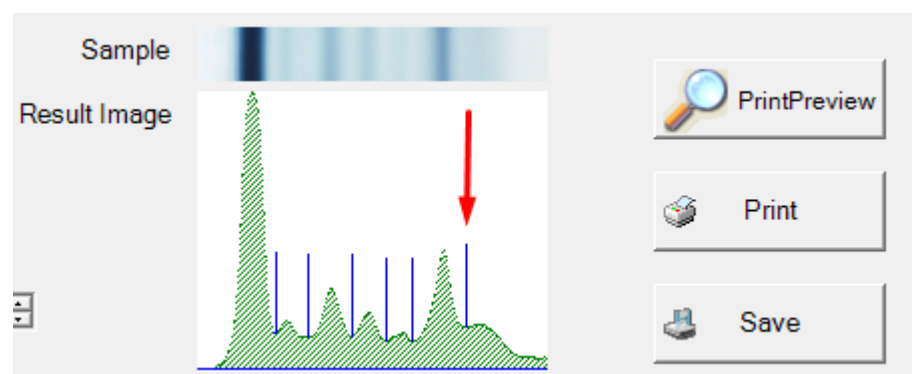




Fig. 2.3

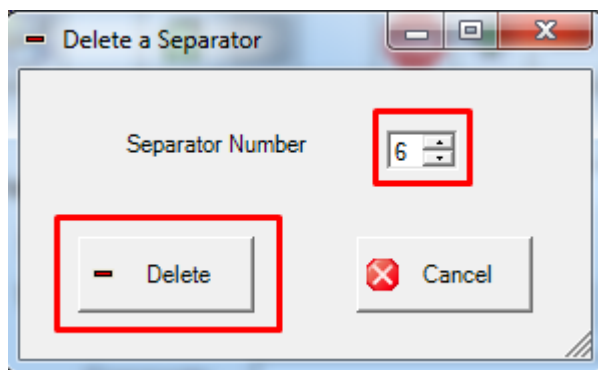
### **Example 3**



More separator /separators

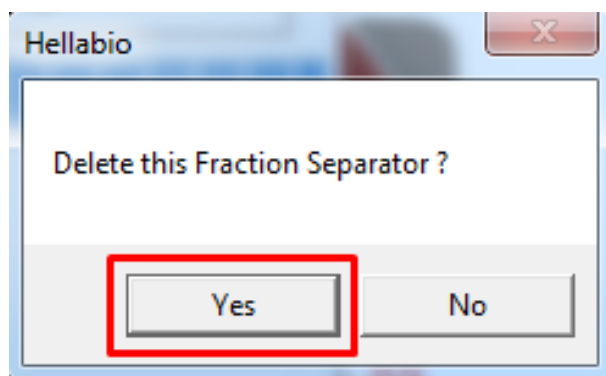
For manually correction, the user must follow the following steps:

- I. Click on the option 
- II. Click on the option 
- III. The following table will display on the desktop (**Fig. 3.1**).



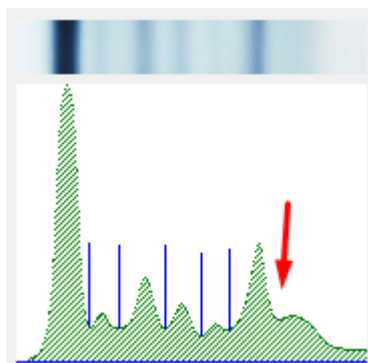
**Fig. 3.1**

- IV. Select the separator you want to delete (**Separator Number**). Click on the option **Delete**.
- V. Alternatively move the mouse over the separator you want to delete. A cross will appear on the separator.
- VI. Right-clicking will display the following table (**Fig 3.2**)



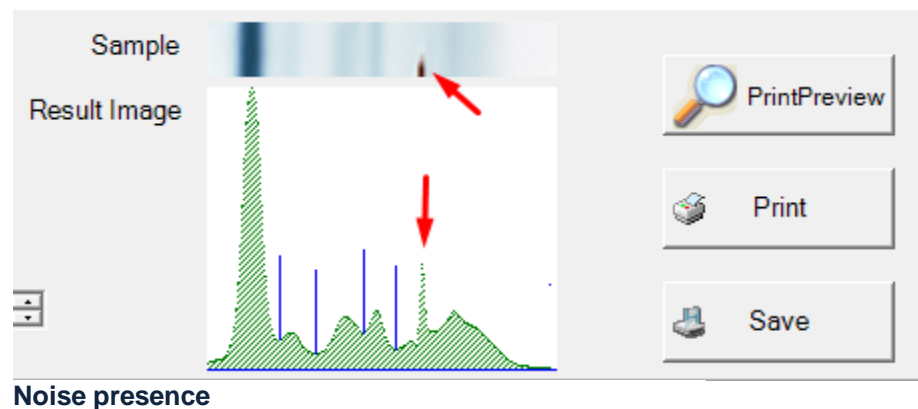
**Fig. 3.2**

- VII. Click on the option **Yes**. The separator has been deleted (**Fig. 3.3**).



**Fig. 3.3**

#### Example 4



For manually correction, the user must follow the following steps:

- I. Click on the option
- II. Move the mouse (right from the peak due to the noise) (**Fig. 4.1**)
- III. Right-clicking will display the following table (**Fig 4.2**)  
Click on the option **Yes** (**Fig. 4.3**).

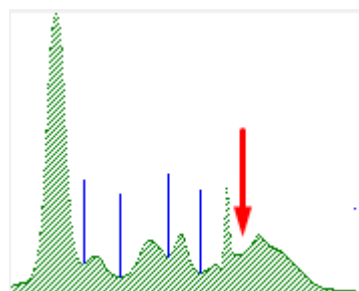


Fig. 4.1

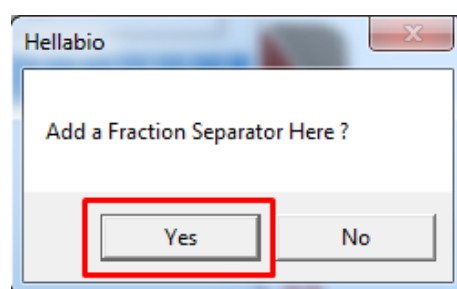


Fig. 4.2

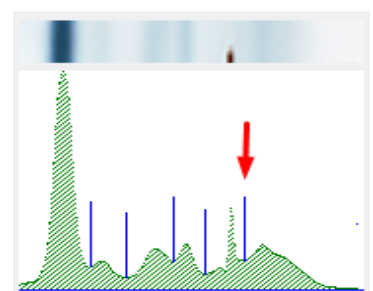


Fig. 4.3

- IV. Click on the option

The following table will display on the desktop (**Fig. 4.4**)

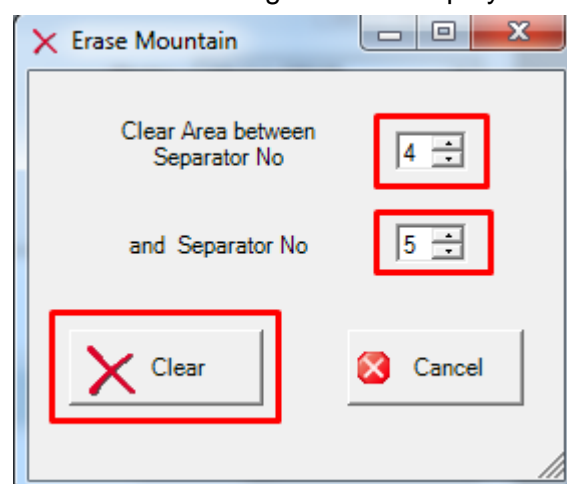
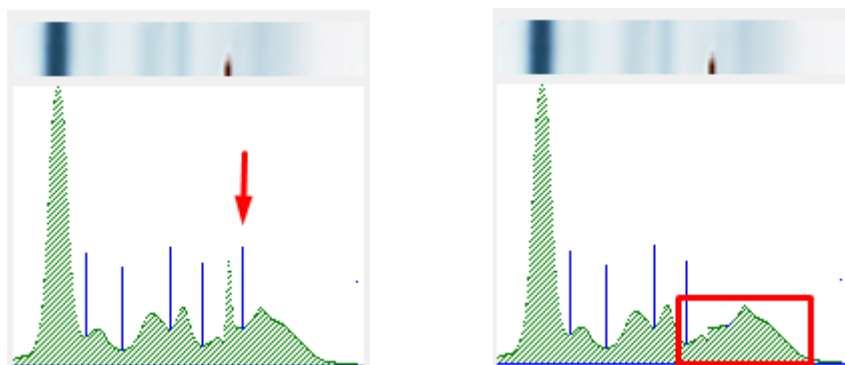


Fig. 4.4

- V. Select the area you want to delete. Click on the option **Clear**.
- VI. Delete the 5<sup>th</sup> separator (**Fig. 4.5**).



**Fig. 4.5**

The above example was used for demonstration purposes only. **Noise should be avoided!** In these cases users are advised to repeat the electrophoresis procedure or check the film (insufficient decolonization).

*If you need further assistance or have any questions related to the HellabioScan program, please do not hesitate to contact our team.*

**Email:** [hellabio@hellabio.com](mailto:hellabio@hellabio.com) &  
[hellabio@thermokoitida.gr](mailto:hellabio@thermokoitida.gr)