

***hiScan***

***hiScan/R***

*densitometers*

*presentation*



## Basic features

**hiScan** and **hiScan/R** are two computerized densitometers capable of reading electrophoresis migrations of Serumprotein, Lipoprotein and Hemoglobin in the micro and semi-micro formats normally used in laboratories.

The **hiScan/R** is a peripheral reader that needs an external computer to operate while the **hiScan** is a self contained unit that is composed by the computerized reader, a monitor, a keyboard and a color ink-jet printer.

Both the instruments are based on the same reading unit and are driven by the same software.

The migration is mounted on an extractable slider in order to simplify its placement. The reading is carried out by inserting the slider into the front slit of the instrument that acquires the pherograms.

The scanning is controlled by a computer (external for hiScan/R, integrated in the hiScan) that manages the operation by means of a friendly software that features a set of pherogram correction tools, many patient report options and the pherogram archive. The archive is stored into the hard disk and is able to save more than ten years of activity.

The following table contains the most relevant features of the instruments

<b>Reading</b>	<i>Format</i>	8 micro migrations 4 semi micro migrations Changeable migration interaxis
	<i>Sampling</i>	Automatic recognition of the pherogram start 12 bit digital sampling Reading time : 8 seconds
	<i>Optics</i>	Programmable high intensity LED source Two silicon photo diodes
	<i>Mechanics</i>	High reliability reached by minimizing the moving parts Stepper motor action
<b>Software</b>	<i>Methods</i>	Three programmable open methods
	<i>Archive</i>	History file ordered by date History file ordered by patient Sample demographics
	<i>Correction</i>	Automatic placement of fractions Manual insertion and deletion of fractions Changeable pherogram start and stop Spurious fraction deletion Manual and automatic correction of the baseline Comment insertion directly on the pherogram
	<i>Display</i>	Many display options Cake diagram to show the fractions True display of the pherogram
	<i>Report</i>	3D representation of the pherogram The pherogram fraction are shown in color Fraction expressed in terms both of percentage and concentration Pathological values in color
	<i>And also...</i>	Interactive on line help Window based software
<b>Hardware</b>	<i>PC</i> <i>(hiScan only)</i>	Integrated Pentium PC High resolution monitor Ink jet printer
	<i>Supply</i>	220V, 50Hz, 70VA
	<i>Dimensions</i>	hiScan base unit 35cm x 31cm x 28cm hiScan/R 28cm x 19cm x 19cm
	<i>Weight</i>	6 kg (hiScan) 1.2kg (hiScan/R)

# The software

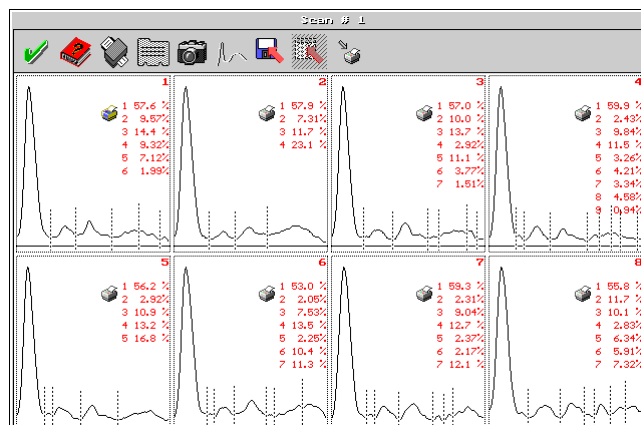
The software is very friendly as it is icon and windows based. Moreover it features an on line help, automatic tool tips that explain the available options and a rational command layout.

After the acquisition, all the sampled pherograms are shown together with the automatically computed minima and the fraction percentages. This way, the operator has an immediate view of the situation to easily identify the pherograms that need manual correction. He can also selectively re sample the pherograms that have not been well read. The system is also capable of automatically reject the wrong migrations by means of a programmable logic.

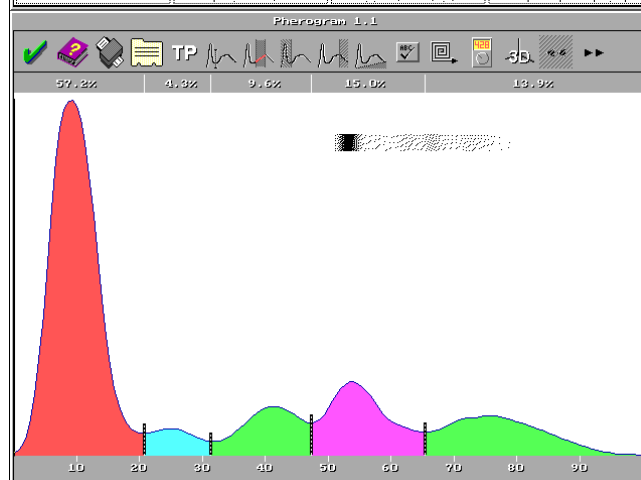
It is possible to modify each sampled pherogram with the sophisticated editor that can move or change minima, cut head or tail of the pherogram, move the baseline, eliminate spurious fractions. Moreover it is possible to add textual comments directly on the pherogram. For example it is possible to point out an abnormal or irregular (monoclonal) fraction placing a comment directly on the pherogram. Each pherogram has associated patient demographics and the total serum protein value.

The results report contains the pherogram with comments, the patient demographics and the numerical results. There are many options for the pherogram presentation, for the demographics and for the assay results. Among the others: fraction colors, 3D representation of the pherogram. It is moreover possible to print a single patient, all the migration in a strip or all the work list of the day.

The work lists are stored day by day on disk and you can query the archive for all the results for a given patient.



Screenshot of all the sampled pherograms



Pherogram Editor

The tools of the toolbar enable the pherogram correction.

## The hardware

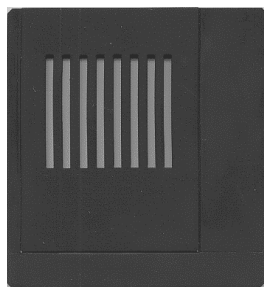
The densitometer has a slit to insert the slider, a light and the power switch. The light indicator guides the operator: it is red when the slider is not to be inserted, green when it should be inserted, black during the pherogram acquisition.

The upper side of the slider is made of metal and features the reading slits to which the film should be aligned and then fixed by means of the included magnets. On the lower side there is a rack for moving it.

Sliders with formats compatible with the different migration standards (micro, semi micro and Paragon™) are available. As a matter of fact, the mechanical arrangement of the reading device makes it independent of the migration standard. To adapt the instrument to another standard you just need to change the slider and perform a simple software configuration step.

The mechanical design of the reader is extremely simple making the device very rugged and of simple maintenance. Besides the reading mechanism, the computer and the other peripheral device find place in the base unit (hiScan only). An optional LAN card is available at request (hiScan only).

### Slider for the sample



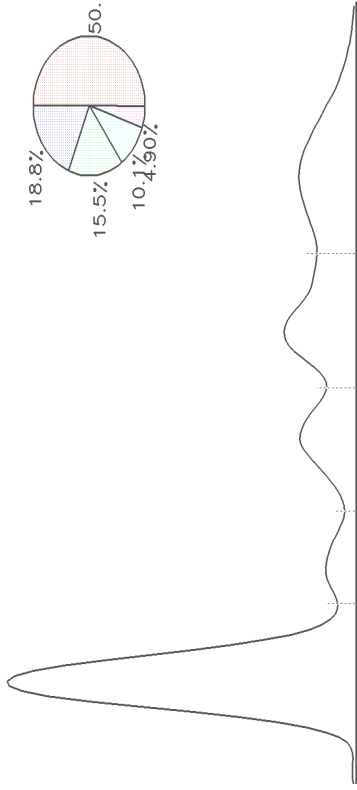
*hiScan/R device*



### hiScan global view



hiScan densitometer



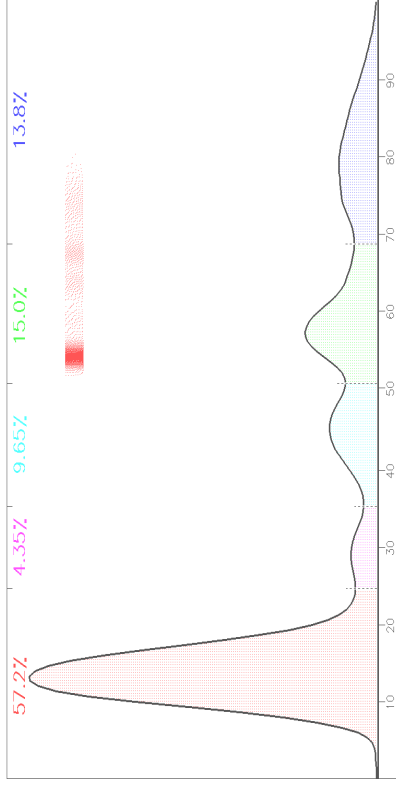
### Electrophoresis of Serumproteins

ID \_\_\_\_\_  
 Surname \_\_\_\_\_  
 Name \_\_\_\_\_  
 DOB \_\_\_\_\_  
 Sex \_\_\_\_\_

Name	Fraction	Normal range	Total P.
1 albumine	50.7 %	57.0 - 68.0	2.46 mg/dl
2 alfa 1	4.90 %	2.0 - 4.5	0.19 mg/dl
3 alfa 2	10.1 %	5.0 - 9.0	0.41 mg/dl
4 beta	15.5 %	9.0 - 13.0	0.65 mg/dl
5 gamma	18.8 %	10.0 - 20.0	0.59 mg/dl
<b>Total Proteins = 4.30 mg/dl</b>			
<b>A/G = 1.03</b>			
<b>MAX O.D. = 1010 mA</b>			

hiScan by hiLab  
 The lab director

hiScan densitometer



### Electrophoresis of Serumproteins

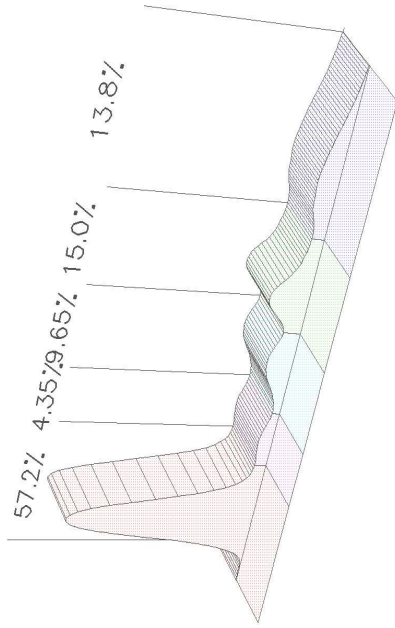
Scan 1 Migration 1 of 2/17/2004  
 ID 1  
 Surname Verdi  
 Name Giuseppe  
 DOB 22/4/1963  
 Sex Male

Name	Fraction	Normal range	Total P.
1 albumine	57.2 %	57.0 - 68.0	2.46 mg/dl
2 alfa 1	4.35 %	2.0 - 4.5	0.19 mg/dl
3 alfa 2	9.65 %	5.0 - 9.0	0.41 mg/dl
4 beta	15.0 %	9.0 - 13.0	0.65 mg/dl
5 gamma	13.8 %	10.0 - 20.0	0.59 mg/dl
<b>Total Proteins = 4.30 mg/dl</b>			
<b>A/G = 1.34</b>			
<b>MAX O.D. = 1075 mA</b>			

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hiScan densitometer



### Electrophoresis of Serumproteins

ID 1  
 Surname Verdi  
 Name Giuseppe  
 DOBIRTH 22/4/1963  
 Sex Male

Name	Fraction	Normal range	Total P.
1 albumine	57.2 %	57.0 - 68.0	2.46 mg/dl
2 alfa 1	4.35%	2.0 - 4.5	0.19 mg/dl
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