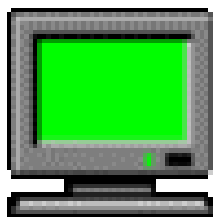


# **HOST MODULE**

**(only for Capillarys/Phoresis version 6.5x & 8.xx  
with SQL Database)**

## **PHORESIS EXTENDED PROTOCOL RS-232C, TCP-IP & FILE-TRANSFER (NETWORK)**



Revision	Description	Date	Author
Rev. 0	First version	-	-
Rev. 1	New version for Rel. 5.6.x and Phoresis with SQL database	March 2012	Sebia Italia/France

# ***INTERFACING PHORESIS TO A HOST COMPUTER***

## ***INTRODUCTION***

This manual provides all the information to interface a Capillarys system or Phoresis scanner to a host computer or LIS (Laboratory Information System) through a RS232C serial link, network TCP-IP connection or via file transfer over network.

It describes the communication protocols and message formats used by Phoresis in receiving and transmitting data.

## ***Contents***

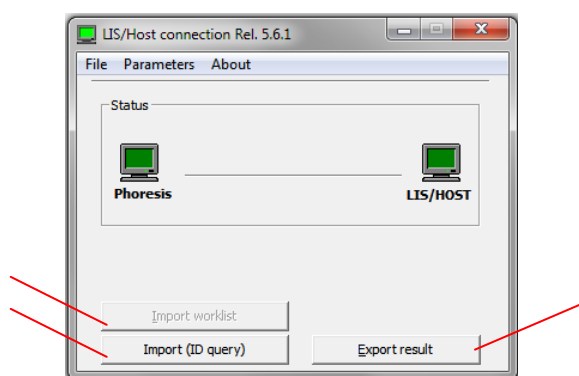
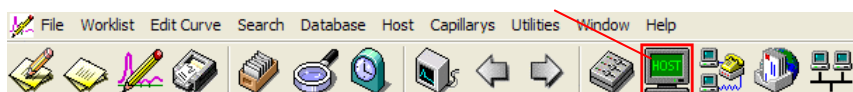
Pag.	3	Rs-232 serial link and TCP-IP connection
Pag	4	Importing a worklist in worklist mode from the Host
Pag	5	Importing a worklist in query mode from the Host (query by patient ID)
Pag	6	Exporting the result to the Host
Pag	12	File-Transfer (Network)
Pag	12	Importing the worklist in worklist (total) mode from the host
Pag	13	Importing the worklist by query (Partial) mode
Pag	15	Exporting the results to the Host (Result file from Phoresis)
Pag	19	Setting parameters
Pag	25	APPENDIX 1 Analysis program codes
Pag	26	APPENDIX 2 Connector pin assignment
Pag	27	APPENDIX 3 CRC 32 calculation (in C language)
Pag	28	APPENDIX 4 Optional Flags transmission
Pag	29	APPENDIX 5 IF image transmission
Pag	29	APPENDIX 6 ELP image transmission
Pag	30	APPENDIX 7 Attached Card data import
Pag	32	APPENDIX 8 HbA1C program details

# RS-232C SERIAL LINK AND TCP-IP CONNECTION

The RS-232C serial link and TCP-IP connection consists of message exchange between Capillaries/Phoresis and the host computer.

Through these messages, it is possible to import either the entire worklist in one time (**Worklist or Total mode**) or patient by patient (**Query or Partial mode**) according to the present patient ID numbers (entered through the keyboard or scanned with the tube barcode reader) in the Phoresis worklist and to export after running the samples the corresponding patient results.

The operator has to click on the Host icon on the main screen, and then select either **Import worklist** or **Import (ID query)** according to the setting to import the patient data or **Export results** to transmit the sample results and thus for the **selected analysis program** and **current date**.



6 types of messages allow the host and Phoresis to communicate together:

- MSG1** Worklist request (or Total request)
- MSG2** Transfer OK (**ACK**)
- MSG3** Demographic data of a single patient
- MSG4** Transfer error (**NACK**)
- MSG5** Result data of a single patient
- MSG6** Query request (or Partial request of a single patient by patient ID number)
- MSG7** No data (**EOT**)

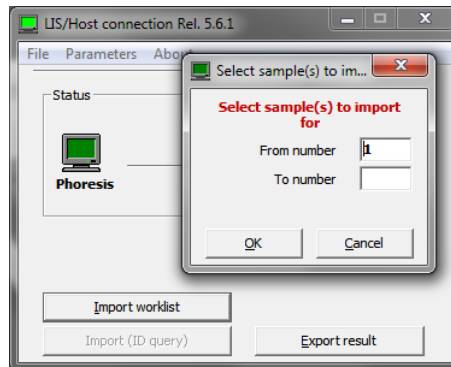
All messages start with a **STX** character (ASCII 02h) and end with an **ETX** character (ASCII 03h).

The last patient to download to Phoresis in Worklist mode after a MSG3 request and the last patient analysis results uploaded (MSG5) to the Host end with **EOT** character (ASCII 04h) instead of ETX in order to indicate to the receiver that there are no more patients to transmit.

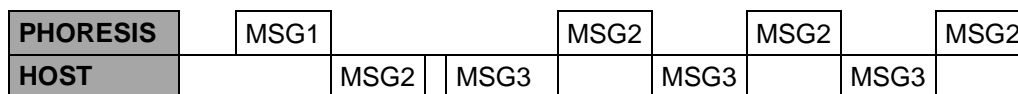
# IMPORTING A WORKLIST IN WORKLIST MODE FROM THE HOST

The Worklist or Total mode allows the operator to download the patient demography of all the patients or a group of patients by indicating the start and end sample numbers (e.g. 1 to 50 or 51 to 51 when it is an emergency patient) and thus for the **selected analysis program** and **current date**.

The operator has to click on the *Host* icon, select *Import worklist*, enter the start and end sample numbers and confirm with *OK* as shown on the following screen before starting downloading the patient data.



## Communication protocol:



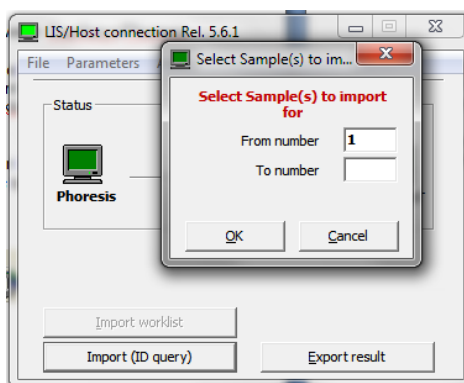
## Notes:

- Phoresis sends a MSG1 to the Host and waits for a MSG2, then waits for the MSG3.
- When Phoresis has received correctly a MSG3 from the Host, it answers with a MSG2 (ACK) and thus for all the patients downloaded. In case of wrong reception, Phoresis answers with the MSG4 (NACK) and consequently the Host retransmits the MSG3 for a max of 3 times then goes to the next patient.
- When the Host does not have anymore samples to download to Phoresis, the last character of MSG3 becomes **EOT** (ASCII 04h) instead of the **ETX** (ASCII 03h) character transmitted after each of the previous samples.
- When the operator does not know the number of samples to download, he has to enter **9999** as the last sample number.
- Every messages have a **fixed length**.
- This mode is highly not recommended for the use of instruments provided with a barcode reader as Minicap, Capillrys and Assist.
- This Mode is unavailable in TCP-IP connection.

## IMPORTING A WORKLIST IN QUERY MODE FROM THE HOST (QUERY BY PATIENT ID)

The Query or Partial mode allows the operator to download the patient data of the **selected analysis program** and **current date** after entry of the patient ID numbers first in the worklist.

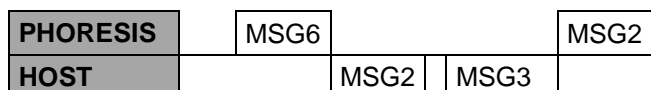
The patient ID numbers can be entered either from the keyboard or a barcode reader from *Worklist by single sheet* or *Worklist by table* menu. Once the patient ID numbers have been entered, the operator has to click on the *Host* icon, select *Partial request* enter the start and end sample numbers and confirm with *OK* as shown on the following screen before starting downloading the corresponding patient data.



### Note:

To enter the patient ID numbers with a barcode reader, select *Worklist by single sheet* and uncheck all the fields except *ID number* from *Options* menu. To verify all the worklist fields once the samples have been downloaded, select *Worklist by table* and *View all*.

### Communication protocol:



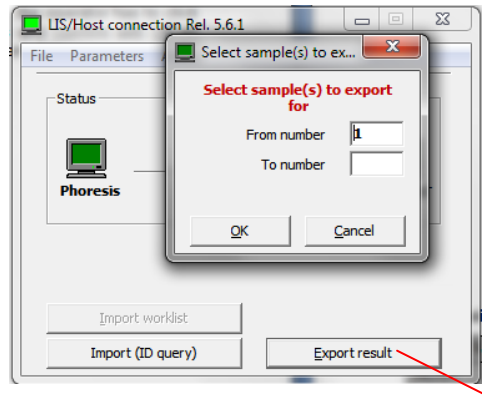
### Notes:

- Phoresis sends a MSG6 to the Host and waits for a MSG2, then waits for the MSG3.
- When Phoresis has received correctly a MSG3 from the Host, it answers with a MSG2 (ACK), and thus for all the patients downloaded. In case of wrong reception, Phoresis answers with the MSG4 (NACK) and consequently the Host retransmits the MSG3 for a max of 3 times then goes to the next patient.
- When the Host does not have patient data for a ID, should send MSG7 instead of MSG3.
- **The Sample number (position in the Worklist) is not used in Query reception since it is given by Phoresis. The Host should return 0000 for this field, if a different value is transmitted, Phoresis will ignore it.**

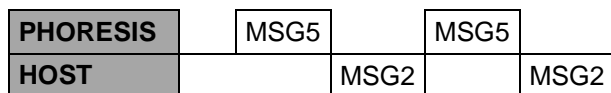
## EXPORTING THE RESULTS TO THE HOST

This procedure allows the operator to upload the whole patient results of the **selected analysis program** for the **current date** to the Host once the samples have been run and edited.

The operator has to click on the *Host* icon, select *Export results* then Phoresis asks for the start and end sample numbers to export as shown on the following screen:



### Communication protocol:



### Notes:

- Phoresis starts the transmission sending MSG5 (first patient) then waits for MSG2 (ACK) from the Host, then continues with the next MSG5 (next patient) and waits again for MSG2, and thus up to the last sample selected by the operator.
- If Host answers a MSG4 (NACK), Phoresis retransmits the previous patient results and waits again for the MSG2 (ACK) for max. 3 times then goes to the next patient results.
- When Phoresis does not have anymore samples to transmit to the Host, the last character of MSG5 becomes **EOT** (ASCII 04h) instead of the **ETX** (ASCII 03h) character transmitted at the end of each previous sample.
- Every record as a fixed length

**MESSAGE 1 DESCRIPTION (MSG1)**

No.	Description	Start	Length	Note
1	STX	1	1	ASCII 02h
2	Analysis program code	2	1	Letter from A to Z , 0 to 9 ( <a href="#">see index 1</a> )
3	Start sample number	3	4	Aligned right e.g. 0001 (1)
4	End sample number	7	4	Aligned right e.g.0010 (9999 or nothing)
5	ETX	11	1	ASCII 03h
		<b>TOTAL</b>	<b>11</b>	<b>bytes</b>

**MESSAGE 2 DESCRIPTION (MSG2)**

No.	Description	Start	Length	Note
1	STX	1	1	ASCII 02h
2	ACK	2	1	ASCII 06h
3	ETX	3	1	ASCII 03h
		<b>TOTAL</b>	<b>3</b>	<b>bytes</b>

**MESSAGE 3 DESCRIPTION (MSG3)**

No.	Description	Start	Length	Note
1	STX	1	1	ASCII 02h
2	Analysis program code	2	1	Letter from A to Z , 0 to 9 ( <a href="#">see index 1</a> )
3	Sample number	3	4	Aligned right e.g. 0001
4	Patient ID number	7	15	Alphanum. charact., aligned left and spaces
5	Patient Name	22	30	Alphanum. charact., aligned left and spaces
6	Date of birth	52	8	DDMMYYYY
7	Sex	60	1	M or F
8	Age in years	61	3	Aligned right e.g. 015
9	Department	64	20	Alphanum. charact., aligned left and spaces
10	Sample date	84	8	DDMMYYYY
11	Concentration (e.g. total protein)	92	5	Not fixed with a decimal separator: "." (2Eh)
12	Free 1	97	30	Alphanum. charact., aligned left and spaces
13	Free 2	127	30	Alphanum. charact., aligned left and spaces
14	Free 3	157	30	Alphanum. charact., aligned left and spaces
15	Free 4	187	30	Alphanum. charact., aligned left and spaces
16	Free 5	217	30	Alphanum. charact., aligned left and spaces
17	<b>ETX or EOT</b>	247	1	ASCII 03h or 04h for the last sample
		<b>TOTAL</b>	<b>247</b>	<b>bytes</b>

**MESSAGE 4 DESCRIPTION (MSG4)**

No.	Description	Start	Length	Note
1	STX	1	1	ASCII 02h
2	NACK	2	1	ASCII 15h
3	ETX	3	1	ASCII 03h
		<b>TOTAL</b>	<b>3</b>	<b>bytes</b>

## MESSAGE 5 DESCRIPTION (MSG5)

No.	Description	Start	Length	Note
1	STX	1	1	ASCII 02h
2	Program code	2	1	Letter from A to Z , 0 to 9 ( <a href="#">see index 1</a> )
3	Sample number	3	4	Aligned right e.g. 0001
4	Patient ID code	7	15	Alphanum. charact., aligned left and spaces
5	Patient Name	22	30	Alphanum. charact., aligned left and spaces
6	Date of Birth	52	8	DDMMYYYY
7	Sex	60	1	M or F
8	Age in years	61	3	Aligned right e.g. 015
9	Department	64	20	Alphanum. charact., aligned left and spaces
10	Sample date	84	8	Format DDMMYYYY
11	Concentration (e.g. total protein)	92	5	Not fixed with a decimal separator "." (2Eh)
12	Measurement unit of concentration	97	8	Alphanum. charact., aligned left and spaces
13	Free field 1	105	30	Alphanum. charact., aligned left and spaces
14	Free field 2	135	30	Alphanum. charact., aligned left and spaces
15	Free field 3	165	30	Alphanum. charact., aligned left and spaces
16	Free field 4	195	30	Alphanum. charact., aligned left and spaces
17	Free field 5	225	30	Alphanum. charact., aligned left and spaces
18	Operator ID	255	3	Alphanum. charact. e.g. JON
19	Date of Analysis	258	8	Format DDMMYYYY
20	Number of fractions (max. 10)	266	2	Aligned right e.g. 06
21	Fraction 1 name	268	10	Alphanum. charact., aligned left and spaces
22	Fraction 2 name	278	10	Alphanum. charact., aligned left and spaces
23	Fraction 3 name	288	10	Alphanum. charact., aligned left and spaces
24	Fraction 4 name	298	10	Alphanum. charact., aligned left and spaces
25	Fraction 5 name	308	10	Alphanum. charact., aligned left and spaces
26	Fraction 6 name	318	10	Alphanum. charact., aligned left and spaces
27	Fraction 7 name	328	10	Alphanum. charact., aligned left and spaces
28	Fraction 8 name	338	10	Alphanum. charact., aligned left and spaces
29	Fraction 9 name	348	10	Alphanum. charact., aligned left and spaces
30	Fraction 10 name	358	10	Alphanum. charact., aligned left and spaces
31	Fraction 1 % value	368	5	Not fixed with a decimal separator "." (2Eh)
32	Fraction 2 % value	373	5	Not fixed with a decimal separator "." (2Eh)
33	Fraction 3 % value	378	5	Not fixed with a decimal separator "." (2Eh)
34	Fraction 4 % value	383	5	Not fixed with a decimal separator "." (2Eh)
35	Fraction 5 % value	388	5	Not fixed with a decimal separator "." (2Eh)
36	Fraction 6 % value	393	5	Not fixed with a decimal separator "." (2Eh)
37	Fraction 7 % value	398	5	Not fixed with a decimal separator "." (2Eh)
38	Fraction 8 % value	403	5	Not fixed with a decimal separator "." (2Eh)
39	Fraction 9 % value	408	5	Not fixed with a decimal separator "." (2Eh)
40	Fraction 10 % value	413	5	Not fixed with a decimal separator "." (2Eh)
41	Fraction 1 conc. value	418	5	Not fixed with a decimal separator "." (2Eh)
42	Fraction 2 conc. value	423	5	Not fixed with a decimal separator "." (2Eh)
43	Fraction 3 conc. value	428	5	Not fixed with a decimal separator "." (2Eh)
44	Fraction 4 conc. value	433	5	Not fixed with a decimal separator "." (2Eh)
45	Fraction 5 conc. value	438	5	Not fixed with a decimal separator "." (2Eh)
46	Fraction 6 conc. value	443	5	Not fixed with a decimal separator "." (2Eh)
47	Fraction 7 conc. value	448	5	Not fixed with a decimal separator "." (2Eh)
48	Fraction 8 conc. value	453	5	Not fixed with a decimal separator "." (2Eh)



49	Fraction 9 conc. value	458	5	Not fixed with a decimal separator "." (2Eh)
50	Fraction 10 conc. value	463	5	Not fixed with a decimal separator "." (2Eh)
51	Peak 1 name	468	10	Alphanum. charact., aligned left and spaces
52	Peak 2 name	478	10	Alphanum. charact., aligned left and spaces
53	Peak 3 name	488	10	Alphanum. charact., aligned left and spaces
54	Peak 4 name	498	10	Alphanum. charact., aligned left and spaces
55	Peak 1 % value	508	5	Not fixed with a decimal separator "." (2Eh)
56	Peak 2 % value	513	5	Not fixed with a decimal separator "." (2Eh)
57	Peak 3 % value	518	5	Not fixed with a decimal separator "." (2Eh)
58	Peak 4 % value	523	5	Not fixed with a decimal separator "." (2Eh)
59	Peak 1 conc. value	528	5	Not fixed with a decimal separator "." (2Eh)
60	Peak 2 conc. value	533	5	Not fixed with a decimal separator "." (2Eh)
61	Peak 3 conc. value	538	5	Not fixed with a decimal separator "." (2Eh)
62	Peak 4 conc. value	543	5	Not fixed with a decimal separator "." (2Eh)
63	Pathological Flag	548	1	0 = Normal , 1 = Pathological
64	Ratio 1 (e.g. A/G for the proteins)	549	5	Not fixed with a decimal separator "." (2Eh)
65	Ratio 2	554	5	Not fixed with a decimal separator "." (2Eh)
66	Comment	559	230	Alphanum. charact., aligned left and spaces
67	Reference pattern flag	789	1	0 = Normal pattern , 1 = Reference pattern
68	QC sample flag	790	1	0 = Normal sample , 1 = QC sample
<b>69</b> <b>82</b> <b>124</b>	Optional fields	--	--	Curve Programmable fields + the attached card comment Extended comment
69/82/124/125	ETX or EOT	791/XXX	1	ASCII 03h or 04h for the last sample

**TOTAL Variable 791 bytes without optional fields**  
**GLOBAL/POSITION: 790 + 1 = 791 bytes/Line**

#### MESSAGE 6 DESCRIPTION (MSG6)

No.	Description	Start	Length	Note
1	STX	1	1	ASCII 02h
2	Program Code	2	1	Letter from A to Z , 0 to 9 ( <a href="#">see index 1</a> )
3	Patient ID number	3	15	Alphanumeric. character., aligned left and spaces
4	ETX	18	1	ASCII 03h

**TOTAL 18 bytes**

#### MESSAGE 7 DESCRIPTION (MSG7)

No.	Description	Start	Length	Note
1	STX	1	1	ASCII 02h
2	EOT	2	1	ASCII 04h
3	ETX	3	1	ASCII 03h

**TOTAL 3 bytes**

## Optional fields for the curve

69	Number of dots of the curve	791	4	Aligned right e.g. 0300
70	Curve scale flag	795	1	A = Automatic scale, M = Manual scale
71	Curve scale factor	796	4	Aligned right with zero (from 0100 to 1000)
72	Start Peak 1 Coord. (peak position)	800	4	Aligned right e.g. 0127
73	End Peak 1 Coord. (peak position)	804	4	Aligned right e.g. 0127
74	Start Peak 2 Coord. (peak position)	808	4	Aligned right e.g. 0127
75	End Peak 2 Coord. (peak position)	812	4	Aligned right e.g. 0127
76	Start Peak 3 Coord. (peak position)	816	4	Aligned right e.g. 0127
77	End Peak 3 Coord. (peak position)	820	4	Aligned right e.g. 0127
78	Start Peak 4 Coord. (peak position)	824	4	Aligned right e.g. 0127
79	End Peak 4 Coord. (peak position)	828	4	Aligned right e.g. 0127
80	Curve dots	832	Max4800	YYYY format, see after
81	Separator " " (pipe)	2032	1	ASCII 7Ch

**TOTAL Variable 1242 bytes for a curve made of 300 dots.**

***The length of the curve optional fields depends of the number of dots of the curve:***

- Number of dots (No. 69)  
Max. 1200 dots.

- Curve scale flag (No. 70)

"A" = Automatic, the scale is determined by the max. (Y) Amplitude value of the curve (curve full scale).

"M" = Manual, the scale is multiplied by a percentage factor of the max. value.

- Curve scale factor (No. 71)

A number from 100% to 1000% to redraw the curve with the new manual scale.

- Start/End Peak coord. (No. 72-79) peak position

4 couples of coordinate values indicating the start and end positions of the 4 peaks (monoclonal peaks) on the curve.

Note that in the latest versions of Phoresis / Capillarys is possible to highlight up to 10 areas, but only the first four areas will be sent to LIS.

- Curve dots (No. 80)

A set of dots for the curve coded under the following format: **YYYY**

**X** representing the type of dot:

0 = ASCII (30h) Normal dot

8 = ASCII (38h) Dot corresponding to a minimum separator.

4 = ASCII (34h) Dot corresponding to a manually deleted minimum separator.

C = ASCII (43h) Dot corresponding to a manually inserted minimum separator.

1 = ASCII (31h) Dot corresponding to a deleted fraction.

5 = ASCII (35h) Dot corresponding to a deleted fraction and deleted minimum separator.

**YYY** (hexadecimal value) indicating the Y amplitude of the dot (right aligned, min. = 000, max. = FFF).

- Separator character (No. 81)

"|" **pipe** char. (ASCII 7Ch) to indicate to the host the last dot of the curve.

- The curve consists today of 300 dots, so it means that it has a total length of 1200 characters, and the whole optional fields for the curve has a total length of 1242 bytes. In the future, the number of dots of the curve could be increased from 300 up to 1200 dots (4800 characters).

### ***Additional field transmission: 40 programmable fields + the attached card comment***

No.	Description	Start	Length	Note
82	** (2 Characters 2Ah)	791	2	Indicates the additional field transmission
83	Programmable field #1	793	15	Alphanum. charact.
84	Programmable field #2	808	15	Alphanum. charact.
85	Programmable field #3	823	15	Alphanum. charact.
86	Programmable field #4	838	15	Alphanum. charact.
87	Programmable field #5	853	15	Alphanum. charact.
88	Programmable field #6	868	15	Alphanum. charact.
89	Programmable field #7	883	15	Alphanum. charact.
90	Programmable field #8	898	15	Alphanum. charact.
--	-----	----	---	---
120	Programmable field #38	1348	15	Alphanum. charact.
121	Programmable field #39	1363	15	Alphanum. charact.
122	Programmable field #40	1378	15	Alphanum. charact.
123	Attached card comment	1393	256	Alphanum. charact.
<b>TOTAL</b>		<b>858</b>	<b>bytes</b>	

The content configuration of the 40 programmable fields can be done only by modification of the host.ini file (into the Host folder).

### ***Host.ini file example to transmit the additional Capillarys data***

```
[PROTOCOLLO]
MOD0=RS232
TIPO=Phoresis Extended
LETTERA=S
RX_MODE=WORKLIST
REALTIME=0
RECALL_MODE=1

[PHORESIS]
CURVA=0
COMMENTO_ESTESO=0
OPTIONAL_FIELDS=0
CRC_CHECK=0
IMAGE_IF=0
AUTOSEQUENCE=0
NUMERIC_ID=0
FILE_CARD=0
FORCE_SEQUENCE=0
OPZ_FIELD1=DO_MAX
OPZ_FIELD2=NR_CAPILLARY
OPZ_FIELD3=RACK_NR
OPZ_FIELD4=ANALYSIS_TIME
OPZ_FIELD5=MIGRATION_TIME
OPZ_FIELD6=DELAY_TIME
...
```

The additional instructions to transmit the programmable fields (corresponding to Capillarys here) are in bold characters.

### ***Optional field for the extended comment***

124	Extended comment	--	max3000	Alphanum. charact. With max 3000 charact.
-----	------------------	----	---------	---

This optional field has a variable length from 0 to 3000 characters. All CR+LF (ASCII 0Dh+0Ah) entered in the extended comment will be converted in RS characters (ASCII 1Eh).

## FILE-TRANSFER (NETWORK)

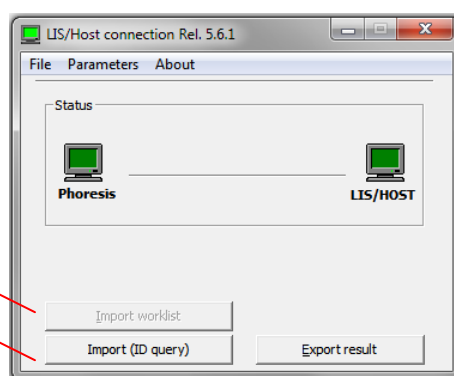
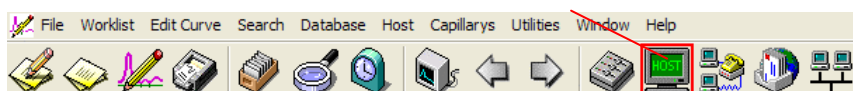
The connection via File Transfer happens through read/write of files in a folder shared in network between Phoresis and the Host.

Two files, of configurable path and name, one containing the Worklist data and the other one, the result data are in ASCII format with a structure of record, will be read therefore from a common text editor.

This file containing the patient demography of all the samples to scan is generated by the Host.

The record has a fixed length.

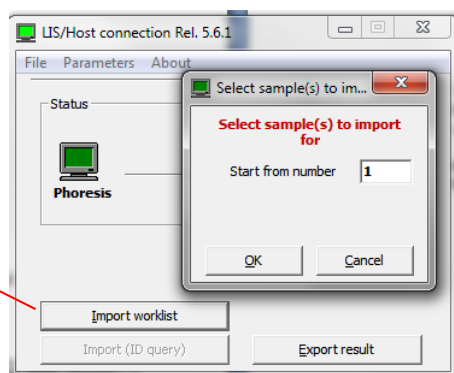
The operator has 2 options to download the worklist of the **selected analysis program** for the **current date**:  
Worklist (Total) mode or Query (Partial) mode



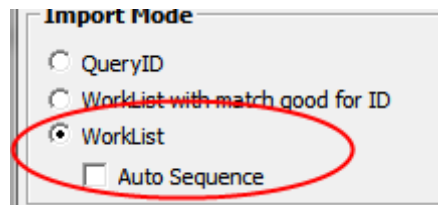
## IMPORTING THE WORKLIST IN WORKLIST (TOTAL) MODE FROM THE HOST

The Worklist or Total mode allows the operator to download the patient demography of all the patients or a group of patients to run on the system by indicating the start and end sample numbers (e.g. 1 to 50 or 51 to 51 when it is an emergency patient) and thus for the **selected analysis program** and **current date**.

The operator has to click on the *Host* icon, select *Import worklist*, sets from which sequence should begin the import of the data and confirm with *OK* as shown on the following screen before starting downloading the patient data.



- This mode is highly not recommended for the use of instruments provided with a barcode reader as Minicap, Capillrys and Assist.
- Note that changing the value 'Start from Number' implies that the received data is shifted from the original sequence of a value equal to that indicated.  
For example: if you enter 10 in 'Start from Number' and the file contains 10 records, from 1 to 10, the samples will be imported in positions start from sequence 10 to sequence 20.
- There is a configuration to force the sequence of all records in the file.  
When Auto Sequence is enabled the sequence will depend by absolute row position in the file and not by Sample number.



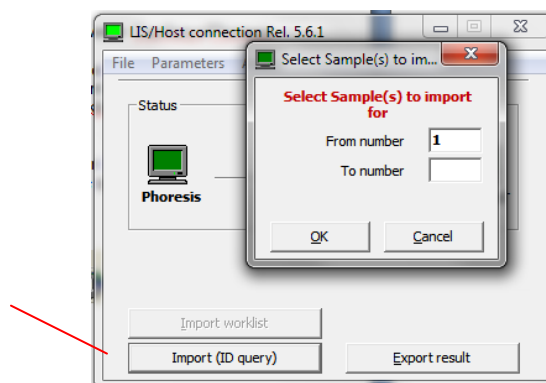
S0002922222222	PATIENT 2 NAME	01011960F040DEPARTMENT
28012000078.5	FREE FIELD 1	FREE FIELD 2
FREE FIELD 4	FREE FIELD 5	FREE FIELD 3
S0003933333333	PATIENT 3 NAME	01011970F030DEPARTMENT
28012000078.5	FREE FIELD 1	FREE FIELD 2
FREE FIELD 4	FREE FIELD 5	FREE FIELD 3

Two example records will be imported into sequence number 1 and 2 instead of sequence 2 and 3.

## IMPORTING THE WORKLIST BY QUERY (PARTIAL) MODE

The Query or Partial mode allows the operator to download the patient data after entry of the patient ID numbers first in the Worklist. The patient ID numbers can be entered either from the keyboard or a barcode reader from *Worklist by single sheet* or *Worklist by table* menu.

Once the patient ID numbers have been entered, the operator has to click on the *Host* icon, select *Import (ID query)*, enter the start and end sample numbers and confirm with *OK* as shown on the following screen before importing the corresponding patient data.



### Note:

To enter the patient ID numbers with a barcode reader, select *Worklist by single sheet* and uncheck all the fields except *ID number* from *Options* menu.

To verify all the worklist fields once the samples have been downloaded, select *Worklist by table* and *View all*.

## RECORD DESCRIPTION

No.	Description	Start	Length	Note
1	Analysis program code	1	1	Letter from A to Z , 0 to 9 (see index 1)
2	Sample number	2	4	Aligned right e.g. 0001
3	Patient ID number	6	15	Alphanum. charact. aligned left and spaces
4	Patient Name	21	30	Alphanum. charact. aligned left and spaces
5	Date of birth	51	8	DDMMYYYY
6	Sex	59	1	M or F
7	Age in years	60	3	Aligned right e.g.. 015
8	Department	63	20	Alphanum. charact. aligned left and spaces
9	Sample date	83	8	DDMMYYYY
10	Concentration (e.g. total protein)	91	5	Not fixed a decimal separator "." (2Eh)
11	Free 1	96	30	Alphanum. charact. aligned left and spaces
12	Free 2	126	30	Alphanum. charact. aligned left and spaces
13	Free 3	156	30	Alphanum. charact. aligned left and spaces
14	Free 4	186	30	Alphanum. charact. aligned left and spaces
15	Free 5	216	30	Alphanum. charact. aligned left and spaces
16	CR+LF	246	2	ASCII 0Dh + 0Ah
<b>TOTAL</b>			<b>247</b>	<b>bytes</b>

**Example of protein worklist with 4 samples** (analysis program code: S)

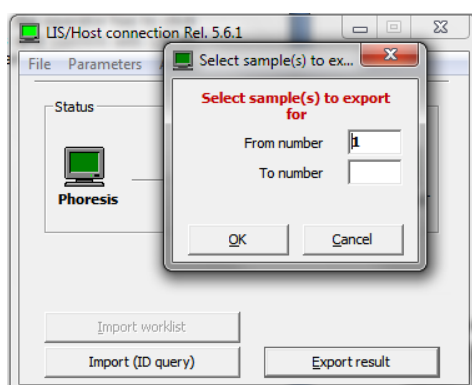
S00019111111111	PATIENT 1 NAME	01011950M050	DEPARTMENT
28012000078.5	FREE FIELD 1	FREE FIELD 2	FREE FIELD 3
FREE FIELD 4	FREE FIELD 5		
S00029222222222	PATIENT 2 NAME	01011960F040	DEPARTMENT
28012000078.5	FREE FIELD 1	FREE FIELD 2	FREE FIELD 3
FREE FIELD 4	FREE FIELD 5		
S00039333333333	PATIENT 3 NAME	01011970F030	DEPARTMENT
28012000078.5	FREE FIELD 1	FREE FIELD 2	FREE FIELD 3
FREE FIELD 4	FREE FIELD 5		
S00049444444444	PATIENT 4 NAME	01011980M020	DEPARTMENT
28012000078.5	FREE FIELD 1	FREE FIELD 2	FREE FIELD 3
FREE FIELD 4	FREE FIELD 5		

# EXPORTING THE RESULTS TO THE HOST (RESULT FILE FROM PHORESIS)

This file is generated by Phoresis after selection of the patients to export by the operator.  
It contains all the numerical results and demographic patient data.  
It consists of a sequential ASCII record with a fixed length when the optional fields are not selected or a variable length when they are selected.

The procedure allows the operator to upload the whole patient results of the **selected analysis program** for the **current date** to the Host once the samples have been run and edited.

The operator has to click on the *Host* icon, select *Export results*, enter the start and end sample numbers to upload and confirm with OK as shown on the following screen:



## RECORD DESCRIPTION

No.	Description	Start	Length	Note
1	Program code	1	1	Letter from A to Z , 0 to 9 (see index 1 )
2	Sample number	2	4	Aligned right e.g. 0001
3	Patient ID number	6	15	Alphanum. caract. aligned left and spaces
4	Patient Name	21	30	Alphanum. caract. aligned left and spaces
5	Date of Birth	51	8	Format DDMMYYYY
6	Sex	59	1	M or F
7	Age in years	60	3	Aligned right e.g. 015
8	Department	63	20	Alphanum. caract. aligned left and spaces
9	Sample date	83	8	Format DDMMYYYY
10	Concentration (e.g. total protein)	91	5	Not fixed decimal separator "." (2Eh)
11	Measurement unit of concentration	96	8	Alphanum. caract. aligned left and spaces
12	Free field 1	104	30	Alphanum. caract. aligned left and spaces
13	Free field 2	134	30	Alphanum. caract. aligned left and spaces
14	Free field 3	164	30	Alphanum. caract. aligned left and spaces
15	Free field 4	194	30	Alphanum. caract. aligned left and spaces
16	Free field 5	224	30	Alphanum. caract. aligned left and spaces
17	Operator ID	254	3	Alphanum. character e.g. JON
18	Date of Analysis	257	8	DDMMYYYY
19	Number of fractions (max.10)	265	2	Aligned right with e.g. 06
20	Fraction 1 name	267	10	Alphanum. caract. aligned left and spaces
21	Fraction 2 name	277	10	Alphanum. caract. aligned left and spaces
22	Fraction 3 name	287	10	Alphanum. caract. aligned left and spaces
23	Fraction 4 name	297	10	Alphanum. caract. aligned left and spaces
24	Fraction 5 name	307	10	Alphanum. caract. aligned left and spaces
25	Fraction 6 name	317	10	Alphanum. caract. aligned left and spaces
26	Fraction 7 name	327	10	Alphanum. caract. aligned left and spaces
27	Fraction 8 name	337	10	Alphanum. caract. aligned left and spaces
28	Fraction 9 name	347	10	Alphanum. caract. aligned left and spaces
29	Fraction 10 name	357	10	Alphanum. caract. aligned left and spaces
30	Fraction 1 % value	367	5	Not fixed with a decimal separator "." (2Eh)
31	Fraction 2 % value	372	5	Not fixed with a decimal separator "." (2Eh)
32	Fraction 3 % value	377	5	Not fixed with a decimal separator "." (2Eh)
33	Fraction 4 % value	382	5	Not fixed with a decimal separator "." (2Eh)

34	Fraction 5 % value	387	5	Not fixed with a decimal separator "." (2Eh)
35	Fraction 6 % value	392	5	Not fixed with a decimal separator "." (2Eh)
36	Fraction 7 % value	397	5	Not fixed with a decimal separator "." (2Eh)
37	Fraction 8 % value	402	5	Not fixed with a decimal separator "." (2Eh)
38	Fraction 9 % value	407	5	Not fixed with a decimal separator "." (2Eh)
39	Fraction 10 % value	412	5	Not fixed with a decimal separator "." (2Eh)
40	Fraction 1 conc. value	417	5	Not fixed with a decimal separator "." (2Eh)
41	Fraction 2 conc. value	422	5	Not fixed with a decimal separator "." (2Eh)
42	Fraction 3 conc. value	427	5	Not fixed with a decimal separator "." (2Eh)
43	Fraction 4 conc. value	432	5	Not fixed with a decimal separator "." (2Eh)
44	Fraction 5 conc. value	437	5	Not fixed with a decimal separator "." (2Eh)
45	Fraction 6 conc. value	442	5	Not fixed with a decimal separator "." (2Eh)
46	Fraction 7 conc. value	447	5	Not fixed with a decimal separator "." (2Eh)
47	Fraction 8 conc. value	452	5	Not fixed with a decimal separator "." (2Eh)
48	Fraction 9 conc. value	457	5	Not fixed with a decimal separator "." (2Eh)
49	Fraction 10 con. value	462	5	Not fixed with a decimal separator "." (2Eh)
50	Area 1 name	467	10	Alphanum. charact. aligned left and spaces
51	Area 2 name	477	10	Alphanum. charact. aligned left and spaces
52	Area 3 name	487	10	Alphanum. charact. aligned left and spaces
53	Area 4 name	497	10	Alphanum. charact. aligned left and spaces
54	Area 1 value %	507	5	Not fixed with a decimal separator "." (2Eh)
55	Area 2 value %	512	5	Not fixed with a decimal separator "." (2Eh)
56	Area 3 value %	517	5	Not fixed with a decimal separator "." (2Eh)
57	Area 4 value %	522	5	Not fixed with a decimal separator "." (2Eh)
58	Area 1 conc. value	527	5	Not fixed with a decimal separator "." (2Eh)
59	Area 2 conc. value	532	5	Not fixed with a decimal separator "." (2Eh)
60	Area 3 conc. value	537	5	Not fixed with a decimal separator "." (2Eh)
61	Area 4 conc. value	542	5	Not fixed with a decimal separator "." (2Eh)
62	Pathological Flag	547	1	0 = Normal , 1 = Pathological
63	Ratio 1(e.g. A/G for the proteins)	548	5	Not fixed with a decimal separator "." (2Eh)
64	Ratio 2	553	5	Not fixed with a decimal separator "." (2Eh)
65	Comment	558	230	Alphanum. charact. aligned left and spaces
66	Reference pattern flag	788	1	0 = Normal pattern , 1 = reference pattern
67	QC sample flag	789	1	0 = Normal sample , 1 = QC sample
68 81 123	Optional fields	---	---	Curve Programmable fields + the attached card comment Extended comment
68/81/123/124	CR + LF	790/XXX	2	ASCII 0Dh or 0Ah

**TOTAL Variable 791 bytes without optional fields**  
**GLOBAL/POSITION: 789+2 = 791 bytes/Line**



### **Optional fields for the curve**

68	Number of dots of the curve	790	4	Aligned right e.g. 0300
69	Curve scale flag	794	1	A = Automatic scale, M = Manual scale
70	Curve scale factor	795	4	Aligned right with zero (from 0100 to 1000)
71	Start peak 1 Coord. (peak position)	799	4	Aligned right e.g. 0127
72	End peak 1 Coord. (peak position)	803	4	Aligned right e.g. 0127
73	Start peak 2 Coord. (peak position)	807	4	Aligned right e.g. 0127
74	End peak 2 Coord. (peak position)	811	4	Aligned right e.g. 0127
75	Start peak 3 Coord. (peak position)	815	4	Aligned right e.g. 0127
76	End peak 3 Coord. (peak position).	819	4	Aligned right e.g. 0127
77	Start peak 4 Coord. (peak position)	823	4	Aligned right e.g. 0127
78	End peak 4 Coord. (peak position)	827	4	Aligned right e.g. 0127
79	Curve dots	831	max4800	See hereafter
80	Separator " " (pipe)	2031	1	ASCII 7Ch

**TOTAL Variable 1242 bytes for a curve made of 300 dots.**

***The length of the curve optional fields depends of the number of dots of the curve:***

- Number of dots (No. 68)

Max. 1200 dots.

- Curve scale Flag (No. 69)

"A" = Automatic, the scale is determined by the max. (Y) Amplitude value of the curve (curve full scale).

"M" = Manual, the scale is multiplied by a percentage factor of the max. value.

- Curve scale factor (No. 70)

A number from 100% to 1000% to recalculate and redraw the curve with the new manual scale.

- Start/End Peak coord. (No. 71-78) peak position

4 couples of coordinate values indicating the start and end positions of the 4 peaks (monoclonal peaks) on the curve.

Note that in the latest versions of Phoresis / Capillarys is possible to highlight up to 10 areas, but only the first four areas will be sent to LIS.

- Curve dots (No. 79)

A set of dots for the curve coded under the following format: **YYYY**.

**X** representing the type of dot:

0 = ASCII (30h) Normal dot

8 = ASCII (38h) Dot corresponding to a minimum separator.

4 = ASCII (34h) Dot corresponding to a manually deleted minimum separator.

C = ASCII (43h) Dot corresponding to a manually inserted minimum separator.

1 = ASCII (31h) Dot corresponding to a deleted fraction.

5 = ASCII (35h) Dot corresponding to a deleted fraction and deleted minimum separator.

**YYY** (hexadecimal value) indicating the Y amplitude of the dot (right aligned, min. =000, max. =FFF).

- Separator character (No. 80)

"|" pipe char. (ASCII 7Ch) to indicate to the host the last dot of the curve.

- The curve consists today of 300 dots, so it means that it has a total length of 1200 characters, and the whole optional fields for the curve has a total length of 1242 bytes. In the future, the number of dots of the curve could be increased from 300 up to 1200 dots (4800 characters).

### **Additional field transmission: 40 programmable fields + the attached card comment**

No.	Description	Start	Length	Note
81	** (2 Characters 2Ah)	790	2	Indicates the additional field transmission
82	Programmable field #1	792	15	Alphanum. charact.
83	Programmable field #2	807	15	Alphanum. charact.
84	Programmable field #3	822	15	Alphanum. charact.
85	Programmable field #4	837	15	Alphanum. charact.
86	Programmable field #5	852	15	Alphanum. charact.
87	Programmable field #6	867	15	Alphanum. charact.
88	Programmable field #7	882	15	Alphanum. charact.
99	Programmable field #8	897	15	Alphanum. charact.
--	-----	----	---	---
119	Programmable field #38	1347	15	Alphanum. charact.
120	Programmable field #39	1362	15	Alphanum. charact.
121	Programmable field #40	1377	15	Alphanum. charact.
122	Attached card comment	1392	256	Alphanum. charact.
<b>TOTAL</b>		<b>858</b>	<b>bytes</b>	

The content configuration of the 40 programmable fields can be done only by modification of the host.ini file (into the Host folder).

#### **Host.ini file example to transmit the additional Capillary data**

```
[PROTOCOLLO]
MOD0=RS232
TIPO=Phoresis Extended
LETTERA=S
RX_MODE=WORKLIST
REALTIME=0
RECALL_MODE=1
```

```
[PHORESIS]
CURVA=0
COMMENTO_ESTESO=0
OPTIONAL_FIELDS=0
CRC_CHECK=0
IMAGE_IF=0
AUTOSEQUENCE=0
NUMERIC_ID=0
FILE_CARD=0
FORCE_SEQUENCE=0
```

```
OPZ_FIELD1=DO_MAX
OPZ_FIELD2=NR_CAPILLARY
OPZ_FIELD3=RACK_NR
OPZ_FIELD4=ANALYSIS_TIME
OPZ_FIELD5=MIGRATION_TIME
OPZ_FIELD6=DELAY_TIME
```

The additional instructions to transmit the programmable fields (Corresponding to Capillary data here) are in bold characters.

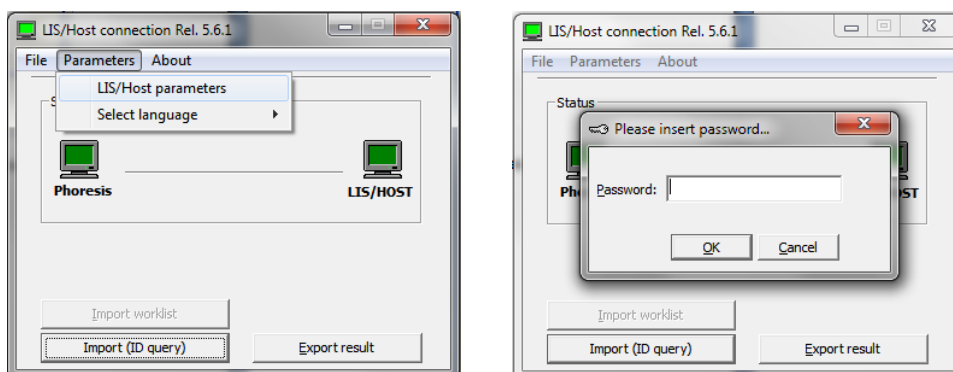
#### **Optional field for the extended comment**

123	Extended comment	--	max3000	Alphanum. charact. With max 3000 charact.
-----	------------------	----	---------	---

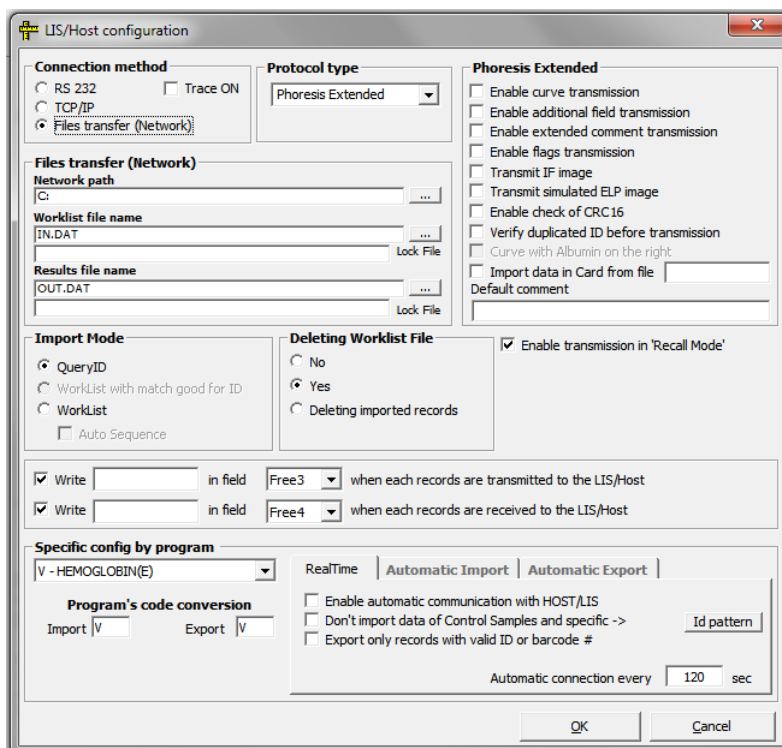
This field has a variable length from 0 to 3000 characters. All CR+LF (ASCII 0Dh+0Ah) entered in the extended comment will be converted in RS character (ASCII 1Eh)

# SETTING PARAMETERS

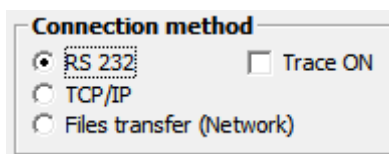
From the main menu, click on *Host* icon, select successively *Parameters* and *Host parameters*,



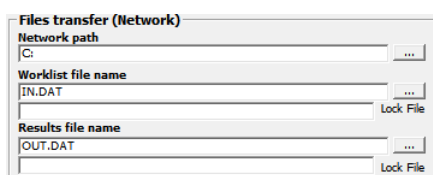
Enter the password **4644** or **free** then the system displays the following screen:



## Connection Method



**File-transfer (Network)**, select the network path, enter the Worklist and result file names, confirm with **OK**, and then restart Phoresis for the changes to be effective.



(Lock file is the name of semaphore files to prevent simultaneous access with LIS)

**TCP/IP** select the Remote Host Address or IP and the remote Host TCP Port, confirm with *OK* then restart Phoresis for the changes to be effective.

(UDP connection mode is present but not supported)

**RS232**, select the COM port, set the baud rate, data bit, parity, stop bit and delays, confirm with *OK* then restart Phoresis for the changes to be effective.

(Delay Answer are milliseconds of waiting time between sent and received messages and vice versa. Time Out is a maximum time to receive a message from LIS. If not arrive in time, Host module will show an error.)

**Trace ON** check-box activates permanently writing of the log files into folder HOST of Phoresis. This file logs all operations of connection with the LIS (outcomes and error of the communication). The log files are daily and are named:

HOSTTRACEYYYYMMDD.LOG

where

YYYY is the year  
MM is the month  
DD is the day

## Protocol Type

When clicking in the *Protocol type* window, the system proposes only Phoresis Extended and *Preference*.

Preference protocol is not described in this manual because It does not give the possibility to use all the capabilities of Phoresis such as the capability to use the date of birth, the laboratory code, the sample collection date, the 5 additional free fields and the operator ID for the Worklist and the capability to transmit the monoclonal peaks and the extended comment to the host.

## Import Mode

**Query ID.** Request to LIS demographic data of patients by ID/Barcode tube

**Worklist with Match good for ID.** Request to LIS a Worklist and it will match Sample with demographic data by ID/Barcode tube. The position of the samples is the same as the instrument read

**Worklist.** Request to LIS a Worklist. Position of samples (Sequence) is the same received from LIS.

**Note:**

*Before writing a record, the Host Module looks for a sample with correspondent ID to merge it with the demographic data received.*

*If the position in which it must be written a demographic data there is a curve without ID or with ID does not match, this last will be moved to the end of the work list.*

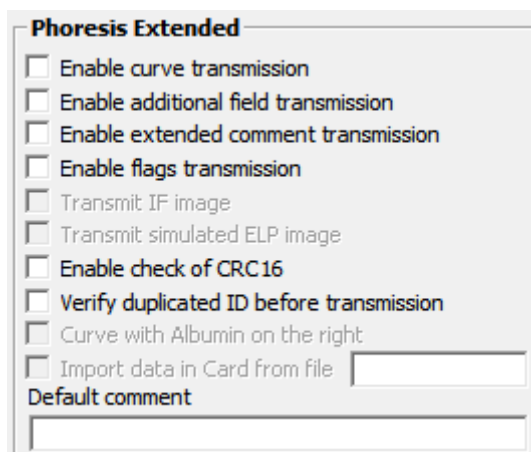
*This mode is not compatible with MiniCap because moving records causes a runtime error on the affected records.*

*Moreover this mode does not allow to work with no ID / barcode on the tube, for example with Hydrasys without sampler Assist.*

*It is possible to disable the displacement of the samples by changing the voice OVERWRITE\_PROGRAM in the section PHORESIS of the file HOST.INI.*

*This entry contains the list of codes of programs which enabled the overwrite function of demographic data. In this way demographic data are written with no check.*

## Phoresis Extended Option



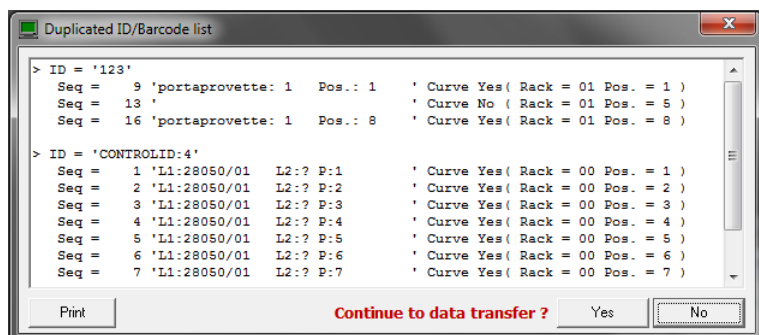
**Phoresis Extended**

- ☐ Enable curve transmission
- ☐ Enable additional field transmission
- ☐ Enable extended comment transmission
- ☐ Enable flags transmission
- ☐ Transmit IF image
- ☐ Transmit simulated ELP image
- ☐ Enable check of CRC16
- ☐ Verify duplicated ID before transmission
- ☐ Curve with Albumin on the right
- ☐ Import data in Card from file
- Default comment

In above frame will be enabled/disabled options of protocol:

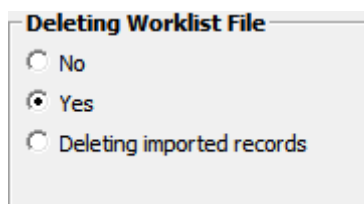
- **Enable curve transmission.** See page 10 in RS232/TCP and page 17 in File Transfer.
- **Enable additional field transmission,** See page 11 in RS232/TCP and page 18 in File Transfer.
- **Enable extended comment transmission,** See page 11 in RS232/TCP and page 18 in File Transfer.
- **Enable flags transmission,** enabled/disabled additional option to transmission of normal range and alarms of fractions value. See Appendix 4.
- **Transmit IF image,** enabled/disabled transmission of image file with scanned IF. This is active only in file transfer mode. See Appendix 5.
- **Transmit simulated ELP image,** enabled/disabled transmission of image file with ELP image (is not a real scanned image but a virtual rebuild). This is active only in file transfer mode. See Appendix 6.

- **Enable Check of CRC16**, enable/disable check and transmission of five characters for CRC. See Appendix 3 for CRC16 calculation)
- **Verify duplicated ID before transmission**, enable/disable a pre transmission of results to check for any duplicate IDs in the worklist. If there are duplicate IDs, Host module will open following window:



- **Curve with Albumin on the right**, this option is active only when Enable curve transmission is checked.
- **Import data in Card from file [File name]**, enable/disable import of specific protein value from LIS into 24 value of Attached Card. See Appendix 7
- **Default comment [comment text]**, allows to specify a default text for all records that have empty comment.

## Deleting Worklist File



This frame is active only for File Transfer Mode.

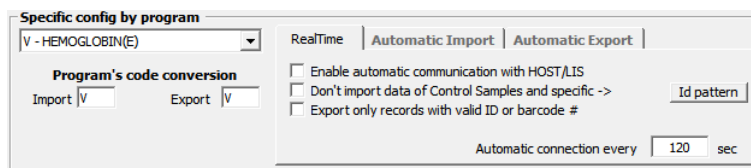
**Warning**, this option should be adjusted based on the operation of the LIS:

**No**, after importation of demographics data the Worklist file will not be deleted. The file size will grow, If LIS doesn't erase it. This slows down the operations of importing data.

**Yes**, after importation of demographics data the Worklist file will be deleted. If the worklist file is partially imported, demographics data not imported will be lost.

**Deleting imported records**, after importation will be removed only the imported records. Into the Worklist file will remain only not imported rows. We suggest to select this mode if you do not know how LIS manages this file and is mandatory if the LIS handles the records in queue.

## Specific config by program



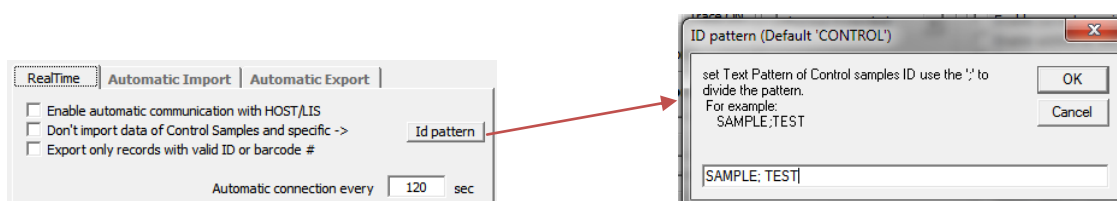
In above frame will be enabled/disable function regarding a specific analysis program

### Program's code conversion

Use this text boxes to force a different code for each analysis program. It could be helpful during instrument model changes because you can manage the communication with no LIS specialist support.

### Realtime

Three Tabs of this frame contain all settings concerning the realtime.

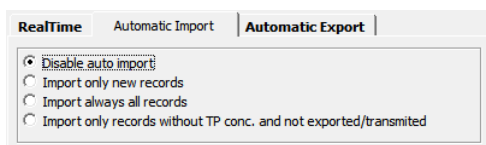


**Enable automatic communication with HOST/LIS**, enable/disable all automatic communication with LIS for selected analysis program.

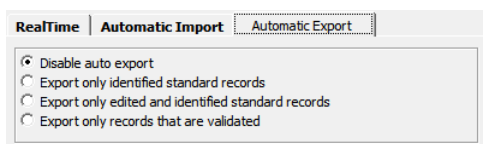
**Don't import data of Control Sample and specific ->[Id Pattern]**, if enable, auto import don't request demographic data for control sample (the QC records are identified by ID on database equal at 'CONTROL\*'). With button [Id Pattern] you can specify a text string that, if found in the ID field, disables automatic import for that sample. For example, typing the string 'SAMPLE, ABC' all records with IDs that start with SAMPLE or ABC will be excluded from automatic import.

**Export only records with valid ID or barcode #**, if enabled, only records with ID/Barcode are automatic exported. Otherwise all samples (even with no ID) will send to LIS.

**Automatic connection every [ ] sec**, this text box specify waiting time in second between connection. Warning, in earlier releases this timing was in milliseconds.



**Automatic Import**, kind of samples imported to LIS regarding import demographic data. Warning, all records just exported will no longer be imported.



**Automatic Export**, , kind of samples exported to LIS regarding import demographic data. Edited records are samples that they are displayed on Edit Curve (no more bold in the work list). Identified records are samples that they have a right number of fractions (in according with Program configuration)  
Warning, all HBA1C samples are identified

## Other setting

☒ Enable transmission in 'Recall Mode'

If Enabled, it will allow to communicate to LIS in recall mode.

<input checked="" type="checkbox"/> Write	<input type="text"/>	in field	Free3	when each records are transmitted to the LIS/Host
<input checked="" type="checkbox"/> Write	<input type="text"/>	in field	Free4	when each records are received to the LIS/Host

This checkbox will allow to write something into Free Field of demographic data after a transmission/reception to LIS. You may specify which free field, for import and export and what to write inside the field. If you leave the text box blank, it will write the time of operation (in format HH:MM:SS)



# APPENDIX 1

## *Analysis program codes*

Codice_prog	Intest
#	β2 Transferrine Electrophoresis
\$	Protein Electrophoresis
@	HbA1c
0	Urin Electrophoresis
1	CSF ISOFOCUSING Electrophoresis
2	Hemoglobin Neonatal Electrophoresis
3	Urin Electrophoresis
4	Protein Electrophoresis
5	Protein Electrophoresis
6	Protein Electrophoresis
7	Hemoglobin Cord Bloods Electrophoresis
8	CSF Electrophoresis
9	IF Penta
A	High Resolution Electrophoresis
B	High Resolution Electrophoresis
C	Protein Electrophoresis
D	Protein Electrophoresis
E	Protein Electrophoresis
F	Protein Electrophoresis
H	HDL Cholesterol Quantification
I	ISO-LDH Electrophoresis
J	Protein Electrophoresis
K	High Resolution Electrophoresis
L	Lipoprotein Electrophoresis
M	ISO-PAL Electrophoresis
N	Transferrin isoforms electrophoresis
O	CSF Electrophoresis
P	Urinary Protein Electrophoresis
Q	ISO-CK Electrophoresis
R	High Resolution Electrophoresis
S	Protein Electrophoresis
T	Hemoglobin Electrophoresis
U	Urinary Protein Electrophoresis
V	Hemoglobin Electrophoresis
W	Urine Electrophoresis
X	Sebia Test Pattern
Y	Total Protein
Z	IF/Bence Jones

## APPENDIX 2

### Connector pin assignment

The output is compatible V 24 and RS 232C from one asymmetric 9 pin male connector (db9 connector or COM port) located at the back of the PC.

Pin No.	Signal	Direction	Description
1	DCD	in	Data Carrier Detect
2	RXD	in	Received Data
3	TXD	out	Transmitted Data
4	DTR	out	Data Terminal Ready
5	GND	-	Ground
6	DSR	in	Data Set Ready
7	RTS	out	Request To Send
8	CTS	in	Clear To Send
9	RI		Ring Indicator

**Note:**

*In normal condition, only pins RX, TX and GND are connected.*

## APPENDIX 3

### CRC CALCULATION (in C language)

The CRC is calculated from the following table\_CRC\_16 which is a table of 256 uint (unsigned integer)

Input data:    Number of bytes to calculate

                Buffer of date where the calculation is made

Output: CRC obtained for the complete buffer

The STX and ETX are not used for the calculation of the CRC

The CRC is a uint (unsigned integer) transmitted with 5 characters (completed with 0 when necessary)

The CRC is calculated on 16 bits

```
uint CalculateCRC16(uint NbBytes,char* Buffer) {
uint Loop,CRC;
uint Table_CRC_16[ 256 ] =

{
0x0000, 0xC1C0, 0x81C1, 0x4001, 0x01C3, 0xC003, 0x8002, 0x41C2,
0x01C6, 0xC006, 0x8007, 0x41C7, 0x0005, 0xC1C5, 0x81C4, 0x4004,
0x01CC, 0xC00C, 0x800D, 0x41CD, 0x000F, 0xC1CF, 0x81CE, 0x400E,
0x000A, 0xC1CA, 0x81CB, 0x400B, 0x01C9, 0xC009, 0x8008, 0x41C8,
0x01D8, 0xC018, 0x8019, 0x41D9, 0x001B, 0xC1DB, 0x81DA, 0x401A,
0x001E, 0xC1DE, 0x81DF, 0x401F, 0x01DD, 0xC01D, 0x801C, 0x41DC,
0x0014, 0xC1D4, 0x81D5, 0x4015, 0x01D7, 0xC017, 0x8016, 0x41D6,
0x01D2, 0xC012, 0x8013, 0x41D3, 0x0011, 0xC1D1, 0x81D0, 0x4010,
0x01F0, 0xC030, 0x8031, 0x41F1, 0x0033, 0xC1F3, 0x81F2, 0x4032,
0x0036, 0xC1F6, 0x81F7, 0x4037, 0x01F5, 0xC035, 0x8034, 0x41F4,
0x003C, 0xC1FC, 0x81FD, 0x403D, 0x01FF, 0xC03F, 0x803E, 0x41FE,
0x01FA, 0xC03A, 0x803B, 0x41FB, 0x0039, 0xC1F9, 0x81F8, 0x4038,
0x0028, 0xC1E8, 0x81E9, 0x4029, 0x01EB, 0xC02B, 0x802A, 0x41EA,
0x01EE, 0xC02E, 0x802F, 0x41EF, 0x002D, 0xC1ED, 0x81EC, 0x402C,
0x01E4, 0xC024, 0x8025, 0x41E5, 0x0027, 0xC1E7, 0x81E6, 0x4026,
0x0022, 0xC1E2, 0x81E3, 0x4023, 0x01E1, 0xC021, 0x8020, 0x41E0,
0x01A0, 0xC060, 0x8061, 0x41A1, 0x0063, 0xC1A3, 0x81A2, 0x4062,
0x0066, 0xC1A6, 0x81A7, 0x4067, 0x01A5, 0xC065, 0x8064, 0x41A4,
0x006C, 0xC1AC, 0x81AD, 0x406D, 0x01AF, 0xC06F, 0x806E, 0x41AE,
0x01AA, 0xC06A, 0x806B, 0x41AB, 0x0069, 0xC1A9, 0x81A8, 0x4068,
0x0078, 0xC1B8, 0x81B9, 0x4079, 0x01BB, 0xC07B, 0x807A, 0x41BA,
0x01BE, 0xC07E, 0x807F, 0x41BF, 0x007D, 0xC1BD, 0x81BC, 0x407C,
0x01B4, 0xC074, 0x8075, 0x41B5, 0x0077, 0xC1B7, 0x81B6, 0x4076,
0x0072, 0xC1B2, 0x81B3, 0x4073, 0x01B1, 0xC071, 0x8070, 0x41B0,
0x0050, 0xC190, 0x8191, 0x4051, 0x0193, 0xC053, 0x8052, 0x4192,
0x0196, 0xC056, 0x8057, 0x4197, 0x0055, 0xC195, 0x8194, 0x4054,
0x019C, 0xC05C, 0x805D, 0x419D, 0x005F, 0xC19F, 0x819E, 0x405E,
0x005A, 0xC19A, 0x819B, 0x405B, 0x0199, 0xC059, 0x8058, 0x4198,
0x0188, 0xC048, 0x8049, 0x4189, 0x004B, 0xC18B, 0x818A, 0x404A,
0x004E, 0xC18E, 0x818F, 0x404F, 0x018D, 0xC04D, 0x804C, 0x418C,
0x0044, 0xC184, 0x8185, 0x4045, 0x0187, 0xC047, 0x8046, 0x4186,
0x0182, 0xC042, 0x8043, 0x4183, 0x0041, 0xC181, 0x8180, 0x4040,
};

CRC=0;
for (Loop=0;Loop<NbBytes;Loop++)
CRC=( ( CRC << 8 ) ^ Table_CRC_16[ (CRC >> 8 ) ^ Buffer[Loop] ] ); return(CRC);
}
```

# APPENDIX 4

## Optional Flags transmission

This option allows alarm flags transmission. The optional field has fixed length of 23 characters:

1-10 characters	Flag for value % of Fraction 1 to 10 (one char. for fraction)
11-20 characters	Flag for value concentration of Fraction 1 to 10 (one char for fraction)
21 character	Flag of Total Protein concentration
22 character	Flag of Rapport Rapp1 (A/G for protein EPH)
23 char	Flag of Rapport Rapp2

It is possible to set-up characters of the flags by 3 values under [PHORESIS] section of HOST.INI:

FLAG_LOW=	define the char used for Low (default 'L')
FLAG_NORMAL=	define the char used for Normal (default 'N')
FLAG_HIGH=	define the char used for High (default 'H')

Warning will be used only one char (the first) of the string

Item FLAG\_MODE under [PHORESIS] section of HOST.INI is used to store the Normal Range:

FLAG_MODE=0	Normal Range from Section NORMAL in HOST.INI
FLAG_MODE=1	Normal Range from Phoresis Config (not yet available)

### Note:

If you use NORMAL section in HOST.INI (see below), the normal range will search by Name of Fraction.

Section [NORMAL], in HOST.INI is used to store the normal value of Fraction, PT and Rapport, usable by Optional Field Flag:

<i>P_FRAZ_n%=Min;Max</i>	Normal Value % for fraction <i>n</i>
<i>P_FRAZ_Name%=Min;Max</i>	Normal Value % for fraction <i>Name</i>
<i>P_FRAZ_n#=Min;Max</i>	Normal Value concentration for fraction <i>n</i>
<i>P_FRAZ_Name#=Min;Max</i>	Normal Value concentration for fraction <i>Name</i>
<i>P_PT=Min;Max</i>	Normal Value for PT (Concentration)
<i>P_RAPP1=Min;Max</i>	Normal Value for Rapport 1 (A/G)
<i>P_RAPP2=Min;Max</i>	Normal Value for Rapport 2

Where:

<i>P</i>	the analysis program code (example J for Protein(e)6)
<i>n</i>	fraction index (1 to 10)
<i>Name</i>	Name of fraction (example 'Albumin' or 'Albumine', based on the selected operator language)
<i>Min</i>	low value of normal range, use . as separator (Es: 5.6)
<i>Max</i>	high value of normal range, use as separator (Es: 34.63)

Example for Protein(e) 6 program (code J):

```
[NORMAL]
J_FRAZ_ALBUMINE%=55.8;66.1
J_FRAZ_ALPHA 1%=2.9;4.9
J_FRAZ_ALPHA 2%=7.1;11.8
J_FRAZ_BETA 1%=4.7;7.2
J_FRAZ_BETA 2%=3.2;6.5
J_FRAZ_BETA%=8.4;13.1
J_FRAZ_GAMMA%=11.1;18.8
J_FRAZ_ALBUMINE#=40.2;47.6
J_FRAZ_ALPHA 1#=2.1;3.5
J_FRAZ_ALPHA 2#=5.1;8.5
J_FRAZ_BETA 1#=3.4;5.2
J_FRAZ_BETA 2#=2.3;4.7
J_FRAZ_BETA#=6.0;9.4
J_FRAZ_GAMMA#=8.0;13.5
J_PT=50.0;80.0
J_RAPP1=1.08;1.86
J_RAPP2=
```

```
J00061102412805      Patient one
11121920F091Department one      2003201253.20g/dl      1
TX                               11:40:59
SB 2103201206Albumine Alpha 1 Alpha 2 Beta 1
Beta 2 Gamma
048.8006.9009.9005.9006.5022.0000.0000.0000.0000.025.96
03.6705.2703.1403.4611.7000.0000.0000.0000.00
000.0000.0000.0000.000.0000.0000.0000.00000.9501.00
00LHNNNH LHNLNN NL
J00071102429106      Patient two
12011956M056Departemt two      1903201280.20g/dl      1
TX                               11:11:35
SB 2103201206AlbuminE Alpha 1 Alpha 2 Beta 1
Beta 2 Gamma
054.4005.1011.7006.4006.9015.5000.0000.0000.0000.043.63
04.0909.3805.1305.5312.4300.0000.0000.0000.001
006.7000.0000.0000.005.3700.0000.0000.00001.1901.00Pres
enza di componente monoclonale gio' tipizzata.
00LHNNHN NHHNHN HN
```

## APPENDIX 5

### IF IMAGE TRANSMISSION

WARNING! This option is valid only for file transfer via network connections.

This option permits to transfer the IF image of the attached card. For each image stored in the attached card, host module will create a file on the network path (same path used by result file). Those files have JPEG extension and they are created under the following format:

PYYYYMMDDNNNNNID.jpg

where:

P is the analysis program code  
YYYYMMDD is the analysis date  
NNNNN is the sequence number of 5 digits right-aligned with zeros  
ID is the tube ID / Barcode with a variable length up to a maximum of 15 characters

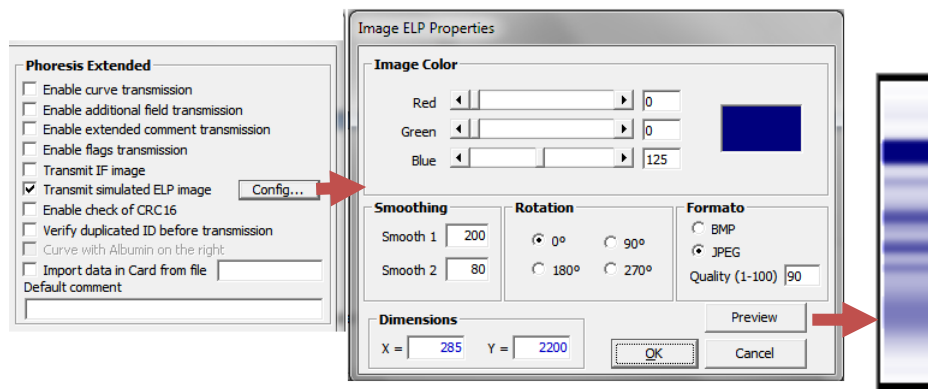
## APPENDIX 6

### ELP IMAGE TRANSMISSION

WARNING! This option is valid only for file transfer via network connections.

This option permits to transfer the mathematical rebuild of the ELP image calculated from the points of the curve.

With the [Config...] button, it's possible to select the parameters of the rebuilt image and the file format



**Image Color**, set base color of the rebuild ELP image.

**Smoothing**, two parameter for calibrate blending simulation of color.

**Rotation**, direction of rebuild migration.

**Format**, set image format and quality of jpeg compression

**Dimension**, set the size in pixel of the image

**[Preview] Button** show parameter modification effect

For each records with curve will be created a file on the network path (with the result file). Those files have JPEG or BMP extensions and they are created under the following format:

PYYYYMMDDNNNNNID.jpg/.bmp

where:

P is the analysis program code  
YYYYMMDD is the analysis date  
NNNNN is the sequence number of 5 digits right-aligned with zeros  
ID is the tube ID / Barcode with a variable length up to a maximum of 15 characters

# APPENDIX 7

## ATTACHED CARD DATA IMPORT

(Active from Rel 4.4.4 of Host Module)

WARNING! This option is valid only for file transfer via network connections.

The attached card is created to store an IF (Immuno Fixation) image and also up to 24 potential other values (fields of data) of specific protein dosage and an extended comment (32000 characters formatted RichText).

The 'Attached Card' window is divided into several sections:

- Patient data:** Includes fields for 'jhon', 'Working date : 02/03/2012', 'No. : 1', and 'ID : '.
- Protein values:** A grid of 24 input fields for various proteins and markers, including IgG, IgA, IgM, IgD, IgE, Alf1AT, Alf1AG, AT III, Alf2M, K free, L free, C3, C4, Fib, Cryo, Alb, HP, PreAlb, Trf, ApoA-1, Trf tau, K tot, L tot, and Rap K/L.
- Comments:** A large yellow text area for extended comments.
- Footer:** Includes buttons for 'Comment lists', 'Options', navigation controls ('Previous', 'Next'), a sample selection dropdown ('Select a sample to be attached with this IF/BJ,CSF,URINE'), 'Print', and 'Close'.

The 24 values (fields of data) can be entered manually. You can also customize the names of the 24 fields based on customer needs.

This window shows a table for manual data entry of the 24 protein values. The table has columns for 'Descr.', 'U/M', 'L', and 'H'.

	Descr.	U/M	L	H
1	IgG			
2	IgA			
3	IgM			
4	IgD			
5	IgE			
6	Alf1AT			
7	Alf1AG			
8	AT III			
9	Alf2M			
10	K free			
11	L free			
12	C3			
13	C4			
14	Fib			
15	Cryo			
16	Alb			
17	HP			
18	PreAlb			
19	Trf			
20	ApoA-1			
21	Trf tau			
22	K tot			
23	L tot			
24	Rap K/L			

At the bottom, there is a checkbox for 'Print image' and 'OK'/'Cancel' buttons.

WARNING the 24 names are common to all programs of analysis and to all records in the database

The option to 'Import data in the card' is used to fill these 24 fields during the acquisition phase of demographic data.

The LIS will provide a second file containing the references of the patient (Sequence Number, Analysis Program, ID / Barcode and date of sampling) and the values of specific proteins.

## SETTING BY HOST.INI

The configuration parameters are only HOST.INI editing in the section [PHORESIS]:

```
[PHORESIS]
FILE_CARD=SPEC.DAT
VAL1=IgG
VAL2=IgM
VAL3=IgK
..
VAL24=K/L
FORCE_SEQUENCE=0
```

**FILE\_CARD** This entry indicates the name of the file that contains the records of specific proteins. The file must be located in the network path (with two files of demographic data).

**VAL1-VAL24** These 24 entries allow the mapping between the codes of the LIS and the values of the card. The codes are alphanumeric for 5 characters long. It is not mandatory to configure all 24 values.

**FORCE\_SEQUENCE** Setting it to '1' to import data by position instead of ID / Barcode. When it is set to '0', the data are imported for ID.

## RECORD STRUCTURE

The file consists of variable length records terminated with CR + LF.  
Each record has a fixed header of 28 characters length for this data:

Program Code	1 character
Sequence	4 characters
ID / Barcode	15 characters
Date Request	8 characters

This header is followed by a variable number (between 1 to 24) of couples 'code / value'. The code is 5 characters and the Value is 15 characters long (Warning only the first 10 characters of value are imported).

N.	Description	Length	Note
1	Program Code	1	Letter from A to Z , 0 to 9 (see appendix 1)
2	Sequence	4	Format 0000
3	ID/Barcode	15	Alphanumeric
4	Request Date	8	DDMMYYYY
5	Analysis Code 1	5	Alphanumeric (example 'IGG')
6	Analysis Result 1	15	Alphanumeric (only first 10 characters are valid, example 'traces')
..	CRLF	2	ASCII 0Dh or 0Ah

Total Length Min 30 characters, max 510 characters (C+LF included)

Couple 5 and 6 are repeated for a max of 24 times.

Each record will have a variable length from a minimum of 30 characters (no value) and a maximum of 510 characters (24 values).

J00012729423	21112006	IgG	0.57	IgA	traces	IgM	traces
IgD 1.23	IgE 5.90		Kappa0.97		Lambda0.35		
Kfree2.80	LFree0.55		K/L 1.41		C3 traces		C4
2.82	Cryo 0.06		PreAl6.65		Alb 3.89		ApoA15.55
J00083478326	21112006	IgG	traces	IgA	traces	IgM	2.33
J00058759746	21112006	IgG	traces	IgA	4.84	IgM	5.47
IgD 4.14	IgE 5.82		Kappatraces		Lambda6.08		
Kfree0.03	LFree7.57		K/L traces		C3 traces		C4
5.93							

# APPENDIX 8

## HBA1C PROGRAM DETAIL (Active from Rel. 5.6.1 of Host Module)

Host Module exported data of HbA1c correctly only from Rel. 5.6.1 and above.  
The default values transmitted by Host are:

1st Fraction : always HbA1c% cal  
2nd Fraction : percentage of the second fraction  
N Fraction : percentage of fraction N  
N+1 Fraction : value in mmol / mol HbA1c  
N+2 Fraction : value of the EAG

The names of primary fractions (HbA1c%, HbA1c in mmol/mol and eAG) are forced with specific labels  
The fractions in concentration are forced to zero value.  
The areas in percent and the areas in concentration are forced to zero value  
The names of areas are null

There is a section in HOST.INI to force the names of primary fractions and activate this mode on other programs:

[HBA1C]	
PROGRAM_CODES=@	Active mode for program code(default '@')
NAME_%CAL=HbA1c%	Force Name of HbA1c % Cal (default HBA1C%)
NAME_MMOL/MOL=HbA1c#	Force Name of HbA1c mmol/mol (default HBA1C#)
NAME_EAG=Eag	Force Name of eAG (default AEG)

Example of transmission without curves:

```
@0008CONTROLID:13    QC Control 1-08021/01                000
00000g/dl
ADM2902201207HbA1c%    Other Hb AHb A0    Hb A2    HbA1c#    eAG
005.6003.3089.6002.3038.0113.9000.0000.0000.0000.000.0000.0000.0000.0000
.0000.0000.0000.0000.00
00.0000.0000.0000.00000.0000.0000.0000.0001.0001.00
01
@00097239645112      patient 1                        000
00000g/dl
ADM2902201207HbA1c%    Other Hb AHb A0    Hb A2    HbA1c#    eAG
007.9002.9086.9002.0063.0181.4000.0000.0000.0000.000.0000.0000.0000.0000
.0000.0000.0000.0000.00
00.0000.0000.0000.00000.0000.0000.0000.0001.0001.00
00
@00107231204233      patient 2                        000
00000g/dl
ADM2902201207HbA1c%    Other Hb AHb A0    Hb A2    HbA1c#    eAG
006.4003.0089.0002.0047.0138.1000.0000.0000.0000.000.0000.0000.0000.0000
.0000.0000.0000.0000.00
00.0000.0000.0000.00000.0000.0000.0000.0001.0001.00
00
@00117231203718      patient 3                        000
00000g/dl
ADM2902201207HbA1c%    Other Hb AHb A0    Hb A2    HbA1c#    eAG
006.6003.3088.3002.1049.0143.3000.0000.0000.0000.000.0000.0000.0000.0000
.0000.0000.0000.0000.00
00.0000.0000.0000.00000.0000.0000.0000.0001.0001.00
00
```