Any communication between two devices is defined on several levels.

Physical Layer

The lowest level is known as the “physical layer”. In order for Platinum to send results to a LIMS system the computer that runs Platinum must be connected to the LIMS with a serial interface cable. Since the computer that runs Platinum is a DTE device, a “null modem cable” may be required to make the connection.

Data Link Layer

This level has procedures for link establishment and release, synchronisation, sequential control, error detection and error recovery.

Platinum supports two data link implementations that lack any of the above. These are called “no protocol” and “Xon / Xoff”. The Xon / Xoff protocol provides only the most basic of synchronisation.

It is strongly suggested that the third protocol, ASTM 1381 (LIS01-A2), be used. This protocol provides for synchronisation as well as error checking. Please refer to the official ASTM 1381 release documents for details on this protocol.

Network Layer, Transport Layer, Session Layer

These layers are of no consequence for communications over serial cables.

Presentation Layer: Sending Data to the LIMS

This level deals with the formatting of the data being sent. Platinum has a number of data items that can be sent to the LIMS. These will be described below. The protocol used is based on ASTM

standard 1394. Please refer to the official ASTM 1394 (LIS2-A2) release documents for details on this protocol.

Under the ASTM 1394 protocol, communication takes place by sending a number of records. Each message sent to the LIMS contains at least the following records:

- Header record
- Patient record
- Order record
- Result record(s)
- Terminating record

There may be multiple patient records, each with one or more order records[1], each with one or more result records.

Following either patient, order, or result records, comment records may be included[2].

Most data items that are sent are sent in the form of Result records.

Header and terminating records follow the ASTM1394 standard precisely.

Header Record

A header record takes this form:

H|\^&||institutionname^Platinum^4.0|institutionaddress||institutiontelephone\r

r indicates a carriage return character (13).

This information is set within File | Customise | Institution Data

[1] IN Platinum, there is always a single order record.

[2] Platinum only includes comment records at the Order record level.

Patient Record

A patient record takes this form:

P|index||demofield1|demofield2|demofield3|…\r

Index gets consecutive values when multiple patient records are sent in a single message.

The order of the demographic fields is identical to the order in which demographic fields are set up in Platinum. Note that Platinum does not follow the strict ASTM1394 standard here.

r indicates a carriage return character (13).

NB Demographic data are sent as part of the patient record only.

Order Record

An order record takes the following form:

O|index|||^^^analysistype\r

Index gets consecutive values when multiple order records are sent for a single patient.

NB analysis type is sent as part of the order record, and is repeated in all result records.

r indicates a carriage return character (13).

Comment Record

The comment record takes this form:

C|index|I|comments\r

Comments can be up to 512 characters in length.

Where:

- **index** gets consecutive values for each comment record
- **r** indicates a carriage return character (13).

Gel Name

The gel name, if selected to be sent, is sent as a comment record:

C|index|I|gelname\r

Where:

- **index** gets consecutive values for each comment record
- **r** indicates a carriage return character (13).

Gel Lot

The gel lot number, if selected to be sent, is sent as a comment record:

C|index|I|gellotnumber\r

Where:

- **index** gets consecutive values for each comment record
- **r** indicates a carriage return character (13).

Gel Expiry

The gel expiry, if selected to be sent, is sent as a comment record:

C|index|I|gelexpiry\r

Where:

- **index** gets consecutive values for each comment record
- **format YYMMDD**

- **r** indicates a carriage return character (13).

Gel ID

The gel ID number, if selected to be sent, is sent as a comment record:

C|index|I|gelIDnumber\r

Where:

- **index** gets consecutive values for each comment record
- **r** indicates a carriage return character (13).

Total Chemistry Value (e.g. Total Protein)

The total chemistry value is sent as a result record, as follows:

R|index|^^^analysistype^Total Chemistry Value|3.00|(mg/l)||||F|||20010730175834\r

Where:

- **index** gets consecutive values for each result record
- **3.00** is the total chemistry value
- **(mg/l)** is the concentration unit as entered in the gel setup
- **F** indicates this is a final result
- **20010730175834** is YYYYMMDDHHMMSS where YYYY is the measurement year, MM is the month, DD is the date, HH is the hour, MM is the minutes, and SS is the seconds.
- **r** indicates a carriage return character (13).

This information is set up through CE System | Configure CE Methods | Chemistry Values

External Chemistry Value

The external chemistry value is sent as a result record, as follows:

R|index|^^^analysistype^External Albumin|0.00|(mg/l)||||F|||20010730175834\r

Where:

- **index** gets consecutive values for each result record
- **0.00** is the external albumin value
- **(mg/l)** is the concentration unit as entered in the gel setup
- **F** indicates this is a final result
- **20010730175834** is YYYYMMDDHHMMSS where YYYY is the measurement year, MM is the month, DD is the date, HH is the hour, MM is the minutes, and SS is the seconds.
- **r** indicates a carriage return character (13).

Band Lists

The user may choose to send band list items as area percentage, concentration, and/or area of each band. These items are sent as follows:

R|index|^^^analysistype^albumin^%|58.19|%||N||F|||20010730175834\r

R|index|^^^ analysistype ^albumin^U|1.75|(mg/l)|1.00-2.00|N||F|||20010730175834\r

R|index|^^^ analysistype ^albumin^I|1162|||||F|||20010730175834\r

Where:

- **index** gets consecutive values for each result record
- **%** indicates the area percentage
- **U** indicates concentration
- **I** indicates band area
- **58.19**, **1.75**, **1162** are the band's relative area, concentration, area
- **%**, **(mg/l)** are the units
- **1.00-2.00** is the result normal range
- **N**, **H**, **L** are result range flags (only N is shown here)
- **F** indicates this is a final result
- **20010730175834** is YYYYMMDDHHMMSS where YYYY is the measurement year, MM is the month, DD is the date, HH is the hour, MM is the minutes, and SS is the seconds.
- **r** indicates a carriage return character (13).

At the end of the band list result records additional records for total values are included:

R|index|^^^ analysistype ^Total^U|3.00|(mg/l)||||F|||20010730175834\r

R|index|^^^ analysistype ^Total^I|1997|||||F|||20010730175834\r

No record for total relative area is included.

For those systems incapable of handling total relative areas other than exactly 100.000% (due to cumulative rounding of fractions), there is an option of Area % out of 100.000%. This subtracts the rounding error from the first peak. Please note that this subtraction will also occur for marked m-spikes. This will lead to different values for the first peak when compared to data output for the option area percentage. Where possible area percentage should be the option selected.

Ratio Values

If ratios are calculated for the bands, they are sent as follows:

R|index|^^^ analysistype ^Ratio|0.94|||||F|||20010730175834\r

- **index** gets consecutive values for each result record
- **Ratio** is the name that was given the ratio
- **0.94** is the calculated ratio
- **F** indicates this is a final result
- **20010730175834** is YYYYMMDDHHMMSS where YYYY is the measurement year, MM is the month, DD is the date, HH is the hour, MM is the minutes, and SS is the seconds.
- **r** indicates a carriage return character (13).

Trace Values

If the user elects to send trace values to the LIMS (trace visible on screen, with x-axis correction applied) and high precision set to off, they are sent as follows:

R|index|^^^ analysistype ^TraceValues|0.0424^0.0420^0.0424^…^0.0391|||||F|||20010730175834\r

Where:

- **index** gets consecutive values for each result record
- **r** indicates a carriage return character (13).

The trace values are separated by the component delimiter character, in this case the caret (^).

Raw Trace Values

If the user elects to send raw trace values (no x-axis correction), with no baseline subtracted, to the LIMS with high precision set to off, they are sent as follows:

R|index|^^^analysistype^RawTraceValues|0.0424^0.0420^0.0424^…^0.0391|||||F|||20010730175834\r

Where:

- **index** gets consecutive values for each result record
- **r** indicates a carriage return character (13).

The raw trace values are separated by the component delimiter character, in this case the caret (^).

Trough Locations

If the user elects to send the trough locations (x-axis coordinate) to the LIMS, they are sent as follows:

R|index|^^^analysistype^Troughs|0^59^1173^…^2634|||||F|||20110706114815\r

Where:

- **index** gets consecutive values for each result record
- **r** indicates a carriage return character (13).

The trough locations are separated by the component delimiter character, in this case the caret (^).

^0^ indicates a trough marker; where this is replaced by a ^2^, this indicates a marked M-spike.

Raw Trough Locations

If the user elects to send the raw trough locations to the LIMS, they are sent as follows:

R|index|^^^analysistype^RawTroughs|0^192^1424^…^2885|||||F|||20110706114815\r

Where:

- **index** gets consecutive values for each result record
- **r** indicates a carriage return character (13).

The raw trough locations are separated by the component delimiter character, in this case the caret (^).

Baseline Values

If the user elects to send baseline values to the LIMS without the high precision setting on, they are sent as follows:

R|index|^^^analysistype^BaselineValues|0.0124^0.0120^0.0124^…^0.0291|||||F|||20010730175834\r

Where:

- **index** gets consecutive values for each result record
- **r** indicates a carriage return character (13).

The baseline values are separated by the component delimiter character, in this case the caret (^).

Raw Baseline Values

If the user elects to send raw baseline values to the LIMS with the high precision setting on, they are sent as follows:

R|index|^^^analysistype^RawBaselineValues|0.00019845^0.00019845^…^0.00002835|||||F|||20110706114815\r

Where:

- **index** gets consecutive values for each result record
- **r** indicates a carriage return character (13).

The raw baseline values are separated by the component delimiter character, in this case the caret (^).

Scan Image

If the user elects to send the scan image to the LIMS, it is sent as follows:

R|index|^^^ analysistype ^ScanImage|RGBvaluesLine1^RGBvaluesLine2^…^|||||F|||20010730175834\r

Where:

- **index** gets consecutive values for each result record
- **RGBvaluesLine1** hexadecimally coded R, G, B values for each pixel on the first line of the image. For instance: f2eae8f0e8e6f1e9e7 defines three pixels
- **F** indicates this is a final result
- **20010730175834** is YYYYMMDDHHMMSS where YYYY is the measurement year, MM is the month, DD is the date, HH is the hour, MM is the minutes, and SS is the seconds.
- **r** indicates a carriage return character (13).

N.B. For artificially generated capillary scan images the image transmitted is a single line 1 (one) pixel in depth. This image must be stretched to fit the final source location. Scan images of gel origin are transmitted as several image lines, with each line separated by the component delimiter character, in this case the caret (^).

IFE images

If the user elects to send the IFE images to the LIMS, it is sent as follows:

R|index|^^^analysistype^IFE1|RGBvaluesLine1^RGBvaluesLine2^…^|||||F|||20010730175834\r

If applicable, a second IFE image is sent:

R|index|^^^analysistype^IFE2|RGBvaluesLine1^RGBvaluesLine2^…^|||||F|||20010730175834\r

Where:

- **index** gets consecutive values for each result record
- **RGBvaluesLine1** hexadecimally coded R, G, B values for each pixel on the first line of the image. For instance: f2eae8f0e8e6f1e9e7 defines three pixels
- **F** indicates this is a final result
- **20010730175834** is YYYYMMDDHHMMSS where YYYY is the measurement year, MM is the month, DD is the date, HH is the hour, MM is the minutes, and SS is the seconds.
- **r** indicates a carriage return character (13).

Due to the size of the IFE image, the transmission of an IFE image will require a significant volume of data transfer, therefore this must be taken into account.

Truncate To Zero

When truncate to zero is set, negative x-axis values are corrected.

When truncate to zero is not set, trough locations are sent to the LIMS as follows:

R|index|^^^analysistype^Troughs|0^-1^1173^…^2634|||||F|||20110706114815\r

When truncate to zero is set, trough locations are sent to the LIMS as follows:

R|index|^^^analysistype^Troughs|0^0^1173^…^2634|||||F|||20110706114815\r

Where:

- **index** gets consecutive values for each result record
- **r** indicates a carriage return character (13).

The trough locations are separated by the component delimiter character, in this case the caret (^).

Reflex Tested?

If the user elects to send whether the sample has been reflex tested, it is sent as a comment record:

C|index|I|ReflexTested : testname\r

Where:

- **index** gets consecutive values for each comment record
- **r** indicates a carriage return character (13).

Example message

A complete message with selected results for two patients is shown below.

H|\^&||PT|Helena Biosciences Europe^Platinum^4.0|Team Valley Trading Estate, Gateshead, NE11 0SD||+44 (0) 191 4828440\r
P|1|5001|Demog 2|Demog 3|Demog 4|01/01/2001|Demog 6|Demog 7|Demog 8|Demog 9|Demog 10\r
O|1|||^^^spe\r
C|1|I|Text Comment location\r
R|1|^^^spe^Total Protein|85.00|g/L||||F|||20110321113048\r
R|2|^^^spe^Albumin|0.00|g/L||||F|||20110321113048\r
R|3|^^^spe^Albumin^%|56.08|%||N||F|||20110321113048\r
R|4|^^^spe^Albumin^U|47.66|g/L|0.00-0.00|H||F|||20110321113048\r
R|5|^^^spe^Alpha-1^%|4.84|%||N||F|||20110321113048\r
R|6|^^^spe^Alpha-1^U|4.12|g/L|0.00-0.00|H||F|||20110321113048\r
R|7|^^^spe^Alpha-2^%|9.73|%||N||F|||20110321113048\r
R|8|^^^spe^Alpha-2^U|8.27|g/L|0.00-0.00|H||F|||20110321113048\r
R|9|^^^spe^Beta-1^%|8.55|%||N||F|||20110321113048\r
R|10|^^^spe^Beta-1^U|7.27|g/L|0.00-0.00|H||F|||20110321113048\r
R|11|^^^spe^Beta-2^%|6.74|%||N||F|||20110321113048\r
R|12|^^^spe^Beta-2^U|5.73|g/L|0.00-0.00|H||F|||20110321113048\r
R|13|^^^spe^Gamma^%|14.06|%||N||F|||20110321113048\r
R|14|^^^spe^Gamma^U|11.95|g/L|0.00-0.00|H||F|||20110321113048\r
R|15|^^^spe^Total^U|85.00|g/L||||F|||20110321113048\r
R|16|^^^spe^Alb:Globulin|1.28|||||F|||20110321113048\r
P|2|5002|Demog 2|Demog 3|Demog 4|01/01/2001|Demog 6|Demog 7|Demog 8|Demog 9|Demog 10\r
O|1|||^^^spe\r
C|1|I|Text Comment location\r
R|1|^^^spe^Total Protein|65.00|g/L||||F|||20110321113049\r
R|2|^^^spe^Albumin|0.00|g/L||||F|||20110321113049\r
R|3|^^^spe^Albumin^%|55.81|%||N||F|||20110321113049\r
R|4|^^^spe^Albumin^U|36.27|g/L|0.00-0.00|H||F|||20110321113049\r
R|5|^^^spe^Alpha-1^%|4.90|%||N||F|||20110321113049\r
R|6|^^^spe^Alpha-1^U|3.18|g/L|0.00-0.00|H||F|||20110321113049\r
R|7|^^^spe^Alpha-2^%|8.86|%||N||F|||20110321113049\r
R|8|^^^spe^Alpha-2^U|5.76|g/L|0.00-0.00|H||F|||20110321113049\r
R|9|^^^spe^Beta-1^%|6.80|%||N||F|||20110321113049\r
R|10|^^^spe^Beta-1^U|4.42|g/L|0.00-0.00|H||F|||20110321113049\r
R|11|^^^spe^Beta-2^%|2.62|%||N||F|||20110321113049\r
R|12|^^^spe^Beta-2^U|1.70|g/L|0.00-0.00|H||F|||20110321113049\r
R|13|^^^spe^Gamma^%|21.02|%||N||F|||20110321113049\r
R|14|^^^spe^Gamma^U|13.66|g/L|0.00-0.00|H||F|||20110321113049\r
R|15|^^^spe^Total^U|65.00|g/L||||F|||20110321113049\r
R|16|^^^spe^Alb:Globulin|1.26|||||F|||20110321113049\r
L|1\r

Presentation Layer: Asking the LIMS for Demographics and Chemistry Values

This level deals with the formatting of requests to the LIMS to send demographic information, and with the format that the LIMS should use to reply to these requests.

Format of Information Request

Platinum asks the LIMS for information using a **LIS identifier**. The LIS identifier is one of the demographics that were set up using the File | Customise menu option.

The demographic field to be used to query the LIMS is indicated by setting its Field Type to “LIS identifier” or “LIS Identifier/Unique String” (indicating a field that is used both to query the LIMS and to ensure uniqueness of values in the Platinum database). Typically, this field will be a tube number.

Platinum can ask the LIMS for demographic information using one message per worklist line, or one message for all worklist lines. The second method reduces overhead considerably and is preferred. Indicate which format to use by means of the File | Customise | Receiving from LIMS menu option.

The information request has the following format:

- header record
- request record
- [[request record]]
- terminator record

The request record specifies the LIS identifier as follows:

Q|1|5000^^||GelScan||||||||\r

Where “5000” is the LIS identifier.

Example Requests

This example asks for demographics and chemistry values for tubes with identifiers “5000” and “5001”:

H|\^&||PT|Institution Name^Platinum^4.0|Institution Address||Telephone number\r

Q|1|5000^^||GelScan|||||||\r

Q|2|5001^^||GelScan|||||||\r

L|1\r

If separate messages were used for each tube, there would have been two messages:

H|\^&||PT|Institution Name ^Platinum^4.0|Institution Address || Telephone number\r

Q|1|5000^^||GelScan|||||||\r

L|1\r

and

H|\^&||PT|Institution Name ^Platinum^4.0|Institution Address || Telephone number \r

Q|1|5001^^||GelScan|||||||\r

L|1\r

Format of Demographic and Chemistry Value Information

The LIMS should reply to a request for information by sending a message that is formatted as follows:

- header record
  - patient record (for each requested LIS identifier; if the patient is found)
    - order record (if TCV or Albumin records are found)
      - result record for Total Chemistry value (if applicable)
      - result record for External Albumin (if applicable)
      - result record for External Chemistry (if applicable)
  - [[patient record, order record, results records]]
- terminator record

For each request, the LIMS should send exactly one response. If requests are combined into a single message, a single response message is expected. If requests are sent separately for each

demographic, the LIMS should immediately respond to each request. Platinum will not send further requests before it has received a response.

Patient Record

The patient record should be formatted as follows:

P|index||demofield1|demofield2|demofield3|…\r

Index gets consecutive values when multiple patient records are sent in a single message.

The order of the demographic fields is identical to the order in which demographic fields are set up in Platinum. Note that Platinum does not follow the strict ASTM1394 standard here.

r indicates a carriage return character (13).

If no demographics are known, do not send a patient record. A header and terminator record should still be sent.

Order Record

The order record should only be sent if at least one of Total Chemistry Value, External Albumin, Exteral Chemistry is available. It should be formatted as follows:

O|index|||^^^MeasTypeName\r

Index gets consecutive numbers when multiple order records are sent. However, for each patient the index starts at 1.

MeasTypeName is the type of measurement, it is ignored here.

r indicates a carriage return character (13).

Result Record

The result records for Total Chemistry Value, External Albumin and External chemistry should only be sent if they are available. They take the following form:

R|index|^^^MeasType^TCV|value|unit||||flag|||datestamp\r

R|index|^^^MeasType^Albumin|value|unit||||flag|||datestamp\r

R|index|^^^MeasType^IGG|value|unit||||flag|||datestamp\r

Index gets consecutive numbers when multiple result records are sent. However, for each patient the index starts at 1.

MeasType is the type of measurement, it is ignored here.

TCV is the name the LIMS uses for the total chemistry value. This name should be entered in the method / gel definition in Platinum, using either CE System | Configure Methods | Chemistry Values (for capillary methods) or Gel | Configure Gels | Chemistry Values for gel methods. Each method used must be set accordingly.

NB If the LIMS sends a result that does not match this name, the result will be ignored and a warning will be displayed.

Albumin is the name the LIMS uses for the external chemistry value. This name should be entered in the method / gel definition in Platinum, using either CE System | Configure Methods | Chemistry Values (for capillary methods) or Gel | Configure Gels | Chemistry Values for gel methods. Each method used must be set accordingly.

NB If the LIMS sends a result that does not match this name, the result will be ignored and a warning will be displayed.

IGG is the name the LIMS uses for the external immunoglobulin G value. This name should be entered in the method / gel definition in Platinum, using either CE System | Configure Methods | Chemistry Values (for capillary methods) or Gel | Configure Gels | Chemistry Values for gel methods. Each method used must be set accordingly.

NB If the LIMS sends a result that does not match this name, the result will be ignored and a warning will be displayed.

Value is the value of the item.

Unit is the concentration unit. **NB** If it does not match the concentration unit that was entered in the gel definition in Platinum a warning will be displayed, but the value will be accepted. *No unit conversion is attempted.*

Flag is ignored.

Datestamp is ignored.

r indicates a carriage return character (13).

Example LIMS Response

This example contains (in order) a result with known TCV and Albumin values, a result with only a TCV value, and a result with no chemistry values.

H|\^&||PT| Institution Name ^Platinum^4.0|Institution Address || Telephone number\r

P|1|Smith|5001|\r

O|1|||^^^Serum Protein\r

R|1|^^^Serum Protein^Chemistry Value|0.71|g/l||||F|||20010517142352\r

R|2|^^^Serum Protein^Albumin|0.16|g/l||||F|||20010517142352\r

P|2|Johnson|5005|\r

O|1|||^^^Serum Protein\r

R|1|^^^Serum Protein^Chemistry Value|0.22|g/l||||F|||20010517142352\r

P|3|Mordichai|5007|\r

L|1\r

Logging

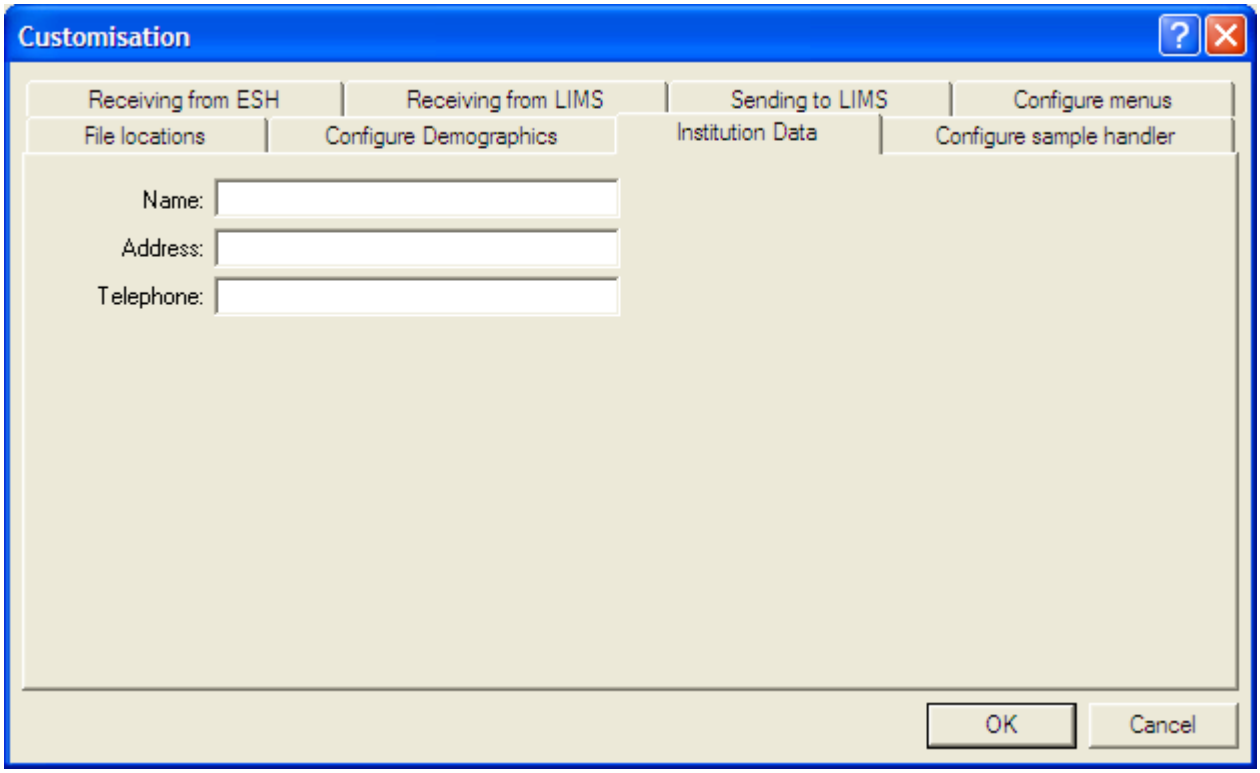
The most recently received message from the LIMS is always stored in the current **Directory for Gel Files** (set using the File | Customise option – default C:\Program Files\Pt\Platinum), under the name **FROMLIMS.log**. This file may be inspected for debugging purposes.

Automated Query

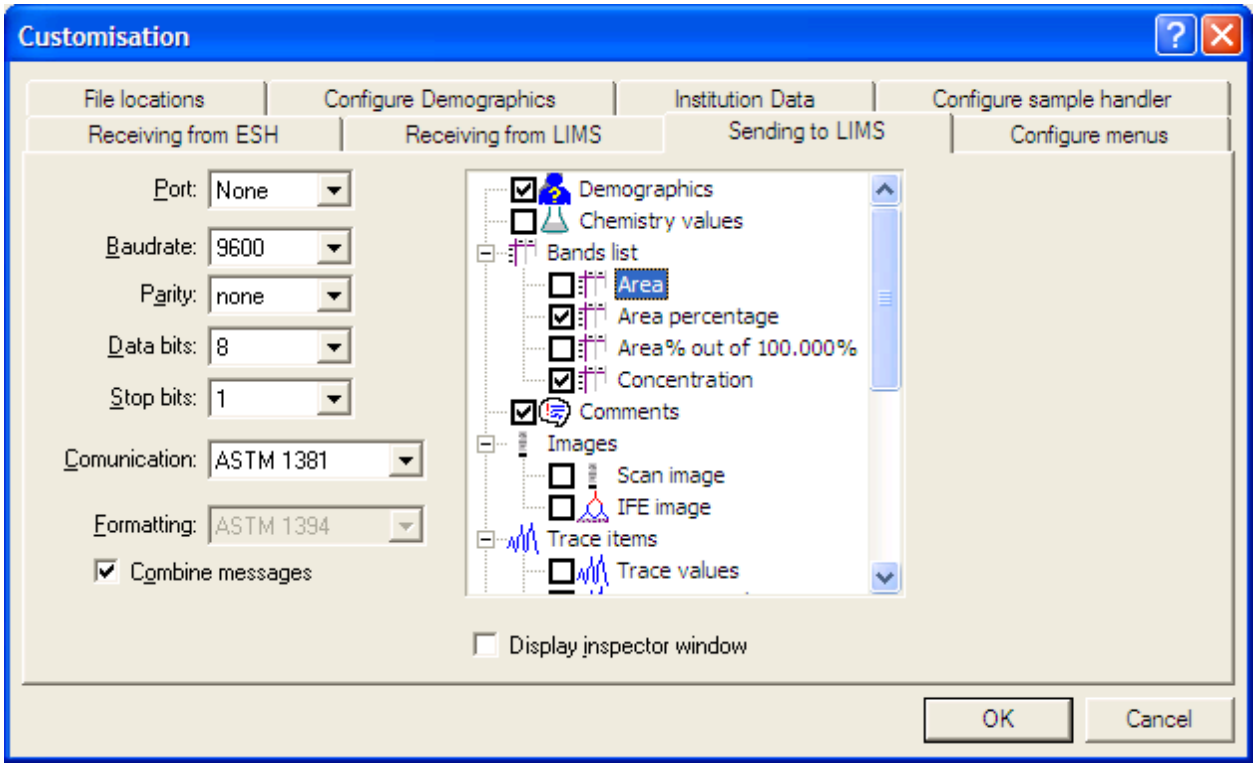
The software has the ability to send an automated query upon generation of a entry in the navigation worklist. This is activated by mean of the tick box “Automatically query LIMS in the Receiving from LIMS tab of File | Customise.

Institution Data Tab

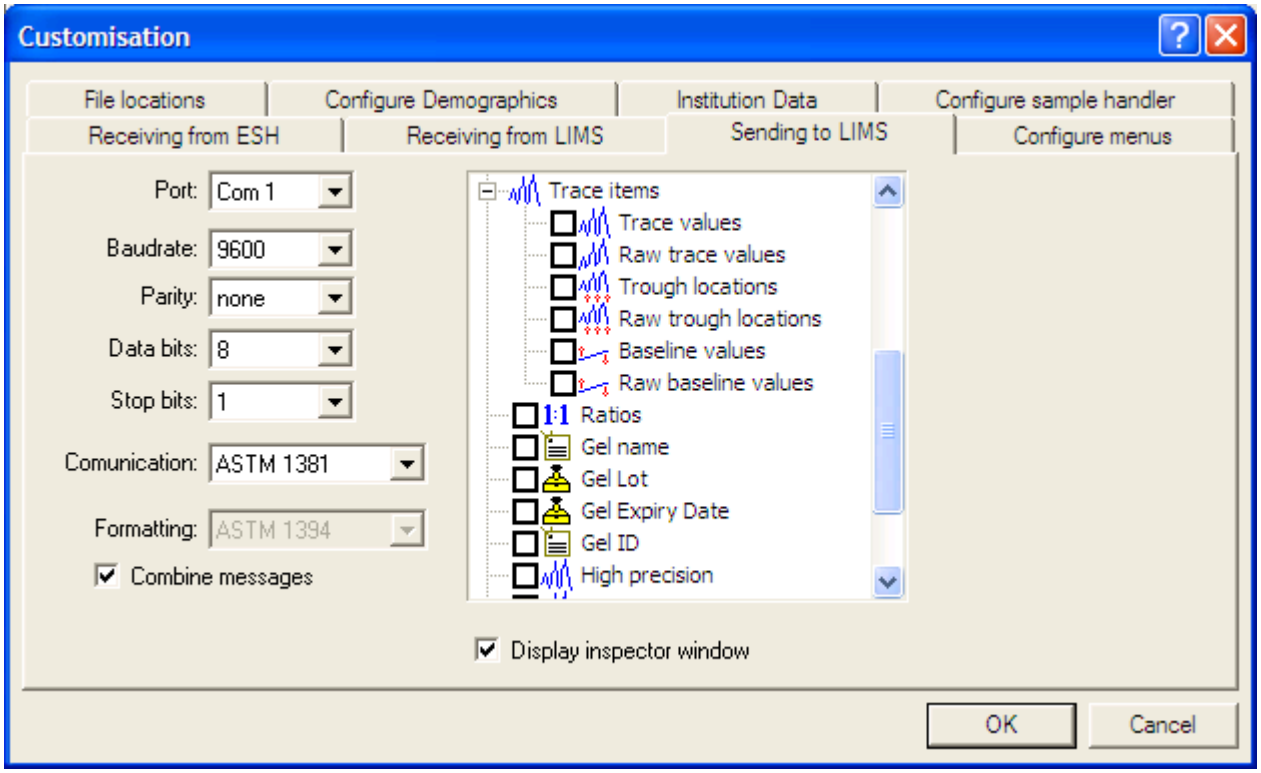
File | Customise | Institution Data



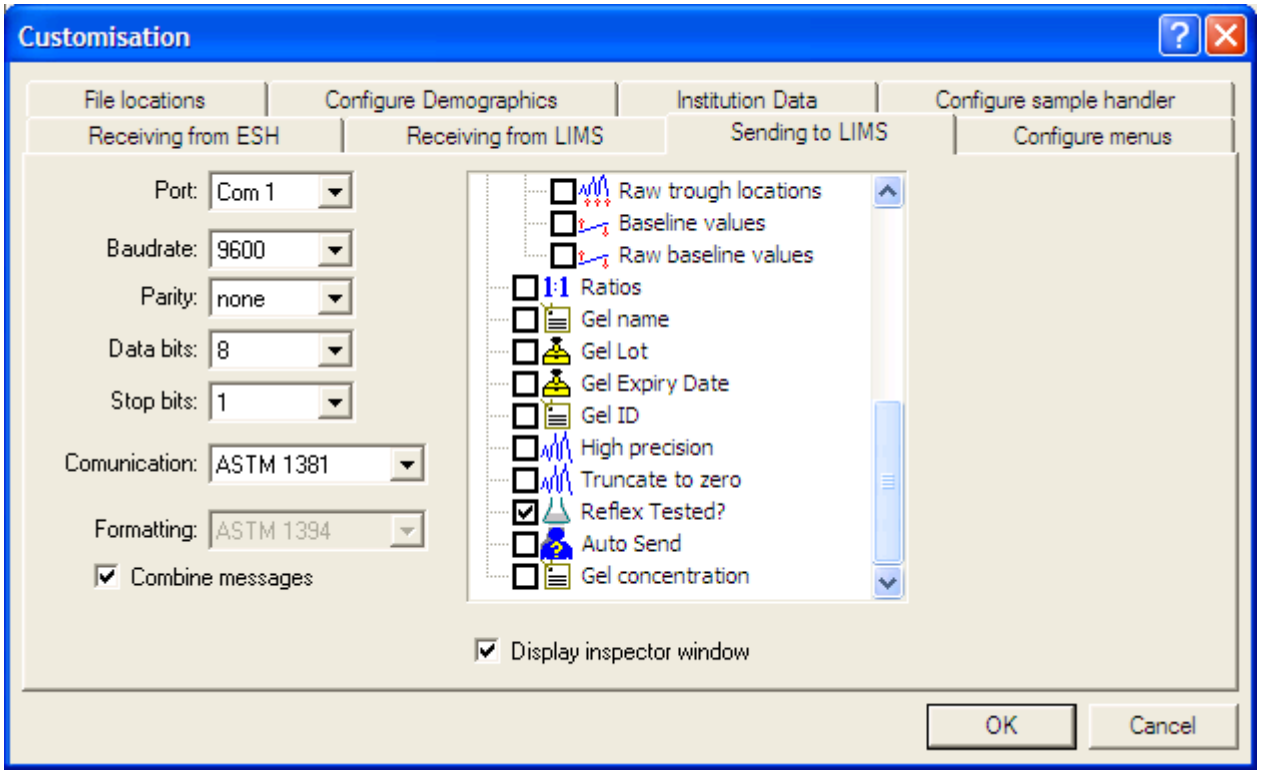
File | Customise | Sending to LIMS (Part 1)



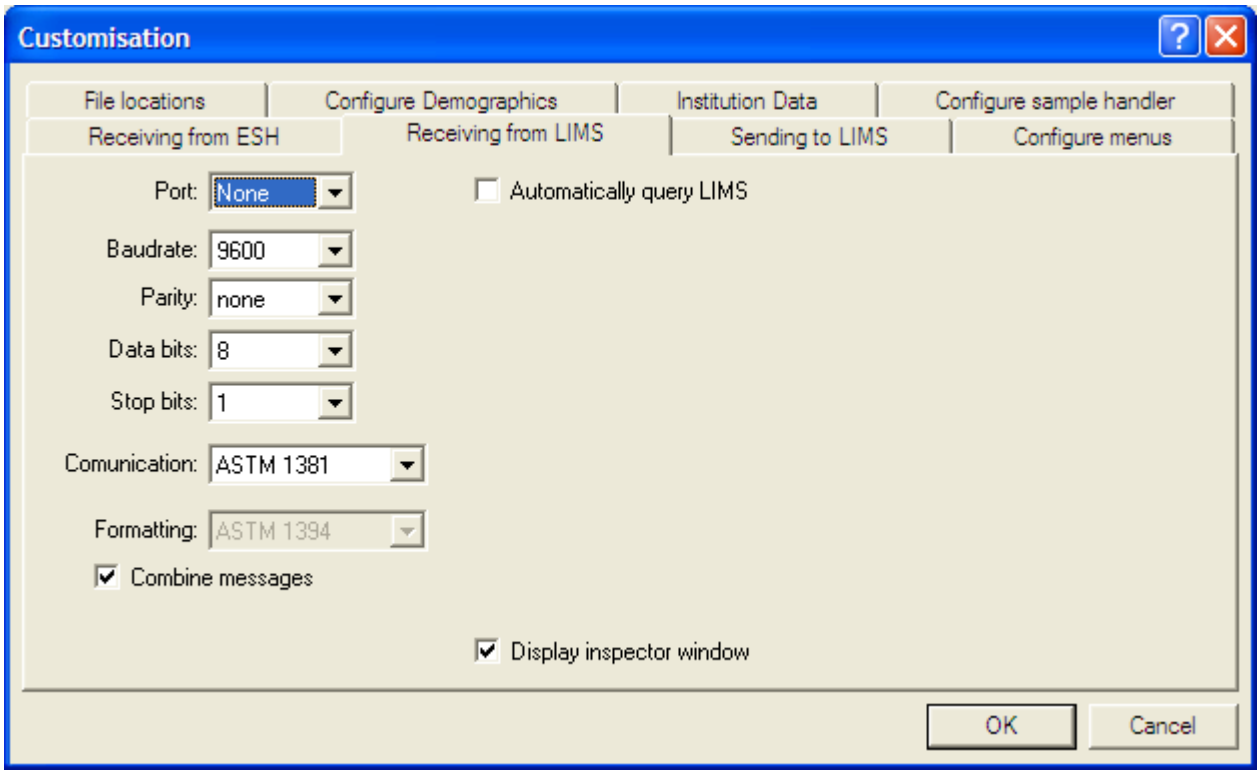
File | Customise | Sending to LIMS (Part 2)



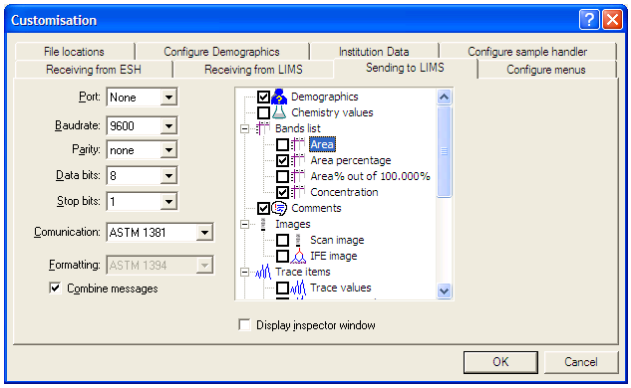
File | Customise | Sending to LIMS (Part 3)

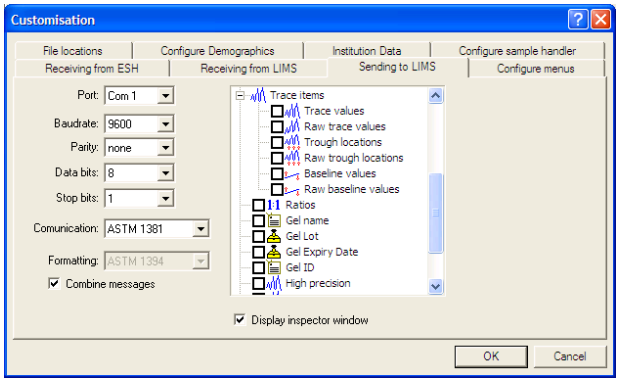


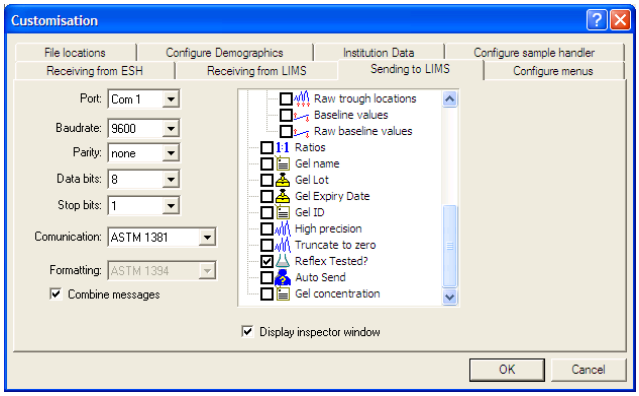
File | Customise | Receiving from LIMS



Sending to LIMS options for Platinum4V are:







Port	Com port the LIMS is connected to the Platinum PC via. (Available: Com1 - Com4).
Baudrate	Transmission rate (Available: 110, 300, 600, 1200, 2400, 4800, 9600, 19200, 38400, 57600, 115200).
Parity	Available: none, odd, even.
Data Bits	Available: 7, 8.
Stop Bits	Available: 1, 2.
Communication	Communication standard applied to the data (Available: No protocol, Xon Xoff, ASTM 1381)
Formatting	Unchangeable from ASTM 1394
Combine Messages	Reduces the amount of data sent by not repeating header messages.
Display Inspector Window	Displays window to show data transfer.
Demographics	As defined by user (one unique demographic must be selected as LIS identifier).
Chemistry Values	Total protein & External chemistry values to be sent to LIMS, only required if not received from LIMS.
Bands List: Area	Integral area of each band.
Bands List: Area percentage	Area % of each band (may be greater or less than 100% due to rounding error).
Bands List: Area % out of 100.00%	Area % of each band (must be exactly 100% any error or m-spike taken from Albumin). *(Only used when an LIS system cannot accept a value that is greater / less than 100%).* ***(Only Area percentage OR area% out of 100.000% should be used, not both).***
Bands List: Concentration	Band concentration in user defined units.
Comments	Any text comments relating to the sample.
Images: Scan Image	Hexadecimal coding of scan image for reconstruction by LIMS.
Images: IFE Image	Hexadecimal coding of IFE image for reconstruction by LIMS.
Trace Items: Trace Values	Copy of trace seen on screen: Y-axis coordinate for each x-axis point of the trace, with X-axis correction applied. The baseline values are pre-subtracted.
Trace Items: Raw Trace Values	Y-axis coordinate for each x-axis point of the trace, without X-axis correction. The baseline values are not pre-subtracted.
Trace Items: Trough Locations	Trough location markers for curve reconstruction with X-axis correction applied. These should be used in tandem with Trace Values.
Trace Items: Raw Trough Locations	Trough location markers for curve reconstruction without the X-axis correction applied. These should be used in tandem with Raw trace values.

Trace Items: Baseline Values	Baseline position measurements for curve reconstruction with X-axis correction applied. These values are not routinely transmitted as they are already subtracted from the trace values.
Trace Items: Raw Baseline Values	Baseline position measurements for curve reconstruction without X-axis correction applied.
Ratios	User defined ratio value e.g. Albumin to Globulin.
Gel Name	Gel Name.
Gel Lot	Lot number of gel input at point of scanning.
Gel Expiry Date	The expiry date of the gel.
Gel ID	Gel ID.
High Precision	When selected (as default) sends values to 8 decimal places. When unselected sends values to 4 decimal places.
Truncate To Zero	Ensures no negative x-axis values for trough locations are sent to the LIMS.
Reflex Tested?	Displays whether sample has been reflex tested – **In order to send this to the LIMS, the comment field must be selected.**
Autosend	Automatic sending to LIMS after a rack has completed data collection.
Gel Concentration	Concentration for gel IFE methods for trays prepared onboard the V8 **– In order to send this to the LIMS, the comment field must be selected.**