

PLATINUM 

helena
Biosciences Europe

Gel Analysis Software
Operator Manual

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Comments or correspondence regarding this manual should be addressed to the manufacturer:

Helena Biosciences Europe
Queensway South, Team Valley Trading Estate, Gateshead,
Tyne and Wear, NE11 0SD
United Kingdom

Tel: +44 (0)191 482 8440
www.helena-biosciences.com
info@helena-biosciences.com



Advena Ltd.
Tower Business Centre,
2nd Flr., Tower Street,
Swatar, BKR 4013 Malta



Licence Agreement Revision History

A copy of the Platinum Gel Analysis Software licence agreement can be found in the following location after installation.

C:\ProgramFiles\Platinum\PlatinumLicense.pdf

Revision History

Amended section:	Date:	Comments:
First Issue	18 Jul 2025	Initial Publication

Acronyms

CV	Coefficient of Variation
IFE	Immunofixation
LIMS	Laboratory Information Management System
LIS	Laboratory Information System
Pt	Platinum
RTF	Rich Text File
SD	Standard Deviation

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Appendix 1

Toolbar functions in Platinum
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Scanner Compatibility

Please contact Helena Biosciences for validated scanner compatibility.

Installation of Scanner

The scanner should be installed according to the instructions provided by the manufacturer.

Ensure the reflective document mat is removed before use.

Placement of the gel alignment template on the scanner

In order to scan transparently, the included Scanner Alignment Guide (REF: 211800) must be placed on the scanner as per the instructions for use provided with the scanner alignment guide.

The origin (0) location is generally located at right rear of the scanner, where the transparency lid joins the base unit.

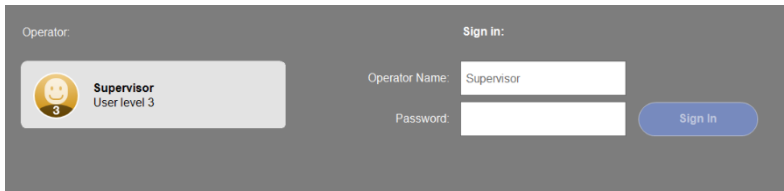
Intended Purpose

Platinum Software is an analytical software package that is used to display, edit and store the result output of numerous clinical kits. Platinum Software can be used as a standalone program or it can be connected to a Helena Clinical Electrophoresis system and/or a laboratory information management system (LIMS). Data imported into Platinum Software can be displayed, peak morphologies assessed and relative area under the curve calculated and thus, provide an operator with qualitative and quantitative information. Results can be stored with patient demographic information in a searchable database. Intended for use by a trained laboratory professional in a clinical laboratory.

1.0 Log in to Platinum

1.1 Initial Log-in Screen

When Platinum is opened, the initial log-in screen will open. A user name and associated password must be entered in order to proceed with using the software.



The initial log-in screen features a dark gray background. On the left, under the label "Operator:", there is a user selection card for "Supervisor" (User level 3) with a yellow smiley face icon and the number 3. On the right, under the label "Sign in:", there are input fields for "Operator Name:" (containing "Supervisor") and "Password:". A blue "Sign In" button is positioned to the right of the password field.

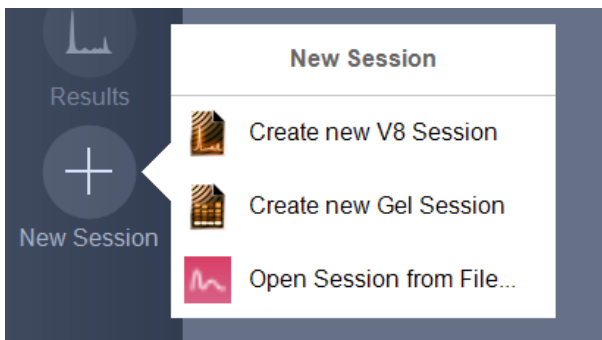
1.2 Initial Window

Once you have logged in, you are given options that will determine the main action of the session:

- You can open a new Gel Session



- Or, open a saved file



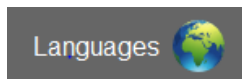
NOTE: 'Create a new V8 session' will only be visible to V8 users

2.0 Platinum Initial Setup (Part 1)

The following settings must be configured before first use of the software to ensure correct operation.

2.1 Language

Selecting the Languages heading on the initial log-in screen page provides a drop down list of available languages.



To select an alternative language click on the language name. A window will appear informing you that the language selected will apply after the software is restarted. Clicking Set Language will close the software immediately and the language selected will be applied on reopening.



Use French after restart.

For the newly selected language to be used, Platinum will restart.

Utilisation du Français après redémarrage.

Le logiciel doit être redémarré pour utiliser la nouvelle langue sélectionnée.
Sortir maintenant?

Set Language

Cancel

2.2 Configuration of Demographics

The software allows up to 10 demographic fields (e.g. Tube Barcode, Patient Identification Number, Name, Date of Birth) to be set. This allows any future results to be searched / filtered by any of the fields set. The demographics apply to all methods used and should be only set once during the initial setup of the software. Log into Plainum Software and select **Configure** > **Customise (Communications)** > **Configure Demographics**

If the system is to be linked to a LIS/LIMS system ensure the demographic fields match identically to those used by the LIMS. The field type for each demographic can be selected from the drop-down list as appropriate for each demographic. The field marked as LIS identifier will be the location for the tube barcode. It is of paramount importance that the demographic field used as a LIS identifier, matches identically the field name being used by the LIS.

Select **one** demographic field for “Use when finding similar data” by selecting the check box. This is usually a unique patient identification number which is used for linking the same patient results together.

Database	Sending to LIMS	Receiving from LIMS	Reports	Configure Demographics	Institution Data	Configure sample handler
Demographics:						
Index		Item	Field Type		Use when finding similar data	
1		Tube ID	LIS Identifier		No	
2		NHS Number	String		Yes	
3		Surname	String		No	
4		Forename	String		No	
5		Gender	String		No	
6		Date Of Birth	String		No	
7		Requestor	String		No	
8		Source	String		No	
9		Hospital Number	String		No	
10		Location	String		No	

NOTE: Users shall report patient results under unique identification to ensure they are not misreporting.

Click the **Save** button and save the file under the name demo.dem in the Platinum folder.

If you wish to Load the previously saved demographics, select the **Load** button and choose the required file to open. This will activate the correct demographic fields.

3.0 Platinum Initial Setup (Part 2)

3.1 Chemistry Values

Platinum allows up to 12 different chemistry values (e.g. Total Protein) to be input manually or imported from a LIMS per scan type.

To set the chemistry values for each scan type, select **Configure > Configure Gels (Methods) > Select the Method Type required > Then Select the Chemistry Values tab**.

Method
SAS-3 SP-60 (300100)

Configure Standard Methods	Method type	Chemistry Value	Geometry	Lanes	Bands	Smoothing/Fit
----------------------------	-------------	-----------------	----------	-------	-------	---------------

Total Chemistry Value name :

External compound name :

Concentration unit :

LIMS Name:

Chemistry item	Name	Unit	LIMS Name
Chemistry 1	IgG	g/L	IgG
+			

Enter the Chemistry Name, Unit and the LIMS Name for each chemistry value. These will be saved automatically.

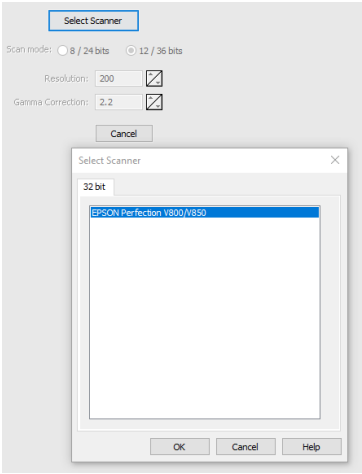
Total Chemistry Value Name will be used to calculate concentrations of bands except when an External Compound Name is entered. All other chemistry values should be input in the chemistry items below.

3.2 Scanner

Once the scanner has been installed, you will be required to select the scanner model. **Select Configure > Scanner Settings (Methods) > Select Scanner.**

Highlight the scanner model.

Note: If two options for the same scanner model are present **do not** select the option ending in WIA.



3.3 Reports

The report template used for each method type must be set prior to scanning the gel. Once a template has been set it will apply to all future scans of that type. To set a report template select, **Configure > Configure Gels (Methods) > Select the Method required > Method Type Tab**

Method

SAS-3 SP.60 (300100)

Configure Standard Methods

Method type

Chemistry Value

Geometry

Lanes

Bands

Smoothing/Filtering

Gain Settings

Lot IDs

Barcode

Controls

Carbamylated Albumin

Analysis Type: serum protein

Tray type:

Measurement type

☒ Normal

☐ Immunotyping

☐ SP-ID (combination)

Gel scanning mode

☒ Transparent

☐ Reflective (opaque)

☐ Mark abnormal results for reflex testing

Reflex test name:

Default Reflex test name:

Report generation

Report definition : C:\Program Files\Platinum\Reports\SAS Serum Protein.rep

Report with IDs :

Use main reports

Do not report

Low Signal Detection

☐ Enabled

Y Threshold: 0

At the bottom of the window is a section titled Report Generation. Select the button marked ... at the end of the Report definition box. This will open a window allowing you to select an appropriate report template. Once selected the report can be edited by selecting the Edit button.

3.4 Normal Patient Ranges

Platinum allows entry of a normal range for patient samples for quantitative methods. To enter these values select **Configure > Configure Gels (Methods) > Select the Method required > Bands Tab**

The normal range can be entered in either % or a concentration unit (as defined by the unit for total protein in the chemistry value setup).

NOTE: Values entered as % must be suffixed with a % symbol.

Method

SAS-3 SP-60 (300100)

Configure Standard Methods	Method type	Chemistry Value	Geometry	Lanes	Bands	Smoothing/Filtering	Gain Settings	Lot IDs	Barcode	Controls	Carbamylated Albumin																																																						
<div> <input type="radio"/> Recognise Bands by Tops <input type="checkbox"/> Forced Fraction Mode </div> <div> <input checked="" type="radio"/> Fixed Fraction Mode </div> <div> <input type="checkbox"/> Tight Right Albumin </div> <div> <input type="checkbox"/> Use coordinate ranges </div> <div> <input type="checkbox"/> Second Pass Peak Detection </div> <div> <input type="checkbox"/> Alpha Right Shoulder Remove </div> <div> <input type="checkbox"/> Migration Warning </div> <div> <input type="checkbox"/> Closer Ends </div> <div> <input type="checkbox"/> Min Peak Relative Area </div> <div> <input type="button" value="Ratio Setup..."/> </div> <div> Gradient Limit : 0.000 <input checked="" type="checkbox"/> </div> <div> Over seconds : 0.0 <input checked="" type="checkbox"/> </div> <div> 0.000 </div> <div> Expressions... </div> <div> Bands : </div> <table border="1"> <thead> <tr> <th>Band</th> <th>Component</th> <th>Low area limit</th> <th>Upper area limit</th> <th>Include in total area</th> <th>Combine with previous/next</th> <th>Opt...</th> <th>Limit ...</th> <th>Col...</th> </tr> </thead> <tbody> <tr> <td>1</td> <td>Albumin</td> <td>0.00</td> <td>0.00</td> <td>*</td> <td>Do not combine</td> <td></td> <td></td> <td></td> </tr> <tr> <td>2</td> <td>Alpha 1</td> <td>0.00</td> <td>0.00</td> <td>*</td> <td>Do not combine</td> <td></td> <td></td> <td></td> </tr> <tr> <td>3</td> <td>Alpha 2</td> <td>0.00</td> <td>0.00</td> <td>*</td> <td>Do not combine</td> <td></td> <td></td> <td></td> </tr> <tr> <td>4</td> <td>Beta</td> <td>0.00</td> <td>0.00</td> <td>*</td> <td>Do not combine</td> <td></td> <td></td> <td></td> </tr> <tr> <td>5</td> <td>Gamma</td> <td>0.00</td> <td>0.00</td> <td>*</td> <td>Do not combine</td> <td></td> <td></td> <td></td> </tr> </tbody> </table>												Band	Component	Low area limit	Upper area limit	Include in total area	Combine with previous/next	Opt...	Limit ...	Col...	1	Albumin	0.00	0.00	*	Do not combine				2	Alpha 1	0.00	0.00	*	Do not combine				3	Alpha 2	0.00	0.00	*	Do not combine				4	Beta	0.00	0.00	*	Do not combine				5	Gamma	0.00	0.00	*	Do not combine			
Band	Component	Low area limit	Upper area limit	Include in total area	Combine with previous/next	Opt...	Limit ...	Col...																																																									
1	Albumin	0.00	0.00	*	Do not combine																																																												
2	Alpha 1	0.00	0.00	*	Do not combine																																																												
3	Alpha 2	0.00	0.00	*	Do not combine																																																												
4	Beta	0.00	0.00	*	Do not combine																																																												
5	Gamma	0.00	0.00	*	Do not combine																																																												

3.5 Control Ranges / Levey-Jennings

Platinum allows entry of ranges for both normal and abnormal control samples. On initial set up of a method, control ranges should be entered by [Configure > Configure Gels \(Methods\) > Select the Method required > Lot IDs Tab.](#)

Method
SAS-3 SP-60 (300100)

Configure Standard MethodsMethod typeChemistry ValueGeometryLanesBandsSmoothing/FilteringGain SettingsLot IdsBarcodeControlsCarbamylated AlbuminRegions/Zones

Barcode entry :

Method Code :

Normal lot ID :

Expiry Date (MM/YYYY) :

Normal Control Total Protein (g/L)

Abnormal lot ID :

Expiry Date (MM/YYYY) :

Abnormal Control Total Protein (g/L)

Band statistics :

B...	Component	Low normal (%)	Upper nor...	Low abnormal...	Upper abnorm...	Mean normal	SD normal	Mean abnor...	SD abn...
1	Albumin								
2	Alpha 1								
3	Alpha 2								
4	Beta								
5	Gamma								
6	M-spike 1								

- To populate the Lot ID page using the barcode on the assay data sheet, click in the Barcode Entry field and scan the barcode using the handheld barcode scanner. This process should be completed for each control.
- To manually populate the Lot ID page:
 - Input the lot numbers from the assay data sheet into the Normal Lot ID and Abnormal Lot ID fields.
 - Input the expiry from the assay data sheet into the Expiry Date fields in the format MM/YYYY.
 - Select the Edit Lot % button to allow data entry for the bands:

Ranges should be entered in as the percentage values shown on the assay data sheet. If concentration is to be applied rather than percentage, input the corresponding value in the Normal Control Total Protein and Abnormal Control Total Protein from the assay data sheet and configure Chemistry Values tab for the control method to include the Total Protein (as per section 3.1).

Normal control ranges should be entered in the column **Low normal / Upper normal**.

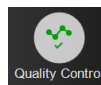
Abnormal Control range should be entered in the column **Low abnormal / Upper abnormal**.

If Levey Jennings analysis is required, then the Mean and Standard Deviation (SD) should be entered in to the **mean normal / abnormal and SD normal / abnormal columns**. These values can only be entered as % and do not require the suffix with a % symbol.

Reselecting the **Edit Lot %** button will lock the entered range.

NOTE: The above data must be entered before scanning a gel. This information cannot be added retrospectively.

NOTE: After initial set up, the control ranges can be updated using the Quality Control Tab in Platinum.



3.6 Default Control Position

Platinum allows a dedicated position on each row to be always automatically marked as a normal or abnormal control. To activate this function select the type of control and the standard lane position in which it will be run through **Configure > Configure Gels (Methods) > Select the Method required > Controls Tab**.

Method

SAS-3 SP-60 (300100)

Configure Standard Methods

Method type

Chemistry Value

Geometry

Lanes

Bands

Smoothing/Filtering

Gain Settings

Lot IDs

Barcode

Controls

Default control

☐ Not used

☒ Normal control

☐ Abnormal contrc

Position:

1

☐ Not used

☐ Normal control

☒ Abnormal contrc

Position:

2

3.7 Display Preferences

The display preferences can be customised by selecting **Configure > Preferences (Appearance) > Bands Tab**.

The options relate to the quantitative data which can be selected to be displayed.

View preferences

Axis Setup Axes Labelling **Bands** Haemoglobin COT Grid N

Peak columns

☐ Peak integral value

☒ Relative Area ☐ 0 ☐ 1 ☒ 2 decimals

☒ Concentration ☐ 0 ☐ 1 ☒ 2 decimals

☒ Concentration range

☐ Top coordinate

☐ Zones / regions

☐ List remaining M-spike values

☒ Statistics

Statistics columns

☒ Area

☒ Relative Area

☒ Concentration

3.8 Report Display

The information visible on hard copy print outs of reports can be selected using the tick boxes in the reports window. To configure the report display select [Configure > Preferences \(Appearance\) > Reports Tab](#).

The screenshot shows the 'View preferences' dialog box with the 'Reports' tab selected. The dialog has a title bar 'View preferences' and a tabbed interface with tabs: 'Area Setup', 'Area Labeling', 'Bands', 'Hemoglobin', 'COT', 'Grid', 'Marker Colours', 'Navigation Work List', and 'Reports'. The 'Reports' tab is active, showing a list of checkboxes for report content. Under 'Multi-Band Columns', the following are checked: Method, Area, Relative Area, Concentration, Band ranges, Tube ID, HC Number, Surname, Forename, Gender, TCV, ECV, Chemistry, and Flagged. Under 'Print to PDF additional support', the PDF directory is set to 'C:\Program Files\Platinum\PDF\'. The 'Automatic Filenaming' checkbox is unchecked, and the 'Tube ID' dropdown is set to 'Tube ID'.


View preferences

Area Setup | Area Labeling | Bands | Hemoglobin | COT | Grid | Marker Colours | Navigation Work List | **Reports**

Multi-Band Columns

- ☒ Method
- ☒ Area
- ☒ Relative Area
- ☒ Concentration
- ☒ Band ranges
- ☒ Tube ID
- ☒ HC Number
- ☒ Surname
- ☒ Forename
- ☒ Gender
- ☐ Date Of Birth
- ☐ Requestor
- ☐ Source
- ☐ Hospital Number
- ☐ TCV
- ☐ ECV
- ☐ Chemistry
- ☒ Tray Position
- ☒ Flagged

Print to PDF additional support

PDF directory : 

☐ Automatic Filenaming

3.9 Operator Levels

Platinum has 3 different operator levels. The Platinum permissions for each user level can be configured through the Operator Access tab by a Level 3 operator only. Setting a check slider to off disables that functionality for a user of that level. To configure the user access, go to [Configure > Operator Access \(Appearance\)](#).

Configure User Access			
	Level 1	Level 2	Level 3
General Functions			
Allow Export	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Allow Trace Visibility	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Allow Usage Logs	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Allow Container Verification	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Printing Functions			
Allow Printing	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Allow Print To Printer	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Allow Print to PDF	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Trace Options			
Allow Trace Editing	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Allow Trace Bands	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Allow Trace Comparisons	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Configure			
Allow Configure	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Allow Configure V8 Systems	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Allow Configure Hardware Calibration	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

NOTE: When logging into Platinum for the first time, the Level 3 operator will be assigned a password set by Helena Biosciences. Please refer to your local distributor/sales representative for further information

3.10 Adding New User

Only users with level 3 (supervisor access) can add a new user.

Operator List						
<div> <div> Operator Entry Login name : <input type="text"/> Full name : <input type="text"/> Date of birth (dd/MM/yyyy) : <input type="text"/> User ID : <input type="text"/> Password : <input type="password"/> User level : <input type="text"/> <input type="button" value="Add User"/> </div> <div> Password requirements Expires in (days) : <input type="text"/> <input type="button" value="v"/> Minimum length : <input type="text"/> <input type="button" value="v"/> <input type="checkbox"/> Must contain letters and numbers </div> </div>						
Login name	Full name	User level	Date of birth	User ID	Password expires	
Supervisor		3			16/02/2999	

- Choose **Configure (Logs and Access) > Manage Operator Accounts**.
- In the dialogue boxes enter the required information according to the field. The criteria of the password, such as minimum length, expiry and format, can be assigned here for added security. (Minimum data required: Login name: Password, User Level).
- After filling in the required fields, choose **Add User**.

3.11 Configuration of Visible Scan Settings

Platinum allows the user to show or hide the types of gels that it is possible to scan to simplify the scanning process. To display only those gels used, select **Configure > Configure Gels (Methods) > Configure Standard Methods Tab**.

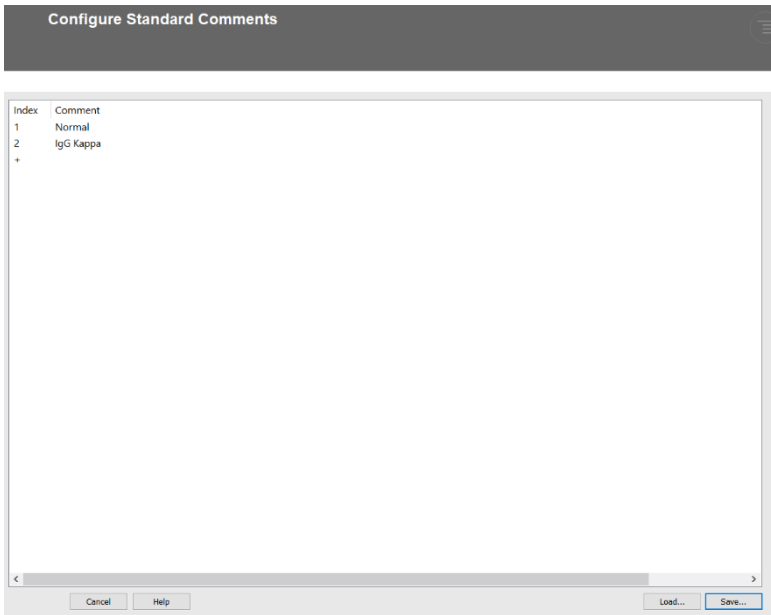
In the usage column next to the gel scan Name select **Hide** to remove this from view or **Main and Reflex** to enable the name to be seen and the method to be scanned.

Method		
SAS-3 SP-60 (300100)		

Configure Standard Methods	Method type	Chemistry Value	Geometry	Lanes	Bands	Smoothing/Filtering
Standard Methods:						
Method	Usage	Name				
1	Main and reflex	SAS-3 SP-60 (300100)				
2	Main and reflex	SAS-3 SP-60 SB (300200)				
3	Main and reflex	SAS-3 IFE-9 (300300) - Serum				
4	Hide	SAS-3 IFE-9 (300300) - Urine				
5	Main and reflex	SAS-3 Urine Analysis (300400)				
6	Hide	SAS-3 Pentavalent Screen 60 (300406)				

3.12 Comments

Platinum allows user pre-configured text comments to be stored within the system. To add comments to the list, select [Configure > Comments \(Reporting\)](#)



Appropriate text can then be entered into the column marked comment. Once complete click Save.

Save the file as `comments.cmt` and if prompted to replace existing file choose [Yes](#).

3.13 Data Backup Location

To allow for a manual backup of the database, a backup location must be defined. To define the location select **Configure > Customise (Communications) > Database > Location for backups** > and select the button ...

Identify the location for the backup within File Explorer.

The screenshot shows the 'Customise' configuration window with the 'Database' tab selected. The 'Location for backups' field is highlighted, showing the path 'C:\Program Files\Platinum\Backups\'. The 'Network Database' checkbox is unchecked. The 'Use old session names' and 'Use V8 name' checkboxes are also unchecked.

Customise

Database | Sending to LIMS | Receiving from LIMS | Reports | Configure Demographics | Institution Data | Configure sample handler

Data

Network Database : ☐

Network Database Location :

Location for new data : ...

Location for backups : ...

Use old session names : ☐

Use V8 name : ☐

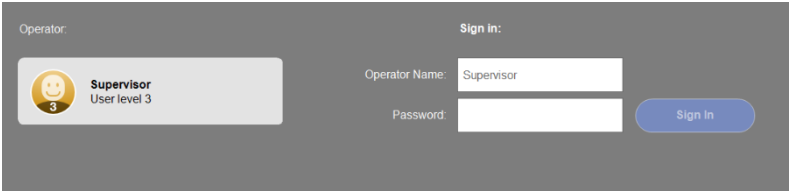
4.0 Quick Start

4.1 How to Scan an Agarose Gel

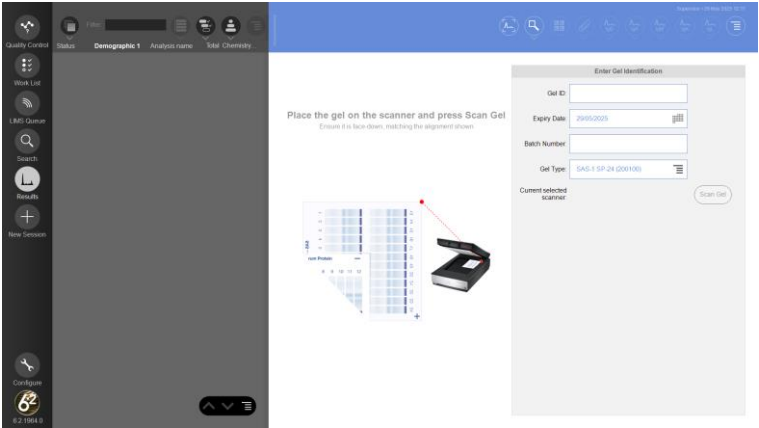
This guide provides a short introduction into the basics of scanning a Helena agarose gel using Platinum Software.

Open the Platinum Software by double clicking the icon on the desktop.

Log into the software using the appropriate username and password.




The Home screen will appear.




Enter the gel identification details on the right hand side of the screen

Enter Gel Identification

Gel ID:

Expiry Date: 

Batch Number:


Gel Type: 

Current selected scanner: Scan Gel


Select the gel type you wish to scan by clicking on the drop down menu for **Gel Type**.

Enter Gel Identification

Gel ID:

Expiry Date: 

Batch Number:

Gel Type: 

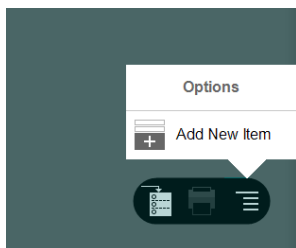
Current selected scanner:

Options

- SAS-3 SP-60 (300100)
- SAS-3 SP-60 SB (300200)
- SAS-3 IFE-9 (300300) - Serum
- SAS-3 Urine Analysis (300400)
- SAS-1 SP-24 (200100)
- SAS-1 SP-24 SB (200200)
- SAS-1 IFE-4 (200300) - Serum
- SAS-1 IFE-4 (200300) - Urine
- SAS-1 Alk Hb (200900)
- SAS-1 Acid Hb (201000)

Select the type of gel you are running from the list. If you wish to enter the patient sample barcodes and demographic information prior to scanning, select the **Worklist** icon on the far left of the screen.

In the worklist window select the **Add New Item** button until the required number of lines are visible for the number of sample positions used.



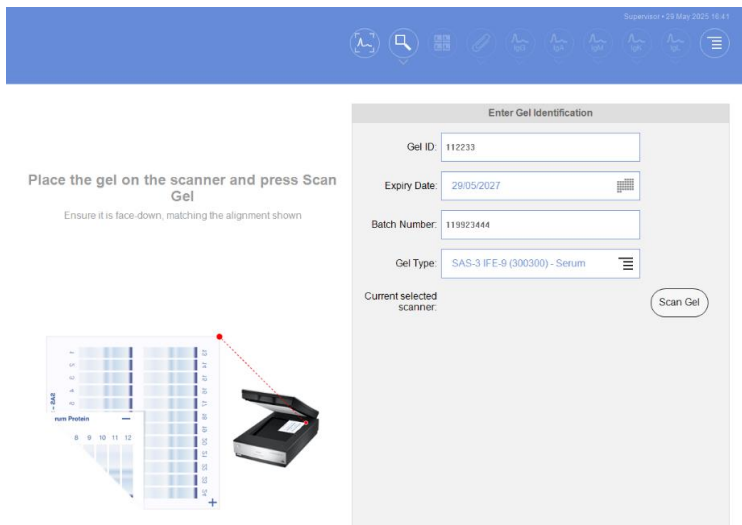
The required data can now be added to the worklist for increased traceability.

NOTE: The worklist can be completed before or after scanning of the gel.

A screenshot of a web form titled 'Enter Gel Identification'. The form has a light grey background. It contains four input fields: 'Gel ID:' with the value '112233', 'Expiry Date:' with the value '29/05/2027' and a calendar icon, 'Batch Number:' with the value '119923444', and 'Gel Type:' with the value 'SAS-3 IFE-9 (300300) - Serum' and a list icon. Below these fields, there is a label 'Current selected scanner:' and a button labeled 'Scan Gel'.

On the gel scan home page there are instructions informing to place the gel face-down on the scanner.

Close the scanner lid and click **Scan Gel**



The gel scan will begin and progress will be shown on screen. Once scanning is complete the gel image will be visible on screen.

4.2 Aligning a Gel Template

Platinum automatically applies a template to gel images. It represents the areas of the gel from which the scan data will be analysed and saved. These are pre-set in the gel-type method configuration and correspond to the particular gel size and sample number. These templates may, however, require slight adjustments to account for slight individual variations.

Aligning a Gel

If after scanning a gel it is found that the template requires adjustment then this is done by selecting the **Align gel** icon.

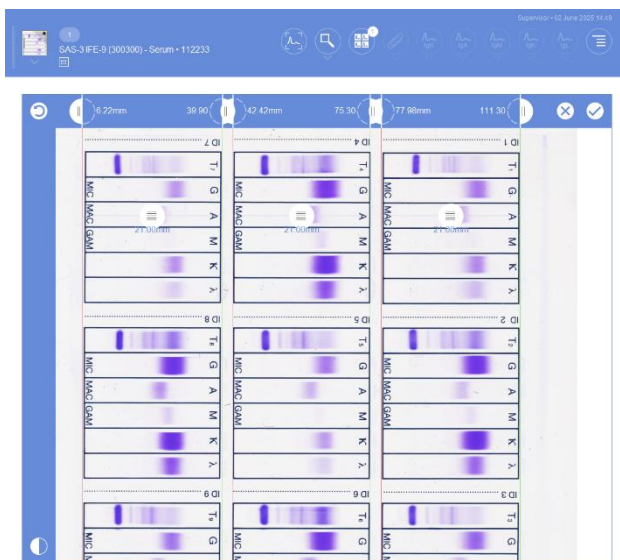




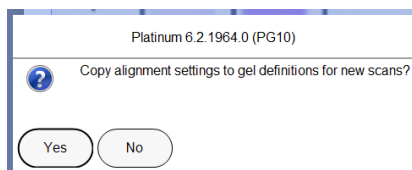
Two vertical markers represent the left-hand (red) and right-hand (green) limits of each row and a single (blue) horizontal marker indicates the centre position of the first sample in each row – with the exception of IFE gels as described below.

Each marker can be positioned either by clicking and dragging with the cursor, or by altering the values that are displayed in the table. These values are in mm, and indicate the distance of the marker from the appropriate axis.

For IFE gels, the blue horizontal line should be positioned through the centre of the **A** on ID1, ID4 and ID7 (top row seen on screen). The green line should be positioned on the top of each ID and the red line on the bottom.



To verify the position of the new template, select the tick icon on the top, right hand side of the screen. The following message will appear:



Selecting **Yes** will save the alignment settings for subsequent gels.

N.B. Result reporting should always be carried out directly from the original gel. The gel is scanned into Platinum only as a record of the result.

4.3 Configure Gels

In Platinum, it maybe necessary to configure the templates that are used in processing samples. These templates are used to specify what the limits for each protein fraction are, default smoothing and filtering levels, and other factors that are interchangeable. This function is only available at Level 3 user access. Please refer to your Helena Biosciences Europe representative for more information.

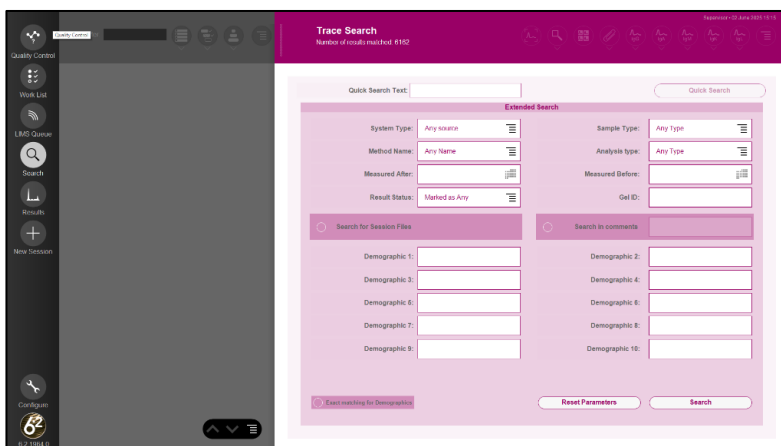
5.0 Common User Functions

5.1 Searching for Data

To locate previous sample results or whole gels in the database, the search tool can be used. Select the Search Icon.



The search page will appear:



To search for individual samples, search in the **Quick Search Text** box, or to search for an entire gel scan search in the **Gel ID** box.

When searching for individual sample results, any of the 10 demographic fields can be used to identify the sample and filter the results. There is an option for selecting **Exact matching for Demographics**.

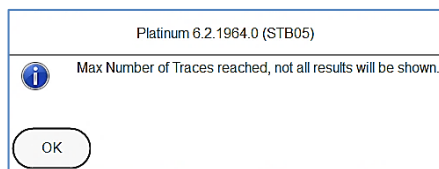
When **Search for Session Files** is selected the demographics are greyed out.

Other search filters include:


- System Type
- Sample Type (Any, Sample, Normal Control, Abnormal Control, Calibrators)
- Method Name (e.g., SAS-1 IFE-4 (200300) – serum)
- Analysis Type (e.g., Serum Protein, IFE)
- Measured Before or Measured After (date)
- Result Status (Marked as Any, Normal, Abnormal, Unsure)
- Search in Comments

By inputting any required demographic filters i.e. patient ID, or other search terms and clicking the **Search** button, a list of search results will appear.

A maximum of 1000 traces can be shown at one time – if more than this is found a dialogue box will appear:



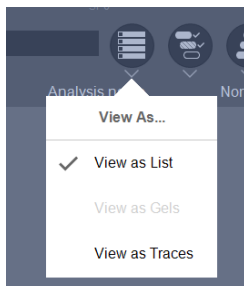
Search results can be filtered in the top left hand corner of the screen.

Once the search results are displayed, basic viewing functions can be carried out. The original session file can be loaded by selecting the **Load Source Data** icon 

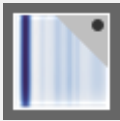

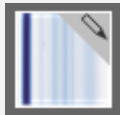
This provides an option to load the original gel to enable more detailed sample editing. Any editing can only be carried out on the original data file.

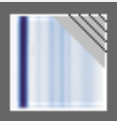
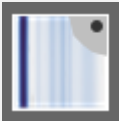
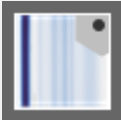



5.2 Editing

When a trace or gel image is first displayed, it is likely that the data will require some form of adjustment so that the correct interpretation of the result(s) can be reported. Every sample trace can therefore be edited to user preferences. To edit a trace, click on the **View as...** button and select **View as List**.






Samples are displayed in the navigation work list and are assigned specific icons to visually show the user the status:

Icon	Editing Status
	The result has been viewed.
	Lane is unedited and may have an unexpected number of peaks/bands or values are out of range.
	Lane has been viewed and edited.

	Result has been hidden from the navigation worklist but 'Show Hidden' has been enabled
	The result has been marked as a Normal Control.
	The result has been marked as an Abnormal Control.
	The result has been marked as 'Normal' by the user.
	The result has been marked as 'Abnormal' by the user.
	The result has been marked as 'Unsure' by the user.

5.2.1 Editing the Baseline

Should it be required to edit the baseline, click the Edit  icon then the Baseline icon . This will allow manual movement of the baseline.


Selecting the  icon on the trace will allow movement of the baseline. Holding down the mouse while moving the baseline allows movement in a horizontal plane up and down.

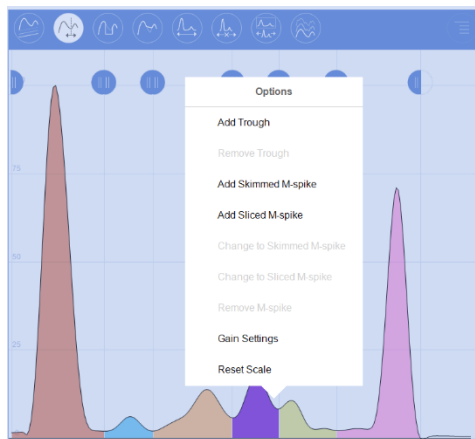


Right clicking over the trace allows the option of adding or deleting a spline node from the baseline.



5.2.2 Editing Peaks

Once a trace is selected, the fractions may be edited by clicking the Edit Peaks icon . Right clicking over a peak on the trace provides specific options that are possible for the selected peak.




Add a Trough Marker

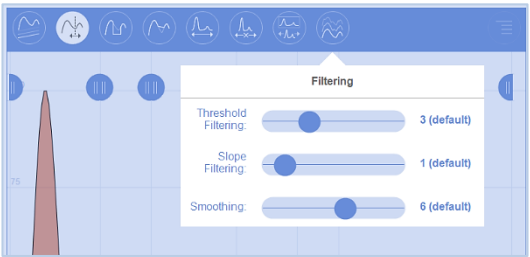
To add an additional trough marker to a trace, move the mouse to the desired location for the marker and right click. Choose **Add trough** from the Options menu, the marker will be placed on the trace. Any further movement can be made by dragging the marker to the correct location within the fraction. (A double arrow will appear when hovering over the trough marker).

Delete a Trough Marker

To delete a surplus trough marker, move the mouse over the surplus marker (a double arrow will appear) and right click. Now choose **Remove Trough** from the drop down menu; the marker will then be removed from the trace.


5.2.3 Smoothing and Filtering

To filter a trace, click the Filter icon  and choose either the option of threshold filtering or slope. The Smoothing option is also available in this menu



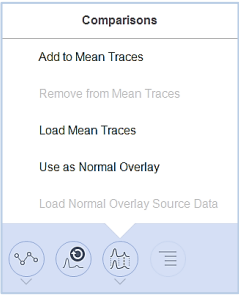
5.3 Overlay Functionality

The overlay function enables comparison of a sample trace against a previously specified 'norm' or against another sample. For the Overlay function select the

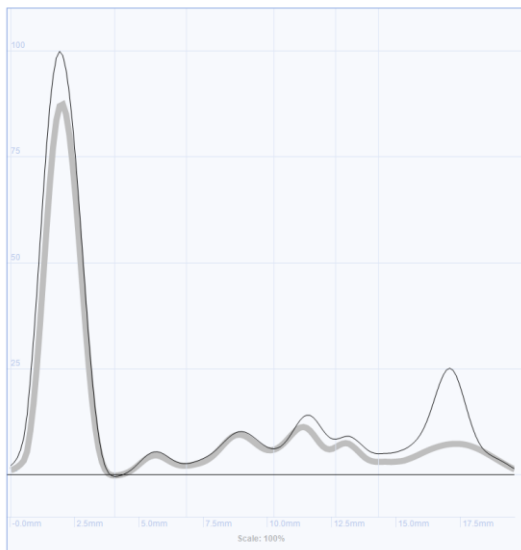
Comparisons icon: 

5.3.1 Normal Overlay

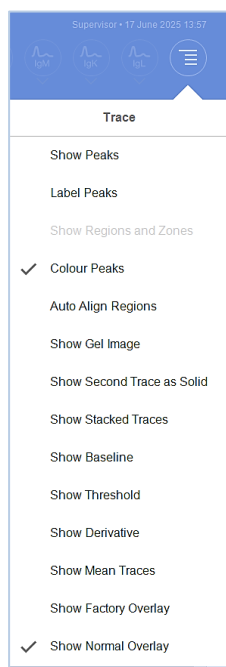
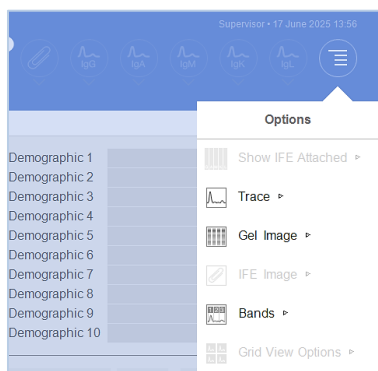
The normal trace is defined by the user, depending on specified laboratory boundary reference ranges. A specific trace can be set as the default normal overlay by clicking on the **Comparisons** icon then selecting **Use as Normal Overlay**.



The defined trace will then be shown in grey whilst the trace being viewed is shown in black:



To switch the normal overlay on/off, go to the top right corner of the screen and select **Options > Trace** and select “**show normal overlay**”.



5.3.2 Overlaying of Sample Traces on Screen

Holding the **SHIFT** key while selecting a second sample trace will also select all samples between the original and the newly selected sample, allowing overlay of the samples.

Holding the **CTRL** key while selecting a second sample will only select the two samples (the original and the newly selected sample), allowing overlay of the two samples. Additional samples can also be selected in the same manner.

5.3.3 Match Shapes

When Overlaying sample traces it may often be necessary to match the overlay from one sample to another. To do this simply highlight two or more traces that you would like to be matched and click the **Edit icon** then select the **Match Shapes** icon



5.3.4 Stretching Samples to Overlay Bands

When overlaying sample traces from different time periods, it may be necessary to stretch a trace to overlay each peak over it's corresponding peak in the second trace.

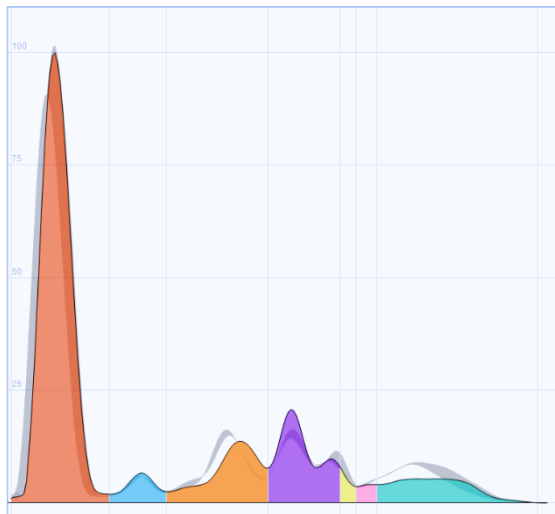
Overlay the required sample traces by holding down the **Ctrl** key whilst selecting from the sample list, select the **Edit icon** then select the **Stretch** icon



Should the sample traces require further manipulation, the trace can be manually stretched by dragging and dropping the three vertical markers which appear on screen.

5.3.5 Mean Traces

Allows a visual range of normal samples to be viewed on screen relative to the currently selected trace.



To add traces to the mean overlay, highlight the sample and select **Comparisons > Add to Mean Traces**.

To view the traces used to compose the mean overlay, select **Comparisons > Load Mean Traces**.

To remove a sample from the Mean Traces, in the screen that shows the list of mean traces, highlight a sample in the list and select **Comparisons > Remove from Mean Traces**.

5.3.6 Trace Regions

Choose the method to be configured in **Configure > Configure Gels (Methods)** and select the **Regions/Zones** tab, enter the Region Names and limits. Suggestions of band(s) that would appear in this region can also be added in the appropriate column.

Method

SAS-3 SP-60 (300100)

Method type

Chemistry Value

Geometry

Lanes

Bands

Smoothing/Filtering

Gain Settings

Lot IDs

Barcode

Controls

Carbamylated Albumin

Regions/Zones

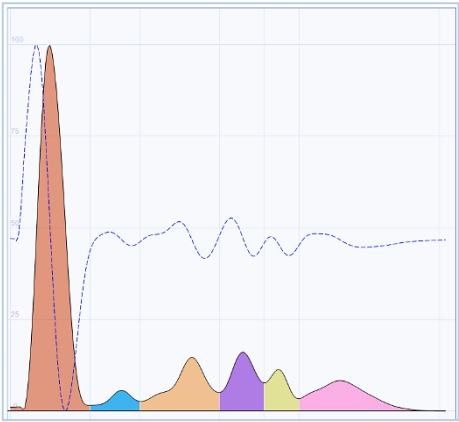
Regions:

Index	Region name	Left limit (%)	Right limit (%)	Colour	Suggestions
1	Albumin	0.0%	0.0%	Red	
2	Alpha-1	0.0%	0.0%	Blue	
3	Alpha-2	0.0%	0.0%	Orange	
4	Beta-1	0.0%	0.0%	Purple	
5	Beta-2	0.0%	0.0%	Yellow	
6	Gamma	0.0%	0.0%	Pink	
+					

5.3.7 First Derivative

Shows the first derivative of the selected trace.

Select **Options > Trace > Show Derivative**. This will show the first derivative of the trace as a dotted line. To remove this, select **Options >Trace > Show Derivative**.



To quantitate a monoclonal protein, it is necessary to isolate the monoclonal band on the trace. There are two possible methods to do this which will give different values of the monoclonal protein: slicing and skimming. If the total protein value of the sample is known and the chemistry value configured (section 3.1), then Platinum will automatically calculate the protein contribution of any marked M-spike.

NOTE: It is recommended that users choose one method or the other, and do not under any circumstances inter-change between methods as this can lead to changes in patient monoclonal quantitation overtime, due to the different methods of measurement used.

5.4.1 Skimmed M-spike

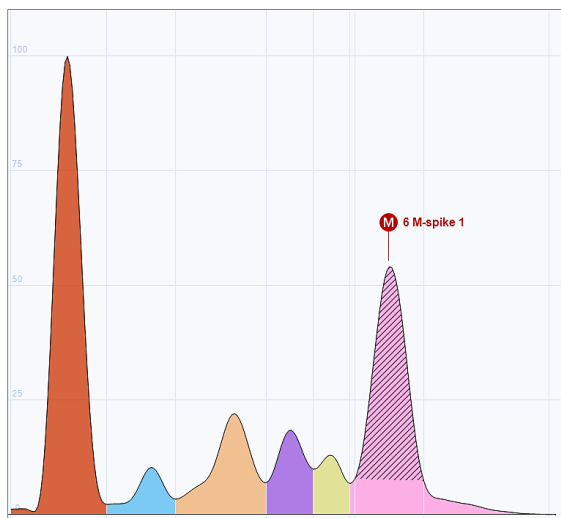
This methodology takes into account the polyclonal background of a sample by allowing the user to estimate the amount of polyclonal background and remove this from the quantitation.

Adding a Skimmed M-spike

Select the **Edit Mode** and **Edit Peaks** icon, then right click on the are of the trace where the monoclonal spike is and select **Add Skimmed M-spike**.

Platinum will then estimate the extent of the monoclonal peak and highlight this area by filling in the trace with 'hashed lines'. To edit the location of the start and end points of the area quantitated, hover the mouse pointer over the trough marker until a double headed arrow appears, then drag and drop until a suitable location is found. Deselect the Edit Mode.

The band list will now contain an extra band called M-spike with additional prefix and suffixes depending on its location in the trace and the number of M-spikes added e.g. Gamma M-spike 1 13.39%.



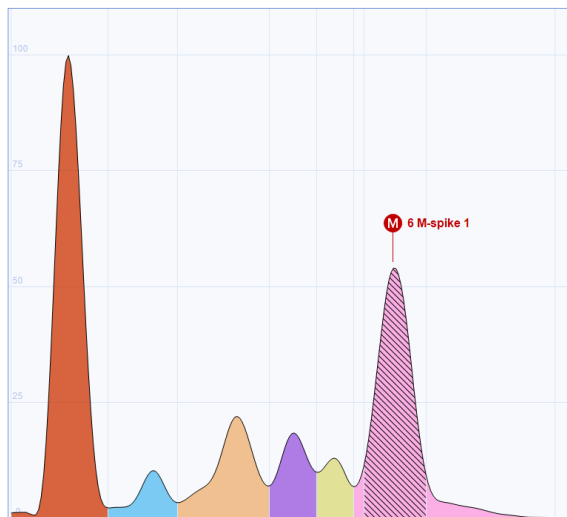
Example of a monoclonal spike quantitated using the skimmed M-spike function

5.4.2 Sliced M-spike

This methodology assumes the monoclonal protein band is the only protein in the gel at this position, and therefore quantitates the band down to the baseline of the trace.

Adding a Sliced M-spike

Select the **Edit Mode**, then **Edit Peaks**. Right click on the monoclonal spike and select **Add Sliced M-spike**. Platinum will then estimate the extent of the monoclonal spike and highlight this area by filling in the trace to the baseline with hashed lines. To edit the location of the start and end points of the area quantitated, hover the mouse pointer over the trough marker until a double headed arrow appears, then drag and drop until a suitable location is found.



Example of a monoclonal spike quantitated using the sliced M-spike function

5.4.3 Removing an M-spike

To remove an un-necessary M-spike, right click the mouse while hovering over the M-spike and choose **Remove M-spike**. The hashed area will then be removed.

5.5 Removing Artefacts from Traces


Artefacts are not common, but are sometimes a problem; these functions enable the removal of an artefact from a trace without disturbing the data.

5.5.1 Slice Data

To edit a trace to remove an unwanted artefact (to the baseline), click the **Slice data** icon. Then, using the mouse, left click and drag the mouse over the area to be removed.



5.5.2 Skim data

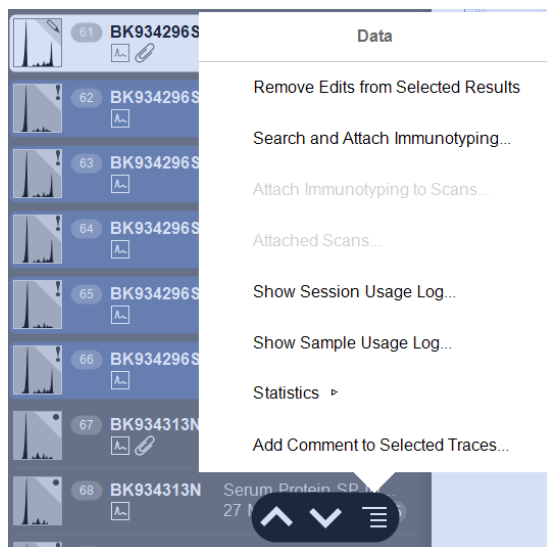
To edit a trace to remove an unwanted artefact whilst maintaining the general progression of the curve (peak to peak), click the **Skim data** icon 

Using the mouse, left click and drag the mouse over the area to be removed, this will be highlighted by a series of vertical bands (releasing the mouse button will complete the process).

5.6 Searching for & Attaching an Immunotyping Result

When using a unique identifier Platinum will automatically link patient results. It is then possible within a single Platinum window to link and display IFE images relating to a specific patient next to the corresponding serum protein trace for use as a reference.

In absence of automatic linking, IFE images can be manually attached to the corresponding serum protein trace. Select the serum protein sample to which the IFE is to be linked, and from the Options menu at the bottom of the sample list, on the left hand side of the trace, left click and select **Data > Search and Attach Immunotyping**.



A search window will appear. Select the Search item (s), then click the search button. Once the results have appeared, highlight any immunotypes (IFE) you wish to link to the serum protein. Click **OK**. The linking will now take place and the window will close.

Search for Immunotyping results to attach

Search

Search item	Low Value	High value
System type	Any source	
Scan type	Any type	
Gel name	Any Name	
Analysis type	Any Type	
Measurement time (dd/MM/yyyy)		
Gel ID		
Measurement status	Normal / abnormal	
Demographic 1		
Demographic 2		
Demographic 3		
Demographic 4		
Demographic 5		
Demographic 6		
Demographic 7		
Demographic 8		
Demographic 9		
Demographic 10		

Sample

Clear

Search

Archive Search

Configure

Help

Close

For additional search criteria select **Configure**.

Search Results

Number of records found: 36

ScanId#	SystemType	Type	GelName	GelType	GelId	Measurement time	UpdateDate	Status
6878	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	250930-1906819-(73144)-2...	04/04/2024 17:...	13/06/2025 10:...	Normal
6879	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	250930-1906819-(73144)-2...	04/04/2024 17:...	21/05/2025 14:...	Normal
6880	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	250930-1906819-(73144)-2...	04/04/2024 17:...	21/05/2025 14:...	Normal
6881	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	250930-1906819-(73144)-2...	04/04/2024 17:...	21/05/2025 14:...	Normal
6882	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	250930-1906819-(73144)-2...	04/04/2024 17:...	21/05/2025 14:...	Normal
6883	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	250930-1906819-(73144)-2...	04/04/2024 17:...	21/05/2025 14:...	Normal
6884	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	250930-1906819-(73144)-2...	04/04/2024 17:...	21/05/2025 14:...	Normal
6885	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	250930-1906819-(73144)-2...	04/04/2024 17:...	21/05/2025 14:...	Normal
6886	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	250930-1906819-(73144)-2...	04/04/2024 17:...	21/05/2025 14:...	Normal
6887	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	240109-1192721-(20240118...	22/01/2024 12:...	21/05/2025 14:...	Normal
6888	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	240109-1192721-(20240118...	22/01/2024 12:...	21/05/2025 14:...	Normal
6889	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	240109-1192721-(20240118...	22/01/2024 12:...	21/05/2025 14:...	Normal
6890	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	240109-1192721-(20240118...	22/01/2024 12:...	21/05/2025 14:...	Normal
6891	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	240109-1192721-(20240118...	22/01/2024 12:...	21/05/2025 14:...	Normal
7039	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	270529-11923444-(112233)...	30/05/2025 17:...	02/06/2025 15:...	Normal
7040	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	270529-11923444-(112233)...	30/05/2025 17:...	02/06/2025 15:...	Normal
7041	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	270529-11923444-(112233)...	30/05/2025 17:...	02/06/2025 15:...	Normal
7042	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	270529-11923444-(112233)...	30/05/2025 17:...	02/06/2025 15:...	Normal
7043	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	270529-11923444-(112233)...	30/05/2025 17:...	02/06/2025 15:...	Normal
7044	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	270529-11923444-(112233)...	30/05/2025 17:...	02/06/2025 15:...	Normal
7045	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	270529-11923444-(112233)...	30/05/2025 17:...	02/06/2025 15:...	Normal
7046	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	270529-11923444-(112233)...	30/05/2025 17:...	02/06/2025 15:...	Normal
7047	Gel Scan	Sample	SAS-3 IFE-9 (300300) - Se...	ife	270529-11923444-(112233)...	30/05/2025 17:...	02/06/2025 15:...	Normal

<

>

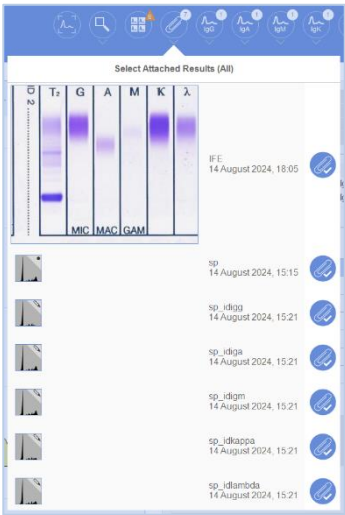
OK

Select All

Deselect All

Cancel

Select the correct sample ID to attach. In the results screen select the paperclip icon to view attached IFE results.

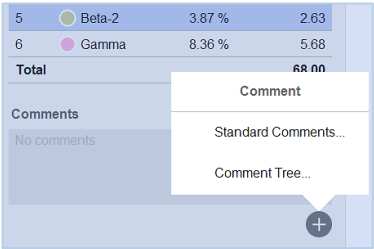


5.7 Result Comments

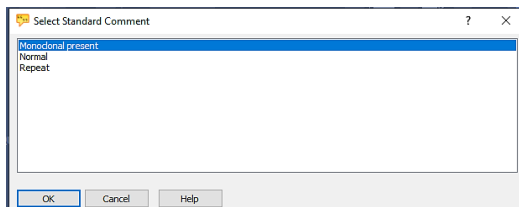
It is possible within Platinum to store predefined comments which can be added to the individual sample records (see section 3.15)

5.7.1 Adding a Comment to a Sample Result

To add a comment to a result, highlight the sample in the results list then add a comment in the comments box under the band data on the right hand side. The comment can be free text or predefined comments.

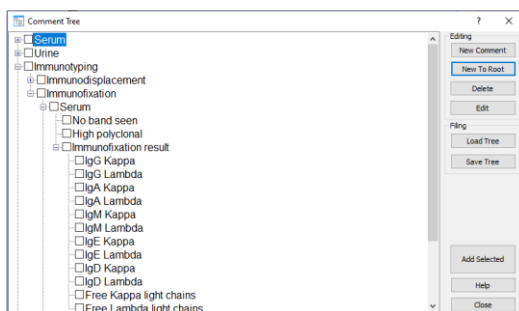


Predefined comments can be added by clicking on the + icon under the comments box. This will allow the user to select a Standard Comment or comment from the Comment Tree. Standard comments can be added by selecting **Configure > Comments (Reporting)**. When this is selected the Standard Comment window will appear.



Highlight the required comment and click **OK**. The comment will appear in the comments window.

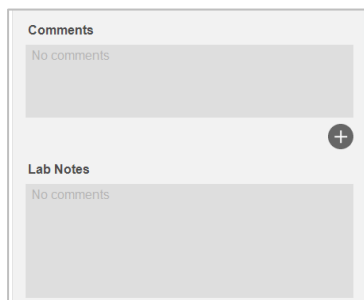
The Comment Tree is a set of predefined comments linked to tests. New comments can be added to the tree under each test by selecting **New Comment** or a new set of comments can be added by selecting **New To Root**.



One other way of adding comments is by the Options menu. Go to **Options > Data > Add Comments to Selected Traces**. Comments can be added to selected samples, or by selecting all, the same comment can be added to all samples in one action.

5.7. Adding Lab Notes to a Sample Result

Users can also add Lab Notes to a sample. This is a free text comment and unlike the text in the Comments box the notes are not sent to LIMS or seen on the report.



The screenshot shows a user interface with two main sections: 'Comments' and 'Lab Notes'. The 'Comments' section at the top has a header 'Comments' and a text area containing 'No comments'. Below this is a '+' icon in a circle. The 'Lab Notes' section below it has a header 'Lab Notes' and a larger text area also containing 'No comments'.

5.8 Levey-Jennings

This function allows the user to verify and track system performance over time through the use of a corresponding control.

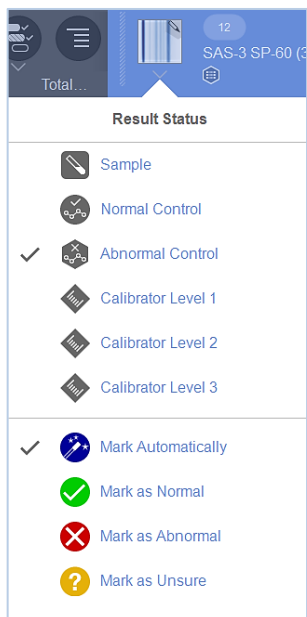
5.8.1 Setting up the Levey-Jennings Analysis (see section 3.5)

5.8.2 Day to day running of controls and Levey-Jennings

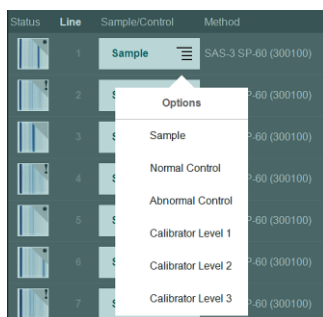
Scan the gel containing the control. (If an abnormal control is to be viewed in the Levey-Jennings plot, then a normal control must also be present on the same gel).


Mark the lane containing the control either using the following options:

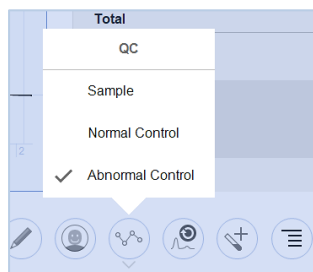
- **Results Status** drop down box



- In the **Worklist** by clicking on the **Sample Options** drop down box

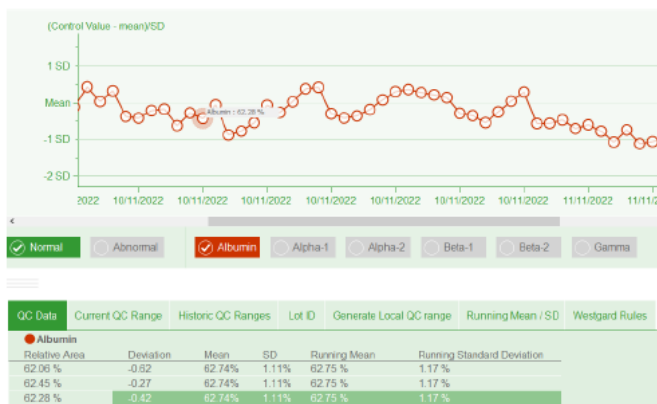


- Selecting the **QC Icon**  on the Menu underneath the trace in the Results Window.



In the QC Suite select the desired Method and the Levey-Jennings plot will be shown on the right hand side of the screen.

Select the control type (Normal or Abnormal) and then input the date range you wish to analyse.



The Levey Jennings window shows all current selected QC data plotted Against a Levey Jennings chart. Hovering the mouse over a point in this chart will show the value of this data point and the raw data will be highlighted in the QC Data tab.

To view the Trace for a specific data point select it in the table and then from the Options menu, select **Load Source Data**.

5.9 Performing Statistics in Platinum

Within Platinum, it is possible to perform basic statistical analysis on the data and to print or display this information.

To compare data from multiple samples, it is necessary to have all of the results in the same analysis window, either on a single gel image, or as the result of a database search. To select all samples for analysis, choose **CTRL + A** or **Options > Select > Select all** or hold down the **Ctrl** key whilst selecting the desired samples.

To display the statistics window after all of the required samples have been selected, from the Options menu choose **Data > Statistics**.

The index of each band is displayed in the Index column with the number of samples n in brackets. The name of each band is indicated in the band column, whilst the remaining columns can be determined in **Configure > Preferences (Appearance) > Bands**. These columns are used to display the mean, standard deviation, and the C.V. for the area, area %, or concentration.

5.10 Report

Patient sample results can be viewed as a report and printed for use by the clinician. Templates can be altered according to preference and type of assay run.

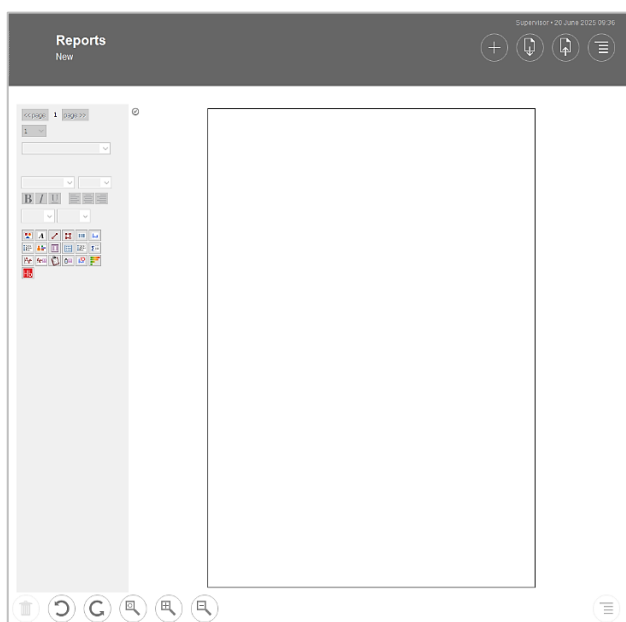
5.10.1 Create new report

In order to create a new report, choose **Configure > Reports (Reporting)**.

This will show a new report window that will display the report template layout with all of the functions that are required to create new templates.

How to create a template layout

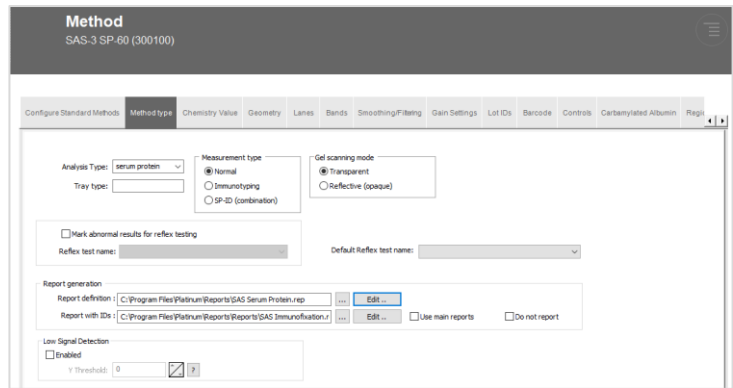
When a template layout is created, a blank page will be displayed with tool buttons on the left hand side. Users can choose what type of result is to be shown, where it is to be situated, and what demographic data is displayed. Data such as peak values and immunofixation images can also be included.



5.10.2 Edit report

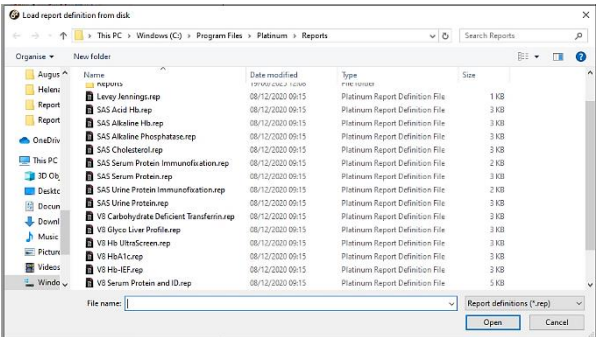
To edit the current method dependent default report, choose **Configure** > **Configure Gels**. Select the method then choose the **Method Type** tab.

Next to the Report definition select **Edit**



This will open the defined report associated with this test.

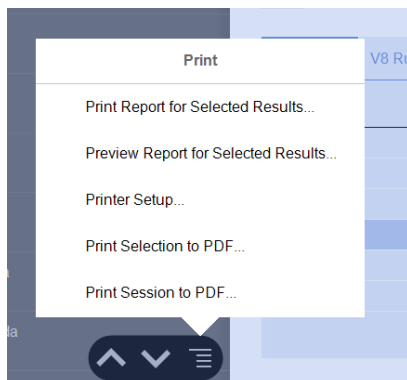
To edit another user selected report template go to **Configure** > **Reporting** > **Reports**. Then select the **Load Source Data** icon



This will bring up a window with a list of saved reports, when one is selected, choose **Open**. This will open the report in a new window with all the required functions to edit the report.

5.10.3 Preview report

To preview a report before printing, select a result in the results page then choose **Options > Print > Preview Report for Selected Results**.



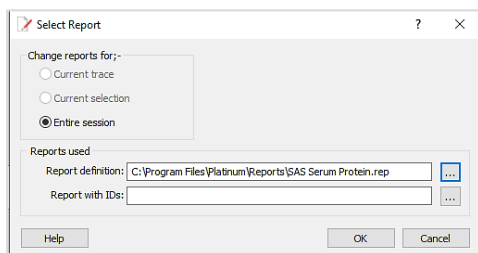
In Platinum it is possible to use user definable reports, but Helena Biosciences also provides an array of default report templates that the user can customise to suit their own needs.


5.10.4 Applying a report definition retrospectively to data

From time to time it may be necessary to use a different report or apply a new report to some old data retrospectively.

With the result highlighted in the results page, select **Configure > Configure Bands (Methods)**.

Select the **Report Selection** button. This will bring up the following window:



Select the  button next to Report Definition. This will bring up the list of reports available. Select the new report type to be assigned to the test.

The default location for the reports files is in the following location:

C:\Program Files\Platinum

Reports with IDs is not applicable to gel scanning. This report definition will be applied to this session only. Select **OK** on the reports box.

5.11 Database

The Platinum database stores all data that is processed and imported.

5.11.1 Backup New Data

To back up new data in Platinum, choose **Configure > Database > Back-up > New and Changed Sessions**.

5.11.2 Backup All Data

To back up all data in Platinum, choose **Configure > Database > Back-up All Sessions**.

5.11.3 Custom Backup Selected Data

Allows a custom search for back up for specific data in Platinum. choose **Configure > Database > Custom Back-up Selected Data**.

5.11.4 Archive

To archive data in Platinum, choose **Configure > Database > Archive**

NOTE: It is not advised to archive MS SQL Server data.

5.11.5 Database Maintenance

To be used as a troubleshooting tool which includes validation of sessions.

5.11.6 Database Backup and Recovery


To backup and recover databases.

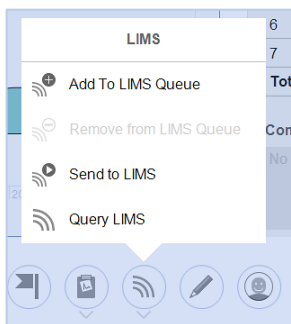
5.12 LIMS

Controlling data to the LIMS/LIS

There are two ways to send data to LIMS/LIS. It can either be to a LIMS Queue, where data can be validated before sending to the LIMS/LIS, or it can be sent directly to the LIMS/LIS.

5.12.1 Sending Data to the LIMS Queue

Results are sent to the LIMS/LIS holding queue so that once a user of suitable seniority has validated the data as acceptable it can be sent to the LIMS database. To send an individual lane or several lanes currently selected to the LIMS queue, highlight the specific results, select the LIMS icon  then select **Add to the LIMS Queue**.



To send the whole CE session or gel scan to LIMS, in the sample list, Select all by either pressing **CTRL + A** or **Options > Select > Select all**. Then select the LIMS icon and choose Send to LIMS.

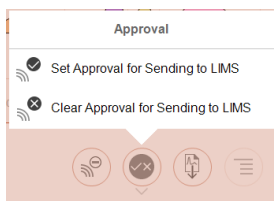
Those samples sent to the LIMS Queue will be marked with a LIMS icon.





5.12.2 Viewing and Releasing Data in the LIMS Queue

To view those samples in the LIMS Queue go to the LIMS Queue window


To approve an individual result to be released from the LIMS Queue, highlight the sample in the worklist then select the Approval icon, followed by **Set Approval for Sending to LIMS**.



To approve multiple selected results to be released from the LIMS queue, highlight the results in the worklist by touching the small trace icon then select the Approval icon, followed by **Set Approval for Sending to LIMS**. Ticks should appear next to the LIMS icon for all selected samples. 

To prevent a previous approved individual sample from being released from the LIMS Queue, select the Approval icon, followed by **Clear Approval for Sending to LIMS** . The tick should then be removed from the Navigation Worklist (NWL).

To do this for multiple results, highlight all the results you wish to remove the approval from by touching the small trace icon in the NWL before selecting **Clear Approval for Sending to LIMS**.

To remove an individual sample from the LIMS queue, **Select the Remove from LIMS Queue** icon . To remove multiple samples, highlight all of the results you wish to remove by touching the small trace icon in the NWL before selecting **Remove from the LIMS queue**.

Once the appropriate results have been authorised to be sent to the LIMS database, select **Send to LIMS**. To display the results sent to LIMS in the NWL, go to the top of the NWL and click **Show** > **Show Only Sent To LIMS**.

5.12.3 Sending Data Directly to LIMS

Results can be sent directly to LIMS / LIS bypassing the use of the queuing system. This is set up in [Configure](#) > [Communications](#) > [Customise](#) > [Sending to LIMS](#).

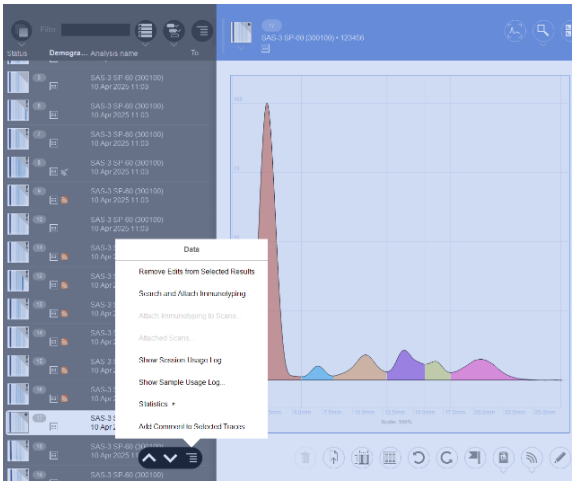
5.13 Usage log

The usage log stores a full history of operator data and decision-making.


5.13.1 Gel Session Usage Log

Shows a list of the user activity for the current active session.

To view this, from the Options menu select [Data](#) > [Show Session Usage Log](#).

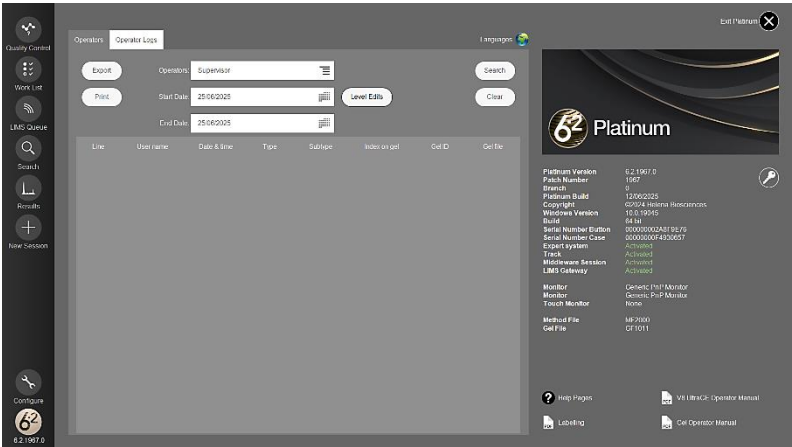


5.13.2 Sample Usage Log

Shows a list of the user activity for the result that is currently selected on screen. To view this, from the Options menu select **Data > Show Sample Usage Log**, or select the  icon.

5.13.3 Operator Usage Log

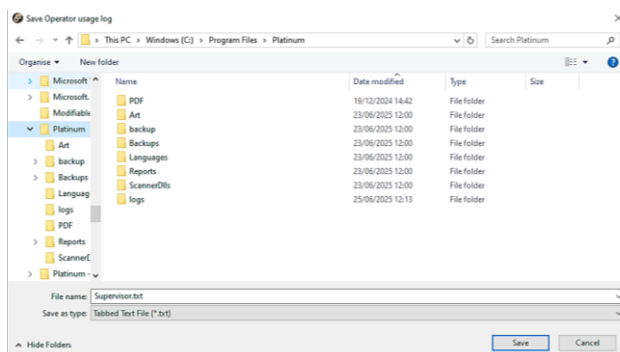
This function allows all viewing/editing functions carried out by a specific user for a defined time period to be identified. To view this, go to the Log in page and enter the search criteria, then select **Search**.



5.13.4 Additional Usage Log Options

Print – the table can be printed by selecting the **Print** button.

Export - The data can be saved as a tabbed txt file by selecting the **Export button**, and entering a file name and location in the appropriate boxes of the **Save As** window.



Appendix 1

Functions in Platinum

New Session: allows the opening of a new gel session, or a session from file. Opening a session from file allows the operator to open files that have been saved in previous sessions or to allow files to be imported from other instruments. This can be used to open previously entered worklists that have not had a scan attached (they are displayed as *.wl0 files).

Search: allows the operator to search for previously saved data along with demographic information. The demographic that is used to call up previous data is set in the demographic configuration.

Results: allows the operator to view the NWL, traces or gel images, Demographics, Band Data, Comments and Lab Notes

Results: Options Menu

Select

Select All: allows the operator to select all results

Select Same: allows the operator to select results of the same type

File

Open: allows the opening of a new V8 session, a new gel session from file.

Open Similar: allows the opening of a new session from file where defined demographics are the same

Save: allows the operator to save the current data without exiting the programme or closing the active window. At user level access, there is no choice as to the file name, or to the destination of the saved data. The data is saved with a unique number relating to the exact time and date the analysis was performed.

Save As: allows the user to select an alternative file name and location when using the **Save** function.

Save to Middleware/ Save Selected to Middleware: These options are only available if Middleware is activated. Please contact your Helena Representative for further details on Middleware.

Export Traces for Selected Results: allows the operator to export traces to a specified location.

Export Reports for Selected Results: allows the operator to export a report to a specified location.

Print

Print Report for Selected Results: print a report of the selected sample on the preconfigured report template.

Preview Report for Selected Results: preview the report for the selected sample on the preconfigured report template.

Printer Setup: allows the configuration of the printer that will be used to print report.

Print Selected to PDF: print a report of the selected sample on the preconfigured report template in the Platinum PDF folder.

Print Session to PDF: print a report of the session on the preconfigured report template in the Platinum PDF folder.

Trace Options: Scan Plot

This function allows the operator to specify options such as the Gain settings, scale and zoom on the scan plot. These options are available by right clicking on the trace.

Gain Settings: Allows the gain settings to be altered for the sample being analysed.

Set Scale: Allows the operator to set the x and y axis on the scan trace image.

Zoom Out: Allows the operator to reverse any Zoom in steps that have been taken.

Reset Scale: This will return the scale of the trace image to the default settings.

Results Page Options

This function allows the operator to specify viewing options for the Trace, Gel image, IFE Image or Band data.

Trace View Options

Auto Align Regions: Lines up regions with where platinum has added trough markers and peaks.

Show Peaks: This adds a trough marker up the middle of each peak for clarification.

Label Peaks: This labels areas on the peak with Albumin, Alpha-1, Alpha- 2, etc, to make differentiation easier.

Colour Peaks: This separates each peak / band area by colour, to further delineate between areas on the trace.

Show Gel Image: This shows a computer generated image of what the trace would look like were it ran on a gel.

Second Trace as Solid: If two traces are compared within the worklist the second trace will be displayed as a solid coloured trace.

Show Stacked Traces: If multiple traces are selected they will be displayed in the trace window stacked one on top of the other.

Baseline: This allows the user to select Baseline settings.

Show Derivative: This allows the operator to view the 1st derivative of the trace.

Show Mean Traces: This overlays the mean traces as specified in previous sessions for comparison with the selected trace.

Show Factory Overlay: This function places the normal overlay used by the operator onto the selected trace for comparison.

Show Normal Overlay: This overlays a user-specified trace on screen.

Gel View Options

This enables the operator to edit the gel image, with respect to colour, magnification and intensity.

Display as Negative: This inverts the gel Image image to a negative picture.

Enhance Contrast: This displays the gel image and scan image in a single colour, which is determined by the darkest pixel point on the scan.

IFE View Options

This enables the operator to edit the IFE image, with respect to colour, magnification and intensity.

Display as Negative: This inverts the IFE image to a negative picture.

Enhance Contrast: This displays the IFE image and scan image in a single colour, which is determined by the darkest pixel point on the scan.

Intensity: This adjusts the level of contrast that is used to display the IFE and scan image.

Display Helper Lines: This displays 3 lines on the IFE image to allow alignment of monoclonal bands.

Bands Options: This allows the operator to choose which data, if any, is displayed in the band list table.

Show Band Integral Value (IF): This allows the operator to select whether or not the peak integral values are displayed in the bands list table next to each band.

Show Band Concentrations: This allows the operator to select whether or not the band concentrations are displayed in the bands list table next to each band.

Show Band Ranges: This allows the operator to select whether or not the normal ranges are displayed in the bands list table next to each band.

Show Band Tops: Used in haemoglobin analysis to identify the x-axis position of the peak top.

Show Band Zones / Regions: Used in Haemoglobin analysis to define potential run positions of different haemoglobin variants.

Preferences: Opens a window that allows alterations to the appearance of features of the analysis window, reports and tables. This is only available to operators with “level 3” user level access.

Quality Control menu

Show Levey-Jennings: this allows the operator to enter in to the Levey-Jennings window. Control data can be searched and displayed in a Levey-Jennings plot.

Show Gel Usage Log: this allowsthe operator to view the actions of other users during a particular session.

Show Sample Usage Log: this allows any operators to scan the usage log for a particular trace, including users and any changes that have been made.

Show Operator Usage Log: this allows any operators with 'Level 3' user level status to search the usage log for information on a particular user or session.

Reagent Statistics: allows the user to query the number of tests that have been carried out using a defined set of analyses or over a range of dates.

Worklist menu

Set Up Work list: allows the operator to set up a work list of patient demographic information. This can be stored for later use when samples are scanned, or it can be implemented immediately if the samples are on board the instrument.

Gel menu

Select Scanner: this enables the user to select a gel scanner for use. Any scanning hardware connected to the computer will be listed.

Select Gel: this allows the user to select which gel tray (SAS-1, SAS-3) and which test type is to be used. Default smoothing, filtering and band set-up can be found in the prompt window also.

Select and Configure Gel: allows the user to make changes to the gel method settings, including Smoothing settings, and default report setting

Scan Parameters: this allows the user to specify the scan mode (8/24 bits or 12/36 bits) and to alter the resolution and gamma correction values.

Scan: this allows the user to enter the ID of the gel tray that is loaded onto the instrument. This can be typed or scanned.

Align Gel: this allows the user to align the gel.

Configure Bands: this enables the operator to configure the bands, and to apply default levels of filtering and smoothing.

Edit Regions / Zones: this allows the operator to edit the regions defined on the gel to clarify individual band regions.

Re-interpret Lane: this allows the operator to re-interpret a selected lane if the result is questionable, or the configuration parameters have been changed.

Re-interpret Gel: this allows the operator to re-interpret an entire gel if the result does not seem right, or the configuration parameters have been changed.

Mark Gel: this allows the user to mark the gel to pick out points of interest.

Search and Attach Immunotyping: this is used to search the database for any previously stored IFE scans for the current sample in the active window. Once found, the IFE is attached so that when the trace data is retrieved the attached IFE is displayed.

Attach Immunotyping to Scans: this is used to search the database for an IFE that will be linked and displayed relating to a specific patient next to the corresponding serum protein gel for use as a reference.

Attached Scans: when viewing an IFE sample this allows the operator to retrieve any samples that have the selected IFE attached.

Statistics: this displays a table of means, standard deviations and CVs for any selected gel data. More than one sample at a time can be selected by keeping the Ctrl key pressed when selecting samples.

Configure Gels: this allows any Level 3 users to configure the set up for gel including smoothing, filtering, band region limits and default gain settings.

Window menu

Session List. Allows quick and easy transition between open platinum sessions.

Trace Display menu

Display gel results as the following options:

As **list**: Shows data as a worklist.

As**Traces**: Shows all results as traces.

As **Gel Image**: Shows all results as a gel image.

Show hidden items: Samples can be hidden from the navigation work list by right clicking and selecting

Hide Selected. When this option is selected hidden samples can be viewed and restored to normal view.

Mark as Sample: the selected sample is marked as a sample.

Mark as Normal Control: the selected sample is marked for use as a normal control.

Mark as Abnormal Control: the selected sample is marked for use as an abnormal control.

Mark as Calibrator: the selected sample is marked for use as a calibrating trace.

Mark Automatically: this is the default selection and all lanes are marked as samples either normal or abnormal dependant on the configuration.

Mark as Normal: this marks the selected patient sample as normal.

Mark as Abnormal: this marks the selected patient sample marked as abnormal.

Mark as Unsure: this marks a patient sample as unsure. If the operator is unsure whether a sample is normal or abnormal, this will flag the sample so that another clinician may view it.

Suspect Levey-Jennings: if a control is in range but there appears to be a trend taking the gel or trace out of range it can be marked as suspect.

Accept Levey-Jennings: this allows the operator to accept the results on a gel or trace and mark it as such even if a control is shown to be out of range.

Add to Mean Traces: this adds a selected trace to those that are used to define the mean values.

Load Mean Traces: this overlays the mean trace for comparison with a selected sample.

Use as Normal Overlay: this allows the operator to select a trace for use as the normal overlay.

Load Normal Overlay Source Data: this loads the source data of the trace being used as the normal overlay.

Smoothing: the smoothing function allows the operator to reduce the effect of and display of noise shown on the trace. This is achieved by plotting the rolling average of results rather than individual points. The degree of smoothing used is on an arbitrary scale and increasing the smooth weight too much can result in an adverse effect on the quantitated values. A default smooth weight can be set in configuration; however it is applied here to selected samples.

Threshold Filtering / Slope Filtering: filtering alters the detection point at which a trough marker is automatically placed on the trace. Filtering is set in configuration, but this function allows individual filtering to be applied to each sample.

Edit menu

Undo: Allows the user to remove any editing on a trace or gel that has taken place.

Redo: If an editing operation has been undone, this function allows it to be redone without performing the operation again.

Edit Baseline: Allows the operator to edit the baseline of the current trace being displayed.

Edit Peaks: Allows the operator to edit the peaks of the current trace being displayed. Peaks are defined at two trough markers, which are automatically placed at the lowest point between two peaks.

Apply Slice: Allows the operator to slice out trace data that is thought to be an anomaly. This could be an artefact in a spike on an otherwise smooth curve. When Apply Slice is checked, the cursor will show as active over the trace. The area to be removed is highlighted by keeping the left mouse button pressed whilst dragging over the required area. The trace is drawn to the baseline rather than peak to peak as in Apply Skim.

Apply Skim: Allows the operator to stretch out trace data that is thought to be an anomaly. This could be an artefact in a spike on an otherwise smooth curve. When Apply Skim is checked, the cursor will show as active over the trace. The area to be removed is highlighted by keeping the left mouse button pressed whilst dragging over the required area.

Apply Stretching: Allows the operator to stretch a selected trace to match that of another i.e a reference trace. When Apply stretch is checked, the outer edges and centre of the trace will be highlighted. Using the left mouse button, these markers can be dragged to the new position and the trace will be scaled to fit.

Remove Stretching: Removes any previous editing applied to the trace.

Match Shapes: Allows you to match two shapes for direct overlay and comparison.

Copy: Allows the operator to copy any of the displayed trace data to be pasted into other Windows applications.

Comments

Add Comment: allows the operator to add a comment to the current sample from a list of predefined comments. The user can also add free hand comments in the comments tile of the active analysis window.

Reporting

New Report Template: This function allows the to create a new report template. See 'Creating a Report' for further details.

Edit Current Report Template: allows the operator to edit the current report template.

Edit Other Report Template: allows the operator to edit a previously created and saved report template.

Preview Current Report: Allows the operator to preview the current report layout associated with the method.

Communications

This submenu allows the operator to configure the settings of Platinum. This can only be accessed under the operator level of 'Level 3'.

Communications > Customise

Database: this is used to define the default directory for saving traces, gels and worklist files. Allows the user to view/configure the Location for new data and the Location for backups. This functions also allows the operator to change the location of the SQL database.

Reports: Shows the default location of Reports

Sending to LIMS: configuration of Platinum to allow communication with a host system and to define what data is sent to LIMS.

Receiving from LIMS: configuration of Platinum to allow communication with a host system and reception of data from LIMS.

Configure Demographics: allows you to define the demographics used for database management and LIS identification.

Institution Data: Input the information as required.

Configure Sample Handler: this enables the operator to confirm that positive patient ID's are used.

Configure Menus: allows the operator to view all menu functions with access levels that are permitted to use each one.

Manage Operator Accounts: Allows operators with "Level 2" operator level access to add, remove or edit all operators on the list of users.

Exit: allows the operator to exit the program and will automatically save any new data or update any editing that has taken place during the session.

Database

Database Information

This provides assorted information about the state of Platinum's database and networking status.

Archive: Allows the user to archive records.

Demographics Merge: The Demographic Merge allows the merging of old database demographics into the current demographic set. It is recommended that demographics are the same across all data. Imported data that has different demographics can be merged into the current demographic set using this tool.

SQL Search

This allows the direct entry of SQL language commands to access the database.

Backup New & Changed Sessions: Backups performed on New and changed sessions.

Custom Backup & Selected Data: Backups can be performed by customising the backup selected data.

Data mine: This functionality allows access to Platinum's data, in a formatted manner, suitable for external evaluation

Database Maintenance: This allows the display of database data and additional maintenance options including Method Table, Comment Table, Session Files and Session/Database Validation.

Database Merge: This functionality allows the merging of multiple existing Platinum databases into the current Platinum database. This is particularly useful when upgrading multiple Platinums to a network solution, with a single combined database. To merge historic platinum databases run the latest Platinum patch to convert them.

Import Database: This allows databases to be imported into Platinum. This function correctly matches the imported trace demographics to the Platinum demographics.

Full Database Search: To locate previous sample results, whole gels or V8 sessions in the database,

Backup All Sessions: Backup all session data.

Backup & Recovery: Creates a full database backup in the user specified directory. Recovery will enable the user to regress to a previous backup. This will overwrite the current database. A database can be reconstructed from the available session files. A directory can be specified then all the session files in that directory are imported into the current database.

Help menu

Platinum Help: Displays help menu.

Open Gel Operator Manual: Open Gel Operator Manual

Product Activation: Allows the user to activate additional Platinum features, including Touch Screen, Networking, Track, Middleware and Expert System.

About Platinum: Displays the Platinum version, including the Patch Number and Serial Number Button.

Notice to Users

Once the Eudamed public website is available, a summary of safety and performance of these devices will be accessible from there.

Definition of Symbols



Authorized representative in the European
Community/European Union

Glossary of software icons

The following software icons have been designed to make operator use simple and efficient.

Main Window Icons



Home Page



Quality Control Window



Quality Control Failed



Quality Control Timed Out



Quality Control Accepted



Quality Control Undefined



Work List



Search Window



LIMS Queue Window



Results Window



New session



Configuration Window

General Icons (Icons that appear in more than one window)



Delete



Undo



Redo



Save



Print



Open



Select



View as Gels



View as List



View as Traces



Sort Traces



Standard Mode



Date



Load Source Data



Reset Zoom



Zoom Out



Zoom In



Zoom



Trace



Show IgM Attached



Show IgL Attached



Show IgK Attached



Show IgG Attached



Show IgA Attached



Show IFE Attached



Show All Attached



IFE Image



Grid Mode



Focus Mode



Gel Image



Copy



Show



Inspector window

Home Page Icons



Language



Help Pages



Gel Operator Manual



Exit Platinum



Product Activation

Quality Control Icons



Rules



Scale to limits



Set Scale



Reset Zoom

Work List Icons



Get Work List Data



Show Pending Trays



Show Conflicts



Add New Item



Show Chemistry Values

LIMS Queue Icons



Send Selected Approved to LIMS



Send Selected to LIMS



Send All to LIMS



Remove from LIMS Queue



Approval



Set Approval for Sending to LIMS



Clear Approval for Sending to LIMS

Search Icons



New Search

Results/Search Results Icons



Sessions



Exit Session



Data



Reinterpret Trace



Copy



QC



LIMS



Add to LIMS Queue



Remove from LIMS Queue



Send to LIMS



Edit



Comparisons



Sample



Normal Control



Abnormal Control



Calibrator (Level 1, 2 or 3)



Mark as Unsure



Mark as Normal



Mark Automatically



Mark as Abnormal



Attach



Attached trace



Detach Trace

Edit Results Icons



Stretch



Slice



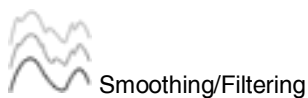
Skim



Edit peaks



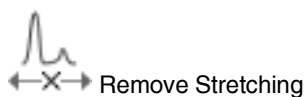
Match Shapes



Smoothing/Filtering



Edit Baseline



Remove Stretching

Gel Icons



Align Gel



Export gel image



Flag



Gel Runtime Parameters



Usage Log



Apply



Cancel



Mark Gel



Revert



Undo



Redo

Navigation Worklist Icons



Comment added



Gel Sample



Gel Normal Control



Gel Abnormal Control



Suspect QC



Accept QC



Sent to LIMS



Approved Sent to LIMS



Pending Send to LIMS



LIMS Approved



No Result in the Database



Previous Monoclonal Result in Database



Previous Normal Result in Database



Previous Abnormal Result in Database



Traces Attached



Host Query



Comments Tree

Tel +44 (0)191 482 8440

info@helena-biosciences.com

www.helena-biosciences.com

Queensway South,
Team Valley Trading Estate, Gateshead,
Tyne and Wear, NE11 0SD, United Kingdom

HL-2-P-3621 (Rev. 1)

www.helena-biosciences.com

