TurboScan Manual

For Version 2.0.3

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1. Introduction

1.1. TurboScan

Congratulations on purchasing one of the premium densitometer systems on the market.
The foundations of the TurboScan densitometer were laid back in 1985 when BIOTEC-FISCHER GmbH already had a densitometer system based on image processing (VID 1D/2D). It was another 12 years before the market for routine analyses in clinical chemistry would be ready for a densitometer system based on image processing. This was precisely when BIOTEC-FISCHER GmbH launched the TurboScan densitometer. You have now purchased the result of over 25 years' experience in the field.
Since TurboScan was launched in 1997 a great deal has changed and there have been many advances. This TurboScan version you now have is the most modern densitometer system in existence for routine use.

1.2. Checklist

The items delivered can vary, depending on the size of your order.
Products supplied as standard for a complete densitometer workstation with PC are listed below:

- PC with keyboard and mouse
- TFT monitor
- Colour printer
- Flatbed scanner with transmitted-light unit
- TurboScan Installations CD
- TurboScan copy protection
- Positioning template for flatbed scanner

1.3. Contact details

If you have any queries about the software or installation, please contact your local dealer or:

BIOTEC-FISCHER GmbH
Daimlerstrasse 6
35447 Reiskirchen
Germany
Tel: +49 (0)6408/6072
Fax: +49 (0)6408/64165
e-mail: info@biotec-fischer.de

2. System requirements

Users who wish to use their own hardware should ensure that the minimum hardware requirements are met.

PC:	Intel Celeron 1.7 GHz processor speed or compatible AMD processor
Memory:	512 MB RAM
Hard disk:	20 GB
USB interface:	2 x USB 2.0
Operating system:	Windows XP with SP2, Windows 2000
Keyboard:	Standard keyboard set to the appropriate language
Mouse:	Standard 2-button mouse with scroll wheel
Monitor:	15'' TFT
Printer:	Any (colour printer or b&w printer are possible)
Scanner:	**Please ask BIOTEC-FISCHER about the up-to-date model in use. You are strongly recommended to use this scanner.**

3. Warranty

The functioning of the TurboScan software has been thoroughly tested. If any faults in the programming are identified, these will be remedied as quickly as possible. An appropriate bugfix is free to TurboScan users. The warranty period is two years from the date of purchase.

Problems that are not based on programming faults do not affect the company's obligation to rectify, exchange or redeem the product.

Failure of TurboScan to operate correctly on the hardware provided by the user does not constitute a fault in the software.

Assistance in resolving the problem can be obtained from the contact address given under 1.3. As a matter of course BIOTEC-FISCHER GmbH also offers an on-site service.

4. Software licence agreement

Like any software, TurboScan is subject to special conditions of use which the TurboScan user accepts when installing the software on a PC. The licence agreement is reprinted here for information purposes [1].

[1] The current version, which may vary from the version printed here, is the valid licence agreement.

Software Licence Agreement

This is a legal agreement between you (hereafter called User) and BIOTEC-FISCHER GmbH (hereafter called BIOTEC-FISCHER GmbH) which contains the Licence for this software program TurboScan (hereafter called PROGRAM).

Use of the program indicates your consent to the conditions and obligations contained in this Agreement between the User and BIOTEC-FISCHER GmbH.

1. The copyright and all other rights existing in connection with the program and all relevant documents are the property of BIOTEC-FISCHER GmbH or the originally authorized person or organization (hereafter called originally authorized person) and entitle BIOTEC-FISCHER GmbH to use the program. The User shall not be entitled to any rights other than those set out in this Agreement.

2. BIOTEC-FISCHER GmbH grants the User a non-transferable, non-exclusive right to use the program. "Use" covers the complete or partial storage of the program on the User's own PC and execution of the program for the sole purpose of utilizing the functions for which the program is intended.

3. The User shall not transfer the aforementioned licence to a third party nor permit third parties to use the program, unless the User has obtained prior written permission to transfer the program from BIOTEC-FISCHER GmbH.

4. The User is NOT entitled to strip, decompile, derive or merge the program with other software, to copy, translate, adapt, alter or modify (wholly or in part) the program. Backtranslation of the program into the form of a source program or into other display forms is equally not permitted.

5. THE PROGRAM IS SUPPLIED "AS-IS" WITHOUT EXPRESS OR IMPLIED GUARANTEES. FURTHERMORE NO GUARANTEE IS MADE OF ITS USABILITY FOR A SPECIFIC PURPOSE NOR THAT THE PROGRAM IS ERROR-FREE. LIABILITY FOR ANY HARMFUL EFFECTS (E.G. CAUSED BY VIRUS TRANSMISSION) ON OTHER PROGRAMS OR DEVICES OF THE USER SHALL BE CONFINED TO GROSS NEGLIGENCE AND INTENT. LIABILITY FOR CONSEQUENTIAL DAMAGE IS EXCLUDED.

6. In the event of a dispute arising between the User and a third party because of use of the program, which results from an infringement of copyright, patent law or any other property right, the User undertakes to settle the dispute at his own cost and shall not assert any claims against BIOTEC-FISCHER GmbH or the originally authorized person.

7. Should it become known that the User has infringed these conditions, BIOTEC-FISCHER shall withdraw the licence from the User. Withdrawal of the licence has no bearing on payments or claims for damages. As a consequence of withdrawal of the licence, the User shall be obliged to delete the entire program including all copies thereof with immediate effect.

5. Installation

To install, insert the Installations CD in the appropriate CD/DVD drive. Installation starts automatically on computers running under XP with standard set-up. If not, select the CD/DVD drive via Windows Explorer and manually run the executable file by double-clicking the left mouse button.

Installation of TurboScan is virtually automatic. The following components will be installed:

- TurboScan software
- BDE database machine
- driver for copy protection

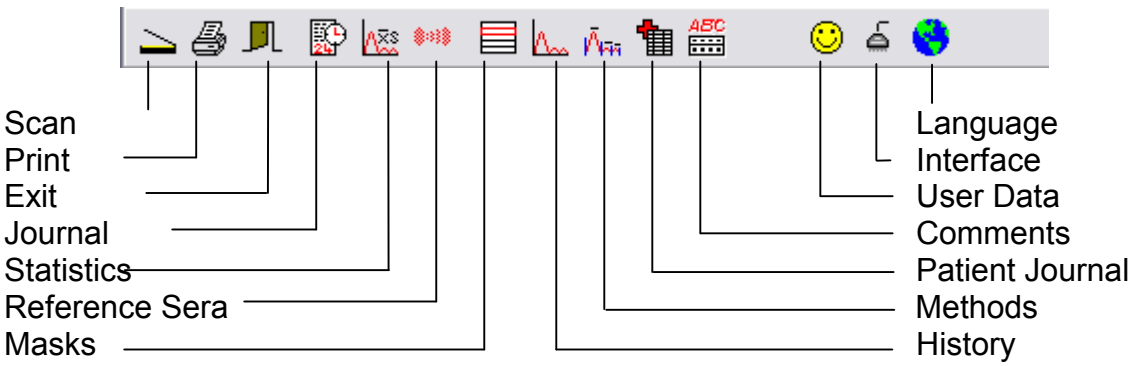
Once installation of the BDE database machine is finished, TurboScan installation can be completed and the system restarted. An Incomplete Installation of the BDE database machine will prevent TurboScan from functioning properly. After the computer is restarted, the copy protection should be connected to the chosen USB port of the computer.

Note for users with their own hardware setup

Please note: in principle, the driver programs should be installed before the device is connected up. If not, there is a possibility of malfunction.

6. TurboScan screen

When the TurboScan software is launched, the following window appears on the screen:



7. TurboScan menu bar

7.1. File

7.1.1. Statistics

The menu selection Statistics opens the menu window for calculating statistical values. See 8.2.5 for detailed description.

7.1.2. Reorganize Database

From time to time it is necessary to reorganize the data in the database. This makes sense if data are added to or deleted from a database over a long period of time. Within a database, a data record is given a status for “deleted”. This record remains in the database until reorganization is carried out. It is only then that the data are actually deleted from the database. Data records with the status “deleted” are assessed by TurboScan as no longer existent and are thus no longer displayed. The status of the reorganization process is indicated by a progress bar in the TurboScan main window.

7.1.3. Print

Selecting this submenu opens the Print Preview window. See 8.2.2 for detailed description.

7.1.4. Exit

Selecting this menu item exits the TurboScan program. All unsaved data will be lost and cannot be recovered when the program is restarted.

7.2. Scan

7.2.1. Start

This submenu launches the scanning process to record a new image. See 8.2.1 for detailed description.

7.3. Management

7.3.1. Masks

Using Mask Management, different reading tracks can be created and written into a database table. See 8.2.7 for detailed description.

7.3.2. Historical Database

All patient data, if entered, are collected in the Historical Database. This database table can be searched for data records using various criteria. See 8.2.8 for detailed description.

7.3.3. Methods

Using Method Management, different methods can be created and written into a database table. See 8.2.9 for detailed description.

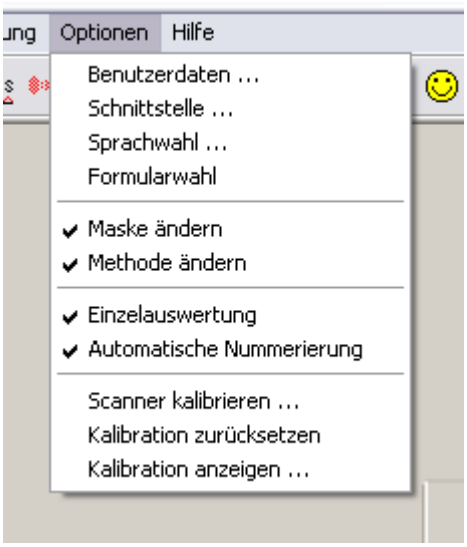
7.3.4. Comments

TurboScan offers you the option of making your own comments for the printout. These comments can later be retrieved from the database and assigned to an analysis. See 8.1.11 for detailed description.

7.3.5. Patient Journal

The Patient Journal is used to record patient data. See 8.2.10 for detailed description.

7.4. Options



7.4.1. User Data

The User Data are used to identify the laboratory which analysed the electrophoreses. These data are reproduced on the printouts. See 8.2.12 for detailed description.

7.4.2. Interface

If the laboratory's own DP is used for managing patient data, this can communicate directly with the TurboScan analysis software. This is where the appropriate port for communication is selected. See 8.2.13 for detailed description.

7.4.3. Language

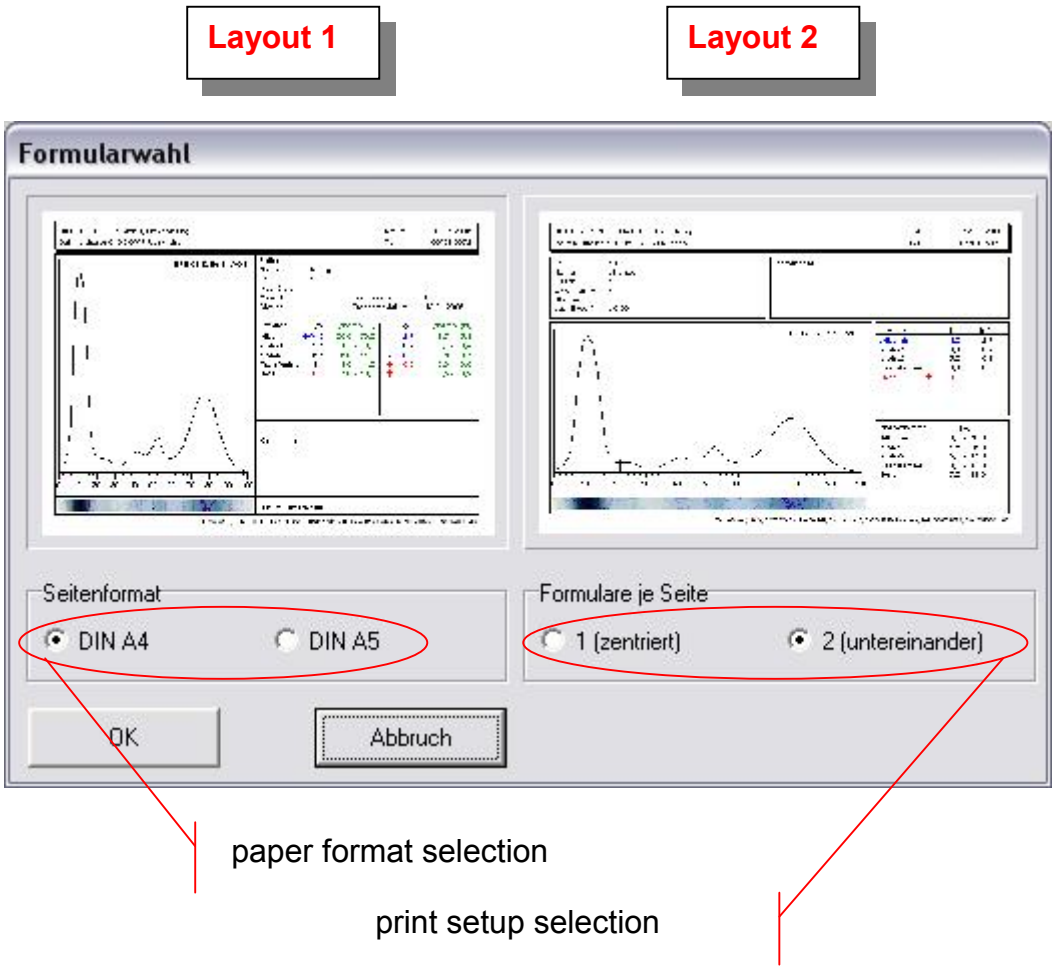
TurboScan is sold very successfully worldwide. With this function, the appropriate language can be selected. See 8.2.14 for detailed description.

7.4.4. Form Selection

TurboScan offers you the option of selecting between 6 different printouts of the results. There are two print layouts for different paper formats available. The opening window shows the two print layouts as a graphic. A single click of the left mouse button on the desired layout immediately activates that layout. The desired paper format can be selected using the radio buttons. The following combinations for print setup are possible:

- single print on DIN A5 landscape
- double print on DIN A4 portrait
- single print on DIN A4 portrait centred

The selection is applied immediately after the layout and paper format have been set.



7.4.5. Change Mask

Masks are the arrangement of the different reading tracks. Depending on the object used, you may store as many masks as you wish for correct analysis. See 8.2.7 ff. for detailed description.

7.4.6. Change Method

Methods are the definition of specific electrophoreses with the relevant names of the fractions and the corresponding normal ranges. TurboScan

allows you to store as many methods as you like and assign these to the analyses, if required. See 8.2.9 ff. for detailed description.

7.4.7. Single Analysis

Single Analysis is linked directly to the mask. TurboScan provides the possibility of mask-dependent management of the Patient Journal. If there is a mask comprising 10 electrophoresis tracks and this menu item has been enabled, only patient data for these 10 tracks on the mask can be input. From a list (which is transmitted by data transfer, where appropriate) only the first 10 data records are accepted. Even when patient data are entered manually, only as many data can be input as there are tracks on the mask. However, this only applies to the mask that is automatically loaded at program startup. This rule does not apply to masks that are automatically created.

Thus a loaded mask may have 10 tracks, for instance, but the automatically created mask only has 8. Ten patient data can hence be input into the Patient Journal, even though only 8 tracks have been analysed. Vice versa, it can also happen that the loaded mask has only 8 tracks while the automatically created mask found 10 tracks. Nevertheless only 8 patient data will be input.

If Single Analysis is not enabled, there is unlimited entry of patient data. A checkmark in front of the menu item indicates that Single Analysis is enabled. If there is no checkmark in front of the menu item, it is not enabled.

To enable or disable Single Analysis, single-click the left mouse button on this menu item. The status changes from ON to OFF with every mouse click.

Single Analysis is only intended for special cases in which the number of electrophoreses to be analysed does not change.

This menu item should not be enabled as a default setting.

7.4.8. Automatic Numbering

Automatic Numbering undertakes the identification of individual samples. If the user does not carry out his own identification of the samples, TurboScan will do this automatically. Every sample is automatically assigned a number, which provides a means of retrieving the analysed samples on the actual day. The automatic ID is made up of 11 digits, the first 4 denoting the year the data record was placed in the database, digits 5 + 6 the month, 7 + 8 the day and the last 3 digits the serial number.

It makes sense to use Automatic Numbering if you do not plan to use any sample identification method of your own.

Automatic Numbering is enabled and disabled by single-clicking the left mouse button on the menu item. Automatic Numbering status is shown by a checkmark in front of the menu item. If there is a checkmark, sample ID

is managed automatically by TurboScan. If there is no checkmark, sample ID must be managed by the user.

7.4.9. Calibrate Scanner

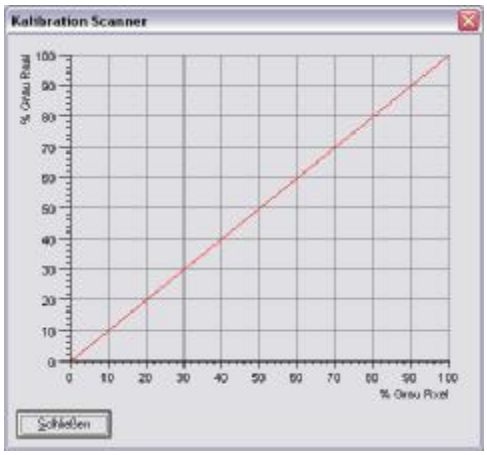
Scanner calibration is not necessary for standard applications. This calibration should only be used for images and analyses in colour spaces that differ from the standard. Further instructions can be obtained from BIOTEC-FISCHER GmbH, on request.

7.4.10. Reset Calibration

Resetting calibration restores the settings to the standard colour space.

7.4.11. Display Calibration

This menu item displays a graph of the current calibration status. The default setting shows a graph with a linear function.



7.5. Help

7.5.1. Index

Selecting this menu item accesses the current manual for help on using TurboScan.

7.5.2. About

When this menu item is selected, general information about the program is displayed. This includes the version number of the current program, the current serial number and a contract address for questions about TurboScan.

8. TurboScan Button Bar

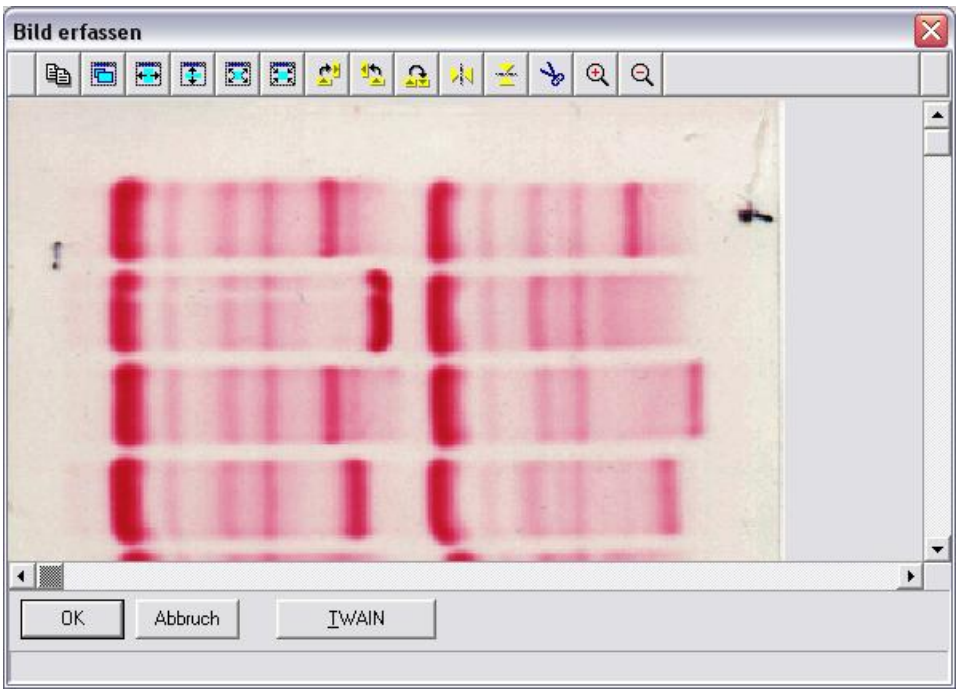
8.1. Scan

8.1.1. Scanner

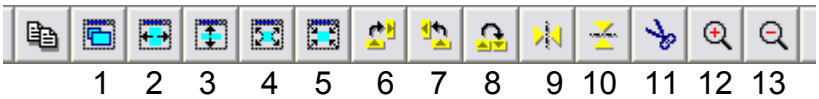
Symbol displayed:

8.1.1.1. Capture image window

Single-clicking the left mouse button starts the procedure to record a new image. First the “Scanned image” window opens and shows the last image scanned.



The button bar at the head of this window can be used to reprocess the current image. However, this is not usually necessary. The following illustration shows the functions of the individual buttons:

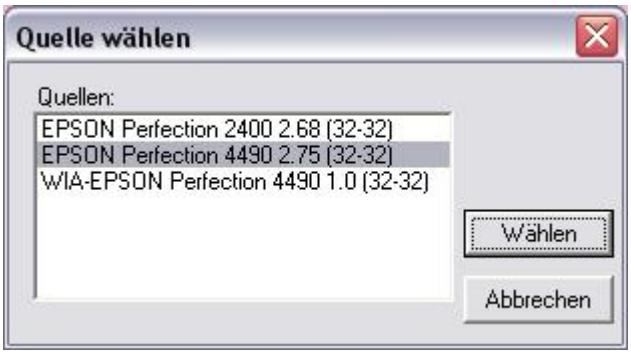


1. Show whole image
2. Show image at maximum width
3. Show image at maximum length
4. Fit image to window
5. Original view of image
6. Rotate image clockwise 90°
7. Rotate image counterclockwise 90°

8. Rotate image 180°
9. Rotate image around longitudinal axis
10. Rotate image around transverse axis
11. Cut out the selected section. To select the section, press and hold the left mouse button. Display the required area by dragging the mouse over it. The area is fixed when the mouse button is released. When the function button is pressed to cut out the section of the image, the area within the frame is cut out and saved as a new image. The original image is overwritten in the process.
    This process **cannot** be reversed.
12. Zoom in
13. Zoom out

8.1.1.2. TWAIN device selection

In order to start recording, the scanner software supplied by the scanner manufacturer should be started on a TWAIN interface basis. Move the mouse pointer onto the TWAIN button and single-click the left mouse button. This opens the window for selecting connected TWAIN devices. To select the desired TWAIN device, position the mouse on the required device and single-click the left mouse button on the selected device. To accept the selected device, click on the “Select” button.

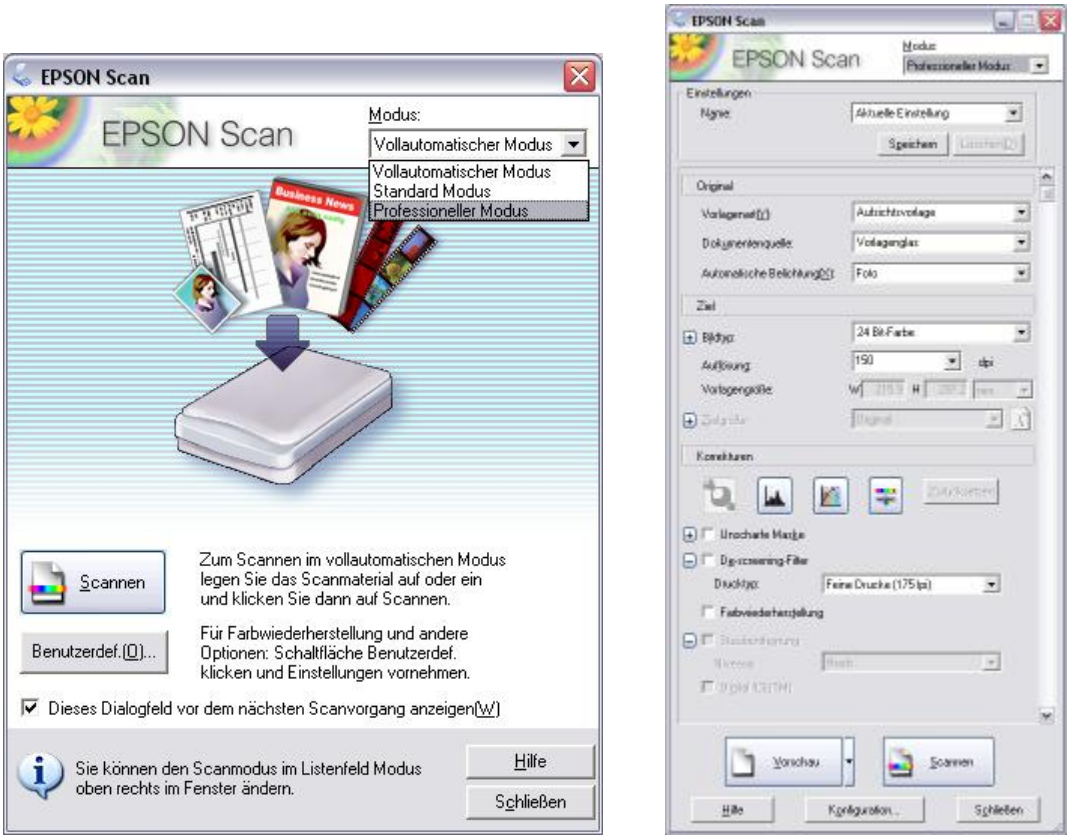


8.1.1.3. EPSON scanner settings[2]

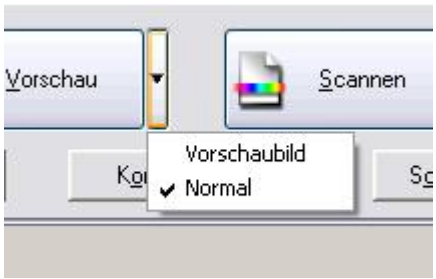
8.1.1.3.1. Scanning mode

When the EPSON TWAIN software is first started up, the system is set up so that the scanning process runs in automatic mode. When the scanning window can be seen on the screen, a selection popup appears in the top part of the screen, which displays “Automatic Mode”. To change this selection, click on the downward arrow of the dropdown menu and select “Professional Mode”.

[2] Example: scanner model EPSON perfection 4490



The window closes and Professional Mode is displayed. To show the preview image correctly, click on the arrow next to the “Preview” button. From the self-opening pop-up, select “Normal” with a single click of the left mouse button.



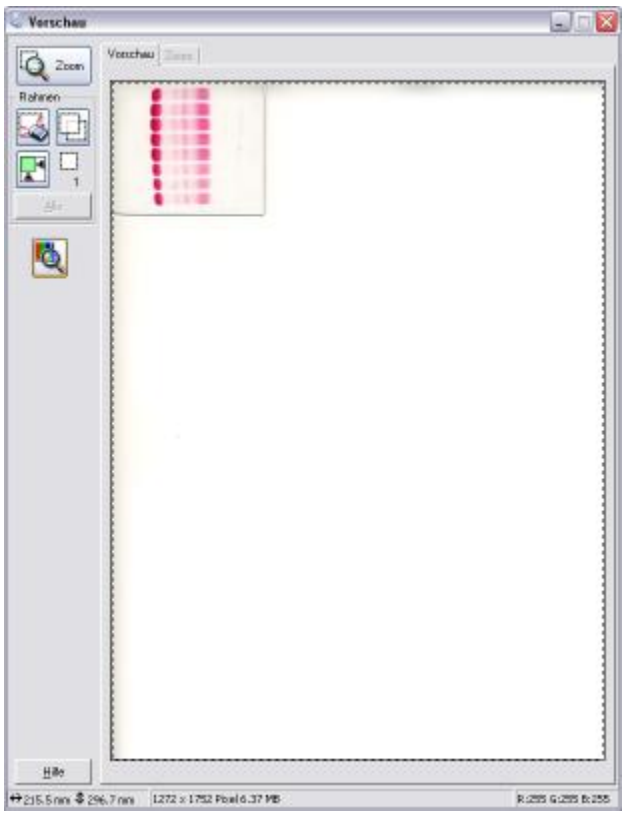
8.1.1.3.2. Basic setting for TurboScan

Use of the scanner is optimized for scanning photographs (negatives and positives) and transparencies. However, use of the flatbed scanner here requires different conditions for correct analysis of electrophoreses. To achieve these conditions, a few settings need to be adjusted to match the required conditions.

First decide on the area to be scanned. To do this, single-click the left mouse button on “Preview”.
The scanner is started up and it scans an overview image, which is displayed in a window on the right next to the Settings window. The overlaid glass plate is displayed at the same time.

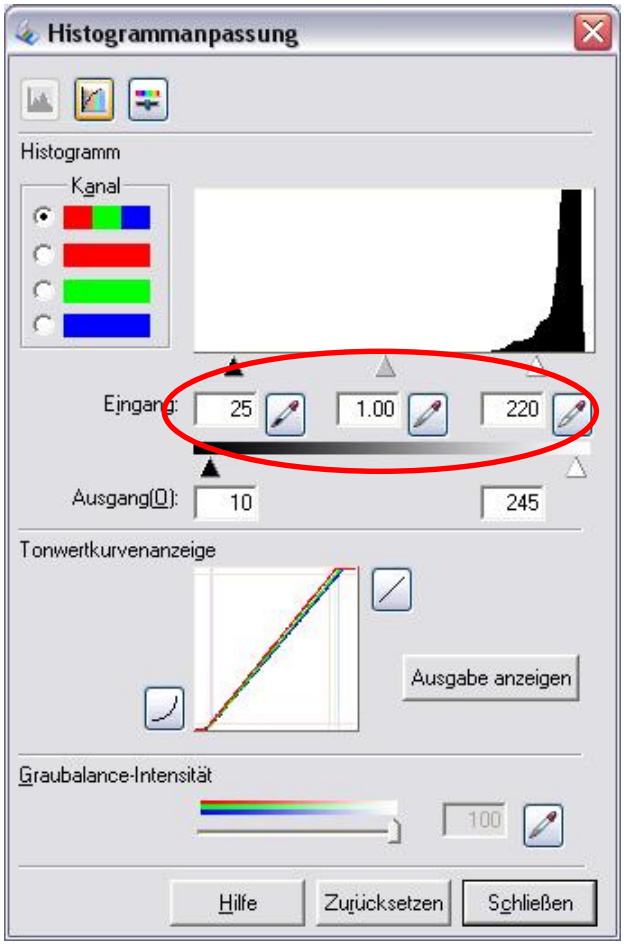
For problem-free routine work, the glass plate always needs to be placed back in the same position. You can use an overlay template (example available as a pdf file) for this purpose or always place the glass plate back at zero on the scanner (as in this example). If using several glass plates, the use of an overlay template is strongly recommended.

Before the technical scanning data can be adjusted, a scanning area has to be defined. To do this, move the mouse pointer onto the top left point. To select the area, press and hold the left mouse button, then drag the mouse pointer down to the bottom right-hand corner. To fix the selection, now release the left mouse button again. The selection is indicated by a dashed line. This now frames the whole preview area.



Next a histogram adjustment is necessary for the scanned images. To do this, single-click the left mouse button on the button for Histogram Adjustment.

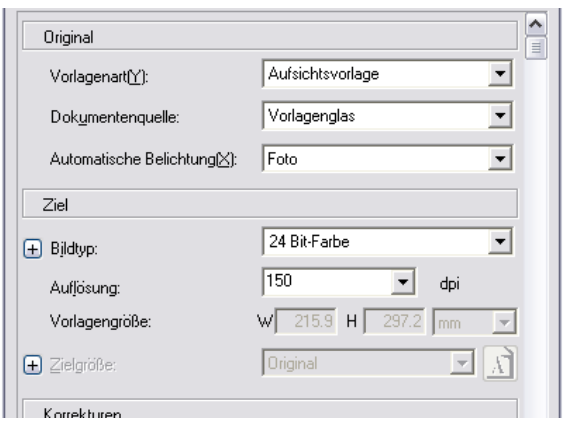
The window that opens after selection shows the current histogram.



For Ponceau S-stained gels and for Amido Black-stained gels, the following values[3] should be entered: Input: 25 / 1.00 / 220 from left to right; Output 10 / 245 from left to right.

No further settings in the Histogram Adjustment are required.
In order to keep these entries, press the “Close” button.

Now the type of original, document source and automatic exposure in dpi still have to be set. The required settings can be read from the following illustration:



For Standard Serum Protein Electrophoreses with the Ponceau S staining method, the following settings are used:

[3] Values may vary, depending on the system used.

Original

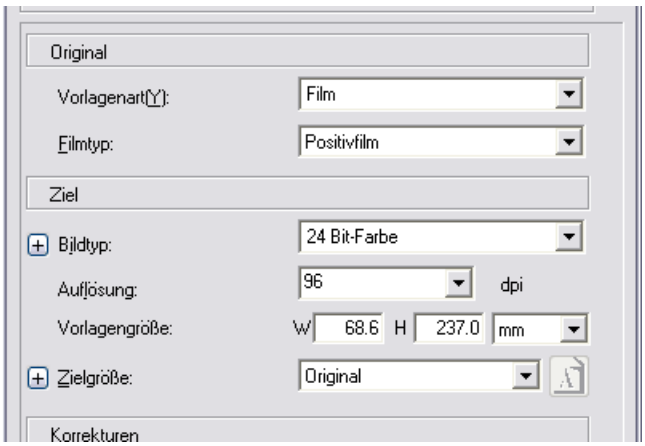
Type of original:	reflection original
Document source:	off-the-glass
Automatic exposure:	photo

Target

Image type:	24-bit colour
Resolution:	150 dpi

Amido Black-stained gels are measured in transmission mode. To do this, detach the white covering upwards from the inside of the cover. For analyses in transmission mode, the use of a positioning template is strongly recommended.

Type of original, document source, automatic exposure as well as image type and resolution should be entered as displayed below:



For Standard Serum Protein Electrophoreses with the Amido Black staining method, the following settings are used:

Original

Type of original:	film
Film type:	positive film

Target

Image type:	24-bit colour
Resolution	96 dpi

Once all the default values have been entered, these can be saved onto the hard disk.

8.1.1.3.3. Save settings

To save what is now the current setting, click on the left mouse button on the “Save” button in the top part of the Scan window. The data record is now saved under the name “Setting 1”[4].

8.1.1.3.4. Restore default settings

If you need to restore the current default settings, you simply have to click on the downward arrow in the popup window in the top part of the Scan window and single-click the left mouse button on the saved setting you wish to select. This deletes all the current settings and activates the settings you have selected.

8.1.1.3.5. Image scanning for Ponceau S-stained objects

You can start working with TurboScan once all the default settings have been made. For serum protein electrophoreses stained with Ponceau-S Red, work in reflection mode. To do this, place the glass plate onto the positioning template, if necessary, or at the zero point of the scanner (in this case the top right-hand corner of the scanner). The glass plate should be positioned so that the albumin bands show on the right and the first electrophoresis track comes to lie at the top edge[5]. Close the scanner cover. With the window still open for Professional Mode, single-click the left mouse button on “Scan”. The scanner is now set in motion and records the object placed on the flatbed.

8.1.1.3.6. Image scanning for Amido Black-stained objects

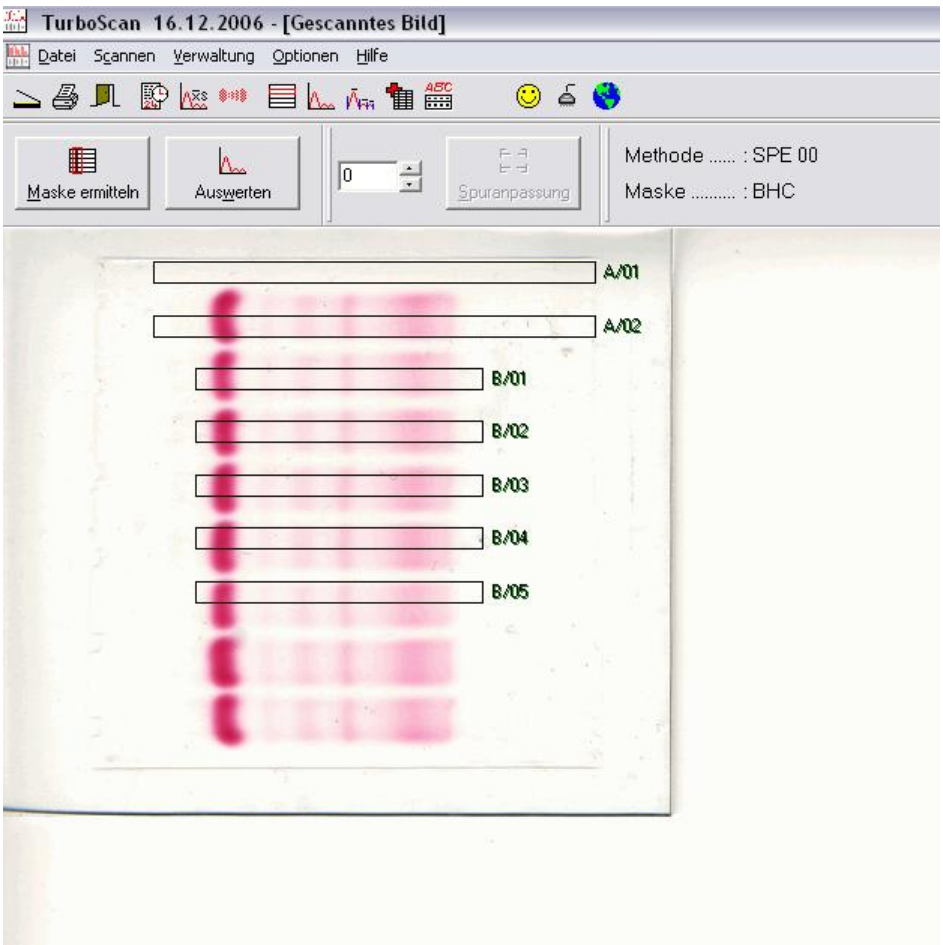
For Amido Black-stained gels, follow the same procedure as for Ponceau S-stained gels. The difference is that, as previously mentioned, scanning should be done in transmission mode. For Amido Black gels with weak staining, the reflection mode may also be used.

[4] The name may change, depending of the number of settings already stored.
[5] The positioning of the electrophoreses may change on alternative scanner models.

8.2. Analyse

8.2.1. Scan and Analyse

After the image has been scanned, the TWAIN window of the scanner closes automatically. The TurboScan window “Capture image” reappears with the image just scanned. If necessary, sections can be selected or the image can be rotated at this stage. Single-click the left mouse button on “OK” to confirm the image and hence transfer the image for analysis.
The Scanned image window opens in maximized mode. If a mask has been activated, the last-used mask appears screened over the image. If the positioning of the glass plate is identical, the mask can be used without any correction.

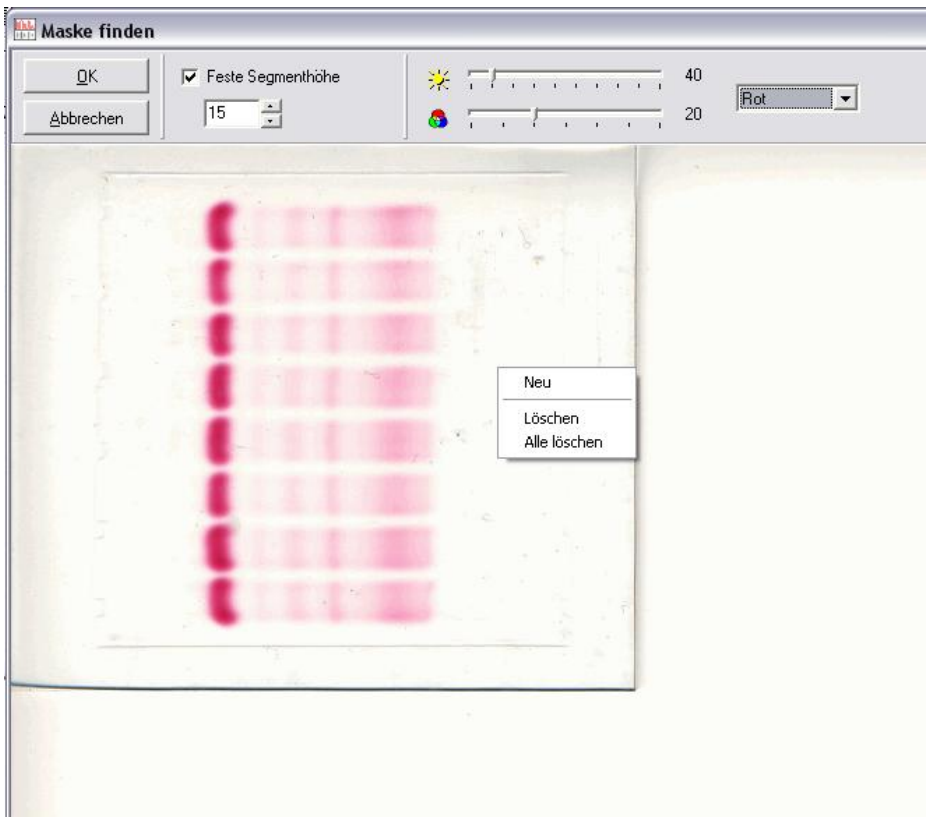


8.2.1.1. Automatically create mask

If you have originals where the content is constantly changing, it makes sense to use the automatic track search. When setting up an object type for the first time, automatic track search can also be used for one-off definition.

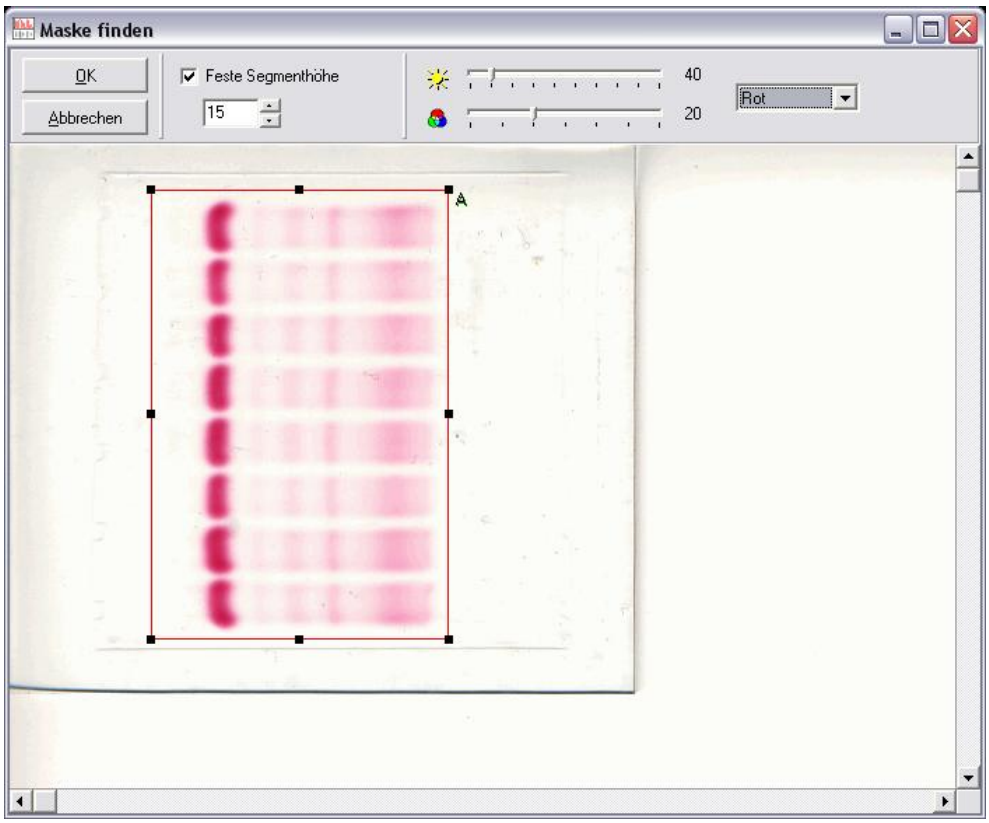
8.2.1.1.1. Mask arrays

To start the automatic mask-finding procedure, single-click the left mouse button on “Get mask”. This opens the “Find mask” window, which shows the current recording and a few functions for automatic track-finding. The fixed segment height indicates how wide each track to be read should be. This is identical for all tracks. If this function is disabled, each track is located individually in the current track width. The “brightness” and “colour intensity” slide controls are used for fine-tuning the track recognition. However, the program offers default settings which are optimized for standard staining methods. These can be selected in the popup selection window.
As the first step in mask creation, an area should be selected within which the TurboScan software is to search the tracks. Single-click the right mouse button inside the image to select this area. A small menu opens right next to the mouse pointer. Single-click the left mouse button on the first menu entry “New” to activate input mode. This is shown by the mouse pointer changing from the standard arrow shape into a cross-shaped cursor.



To select the desired area, position the cursor on the left above the tracks. Now press and hold the left mouse button. Drag the mouse to move the cursor into a position on the right below the electrophoreses. All the electrophoresis tracks should be located within the rectangle you have selected. Now release the left mouse button so that the position of the rectangle remains fixed. An identification letter appears at the top right-

hand corner of the rectangle to enable you to distinguish different areas later.



For correct track-finding, the frame needs to be positioned in the upper and lower border area against the background colour. If this is not the case, tracks may be incorrectly found.

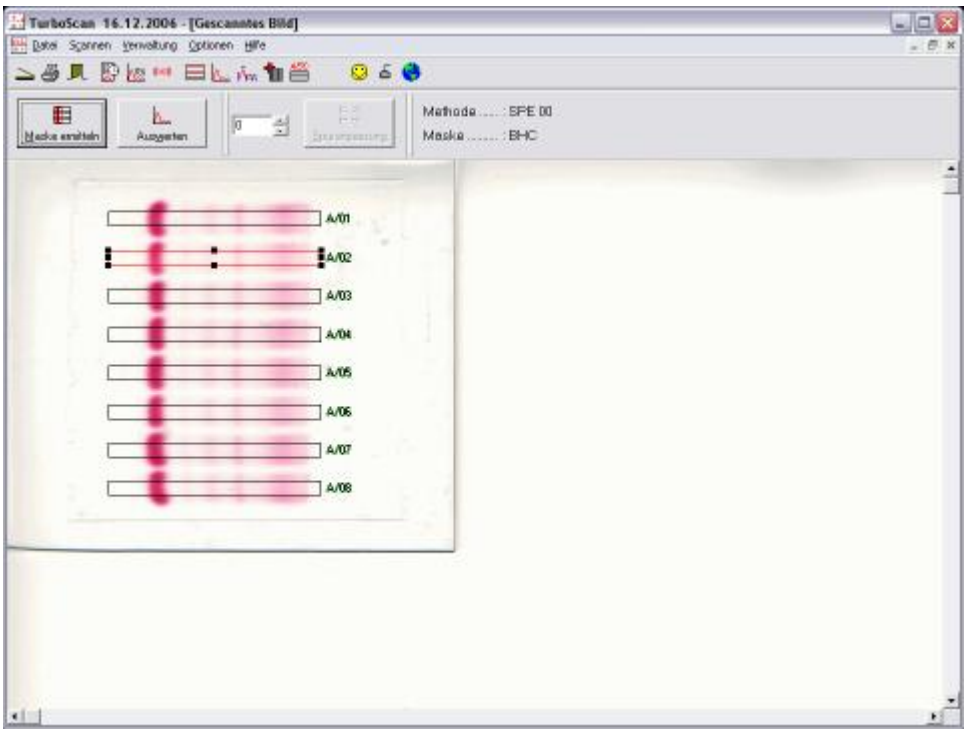
8.2.1.1.2. Segment width

For subsequent adjustment of the area, the black squares can be located with the mouse pointer. The pointer changes into double arrows indicating the direction in which a change can be made. Press and hold the left mouse button to change the frame in the directions indicated by the double arrow. Release the left mouse button to fix the frame in its new position.
Single-clicking the left mouse button on “OK” will start calculation of the tracks. The “Find mask” window closes automatically and the “Scanned image” window reappears with the newly calculated tracks.

8.2.1.1.3. Correction of mask segments

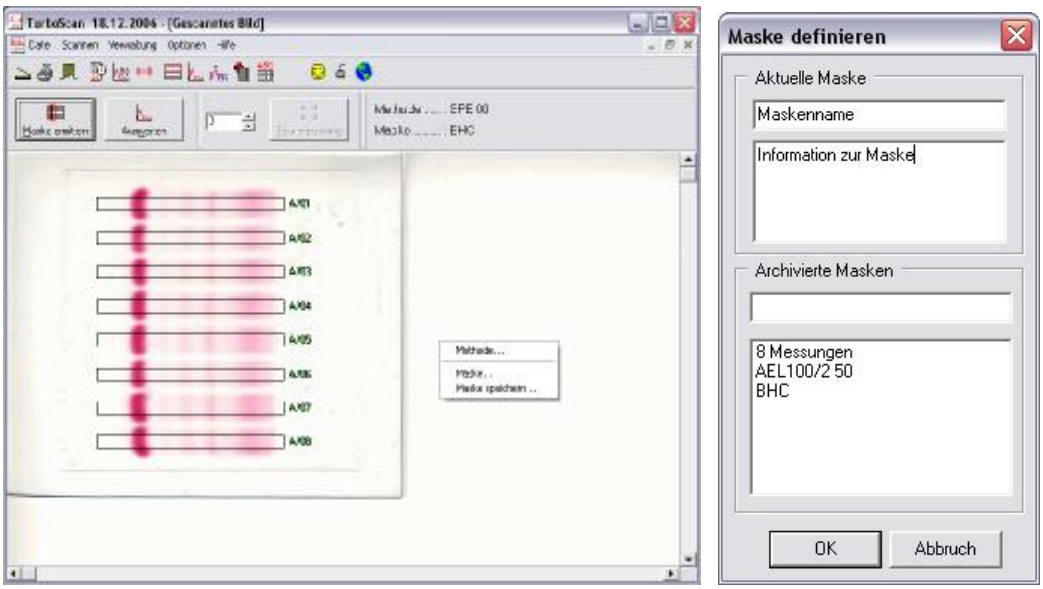
Normally no correction of the automatically located tracks is required. However, if tracks from a stored mask are used, there is a possibility that the tracks will have to be corrected slightly.
The procedure is identical to that of segment correction for automatic track-finding (see 8.2.1.1.2). However, before the correction can be made, the track to be changed must be activated. To do this, position the mouse point within the track to be changed and single-click the left mouse button. The frame of the track turns red and the black correction squares appear at the

corners and in the middle of the sides. The correction can now be done as described above.



8.2.1.1.4. Save mask

As the original objects do not normally change, it is enough to have the tracks found automatically once when the TurboScan software is installed and to save these tracks in a database. The advantage is that the appropriate mask is already loaded every time you start the TurboScan software and the analysis can be carried out immediately.
To save the current mask single-click the right mouse button in the “Scanned image” window. A small menu appears with the mouse pointer. Single-click the left mouse button while the pointer is positioned on the selected menu item “Save mask”: this brings up the reduced window “Define mask”. To input data, activate the “Current mask” field in the top part of the window. To do this, position the mouse pointer in the top narrow entry field and single-click the left mouse button. You can now enter the mask name via the keyboard. For more detailed information, such as selected scanning resolution, number of tracks, electrophoresis equipment used or similar, press the Tab key on the keyboard to skip to the entry field underneath. The desired or necessary information can now be entered via the keyboard.
When you single-click the left mouse button on “OK”, the current mask under the name you have just given it, together with the relevant information, is included in the Masks Database.



From the time it is saved, this mask is accepted as a default mask and automatically loaded after program start-up.

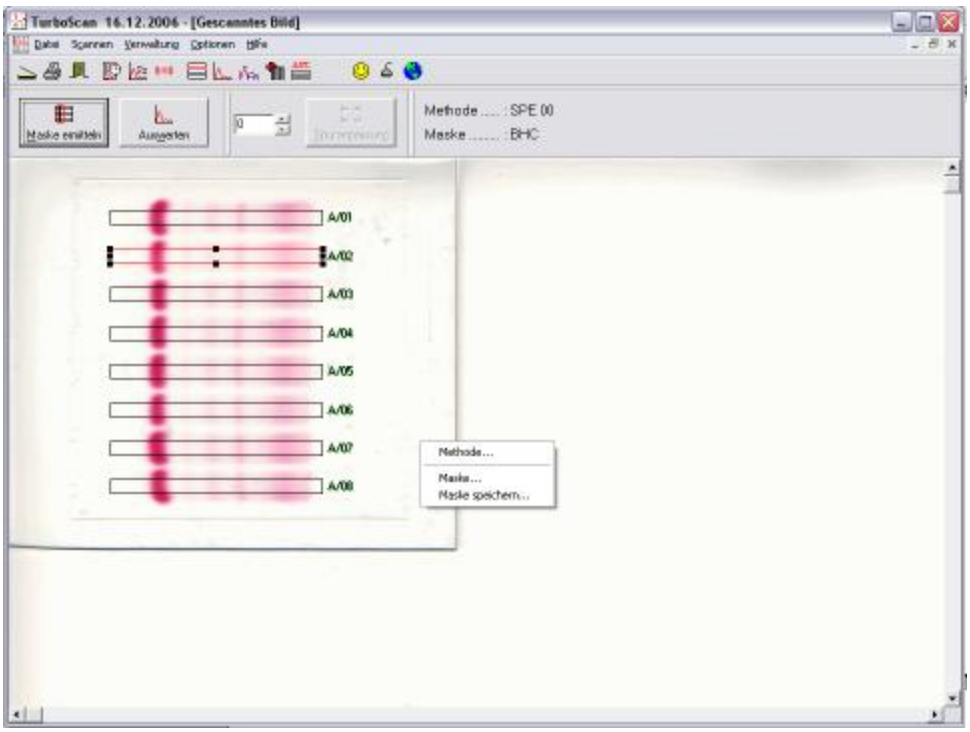
8.2.1.2. Select saved mask

In laboratories with several different analyses, it may be necessary to use different equipment for electrophoresis. This may require a change of mask. Once a mask has first been set up (8.2.1.1 ff. and 8.2.7.ff) and saved, it can be retrieved from the database at any time and used as a default mask. To do this, get the menu on screen as described under 8.2.1.1.4 and activate the selection “Mask”. The enlarged or the reduced selection window for Masks will appear, depending on the setting in the menu item Options.
The currently saved masks are displayed in the bottom left array of the enlarged window or in the bottom array of the reduced “Define mask” window. Double-click the left mouse button with the pointer positioned on a saved mask and the corresponding additional information will appear in the top array. Single-click the left mouse button on “OK” and the information displayed in the top array is. [.....][*]

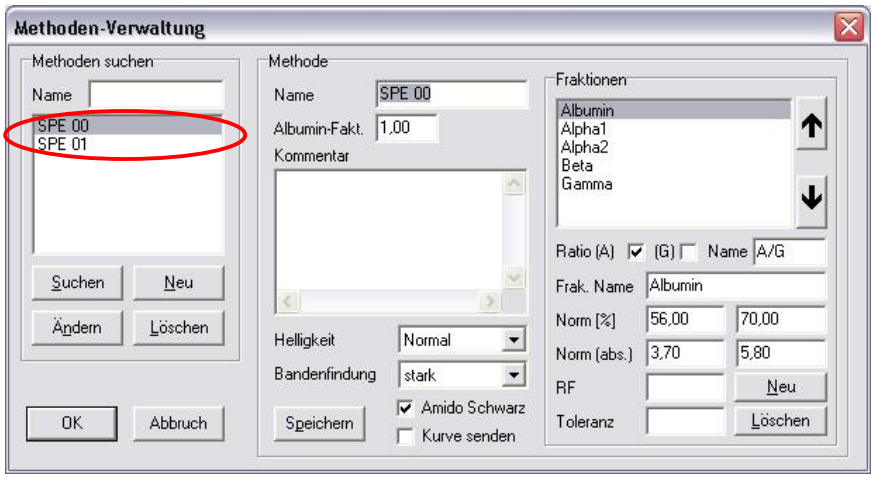
8.2.1.3. Method selection

Depending on the analysis requirements, it may be possible for the type of electrophoresis to change. For example, it may be necessary to switch the method from serum protein to lipoproteins or haemoglobins. To switch the method, single-click the right mouse inside the image in the “Scanned image” window. This opens a small menu. To select the menu point “Method”, move the mouse pointer onto the menu item and single-click the left mouse button.

[*] TRANSLATOR’S NOTE: Sentence is incomplete in the German.

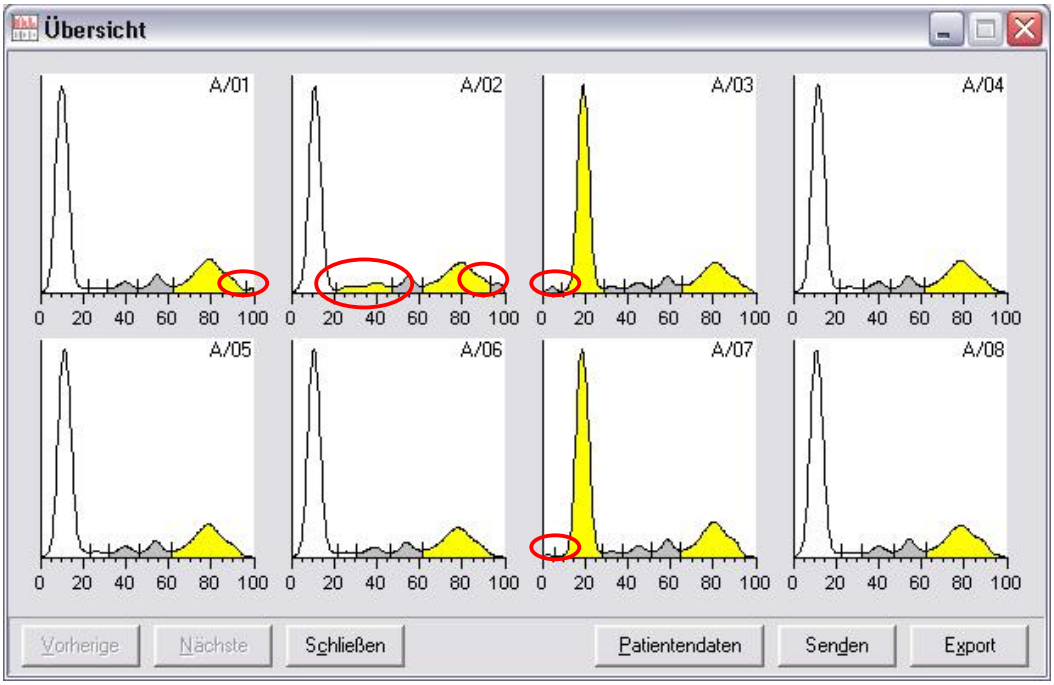


Once the menu point has been selected, the Method Management window appears. All the methods saved up to this point will appear in the left-hand array. To switch method, now simply select the desired method by positioning the mouse pointer on the desired method and single-clicking the left mouse button. Now click “OK” to include the selection in the analysis.



8.2.1.4. Analysis

After selecting the correct method, you can now start the analysis. To do this, simply single-click the left mouse button in the “Scanned image” window. TurboScan takes the current mask and analyses it.
After the calculations are completed, the individual curve profiles are presented in an overview window. Possible corrections may already be identified here. The first 8 curves together with the calculated minimum marks are displayed in the overview window. You will be able to see from this whether all the marks are correct and fully plotted.



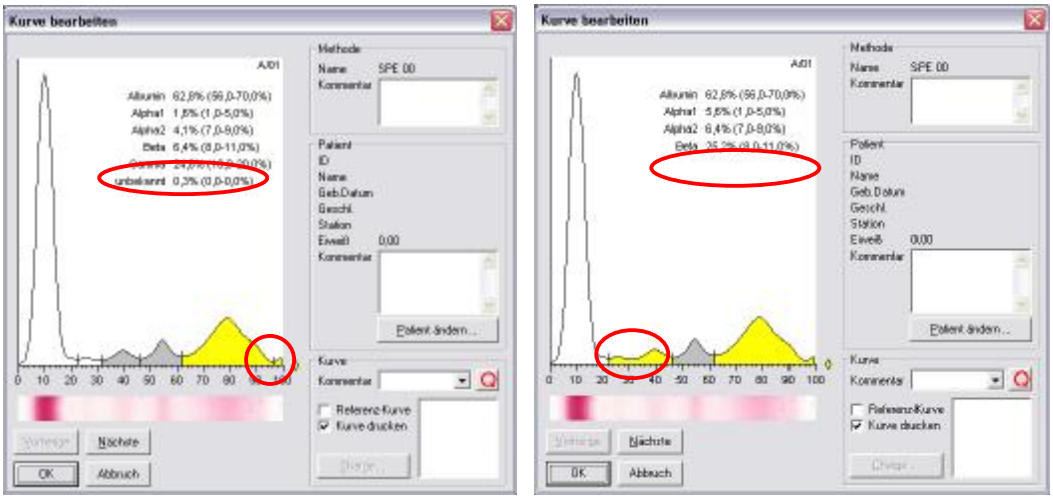
8.2.1.4.1. Correct minimums

In order to correct any incorrectly placed minimum marks, you must switch to Correction mode. To do this, move the mouse pointer onto the curve profile that needs to be corrected. Double-click the left mouse button to open the correction window for the selected curve. Within the graph of the curve profile, the mouse pointer changes to a cross.

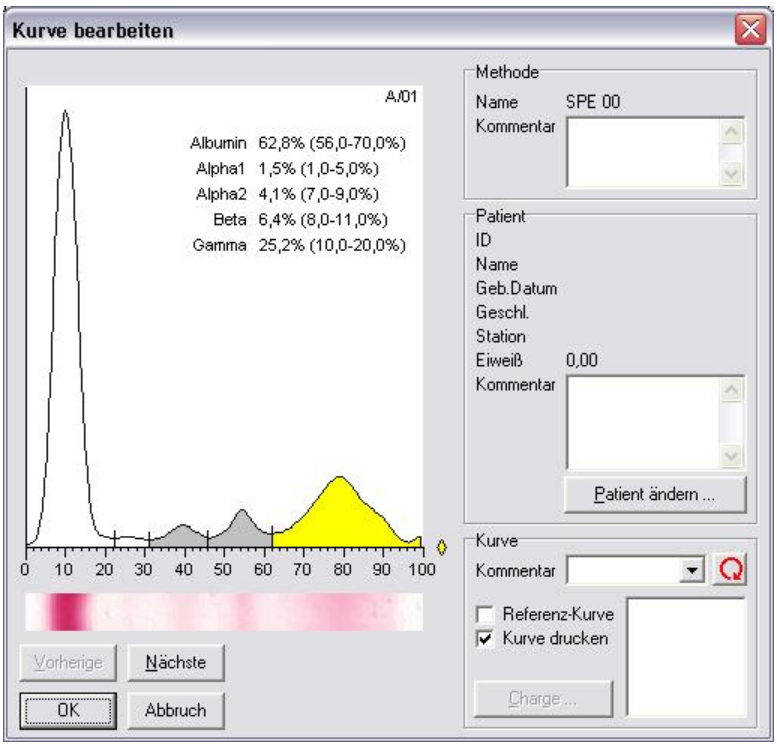
- To delete a minimum mark, position the vertical line of the mouse pointer as accurately as possible over the minimum mark to be deleted. The delete process is executed with a double click on the left mouse button. When double-clicking, make sure you do not move the mouse. If you do, the minimum mark will not be deleted. In this situation, Windows assumes that you are making two separate mouse clicks at different positions.

- To set a minimum mark, place the vertical line of the mouse pointer as accurately as possible at the point where the new minimum mark is to appear. The setting process is executed with a double click on the left mouse button. When double-clicking, make sure you do not move the mouse. If you do, the minimum mark will not be *deleted*.* In this situation, Windows assumes that you are making two separate mouse clicks at different positions.

TRANSLATOR'S NOTE: The German (*..wird keine **Löschung** der Minima Marke vorgenommen*) should probably read "*...wird kein **Setzen** der Minima vorgenommen"* = the minimum mark will not be **set**.



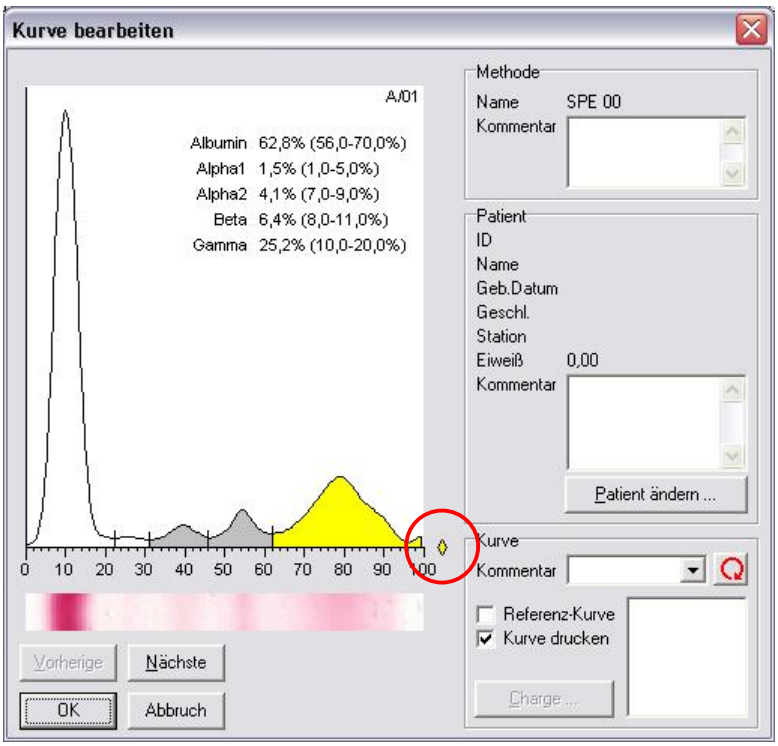
Depending on the defined method, a correction will be needed if a fraction is displayed with the name “unknown”. If this happens, it means that a minimum mark lies too much on the curve.
Conversely, if not all minimum marks are set, not all named fractions will appear in the list.



8.2.1.4.2. Baseline correction

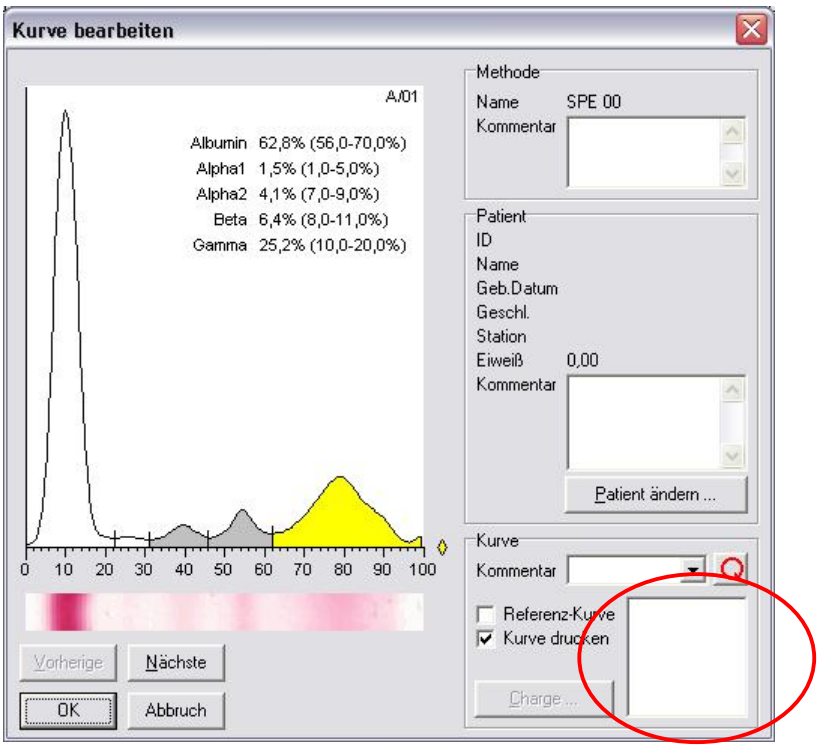
Although TurboScan optimizes the baseline, it may be necessary to correct the baseline. The baseline can be moved up or down parallel to the X-axis. To move the baseline, move the mouse pointer onto the diamond shape on the right next to the X-axis. Now press and hold the left mouse button. Moving the mouse up or down will drag a horizontal line with it, which represents the new baseline.
As soon as the left mouse button is released, the new baseline stays in that position. The position can now be confirmed or rejected via a query window. If the baseline is confirmed, the curve profile will be “cropped” at

that point. The lower part of the curve profile will be deleted and the upper part of the curve profile will be replotted on the X-axis.
Once this change is confirmed with the OK button in the correction window, the change is irreversible.
If you no longer want the baseline correction you have just made, click with the left mouse button on “Cancel” in the correction window. All changes to all the curves up to that point will be rejected.



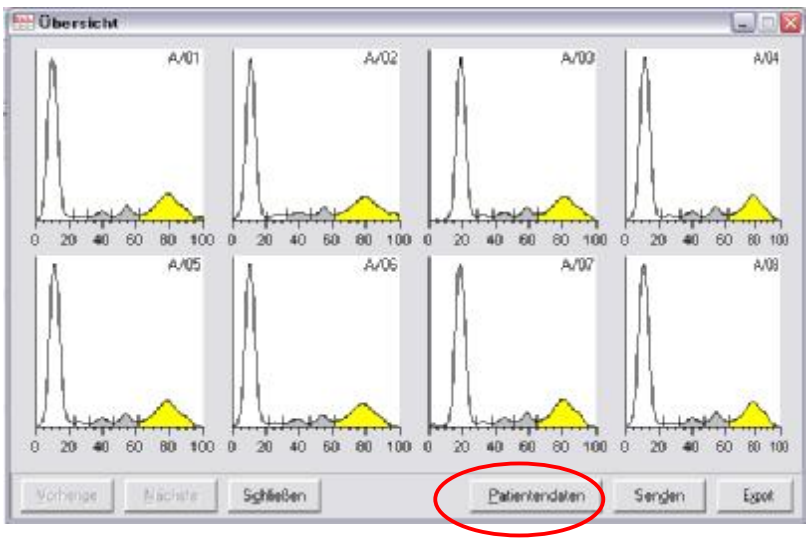
8.2.1.4.3. Comments

TurboScan gives you the option of including your own comments on the printout. The field in the bottom right section of the correction window can be used to do this. In the “Comments” section there is an entry field where free text can be entered. To activate the entry, position the mouse pointer in the field and single-click the left mouse button. A vertical line will blink in the entry field. You can now enter whatever comments you wish via the keyboard.
The entry is immediately active. This means that, as soon as another function is executed or a button is activated in the window, the text is confirmed as it is.
To delete the entry, activate the entry field as described above. You can now select the text and delete it with the “Del” key.



8.2.1.5. Patient Data

After any corrections have been made to the curve profiles, the patients' information can be entered into TurboScan. To do this, single-click the left mouse button on "Patient Data" in the overview window.

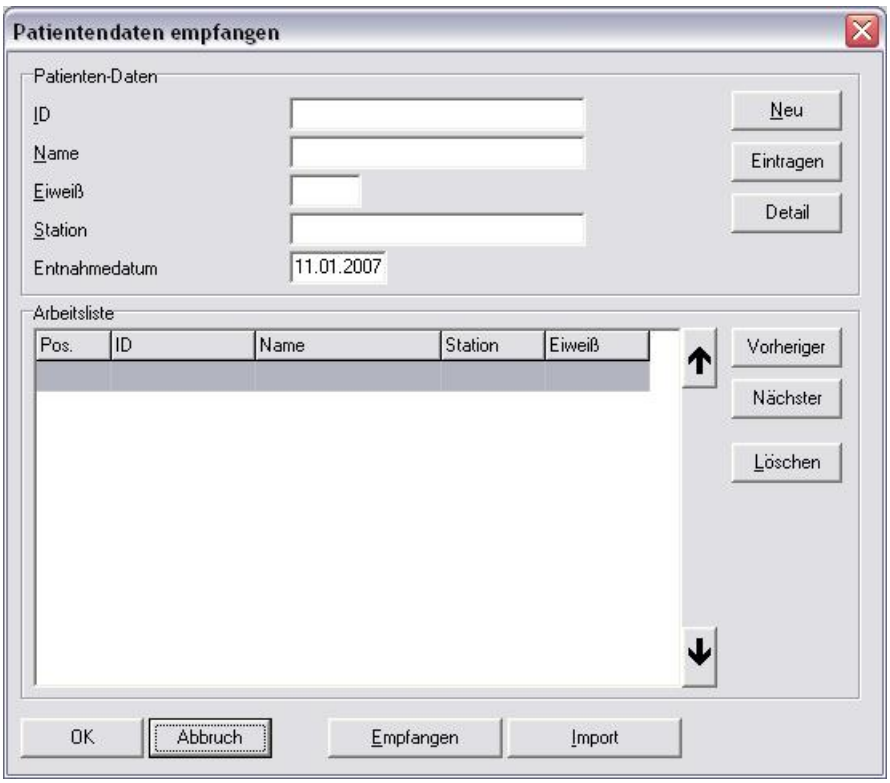


The patient data can either be entered before or after analysis of the electrophoreses.

For entry before analysis, single-click the left mouse button on the symbol in the header bar.

8.2.1.5.1. Patient Data entry

The Patient Journal window opens.



The are 3 possible methods of data entry available:

- via the keyboard
- via ASCII file
- via direct connection to a host

The options via ASCII file transfer and direct connection to a host are described in more detail in section 10 “TurboScan Communication”.

To start data entry, position the mouse pointer on the entry field “ID”[6] and single-click the left mouse button. A vertical cursor appears, which indicates readiness for an entry to be made in the Patient ID field.
You can now start entering data via the keyboard. The information required appears on the left next to the entry fields.
Use the Tab key to move to the next entry field, as usual in Windows[7].

The fields requiring entries have the following content:

ID : Clear identification of the sample

Name : Identification of persons by their name

Protein : The value for the total protein sample

Department : Department or place where the patient is located

[6] If automatic Patient ID allocation is enabled as described under 7.4.8, entry starts in the “Name” field.
[7] Key with the arrows pointing to left and right on the keyboard

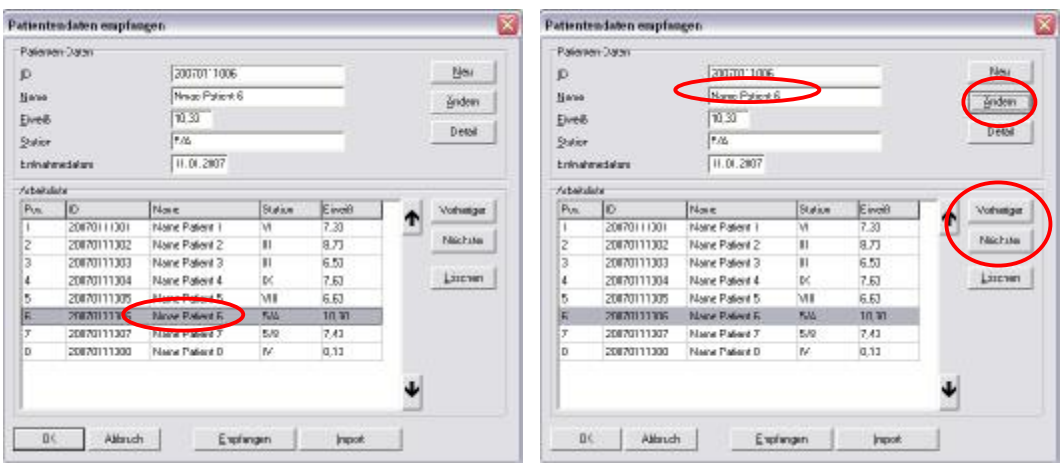
Collection date: The day the blood sample was collected, where this is not the same as the day of electrophoresis. This date is crucial to subsequent searches in the historical database for electrophoreses which were performed on a specific day.

Pressing the Tab key in the “Collection date” field moves the tab stop to the “Enter” button. Confirm the patient’s entry by pressing the ENTER key on the keyboard. The data record just defined appears in the list below the entry field. If the ENTER key is pressed again, the cursor moves again into the “ID” or “NAME” field in the case of automatic numbering.

Repeat this process until all the patient data have been entered. The list is confirmed with the OK button and is cached for any subsequent corrections that may be necessary.
The Patient Journal window re-closes.

8.2.1.5.2. Patient Data correction

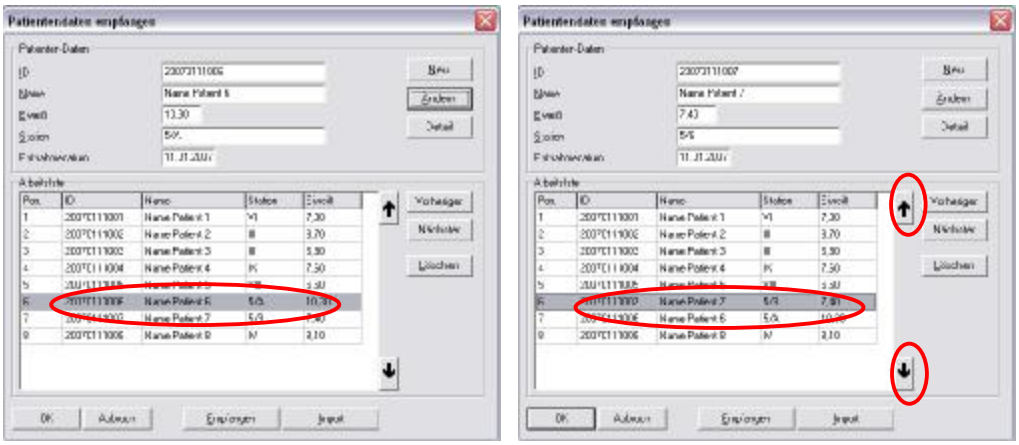
If you need to correct the content of one or more patient data, it can easily be done. Open the window for inputting the Patients Journal, as described above. Highlight the data record to be corrected by positioning the mouse pointer on the appropriate line in the list and pressing the left mouse button. Now the top entry section is filled with the data from the selected line. Any entry field[8] can be changed, as required. Confirm the changes by single-clicking the left mouse button on “Change” while the mouse pointer is positioned over the “Change” button. Any data record can subsequently be changed. The next data record to be changed can selected directly with the mouse or via the “Previous” or “Next” data record buttons. It is also possible to delete individual data records in this mode. The data record to be deleted should be highlighted as described above. Clicking the left mouse button on “Delete” when the mouse pointer is positioned on the “Delete” button will release the selected data record to be deleted. However, before the data record is deleted, the query “Delete this record only?” appears. Answer the query by clicking on “YES” if only this data record is to be deleted. If you click on “NO”, not only the selected data record but the whole list will be deleted. The “Cancel” button interrupts the delete process and no change will be made to the list.



[8] The “ID” field is blocked in the case of automated Patient ID and cannot be changed.

8.2.1.5.3. Correction of patient data – list sequence

It can sometimes happen that the work list does not coincide with the sequence of the electrophoreses. TurboScan allows you to bring the list sequence in line with the actual sequence of electrophoreses. In the following example, samples 6 and 7 were transposed in the electrophoresis.
To correct the list, select the data record in the patient list that is in the wrong position by positioning the mouse pointer on the data record and single-clicking the left mouse button. After selection, click on one of the arrows at the right edge next to the list. Every time you click on the arrow, the selected data record moves down or up one position, depending on the direction of the arrow. When you have finished correcting the position, confirm the corrected list by pressing the “OK” button.
This process can be repeated as often as you like.



8.2.2. Print

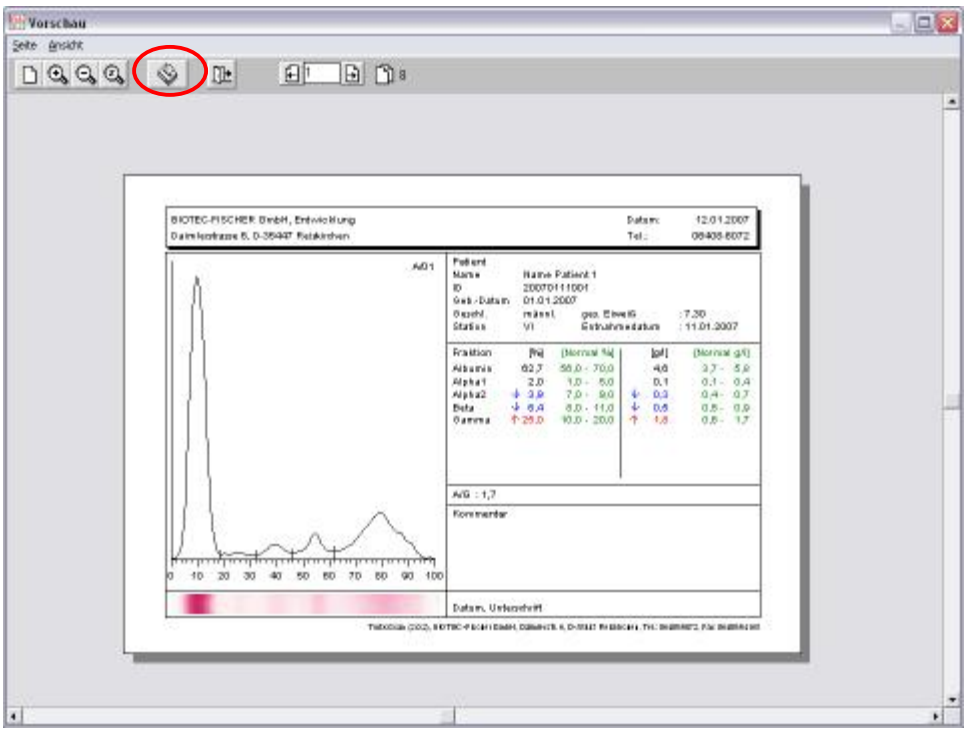
In most cases it is necessary to put the results onto paper so that the analysis can be attached to the patient’s medical records.

8.2.2.1. Prepare to print

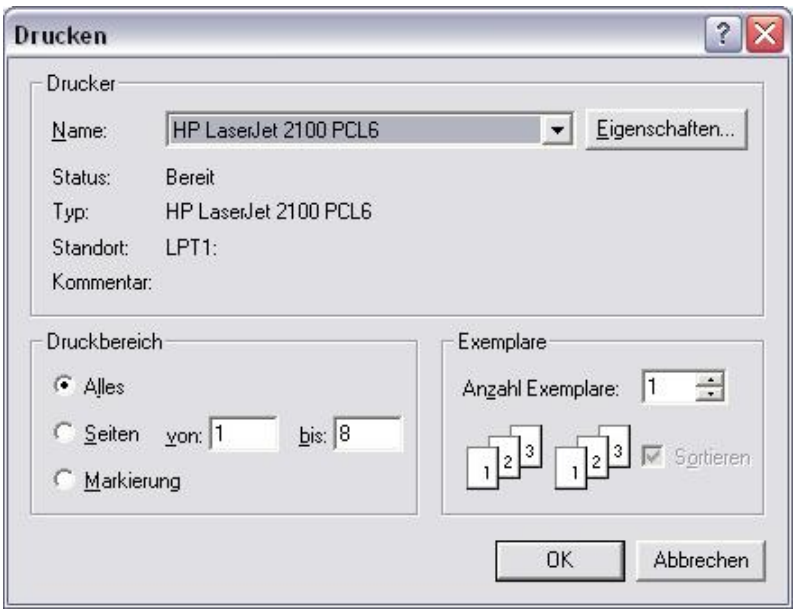
Printing can only take place if the curves and patient data are in the TurboScan memory. This is always the case if the overview window appears with the 8 curves. To make sure that the curve data have also been assigned to the patient data, you must have clicked on “Patient data” in the overview window at least once and re-closed the entry window for the patient data with the “OK” button. You can check whether data have been assigned by double-clicking the left mouse button while the mouse pointer is positioned on one of the curve profiles in the overview window. This opens the correction window. The patient data are displayed on the right side of the correction window. If no data are displayed there, no assignment of the patient data has taken place. If this is the case, you must perform the above procedure.

8.2.2.2. Start print process

Launch the printing process by single-clicking the left mouse button on . This opens the “Print Preview” window. Here the original printout is displayed on the screen.

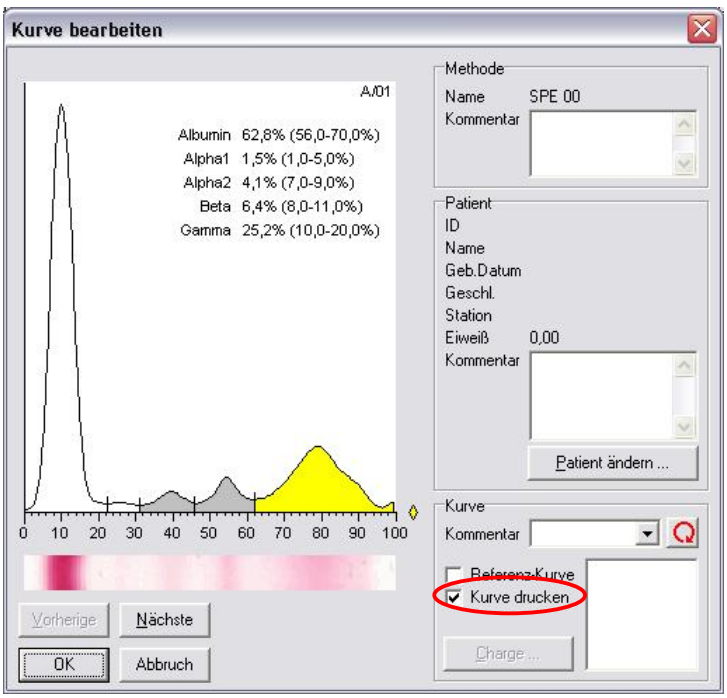


Pressing the printer button in the Print Preview window starts the printer dialogue. Pressing “OK” starts printing of all the curves.



8.2.2.3. Printing restrictions

Individual curves can be excluded from the printing. This is always necessary if an electrophoresis appears to be impossible to analyse or implausible.
For this purpose, Print Enable should be removed in the correction window. To do this, click on the checkmark in the “Print curve” box. The checkmark is now deleted. This curve will not be included in the printing process and therefore will not be printed out.



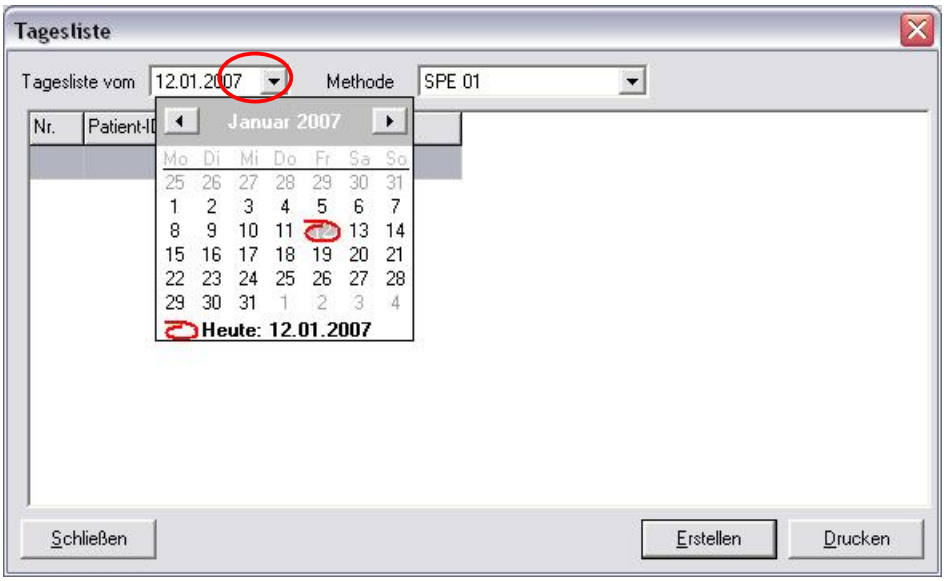
8.2.3. Exit

The Exit button is used to end the TurboScan program. Use this key when analysis of the electrophoreses for that day is completed.

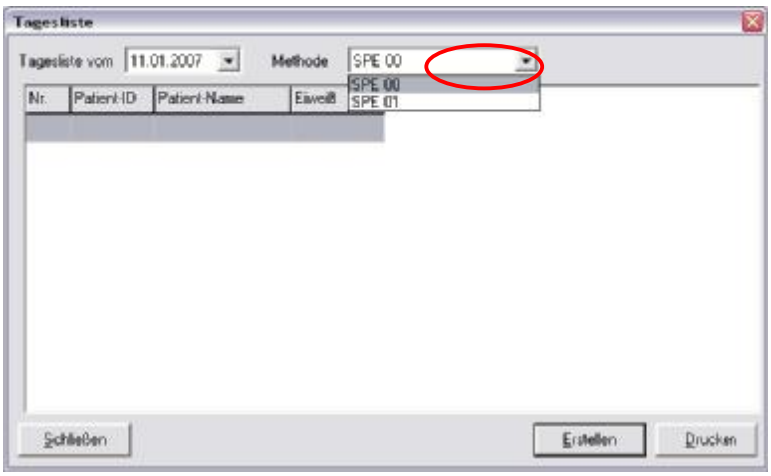
8.2.4. *Journal*

TurboScan can display all the analyses in one day in a “Journal” to provide a summary view. The journal contains only the key data of the analyses which were performed on a specific day by a specific method.

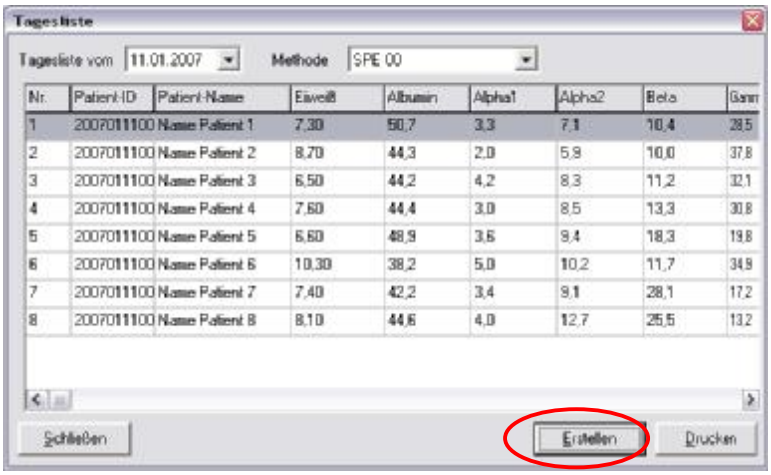
Open the Journal window by single-clicking the left mouse button on the “Journal” button while the mouse pointer is on the Journal symbol. To generate the journal, the required day must first be selected. There is a selection popup in the top section which is opened by single-clicking the left mouse button on the downward-pointing triangle at the right edge of the display. A month’s calendar page appears from which the desired date can be selected.



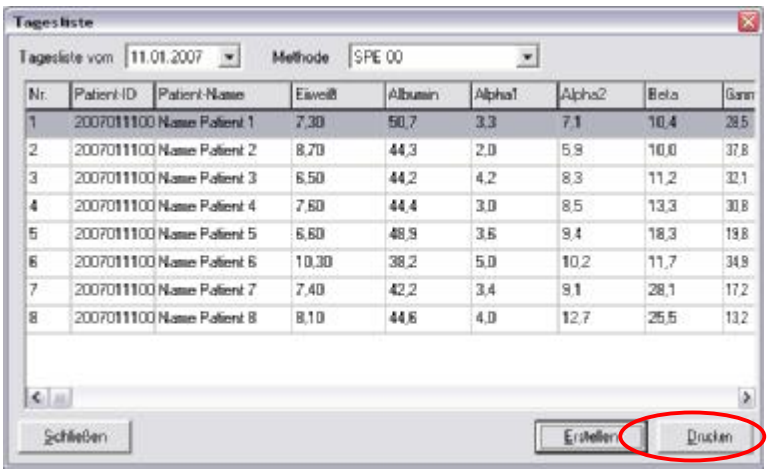
The correct method now needs to be selected to obtain the desired journal. To do this, single-click the left mouse button on the downward-pointing triangle at the right edge of the display to open the method selection popup window. All the methods available in the database will appear. Single-click the left mouse button on the desired method.



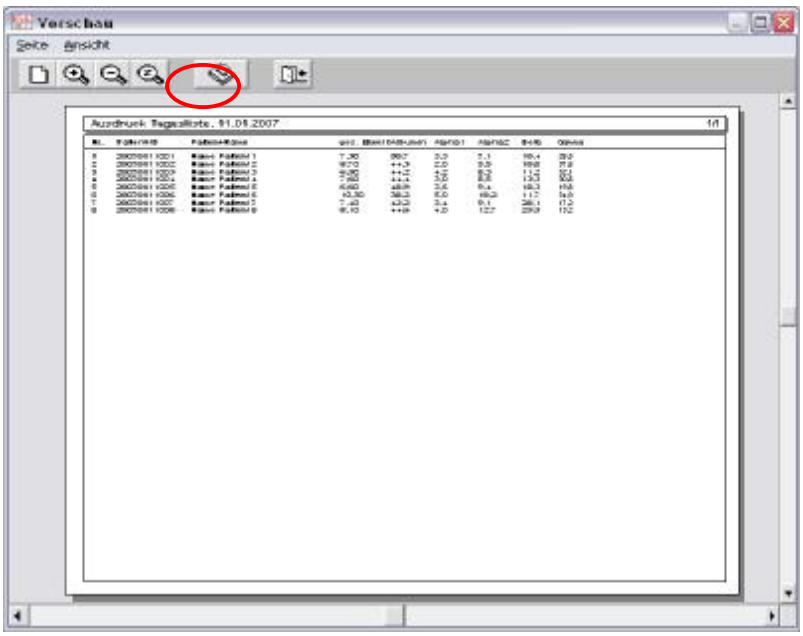
To create the journal with the conditions just selected, single-click the left mouse button on “Create” while the mouse pointer is positioned on the button.

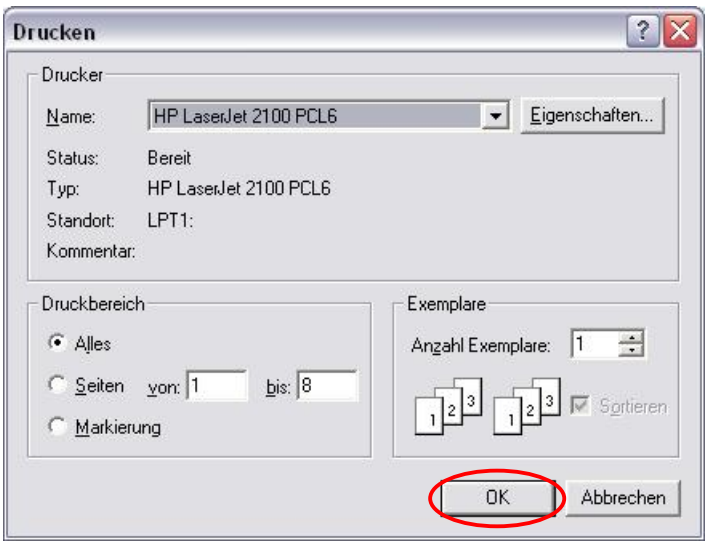


Once created, the journal can be printed out. To start the printout, single-click the left mouse button on “Print” at the bottom right of the Journal window. This opens the Print Preview window.



In the Print Preview window, click on the printer symbol again to open the printer control window. Press the “OK” button and the journal will be printed.





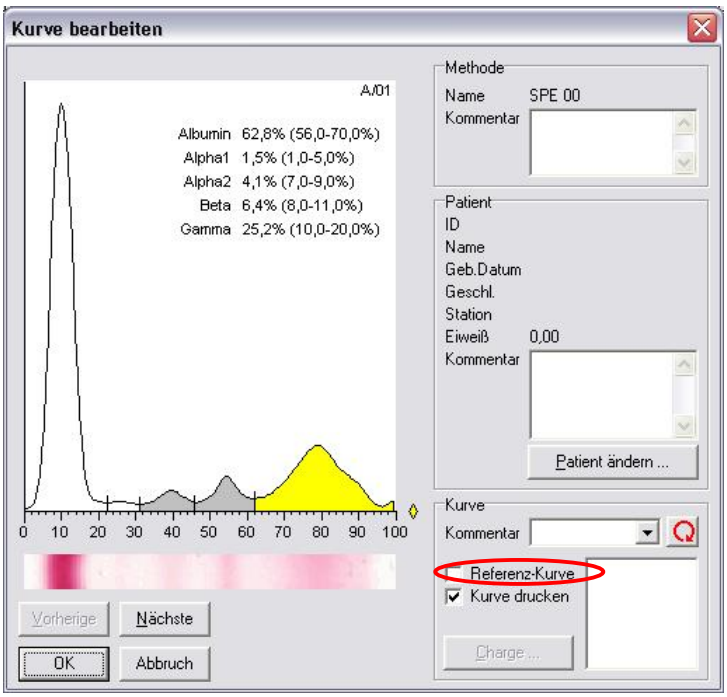
Clicking on the Exit button in the “Print Preview” window will re-close this window. Single-clicking the left mouse button on “Close” in the “Journal” window will close that window. Printing of the journal is completed.

8.2.5. Statistics

To maintain the highest possible quality of electrophoresis and analysis, TurboScan offers Statistics which have now become standard in laboratories. The precision of the electrophoreses and their accuracy can be ascertained and graphically presented with these Statistics.

8.2.5.1. Prepare Statistics

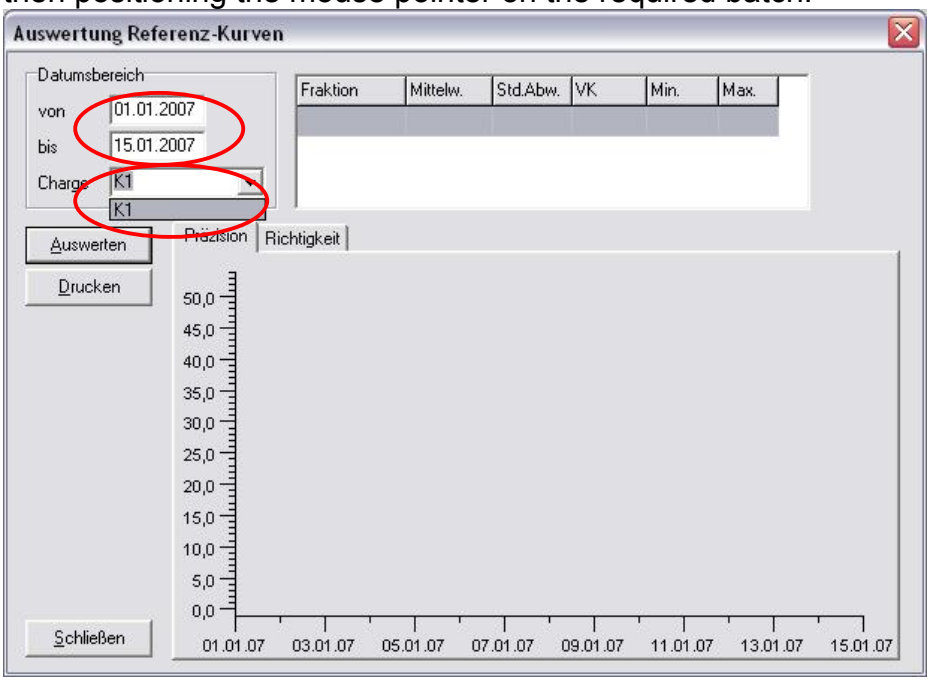
To be able to perform the statistics, data must be made available, based on which the statistics can be generated. To be able to make a reliable statistical statement, it is necessary to include electrophoresis control material at regular intervals. Depending on the frequency of electrophoreses, one track with control material can be loaded with every electrophoresis run. To allow this track to be included in the statistics properly, this track must be checkmarked as a track with control material. This is done in the electrophoresis correction window. In the bottom right section “Curve” there is a checkbox called “Reference curve”. If there is a checkmark alongside this box, the current curve is enabled for the statistics function and will be included in the calculation.



8.2.5.2. Statistical parameters

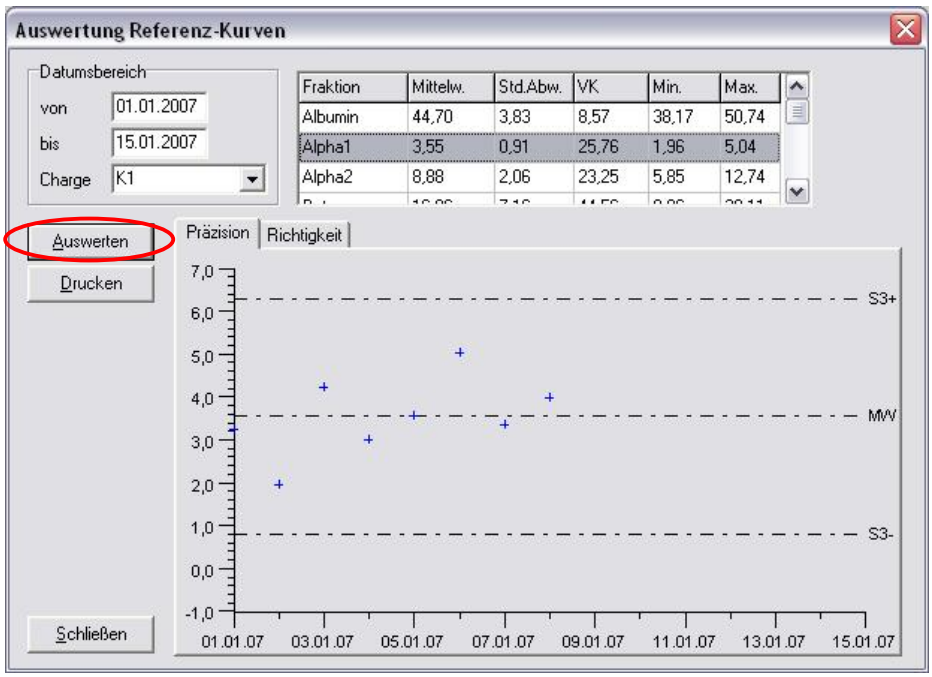
The statistics can be calculated from a freely definable period for each individual batch. Precision is calculated, which is a measure of the reproducibility of the system used. At the same time, accuracy is determined, which provides information about the correct setting of the electrophoresis system, measured by the given values of a control which has been used.

The time setting is entered in the top left section. Here the start time and end time of the statistical period are specified. To ensure correct calculation of the statistics, there must be values with controls during the displayed period.
In the same section, select the desired batch from the selection list popup by single-clicking the left mouse button on the downward-pointing triangle, then positioning the mouse pointer on the required batch.

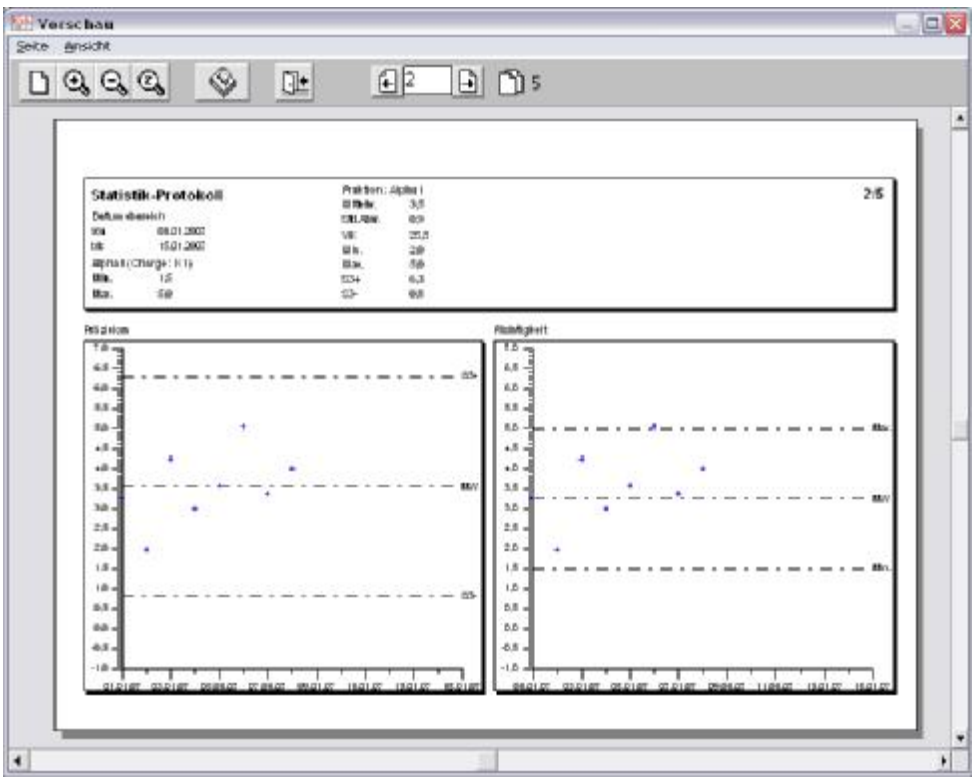


8.2.5.3. Statistical analysis of precision and accuracy

Once the necessary parameters have been selected as described under 8.1.6.2, the analysis can be started. To do this, in the Statistics window single-click the left mouse button when the mouse pointer is positioned on “Analyse”.
The values are immediately calculated in the specified period with the specified batch and the results are graphically displayed in the window.



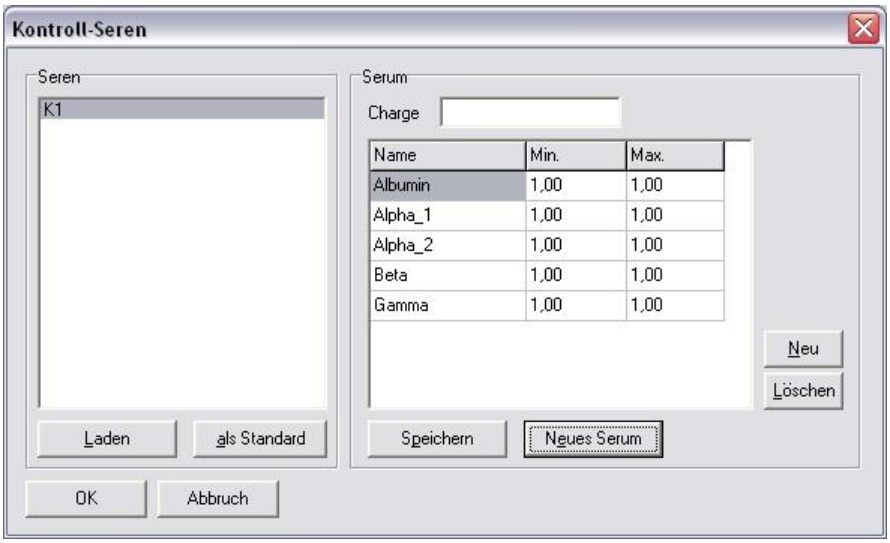
To print out the statistics, single-click the left mouse button on “Print”. The Print Preview window opens, which shows the Print original. A data sheet is printed for each band defined in the method.



8.2.6. *Manage Control Sera*

In order to calculate the accuracy in the statistics, it may be necessary to disclose TurboScan preset data for each individual band. This can be done in the window for managing control sera.

To define control sera, single-click the left mouse button on as soon as the mouse pointer is over the symbol. The entry window for Control Sera opens.

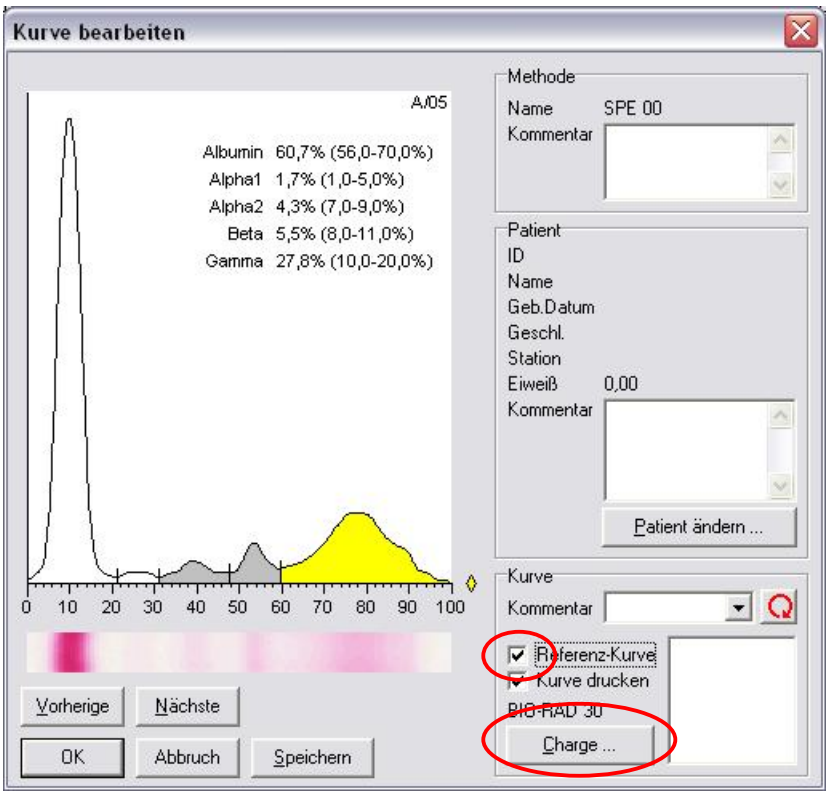


First the control serum should be given a clear name. It is sensible to use an abbreviation for the control in combination with the current batch number. This entry is limited to 10 digits. Single-click the left mouse button on the “Batch” entry field as soon as the mouse pointer is positioned in the entry field.
The fractions Serum Protein Electrophoresis are given as preset in the “NAME” field. However, these can be overwritten during entry. The values in the “MIN” and “MAX” columns should be those given in the packing leaflet of the control used, where the value given in the “MIN” field is the lowest and the value in the “MAX” field the highest value given for the relevant fraction. Once the data have been entered, save the entry just made by single-clicking the left mouse button when the mouse pointer is on the Save key. The data are now stored in the database and can be used.
The selected data record with the control values is loaded into the main memory using the “Load” button. This button is mainly used for correcting the curves.

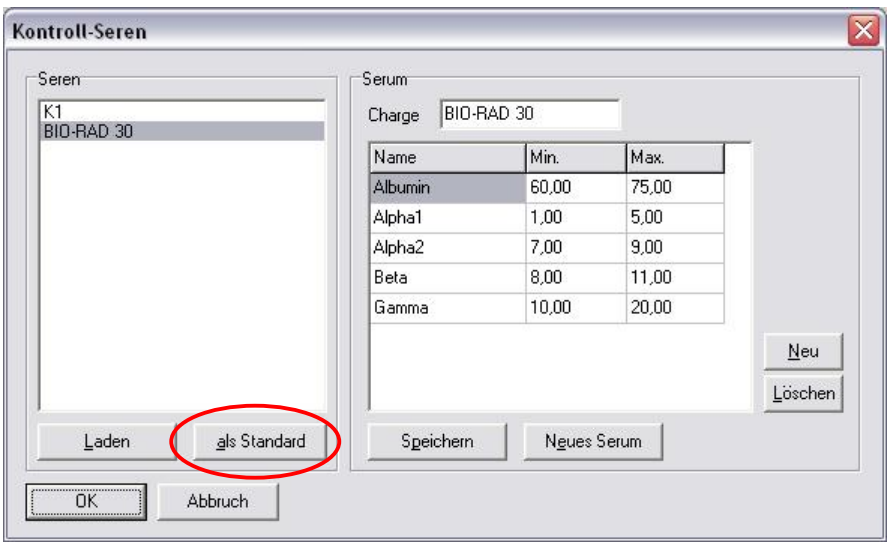
8.2.6.1. Use of control sera

To assign the control values to an analysis, the current curve must be selected as a reference curve in the correction window. To do this, in the

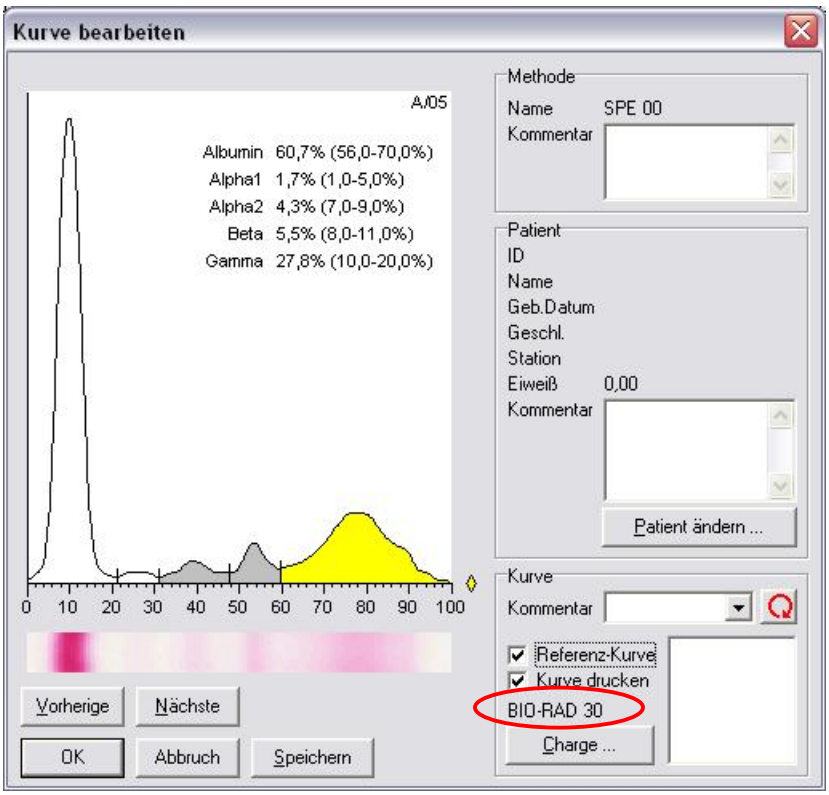
"Curve" section check the box for Reference *sera*[*] by single-clicking the left mouse button. Now the "Batch" key is enabled for selecting the set of values for the current analysis. Next single-click the left mouse button when the mouse pointer is positioned on the "Batch" key.



The window for managing the control sera opens. Single-click the left mouse button on the control used to select it. Single-clicking the left mouse button on "OK" will load the set of values of the selected control and assign them to the current curve. In the curve correction window, the name of assigned set of values is displayed above the "Batch" button.
If you are only working with a control, the selected set of values can be loaded automatically as default by pressing the "...as default" button when the "Batch" button is activated in the correction window.



[*] TRANSLATOR'S NOTE: In the graphic of the software, the checkbox is actually named "Referenz-Kurve", i.e. Reference *curve*.

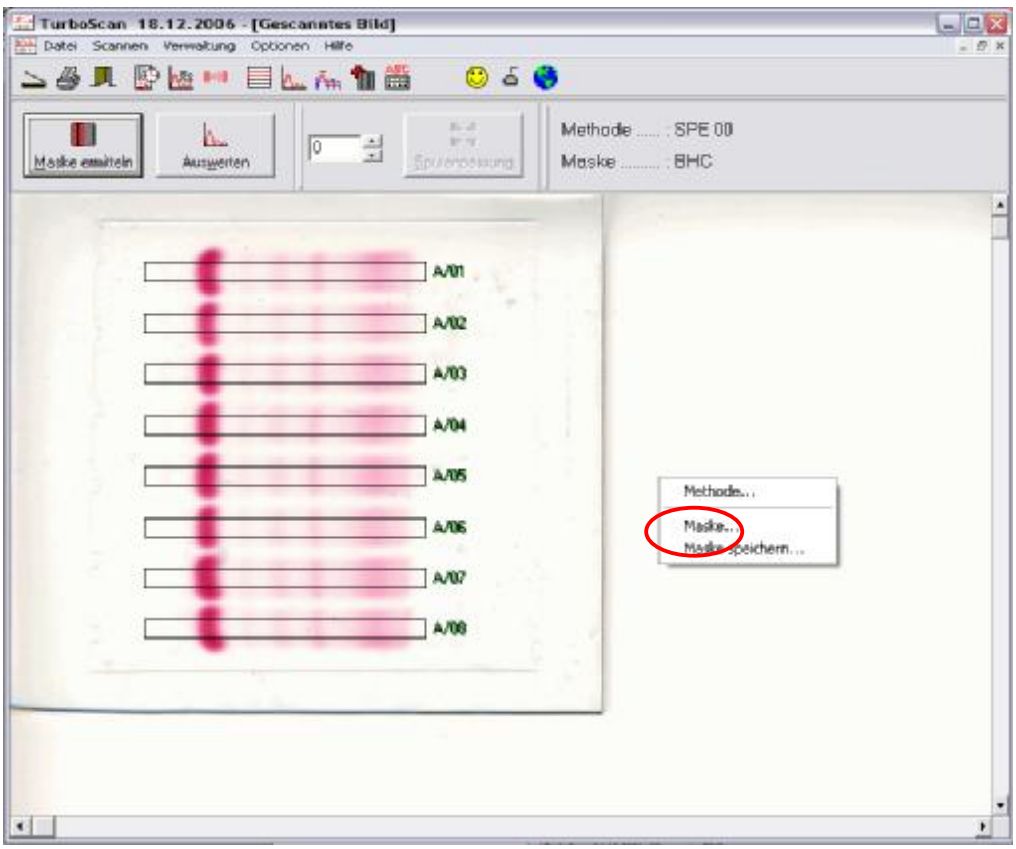

Kurve bearbeiten
A/05
Albumin 60,7% (56,0-70,0%)
Alpha1 1,7% (1,0-5,0%)
Alpha2 4,3% (7,0-9,0%)
Beta 5,5% (8,0-11,0%)
Gamma 27,8% (10,0-20,0%)
0 10 20 30 40 50 60 70 80 90 100
Vorherige
Nächste
OK
Abbruch
Speichern
Methode
Name SPE 00
Kommentar
Patient
ID
Name
Geb.Datum
Geschl.
Station
Eiweiß 0,00
Kommentar
Patient ändern ...
Kurve
Kommentar
Referenz-Kurve
Kurve drucken
BIO-RAD 30
Charge ...

8.2.7. Manage Masks

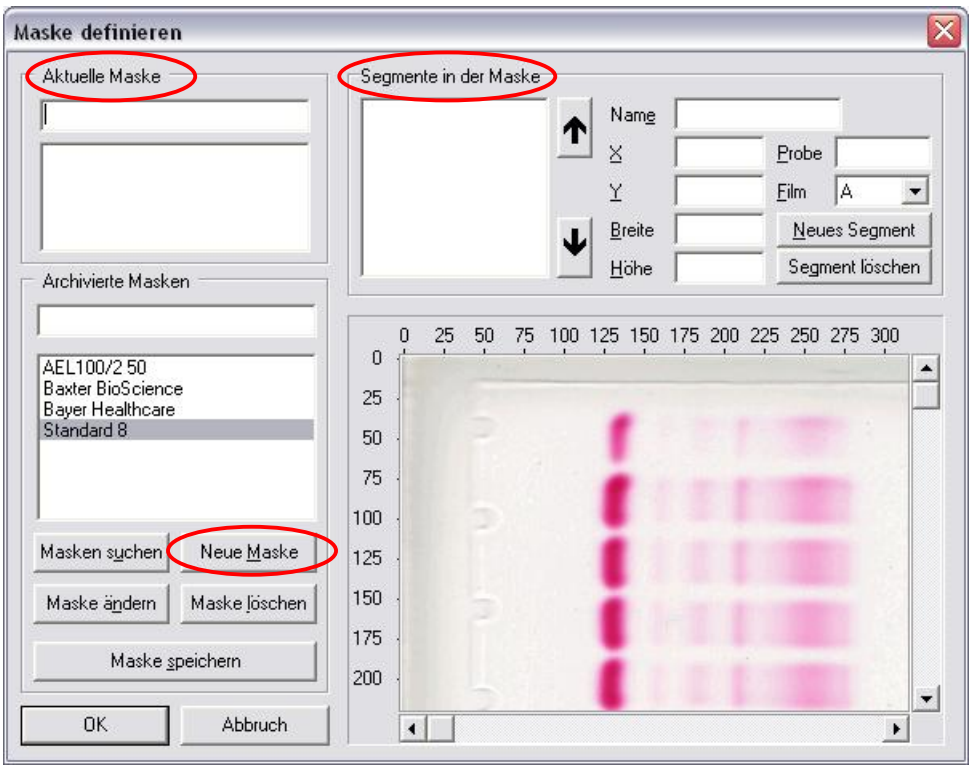
TurboScan not only offers you the option of finding the tracks automatically for analysis, but also defining these manually and saving them in a suitable data record. This procedure should always be chosen if an automatic track search is impeded so much by external circumstances (such as low-contrast staining) that a reasonable automatic search cannot be carried out.
There are no limitations on flexibility within the scanned area.

8.2.7.1. Create new mask

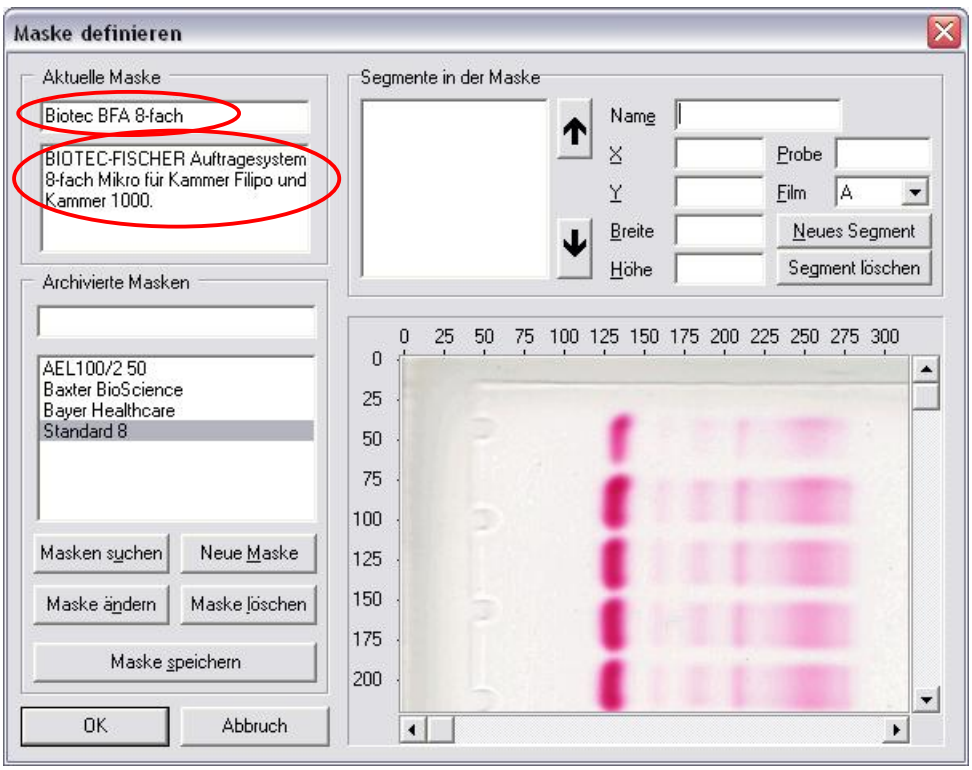
To create a new mask, an image must first be recorded with the object to be analysed (see 8.1.1.3.5 or 8.1.1.3.6). After recording and confirmation of the image in the “Capture image” window, single-click the right mouse button. A small menu appears next to the mouse pointer. Position the mouse pointer on menu item “Mask” and single-click the left mouse button.



The window for creating, processing or deleting masks opens.
Firstly single-click the left mouse button on the “New mask” button. The entry fields in the “Current mask” section and the mask in the “Segment in mask” section are cleared.



Next the name of the new mask should be entered. The name of the mask should be selected so that it can immediately be linked to the scanned object. A more detailed description can be given in the Comments field under the name.



Then the coordinates of the segments for the mask can be defined. The name of the segment, the coordinates and the sample number as well as object name are needed to do this.
The segment name identifies each segment clearly. In other words, when allocating the name, make sure that it is unambiguous and is not entered

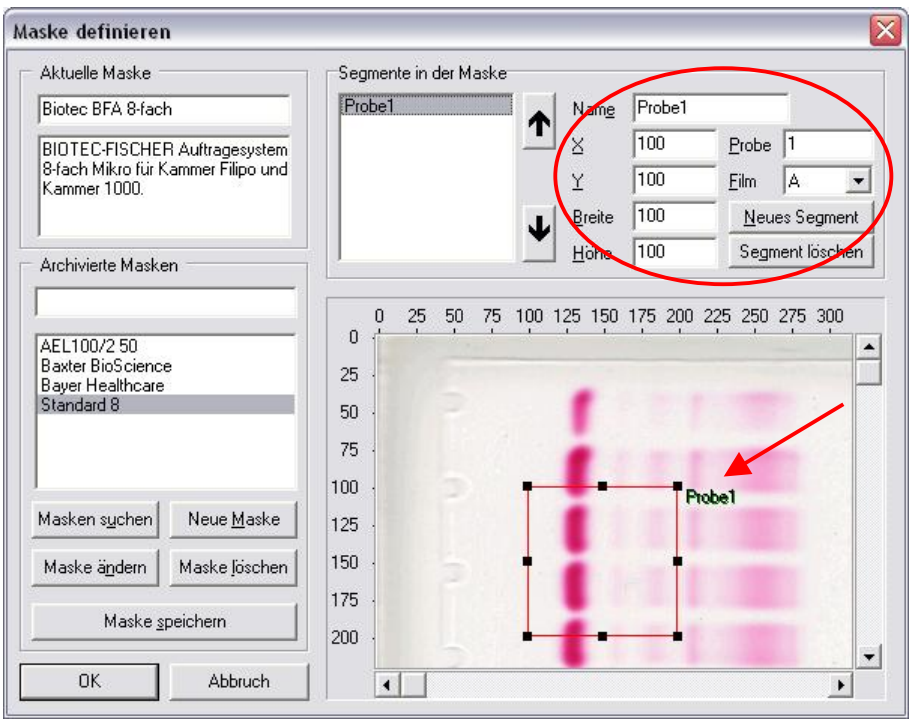
several times. If this happens, TurboScan will not save the “incorrect” segment. It has been found helpful to use a short identifier followed by a numerator.

Example:	Patient 1	or	Track 1	or	T1
	Patient 2		Track 2		T2 ....

Although the coordinates can be read from the axis caption, the accuracy of hitting a point is not very high. It is better to work intuitively here.
In order to work intuitively, a starting basis first has to be created. To do this, enter the following values:

Name: Sample1
X: 100
Y: 100
Width: 100
Height: 100
Sample: 1
Film: A

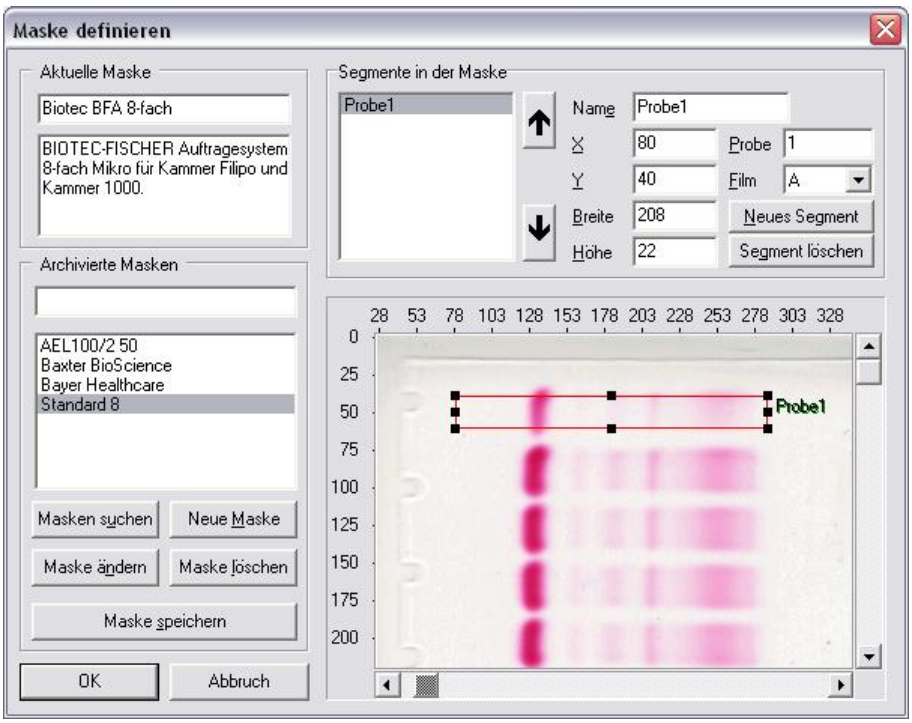
After entering these values, single-click the left mouse button on “New segment”. The above values are now incorporated and the first track is entered in the image.



Sample number and object name, here called “Film”, help to make it easier to assign the individual tracks to the image later.

The reading track just created now has to be placed in the correct position and be given the correct dimensions so that an analysis can take place. Activate the first track by single-clicking the left mouse button when the mouse pointer is positioned inside the track. To move the track, position the mouse pointer inside the track and press and hold the left mouse button. Now move the track so that the top left corner of the track comes to

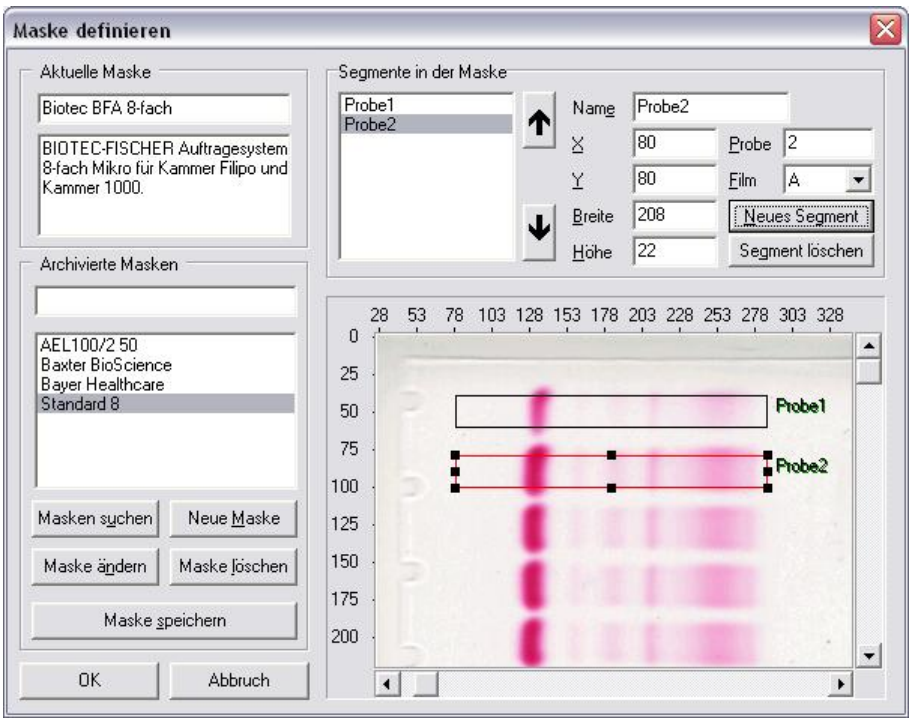
lie just in front of the albumin and the top horizontal line ends at the track. Now the left mouse button can be released. The track is now fixed in the position. To correct the width and height, position the mouse pointer on the bottom right black box. The mouse pointer changes shape to a double-arrow pointing diagonally from top left to bottom right. When the mouse pointer takes on this shape, press and hold the left mouse button. The width and height of the track can now be changed. Position the bottom right corner so that it comes to lie just behind the gamma fraction and the bottom horizontal line ends at the track. The values for X, Y, width and height in the display will change interactively.



For the rest of the tracks to be defined, simply change the fields for Name, Sample and Y. For the second track this would mean:

Name: Sample2
Y: 80
Sample: 2

All other values remain unchanged. As a result of this change, a new track with the name Sample2 is positioned and displayed in parallel below the first track with the same width.



All other tracks are defined by changing the Name, Y and Sample fields.

Tip: The difference in the Y-value from the first to the second track can normally be applied to all the other tracks. As the difference between the first and second Y- value is 40, the third track will have a Y-value of 120, the fourth track a Y-value of 160, etc.

After all the tracks have been defined, position the mouse pointer on “Save mask” and single-click the left mouse button. The mask is now saved.

You can save as many different masks as you like for subsequent use.

8.2.7.2. Load existing mask

As described initially under 8.2.7.1, open the window for managing masks. In the left section of the mask management window, the name of the mask to be activated can now be selected by positioning the mouse pointer on the name and single-clicking the left mouse button. Click on “OK” to confirm the selection just made, which is then incorporated into the program. The mask management window is closed and the mask just selected is active. This mask is now automatically loaded and displayed at every startup of the program. Every mask newly selected in this way automatically becomes the default mask.

8.2.7.3. Change existing mask

As described initially under 8.2.7.1, open the window for managing masks. In the left section of the mask management window, the name of the mask to be changed can now be selected by positioning the mouse pointer on the name and double-clicking the left mouse button. The matching values

for the mask just selected are displayed in the right section “Segment in mask”. Changes can now be made as described under 8.2.7.1. If no new name is entered for the mask, the existing mask will be overwritten with the new data.

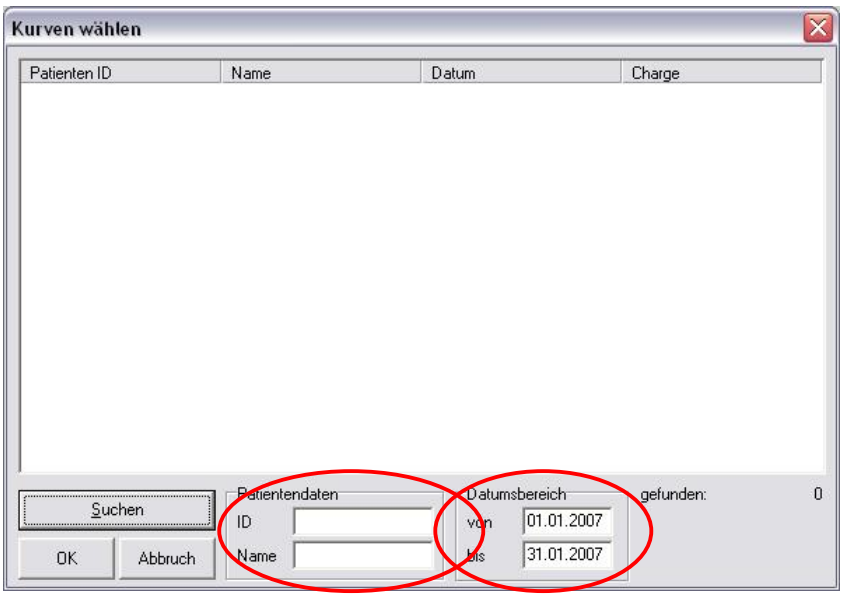
8.2.8. *Database Search*

The database search is used to find analyses from the past or to find analyses of a specific patient from a specific period or some other kind of search for analyses previously performed.

To open the dialogue, single-click the left mouse button on the symbol for sample management . The window for searching by analysis opens.

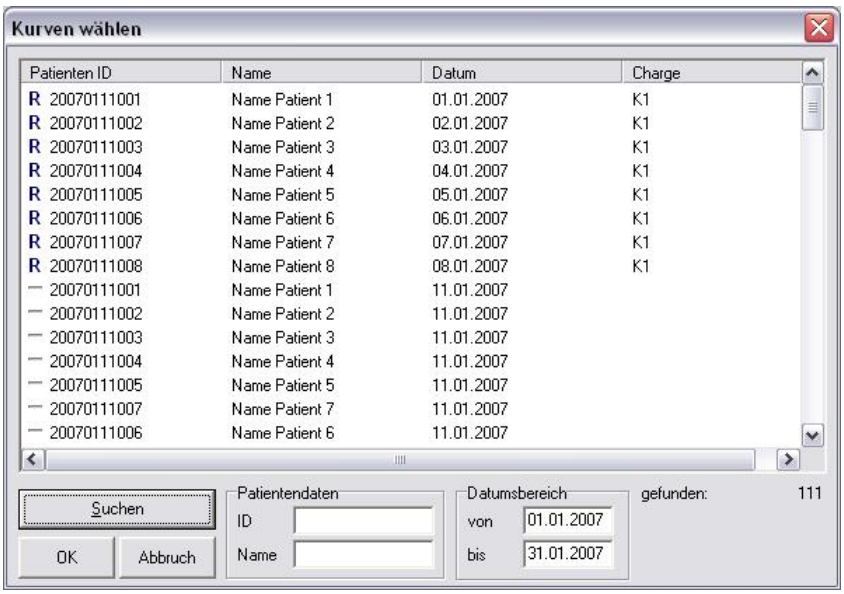
8.2.8.1. Search criteria

So that the search can be designed to meet requirements, information limiting the search needs to be entered. TurboScan automatically presets today's date as a search criterion, but any date can be entered in the date fields. Make sure that the start date is before the end date. As an additional criterion, the database can also be searched by patient ID or by name. You can also combine all 3 criteria in your search.



Start the search by single-clicking the left mouse button on "Search".
If no matches with the specified criteria are found in the database, TurboScan displays a message on the screen that there are no data records with the given criteria.

If the search is successful, the found data records are shown in tabular form in the display array.



8.2.8.2. Selection

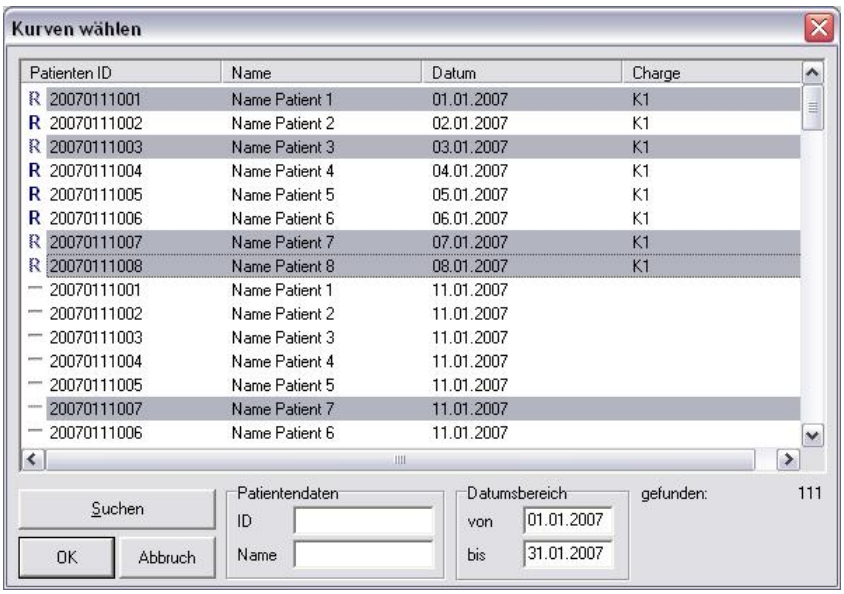
8.2.8.2.1. Grouped selection

After the found data have been displayed, the whole list or just individual data records from the list can be selected and loaded into the main memory.
To select the whole list, first position the mouse pointer on the first line of the list window and single-click the left mouse button. This will have highlighted the first data record. Now position the mouse pointer on the last position in the list. Select the last entry in the list while pressing the Shift key[9] at the same time. This will select all the data records. Groups within the list can be selected in this way. Always select the first and last data record in a group, as described above.
If the list is longer than the window can display, a scroll bar appears on the right of the list, which you can use to scroll to the last data record. To do this, position the mouse pointer on the slider of the scroll bar, press and hold the left mouse button. Moving the mouse downwards will move the list down as well. Now you can release the mouse button.

8.2.8.2.2. Single selection

Single selection involves taking single data records out of the displayed list. To do this, each data record has to be selected separately. To carry out a single selection, for each data record selected, click the left mouse button with the mouse pointer on the relevant data record while pressing the “Ctrl” key on the keyboard.

[9] Key for capital letters



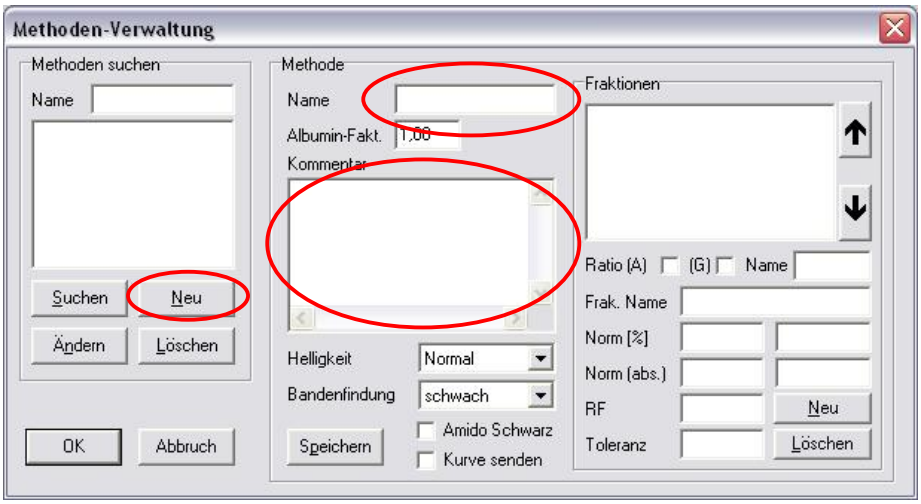
After the data records have been selected, confirm the selection with the “OK” button. The data are retrieved from the database and loaded into the main memory. The data will be available there for subsequent printing, for example.

8.2.9. *Manage Methods*

TurboScan allows you to save electrophoresis methods in a database. This applies to the currently known methods but equally to any that are not yet known at present.
The Method does not specify the procedure but the designation of known fractions linked to a specific procedure. For example, Serum Protein Electrophoresis: this is performed according to specific instructions and the appearance is always the same. The first fraction to appear is albumin, followed by the globulins alpha 1, alpha 2, beta and gamma. This sequence is always the same in the routine procedure.
To open the Manage Methods window, position the mouse pointer on the Manage Methods symbol and single-click the left mouse button. This opens the Manage Methods window.

8.2.9.1. Create new default method

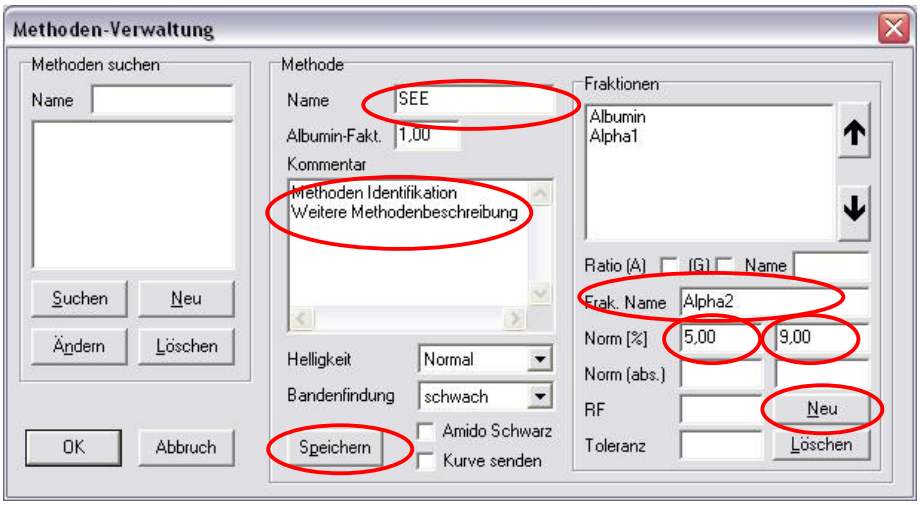
To create a new method, position the mouse pointer on “New” and single-click the left mouse button. Then the first step is to enter the name of the new method in the top entry field in the “Method” section. Make sure that the name of the method identifies the nature of the electrophoresis as much as possible. This will simplify selection of the method later. The entry area field the method name can be used for additional information. The first line of the comments field is included in the eventual printout to document the method used before identification of the track.



After the name of the method has been entered, the method has been identified on the printout and an additional short description has been given, you can now move over to entering the individual fractions. Position the mouse pointer in the “Fract.name” entry field and single-click the left mouse button to start the entry.
Enter the name of the fraction for this method in the “Fract.name” field. Based on the example of Serum Protein Electrophoresis, this would be Albumin[10]. In the “Norm[%]” fields: enter the minimum value of the normal

[10] Variations in subsequent electrophoreses of serum proteins are possible.

range for relative percentages in the left-hand field and the maximum value in the right-hand field. In the “Norm[abs.]” fields: enter the minimum and maximum normal values for the absolute total protein of the relevant fraction. The entries in the “Fract.name”, “Norm[%]” and “Norm [abs.]” fields should be repeated for each fraction and confirmed by clicking on “New” in the “Method” section.

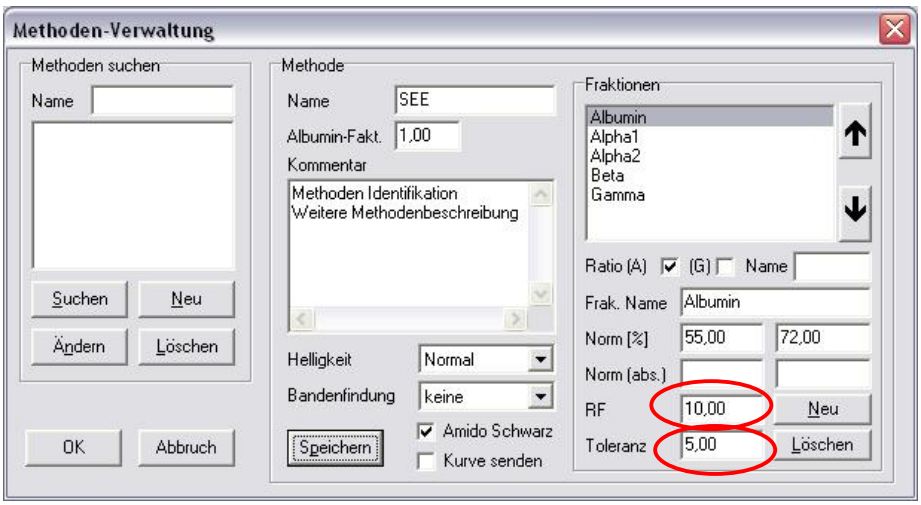


Before saving, take note of sections 8.2.9.3 – 8.2.9.8.

Once all the information has been entered, single-click the left mouse button on “Save”. The method is now stored in the database and can be activated at any time.

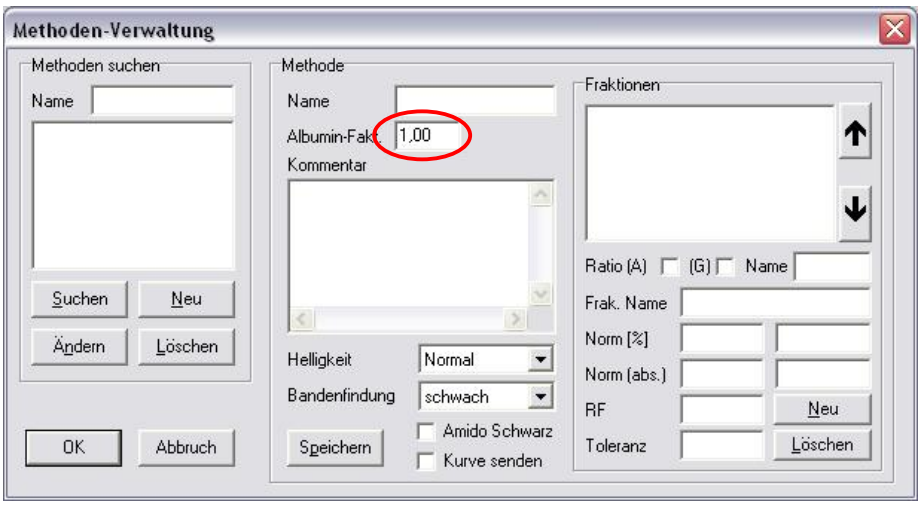
8.2.9.2. Create new position-dependent method

Methods with position-dependent fractions should always be chosen if the appearance or absence of a fraction denotes a normal or pathological condition. In contrast to the normal method, where the sequence of the fractions is always identical, this entry offers a higher degree of flexibility.
A new method with position-dependent fractions is created as described under 8.2.9.1. In addition to this information, the “RF” and “Tolerance” fields are completed.
The “RF” field denotes the position at which a fraction always appears. The % measure on the X-axis is made use of here (see illustrations in 8.2.1.4.1). From the example of the illustrated curve profiles, it can be seen that the albumin fraction is always at the 10% position of the development distance. This value, 10%, is entered in the “RF” field for the fraction albumin. As the fraction albumin is not always found exactly at the 10% position of the development distance, but can also be found at the 8% or 14% positions, an appropriate tolerance value should be entered in the “Tolerance” field. If the value 5 is entered, for example, it means all fractions that are within the range of 10% ± 5%, hence 5% - 15%, are declared as albumin.
These entries are made for each fraction. Thus each fraction is correctly named in the correct position, whether or not it actually appears.



8.2.9.3. Albumin factor

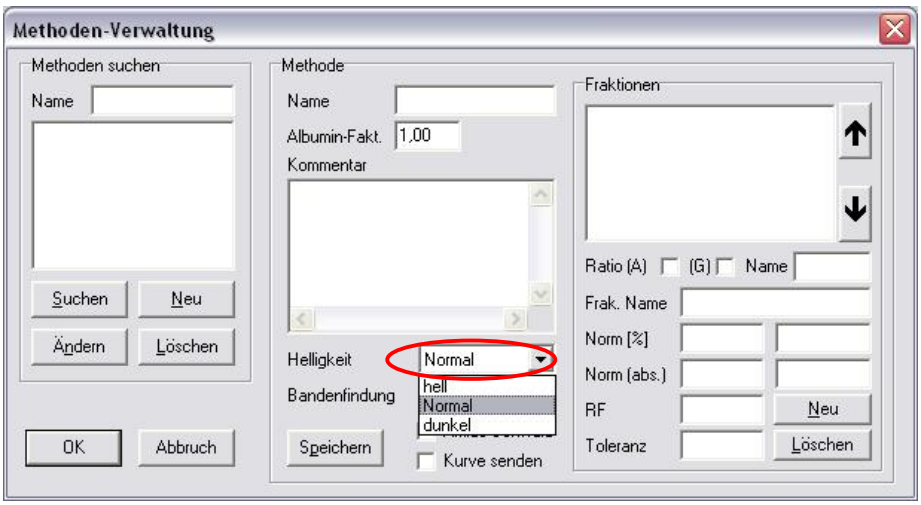
The albumin correction factor originates from the early times of paper electrophoresis. This made up for the fact that the maximum extinction of the albumin band could not be determined. To compensate for this shortcoming, a mathematical method was used to calculate the correct ratio of albumin to globulins.
This factor is still used today for correction of the A/G ratio. The factor 1.00 stands for no correction. If the value is reduced, the ratio shifts in favour of the globulins. If the value is increased, the ratio shifts in favour of albumin.



8.2.9.4. Brightness

Depending on the staining method and recording quality, there may be fluctuations in the staining of the electrophoresis image recorded. If very bright images are being recorded, the “Bright” setting should be selected. Accordingly, the “Dark” setting should be selected for very dark images with a lot of background. For standardized images, the setting should be “Normal”.
Make the brightness selection by positioning the mouse pointer on the small downward-pointing triangle and single-clicking the left mouse button.

A popup window with the selection options Bright / Normal / Dark will now open. Position the mouse pointer on the chosen option and single-click the left mouse button. The setting is now pre-selected. To save this setting in the database, finally single-click on “Save” with the left mouse button.

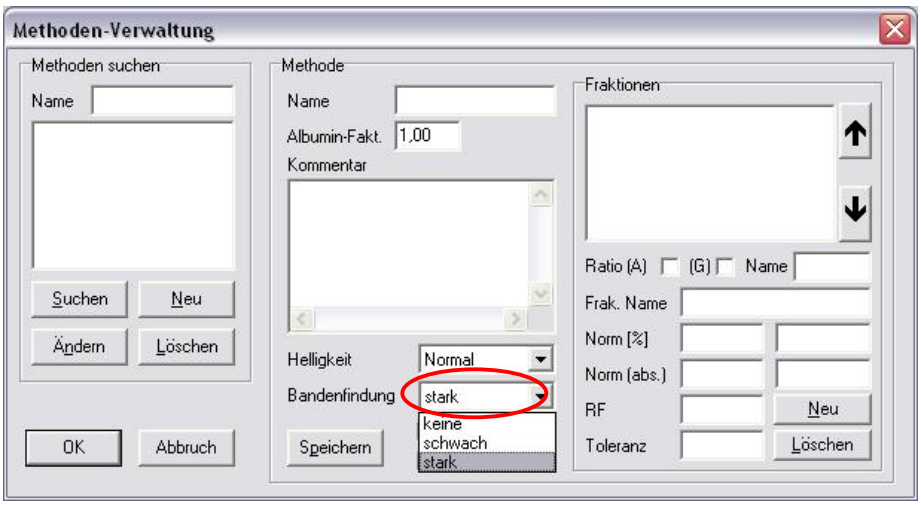


8.2.9.5. Band-finding

TurboScan offers the option of automatic band-finding. The advantage is that a fairly large area is automatically cropped before the first fraction appears. This means the first fraction to appear is always displayed at the start of the curve profile. There are 3 selection options available: none / weak / strong.

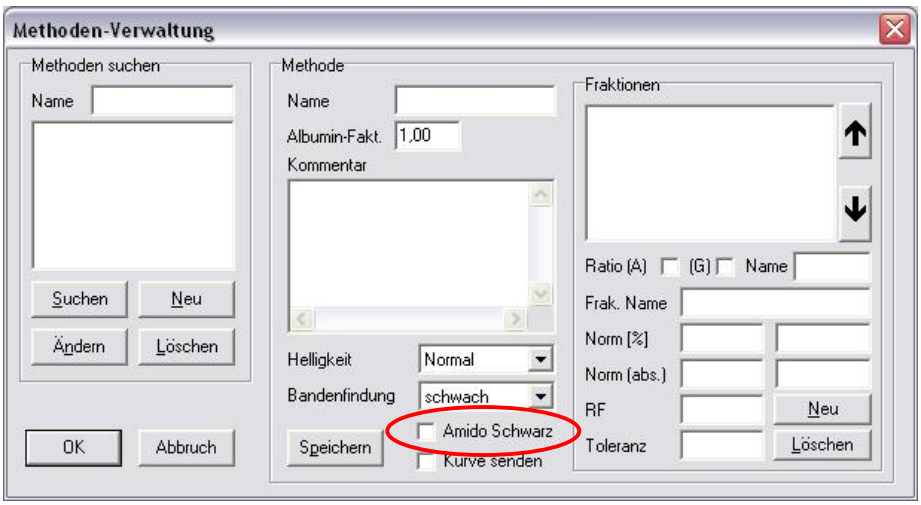
“None” should always be used for methods in which the first fraction may not even appear. If automatic detection were carried out and the first fraction were missing, the subsequent fraction would be erroneously accepted as the first fraction. On the “none” setting, the whole input scanning area is included in the curve profile unchanged.

The “weak” and “strong” settings merely denote the sensitivity of the automatic band-finding. Barely visible fractions are recognized with the “weak” setting. On the “strong” setting, the fraction must already be strongly stained to be recognized as the first fraction. Any noise before the fraction is ignored.



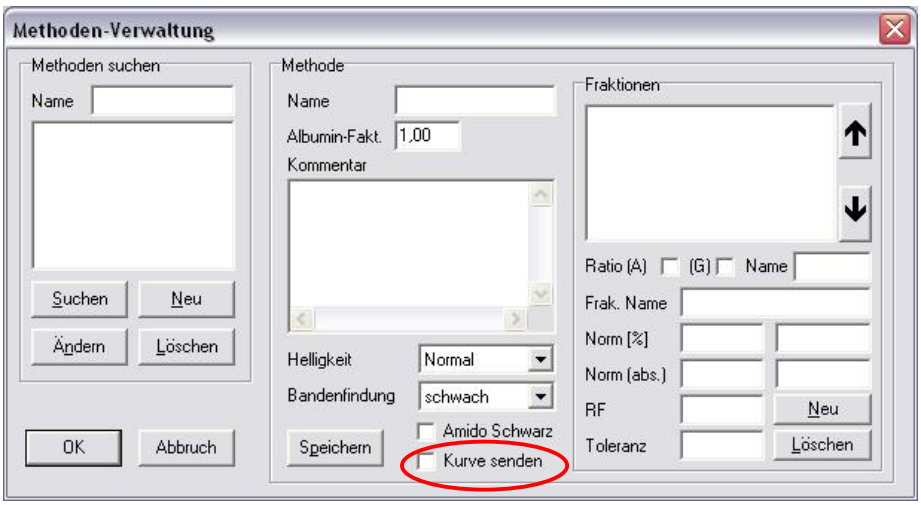
8.2.9.6. Amido Black

The “Amido Black” option is used to correct the background within the track. If this box is not checked, no background correction will take place. This is noticeable as an altered curve profile and hence altered data. On the standard setting, “Amido Black” should be enabled.



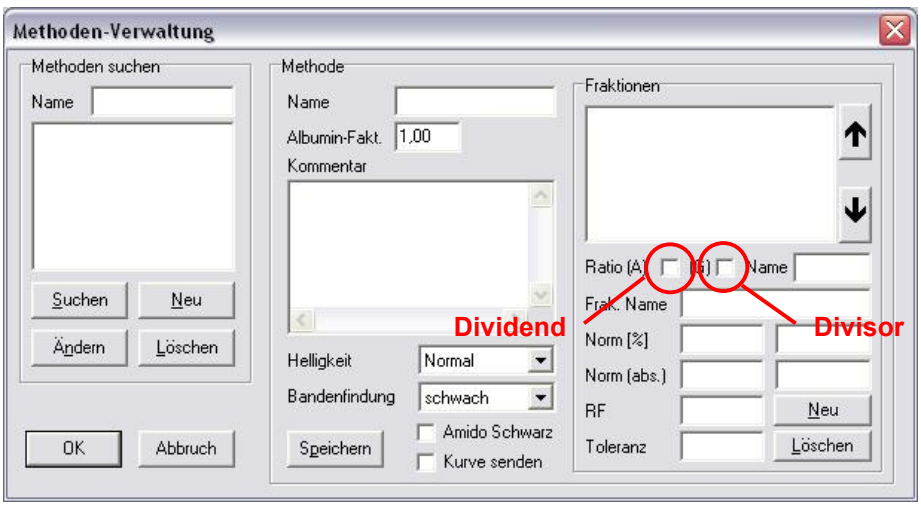
8.2.9.7. Send curve

TurboScan offers as standard two protocols (see section 10. ff) for transferring data by direct communication from workstation to host and back. One protocol involves the transfer of patient data without curve profile and the second protocol contains patient data with curve profile. If “Send curve” is selected, the second protocol with curve profile is automatically transmitted. If “Send curve” is not selected, no curve profile will be transmitted.
Since the protocols differ considerably in structure, you should discuss beforehand with your LIS supplier the extent to which the LIS is able to process the data of curve profiles.



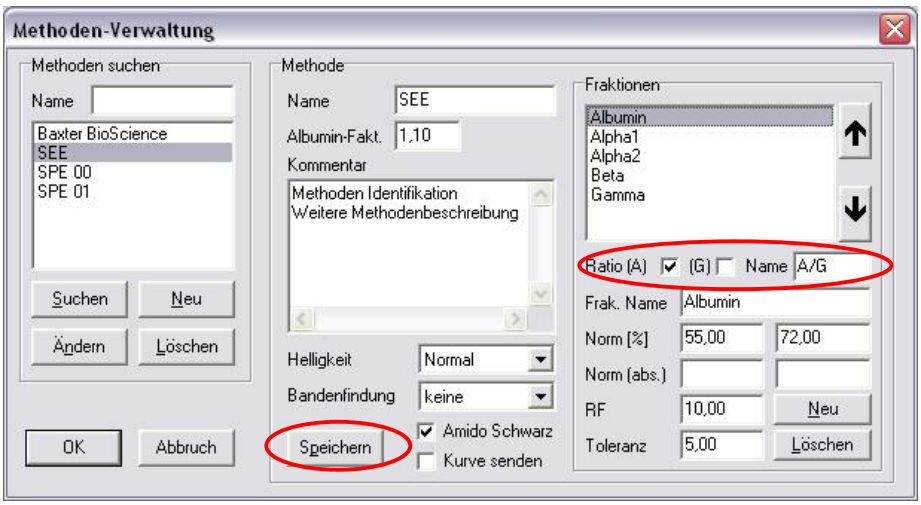
8.2.9.8. A/G ratio

The A/G ratio denotes the relationship between the albumin and the globulins for serum protein electrophoresis: purely mathematically, the albumin is divided by the total of globulins. To achieve this, each fraction (here based on the example of serum protein electrophoresis) has to be defined as the dividend or divisor[11]. Albumin becomes the dividend and globulins alpha1, alpha2, beta and gamma the divisor. The dividend is set in the left-hand checkbox and the divisor on the right of the ratio section. It is not absolutely essential to include all fractions in the calculation. For instance, out of 3 fractions of lipoprotein fractions, only 2 might be calculated for the ratio of LDL to HDL. The VLDL fraction would then be ignored in the calculation.



To make sure the printout of the calculation can be clearly assigned, the ratio can be given a name in the “Name” entry field. For serum protein electrophoresis, it is “A/G” which can be entered here.

[11] Dividend stands above the fraction bar, the divisor below; the result is called the quotient.



To activate the relevant field as the dividend or divisor, position the mouse pointer on the appropriate field and single-click the mouse button. The box now shows a checkmark. To enter the name, position the mouse pointer on the Name entry field and single-click the left mouse button. Now enter the description via the keyboard. To integrate the entry into the method, single-click the left mouse button on “Save”.

8.2.9.9. Change method

The method is changed in the same way as creating a new method, except that the individual fields already have a default value.
To select the method to be changed, position the mouse pointer on the desired method and double-click the left mouse button. Enter the relevant values for the selected method in the “Method” section. The current method can now be altered as previously described in 8.2.9.1 ff. The change can be saved via the “Change” button or directly via the “Save” button.

8.2.9.10. Switch method

To switch from the current method, position the mouse pointer on the method to be activated and singe-click the left mouse button. Confirm the entry by single-clicking the left mouse button on “OK”. The method just selected is active and is automatically loaded with the next startup of the TurboScan program.

8.2.9.11. Delete method

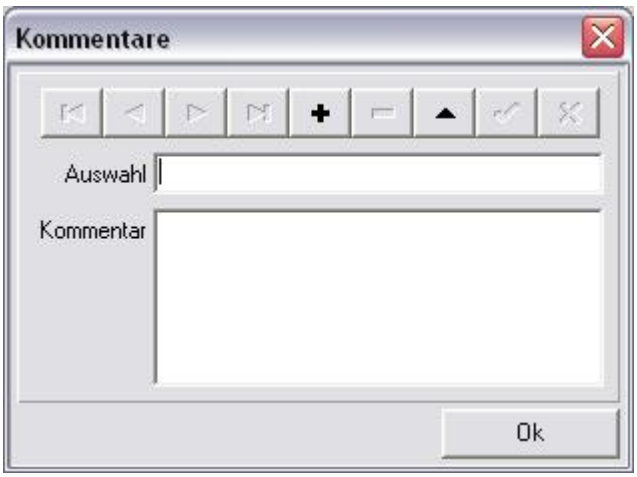
To delete a method, position the mouse pointer on the method to be deleted and single-click the left mouse button. Confirm the entry by single-clicking on “Delete” with the left mouse button. The method just selected is deleted and can no longer be selected.

8.2.10. *Patient Journal*

See (8.2.1.5.1 ff.)

8.2.11. *Comments Database*

The Comments database helps to predefine comments on individual electrophoreses that constantly recur. The comments entered here are available for later output on the print form and are displayed in the Comments field.
Open the dialogue window for processing comments by single-clicking the left mouse button on .



8.2.11.1. Enter and save new comments

To add new comments to the database, you first need to enter a selection ID code in the “Selection” field. To do this, position the mouse pointer on the “Selection” entry field and single-click the left mouse button. You can now enter the title of the comments. To enter the actual comments, position the mouse pointer inside the “Comments” entry field and single-click the left mouse button. You can now enter the actual comments. To confirm the comments, single-click on with the left mouse button.

8.2.11.2. Select comments

If there are several comments in the database, these can be displayed individually via the navigation buttons. The following functions are available for navigation:

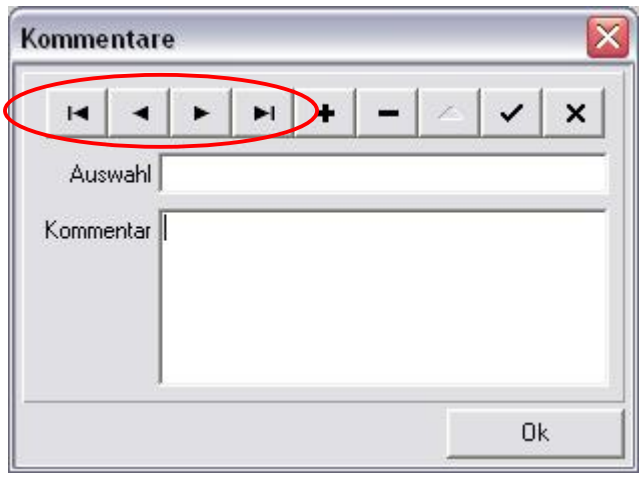
skip to first data record

skip to previous data record

skip to next data record

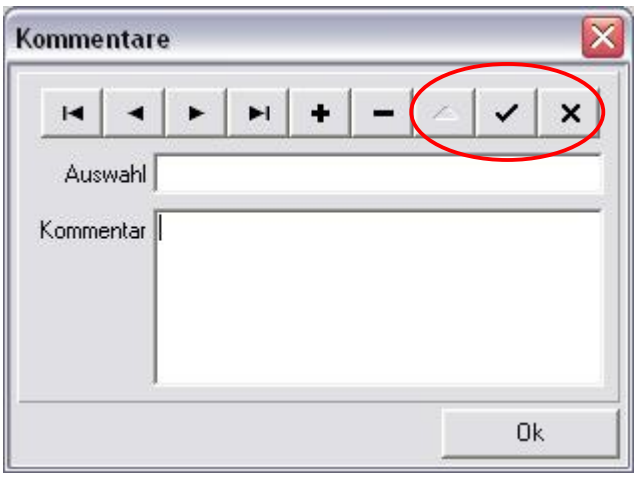
skip to last data record

The current data record is displayed with its ID code in the Selection field and with the comments text in the “Comments” field.



8.2.11.3. Change comments

Comments can be altered directly via the display in the “Comments” field or by first clicking on the button. To accept changes, single-click the left mouse button on .
Corrections that have not yet been accepted with the confirmation button, can be reversed by single-clicking the left mouse button on .



8.2.11.4. Delete comments

To delete a comment, select the data record to be deleted using the navigation buttons. Single-clicking the left mouse button on - will delete the current data record from the database.

8.2.11.5. Closing Enter Comments

Enter Comments is closed by single-clicking the left mouse button on “OK“. The window for managing comments closes.

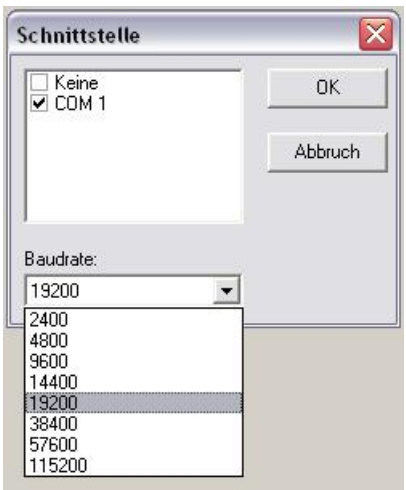
8.2.12. User Data

Entering User Data helps to identify the printout. The data given in User Data are displayed in the header of each report.

To enter data, position the mouse pointer on the “Hospital” entry field and single-click the left mouse button. The entry can now be made via the keyboard. To skip to the next field, press the “Tab” key[12] on the keyboard. Confirm the entry by single-clicking the left mouse button on “OK”.

8.2.13. Interface

The interface is used for direct communication with an external HOST PC. So that the systems are able to communicate with each other, the workstation interface and the speed of data transfer must first be established. The speed of data transfer should be agreed beforehand with the LIS manufacturer. The workstation interface to be used will depend on the hardware being used.



As a serial interface is provided for data transfer, the transfer rate is limited to the values given in the drop-down menu. The usual transfer speed is 9600. However, a higher data transfer rate should not pose any problems for TurboScan. A transmission speed of up to 115200 baud has been tested.

8.2.14. Language

TurboScan is sold worldwide. In order to guarantee the greatest possible service and usability, all the texts and messages have been translated into several different languages. To select the appropriate language, single-click the left mouse button on . This opens the window for language

[12] The key on the left of the keyboard with two arrows pointing in opposite directions

selection. You can directly change the operating language of TurboScan by opening the drop-down menu and selecting the language
No guarantee can be given that languages written with non-Latin letters will function perfectly.

9. Routine program run

The routine program run is intended to show how to handle TurboScan during normal operation. This does not include a description of the individual menu items. It is assumed that TurboScan has already been started and the Welcome image is appearing on the screen.

1. Place objects in the flatbed scanner
2. Press the “SCAN“ button
3. Press the “TWAIN” button
4. Press “Scan” in the TWAIN window
5. Confirm the image with “OK”
6. Press “Acquire mask”
7. Pull frame around the electrophoresis
8. Confirm with “OK”
9. Press the “Analyse” button
10. Double-click on a curve profile in the summary window
11. Correct the minimum marks, if necessary
12. Accept corrections with “OK”
13. Press “Patient data”
14. Enter the patient data
15. Confirm the patient data with “OK”
16. Press the “Print” button
17. Press the “Print” button in the summary window
18. Start Print Jobs by pressing “OK”
19. Close the Print Preview window
20. Press “Exit” in the summary window

10. TurboScan communication

10.1. Conventions

Data transfer takes place in two directions: patient data are transferred from the host to the PC; analysis data are sent back from the PC. In each case, a communication process is initiated by the PC, the host is constantly on stand-by.
A communication process is initiated by the PC sending a defined byte to the host and the host then sending the appropriate response. All user data are sent as ASCII characters.
The following parameters are used for serial communication:

- baud rate 2400 - 115200
- 8 data bits
- no parity
- 1 stopbit

Date format

A date is always transmitted without date separators but with leading zeros; the set sequence for date information is DDMMYYYY. This means that each side can work with whichever date separator is applicable, without influencing the other side.

Examples:

Sender	Sent
01.03.2007	01032007
1.3.07	01032007
1 March 07	01032007
3/1/2007	01032007

Format for floating-point values

Numerical values, e.g. for the information ‘Total Protein’ of a patient, are always multiplied by 1000 on the sender’s side and the numerical value (as an ASCII sequence) is then sent without decimal separators. The recipient side converts the received ASCII sequence into a numerical value and divides it again by 1000. This means that each side can work with whichever decimal separator is applicable without influencing the other side.

Examples:

Sender	Sent
10.362	10362
0.023	23
42	42000

Sex

The sex of a patient is transmitted as 1 character. Only the following are permitted:

m/M	male
f/F	female
blank or x/X	sex not known

10.2. ASCII data transfer by file

10.2.1. Import file (host to TurboScan)

ASCII file, 1 patient per line, all fields separated by tabulator (ASCII 9), each line closed with <CR><LF>. Blank lines within the file are ignored.

<ID> Tab <NAME> Tab <DateBirth> Tab <PROTEIN> Tab <DEPT> Tab <SEX> <CR><LF>

The date of birth is given in the format DDMMYYYY (**no** date separators). The 'Protein' figure is multiplied by 1000 by the host, then divided by 1000 again when input (**no** decimal separators).

The following characters are permitted for indicating the patient's sex:

<F> = female,
<M> = male,
<> = undefined

10.2.2. Export file (TurboScan to host)

ASCII file, 1 sample per line, all fields separated by tabulator (ASCII 9), each line closed with <CR><LF>.

Samples to which no patient is assigned are **not** exported.

<Patient ID> Tab <No. fractions> Tab

for each fraction the following fields:

<Fraction name> Tab <Fraction percentage> Tab
<Method name>

The 'Fraction percentage' number is multiplied by 1000 by the PC and stored in the file without decimal separators. The host has to divide this figure by 1000 again to reach the percentage figure again.

10.3. Data transfer without curve data

10.3.1. Data transfer host to TurboScan

The patient data for the current work list are transferred, the sequence of the data records matching the sequence of the patients in the work list.

PC: **[ENQ]** (request byte)
HOST: **[ACK]** (start data transfer)
[STX] - data record - **[ETX]**
[STX] - data record - **[ETX]**
...
[STX] - data record - **[ETX]**
[EOT] (end data transfer)

The structure of a single data record (per patient) is as follows:

[STX] Patient ID **[LF]**
Patient name **[LF]**
Date of birth (see above for format) **[LF]**
Protein (see above for format) **[LF]**
Department **[LF]**
Sex (see above for format)
[ETX]

On the PC a report is issued each time (data received error-free / with errors).
If the data are correctly received at the PC, the data are automatically assigned to the samples in the correct sequence.

NOTE:
The upper limit of 50,000 characters applies to transfer from host to PC.

10.3.2. Data transfer TurboScan to host

Once the data received from the host are assigned to the individual samples and the samples have been re-corrected (if necessary), the analysis results can be sent back from the PC to the host.

PC: **[SOH]** (request byte)
HOST: **[ACK]** (signals readiness)
PC: **[ACK]** (start data transfer)
[STX] - data record - **[ETX]**
[STX] - data record - **[ETX]**
...
[STX] - data record - **[ETX]**
[EOT] (end data transfer)
HOST: **[ACK]/[NAK]** (acknowledgement byte positive / negative acknowledgement)

The structure of a single data record (per sample) is as follows:

[STX] Patient ID **[LF]**
Number of fractions (without multiplication by 1000!) **[LF]**
for each fraction the following data:
Name of fraction **[LF]**
calculated value for fraction (see above for format) **[LF]**
Method name **[ETX]**

On the PC, once transmission is completed, a report is issued on whether the transmission was positively or negatively acknowledged by the host.

NOTE:
The upper limit of 50,000 characters applies to transfer from PC to host. Data on samples to which a patient has not yet been assigned on the PC will **not** be sent back to the host because these data cannot be assigned by the host.

10.4. Data transfer with curve data

10.4.1. Data transfer host to TurboScan

10.4.2. Data transfer TurboScan to host

Once the data received by the host have been assigned to the individual samples and the samples have been re-corrected (if necessary), the analysis results can be sent back from the PC to the host.

PC: **[SOH]** (request byte)
HOST: **[ACK]** (signals readiness)
PC: **[ACK]** (start data transfer)
[STX] - data record - **[ETX]**
HOST: **[ACK]**
PC: **[STX]** - data record - **[ETX]**
HOST: **[ACK]**
PC: **[STX]** - data record - **[ETX]**
HOST: **[ACK]**
....
HOST: **[ACK]**
PC: **[EOT]** (end data transfer)
HOST: **[ACK]/[NAK]** (acknowledgement byte positive / negative acknowledgement)

The structure of a single data record (per sample) is as follows:

[STX] Patient ID **[LF]**
Number of fractions (without multiplication by 1000!) **[LF]**
for each fraction the following data: Name of fraction **[LF]**
Method name **[LF]**
for each fraction the following data: calculated value of fraction (multiplied by 1000) **[LF]**
Number of minimum marks **[LF]**

per minimum mark minimum mark position (X-values) **[LF]**
Number of measuring points (number of X-values) **[LF]**
per X-value measuring point (Y-values) (multiplied by 1000) **[LF]**
[ETX]

On the PC, once transmission is completed, a report is issued on whether the transmission was positively or negatively acknowledged by the host.

NOTE:
Data on samples to which a patient has not yet been assigned on the PC will **not** be sent back to the host because these data cannot be assigned by the host.

11. Important notes on PC hardware

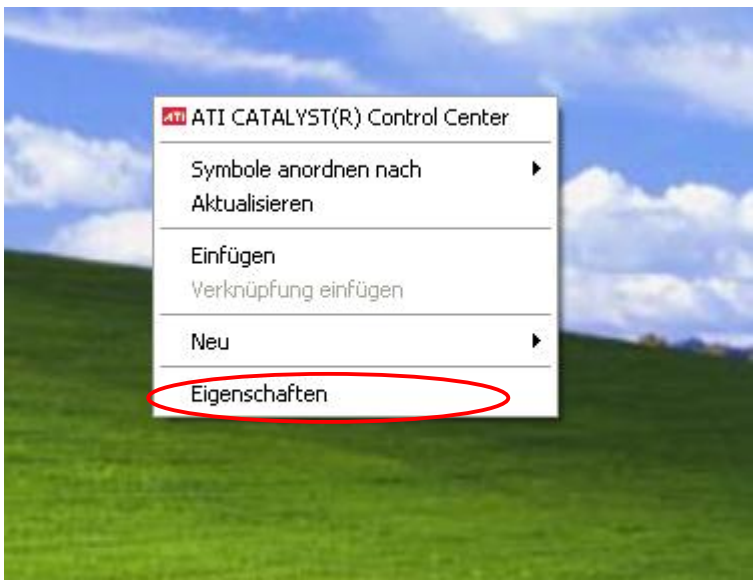
11.1. Safety connector for printer interface

A standard PC as described in section 2 is used to operate TurboScan. For existing systems that have a copy protection connector for the printer interface, it is essential to ensure that the printer interface (set in BIOS) is set to SPP or EPP.
The ECP setting may cause problems. It is possible that the safety connector might not be recognized or the printer might not function properly.

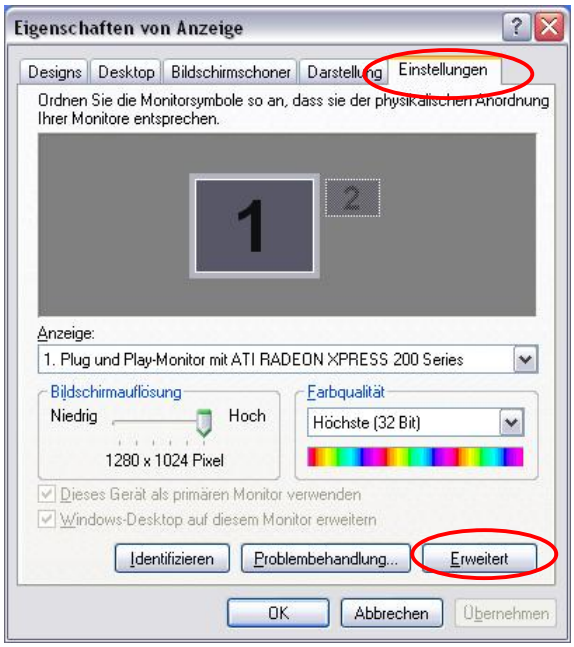
11.2. Graphics card with 3D acceleration

Thanks to the play instinct of human beings, the development of imaging components in PCs has advanced rapidly. Of course, this is not without its repercussions for all the other programs being using on a PC. TurboScan is also affected by this. Depending on the manufacturer and type of graphics card, it can happen that graphic images generated by TurboScan are partly destroyed by smoothing and 3D filtering. This is mainly evident in the correction window of the curve profiles. The curves are partly broken or completely absent.
To prevent this problem caused by the graphics card, the performance of the graphics card must be restricted via a setting in Windows XP. This is done as follows:

1. Position the mouse pointer on an empty area of the Desktop and single-click the right mouse button. A menu opens on the Desktop.

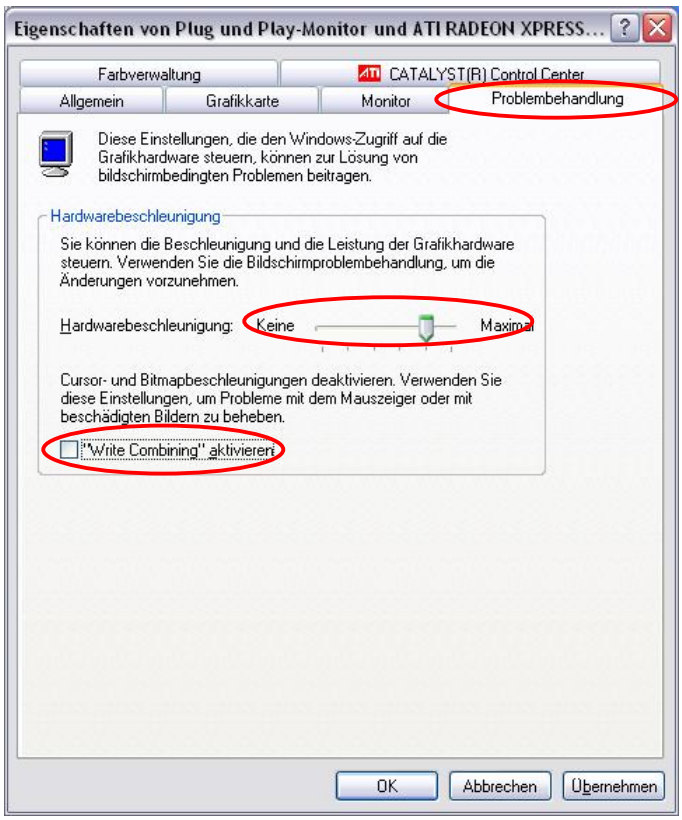


2. Select the menu item “Properties”. The “Display Properties” menu opens.



Click on the “Settings” tab for the correct selection.

3. Click on “Advanced”. The menu for the graphics card advanced settings opens.



Select the “Troubleshoot” tab. If enabled, the “Enable write combining” setting should be disabled and the slide control for “Hardware acceleration” should be moved at least 1 level further to the left.

4. Confirm this setting with the “OK” button.

Once you have performed the above steps, all existing problems in displaying the curve profile caused by the graphics card should be remedied and all images should appear normal again.

I. Hardware not supplied by BIOTEC-FISCHER

In principle, you may assume that each of the hardware items described in section 2. can be used with TurboScan. However, since there are countless combinations of a wide variety of hardware and it is impossible to test absolutely every combination, BIOTEC-FISCHER GmbH clearly cannot guarantee that hardware not supplied by BIOTEC-FISCHER will also function perfectly. Our Technical Customer Services will be happy to offer you their expertise. Problems can be discussed and may even be resolved over the telephone. If necessary, you can also order an on-site service.

Appendix

I. Example of data transfer with curve profile (8 analyses)

= patient ID with leading control characters

= number and name of the individual fraction with followed values

= name of method

= positions of minimum marks

= number of X-values and Y-value per X-position of the curve

• • 1234 567890	10011	8880	13253	7145	12036
5	15174	9485	14033	6632	12076
Albumin	22440	10142	14724	6334	12100
56697	31932	10719	15297	6265	12093
Alpha1	43175	11109	15717	6251	11999
6130	54935	11243	15901	6371	11853
Alpha2	65930	11146	15896	6612	11600
11461	75204	10870	15734	6781	11227
Beta	81695	10355	15370	6863	10916
10493	85313	9562	14886	6951	10374
Gamma	87072	8651	14484	7006	9644
15217	87857	7960	13933	7072	8949
SPE 02	88151	7516	13232	7167	8352
6	88231	7132	12644	7299	7677
0	88178	6807	12479	7418	6911
38	87821	6594	12695	7618	6187
57	86638	6472	13348	7909	5496
85	83634	6381	14441	8178	4758
106	77747	6411	15985	8405	4035
161	69171	6520	17816	8677	3313
162	58759	6584	19660	8971	2686
900	47379	6745	21199	9391	2257
907	36373	7024	21946	9861	1901
958	27031	7361	21755	10176	1470
1097	19994	7718	20519	10425	1055
1394	15081	8200	18294	10674	675
1974	11838	8874	15818	10926	466
2856	9896	9613	13323	11172	276
4251	8779	10446	10964	11485	0
6466	8403	11364	9106	11754	• • 1234 567891
	8450	12308	7845	11937	

5
Albumin
62781
Alpha1
4271
Alpha2
9894
Beta
8830
Gamma
14222
SPE 02
6
0
38
56
87
107
164
165
679
734
850
1060
1372
1882
2643
3848
5784
9004
14118
21603
31282
42821
54888
66162
75417
81249
83804
84661
84904
84950
84743
83525
80060
73845
64644
53279
41244
30308
21464
14838
10579

8004
6521
5475
4866
4646
4616
4627
4689
4991
5506
5996
6237
6266
6260
6217
6005
5507
4963
4527
4100
3716
3553
3499
3493
3498
3522
3592
3745
3981
4193
4412
4654
4926
5215
5606
5975
6216
6512
7025
7577
8154
8763
9143
9283
9325
9335
9338
9339
9339
9340
9333
9246
8921

8450
8360
8465
8681
9209
9999
11330
12681
13660
14349
14257
13496
12425
10925
9248
7636
6293
5220
4571
4097
3811
3687
3696
3803
3890
4059
4284
4449
4584
4641
4710
4824
4928
5066
5257
5425
5695
5989
6147
6230
6297
6433
6700
7096
7492
7816
8143
8484
8637
8786
8983
9046
8953

8776
8629
8589
8382
8039
7569
7027
6555
6230
5845
5359
4764
4057
3599
3192
2687
2276
1987
1716
1454
1258
960
509
190
68
0
• • 1234
567893
5
Albumin
61723
Alpha1
4720
Alpha2
10557
Beta
9067
Gamma
13932
SPE 02
6
0
39
58
90
110
166
167
152
189
297
454
698

993
1399
2240
3600
5886
9449
14750
22677
33119
45003
57012
67539
75248
79331
80785
81207
81316
81342
81344
81262
80544
77573
70984
61702
50046
37898
27291
18987
13271
9528
7281
6047
5390
5044
5017
5190
5386
5684
6162
6648
7017
7180
7171
7007
6643
6067
5429
4973
4637
4281
3875
3621
3448

3392
3411
3523
3776
4106
4332
4468
4577
4662
4853
5173
5495
5900
6479
6997
7318
7753
8476
9238
9804
10221
10468
10619
10649
10644
10586
10401
10147
9989
9730
9445
9206
9141
9359
10024
11052
12410
13812
14936
15722
15779
15133
13855
12006
10078
8172
6795
5636
4997
4703
4532
4414
4374

4413	444	37105	9098	6476	166
4502	299	26650	9012	6676	1116
4572	120	18462	8716	6705	1189
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5972	8557	4379	10146	5542	31063
6298	Gamma	4567	11302	5232	42850
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