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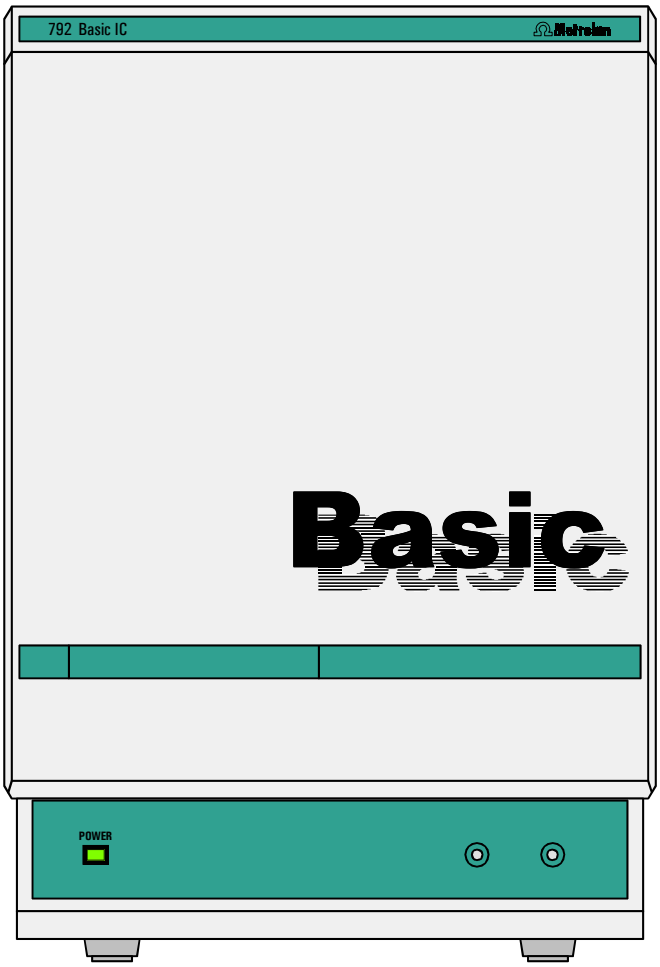
792 Basic IC

Program «792 PC Software 1.0»



8.792.1003 Instructions for Use

11.04.2001 / dö

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1 Introduction

1.1 Instrument description

The **2.792.0020 Basic IC with suppressor module** is a PC-controlled system for ion chromatographic analyses. The extremely compact housing of the 792 Basic IC contains everything needed to carry out ion chromatography at a high quality level:

- **Injection valve** – for individual injections
- **High-pressure pump** – extremely low-pulsation double piston pump with a flow range from 0.2 … 2.5 mL/min and a maximum pressure of 25 MPa (250 bar)
- **Column chamber** – the perfect insulation of the housing provides not only thermally stable conditions for the separation column but also shields the system against electromagnetic interference
- **Columns** – whether anion columns with or without suppression, separation columns for cations or organic acids – the 792 Basic IC can accommodate them all
- **Suppressor** – integrated Metrohm Suppressor Module (MSM), pressure-resistant, with fully automatic regeneration, highest performance and optimal reproducibility
- **Peristaltic pump** – integrated two-channel peristaltic pump with a flow rate of 0.5 … 0.6 mL/min for regeneration and rinsing of the suppressor module
- **Detector** – conductivity detector with outstanding temperature stability. The detector temperature of 40 °C varies by less than 0.01°C.

All components, which come into contact with eluent and sample are metal-free.

The **operation** of the 792 Basic IC takes place via a PC connected to the RS232 interface with the help of the control and evaluation program «**792 Basic IC**». This PC program can be used to open prepared systems for recording and evaluating chromatograms and modify them if need be. Time programs can also be created in which a large number of instrument functions can be triggered for each program step.

The operating software for the 792 Basic IC meets all the requirements you could place today on a modern integration software: single or multi-point calibration, internal or external standard, selectable algorithms for non-linear calibration, various integration modes with integration parameters and integration events, different methods for peak recognition, peak editor, free scaling, superimposing several chromatograms, batch reprocessing; a powerful and GLP-conform report generator with output interfaces for monitor, printer and external databases.

1.2 Parts and controls

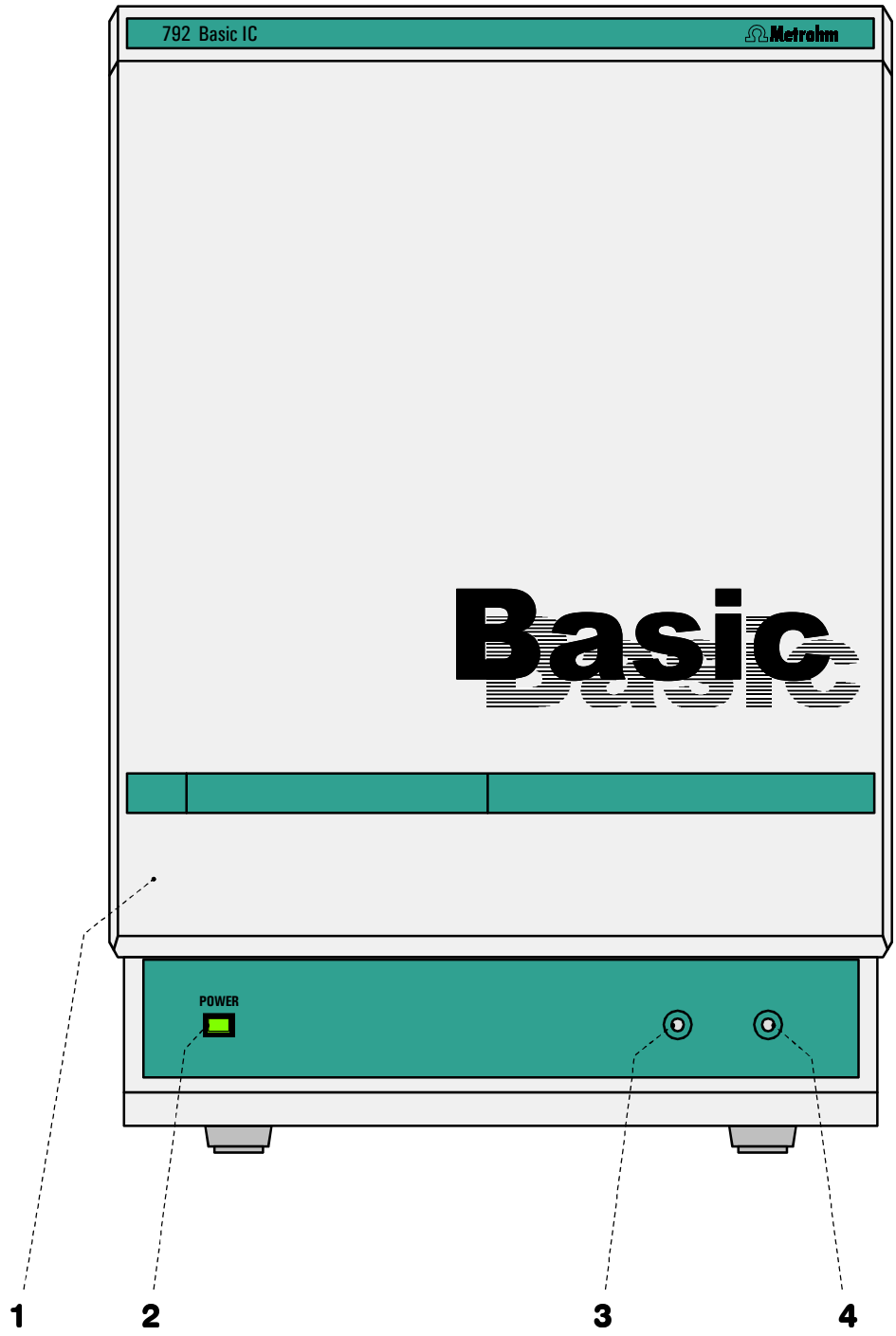


Fig. 1: Front of the 792 Basic IC

1	**Door to interior**	**3**	**Feedthrough for syringe tubing** for connection of the 6.2816.020 syringe used für aspirating the sample
2	**Mains pilot lamp** lit up when instrument switched on	**4**	**Feedthrough for aspirating tubing**

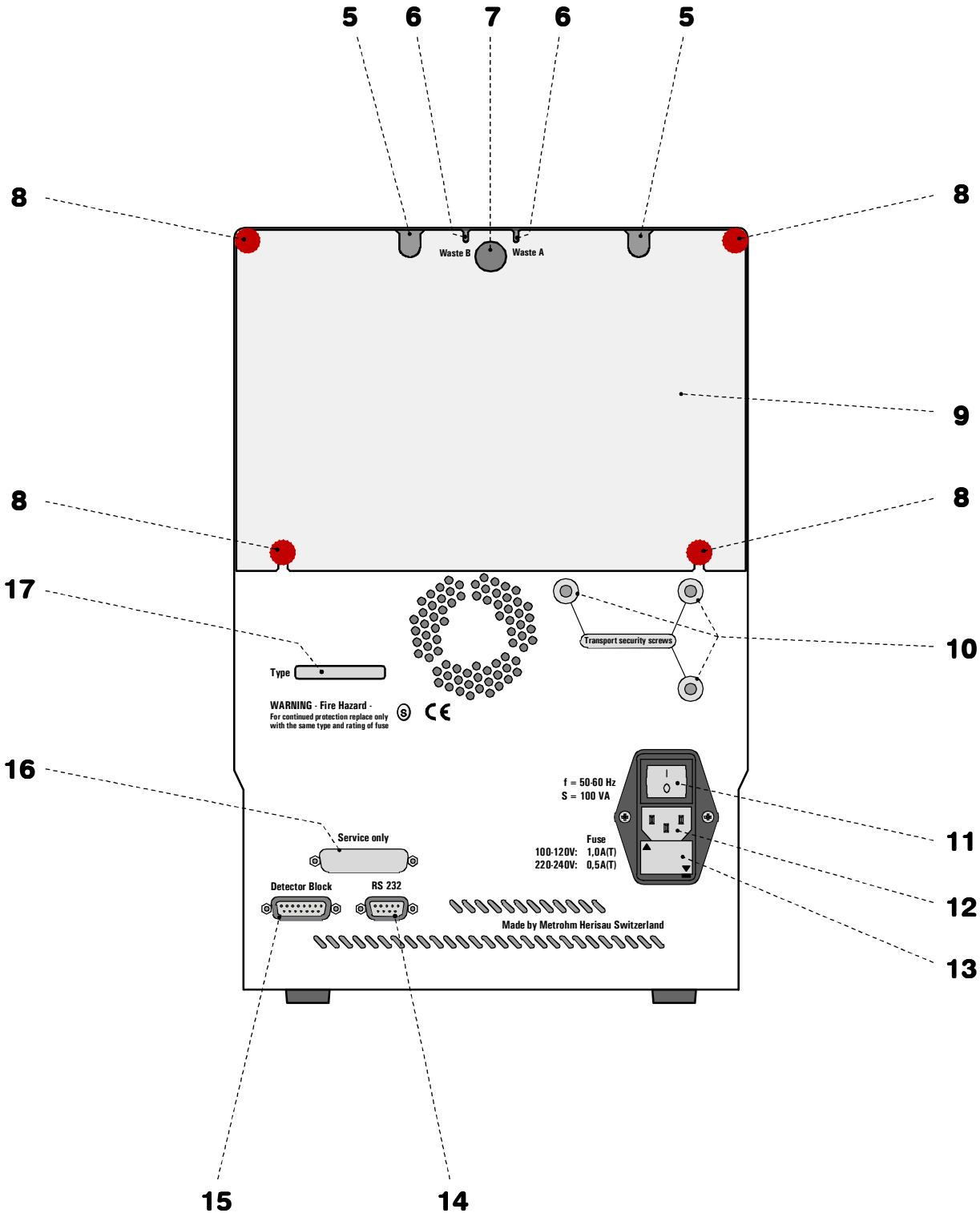


Fig. 2: Rear of the 792 Basic IC

5 **Opening for detector cable**

6 **Opening for outlet capillaries**
for discharge of eluent, regeneration solution, and rinsing solution from the inner compartment

7 **Rear panel opening**
(closed with plastic stopper) for additional supply and discharge lines to and from the inner compartment

8 **Knurled screw**
for fastening the rear panel **9**

9 **Detachable rear panel**
access to upper part of inner compartment

10 **Transport security screws**
to secure the pump head when the instrument is transported

11 **Mains switch**
to switch instrument on and off:
I = ON 0 = OFF

12 **Mains connection plug**
mains connection, see *section 2.4*

13 **Fuse holder**
changing the fuses, see *section 2.4*

14 **RS232 interface**
connection of the PC

15 **Connection for detector block**

16 **Connection**
To be used only for Metrohm Service!

17 **Serial number**

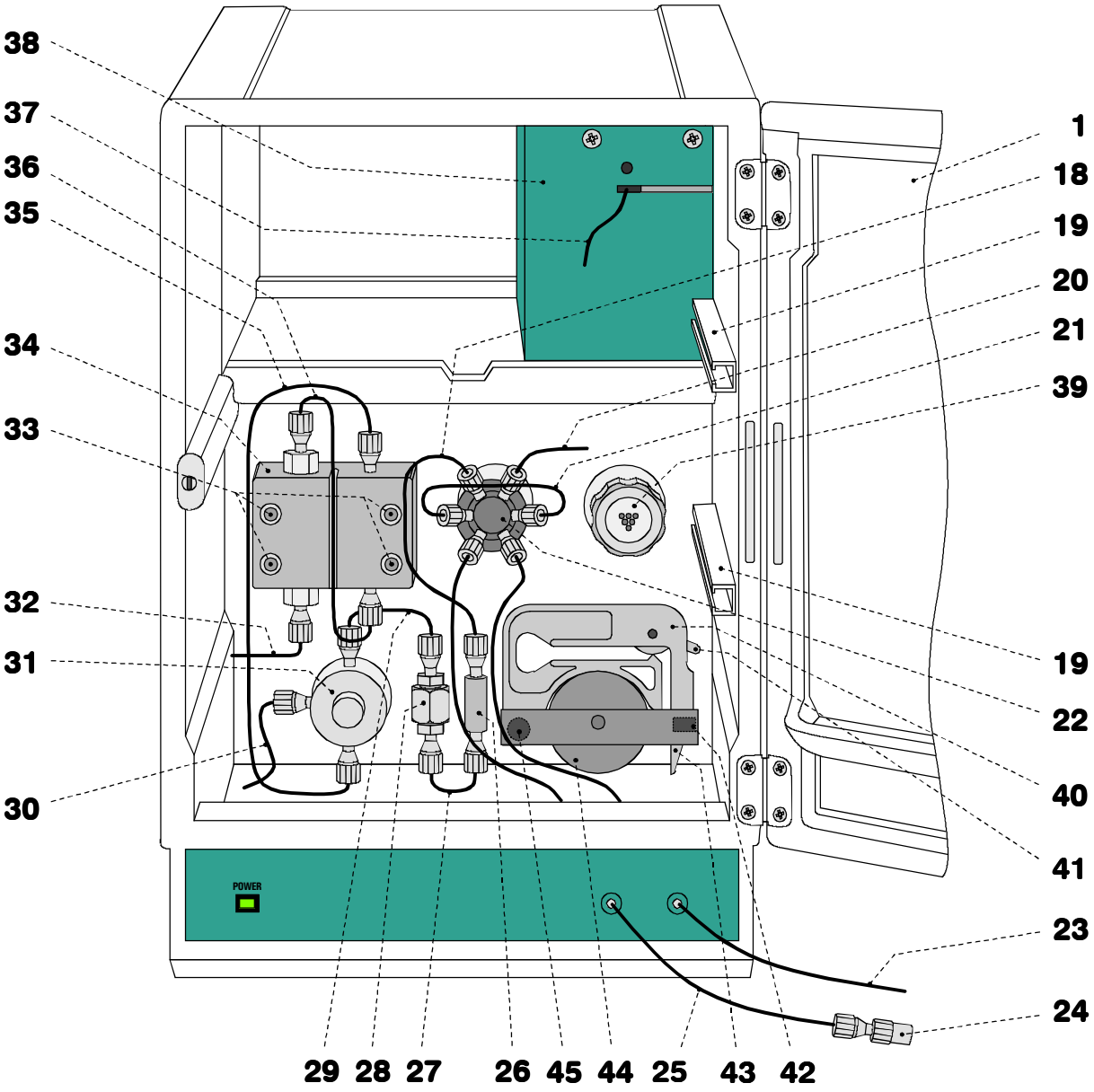


Fig. 3: Interior of the 792 Basic IC (with permanently attached accessories and 1.733.0110 Detector block)

1 **Door to interior**

18 **Inlet capillary for injector**
PEEK capillary,
length L = 24 cm

19 **Mounting rail**
for 6.2027.0X0 column holder

20 **Column connection capillary**
PEEK capillary,
length L = 30 cm

21 **Sample loop 20 µL**
6.1825.210 PEEK sample loop

22 **Injection valve**

23 **Aspirating tubing**
PTFE tubing for aspirating the sample;
length L = 65 cm

24 **Coupling (6.2744.120)**
for connection of the 6.2816.020 syringe

25 **Syringe tubing**
PTFE tubing for connection of the syringe,
length L = 35 cm

26 **PEEK coupling (6.2744.040)**

27 **Connection capillary**
PEEK capillary,
length L = 13 cm

28 **Filter unit PEEK (6.2821.100)**

29 **Connection capillary**
PEEK capillary,
length L = 13 cm

30 **Connection capillary**
PTFE capillary for connection of the 6.2816.020 syringe,
length L = 70 cm

31 **Purge valve**

32 **Aspirating capillary**
Connection for 6.1834.010 aspirating tubing

33 **Fastening screws**
for pump head **34**

34 **Pump head (6.2824.100)**

35 **Connection capillary**
Connection pump head – purge valve, fixed mounting

36 **Connection capillary**
in pump head, fixed mounting

37 **Inlet capillary for detector block**
PEEK capillary, fixed mounting

38 **Detector block (1.732.0110)**

39 **Suppressor module**
(inlet and outlet capillaries are not shown)

40 **Tubing cartridge (6.2755.000)**
for 6.1826.060 pump tubing

41 **Contact pressure lever**
for adjusting the contact pressure

42 **Holding clamp**
for locking the tubing cartridge into place

43 **Snap-action lever**
for releasing the tubing cartridge

44 **Pump drive**
roller head with contact rollers

45 **Mounting pin**
for attaching the tubing cartridges

1.3 Information on the Instructions for Use

Please read through these Instructions for Use carefully before you put the 792 Basic IC into operation. The Instructions for Use contain information and warnings to which the user must pay attention in order to assure safe operation of the instrument.

1.3.1 Organization

These **8.792.1003 Instructions for Use** for the 792 Basic IC provide a comprehensive overview of the installation, startup procedure, operation, fault rectification and technical specifications of this instrument. The Instructions for Use are organized as follows:

Section 1 **Introduction**
General description of instrument, parts and controls and safety notes

Section 2 **Installation**
Installation of accessories and putting instrument into operation

Section 3 **Operating tutorial**
Introduction to the operation using an example

Section 4 **Operation**
Detailed description of the operation

Section 5 **Notes – Maintenance – Faults**
Notes on ion chromatography, maintenance, fault rectification, diagnostic tests, validation

Section 6 **Appendix**
Technical data, standard equipment, options, warranty, declarations of conformity, index

To find the required information on the instruments, you will find it an advantage to use either the **Table of contents** or the **Index** at the back.

As a supplement to the Instructions for Use, the **8.732.2003 Metrohm Monograph "Ion chromatography"** is also supplied. This provides an introduction to the theoretical fundamentals and general information on separating columns and sample pretreatment.

The **8.792.5003 Metrohm Monograph "Practical Ion Chromatography"** is a practical textbook, which provides an illustrative introduction to the basic principles of ion chromatography and also describes 22 experiments covering the whole world of ion chromatography.

The **8.732.2013 IC Applications Collection** is also supplied; this contains all the **Application Notes** on the subject of ion chromatography.

1.3.2 Notation and pictograms

The following notations and pictograms (symbols) are used in these Instructions for Use:

Range	**Menu item, parameter or entry value**
SYSTEM STATE	**Program window**
<OK>	**Button**
[Ctrl]	**Key**
35	**Part or control of 792**
	**Hazard** This symbol draws attention to a possible danger to life or of injury if the associated directions are not followed correctly.
	**Warning** This symbol draws attention to possible damage to instruments or instrument parts if the associated directions are not followed correctly.
	**Caution** This symbol marks important information. First read the associated directions before you continue.
	**Comment** This symbol marks additional information and tips.

1.4 Safety notes

1.4.1 Electrical safety

While electrical safety in the handling of the 792 Basic IC is assured in the context of the specifications IEC 1010-1 (protection class 1, degree of protection IP20), the following points should be noted:

- **Mains connection**

*Setting of the **mains voltage**, checking the **mains fuse** and the **mains connection** must be effected in accordance with the instructions in section 2.4.*

- **Opening the 792 Basic IC**

*If the 792 Basic IC is connected to the power supply, the instrument must not be opened nor must parts be removed from it, otherwise there is a danger of coming into contact with components which are live. Hence, always disconnect the instrument from all voltage sources before you open it and ensure that the **mains cable is disconnected from mains connection** **12** !*

- **Protection against static charges**

Electronic components are sensitive to static charging and can be destroyed by discharges. Before you touch any of the components inside the 792 Basic IC, you should earth yourself and any tools you are using by touching an earthed object (e.g. housing of the instrument or a radiator) to eliminate any static charges which exist..

1.4.2 General precautionary rules

- **Handling of solvents**

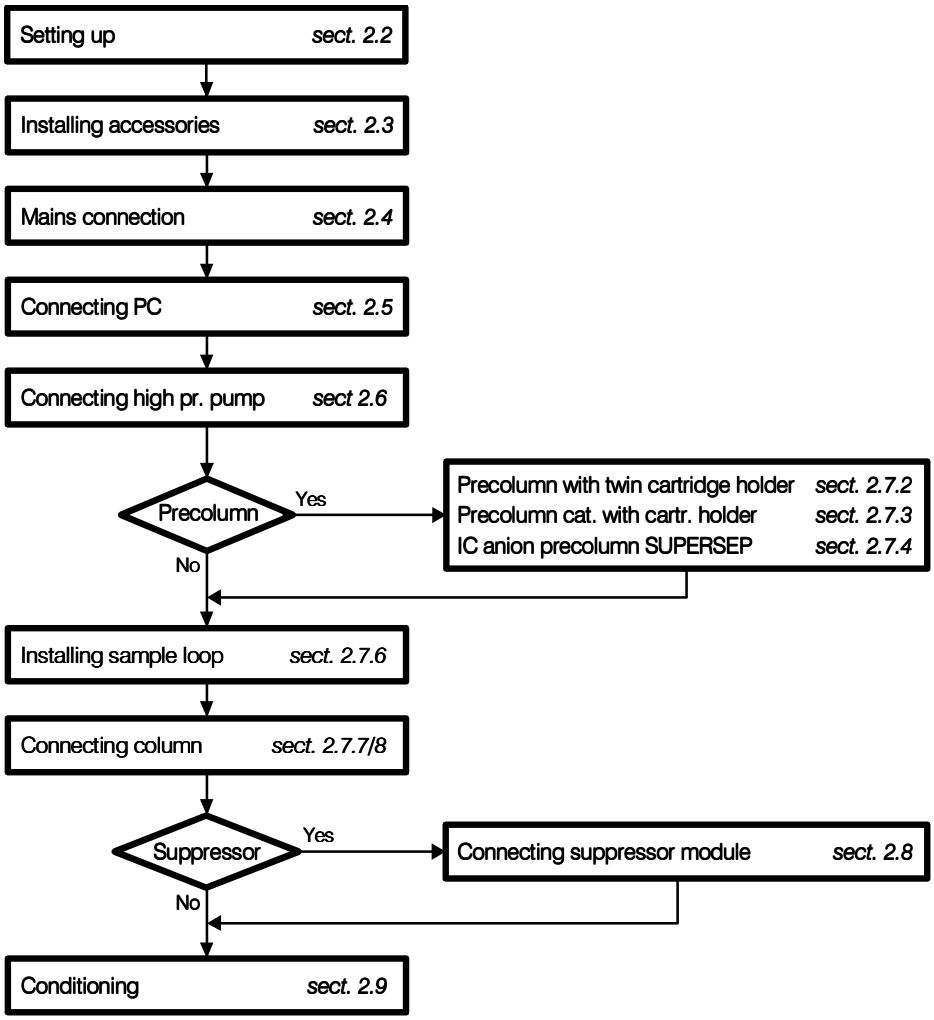
Check all lines of the IC system periodically for possible leaks. Follow the relevant instructions regarding the handling of flammable and/or toxic solvents and their disposal.

2 Installation

2.1 Overview

2.1.1 Flow chart

The following flow chart provides an overview of all installation work. You will find more detailed information in the relevant sections.



2.1.2 Connections in the 792 Basic IC

The two following illustrations show the internal connections in the 792 Basic IC in schematic form. The meanings of the various numbered components are given in the detailed illustrations and descriptions in *sections 2.2 – 2.9*.

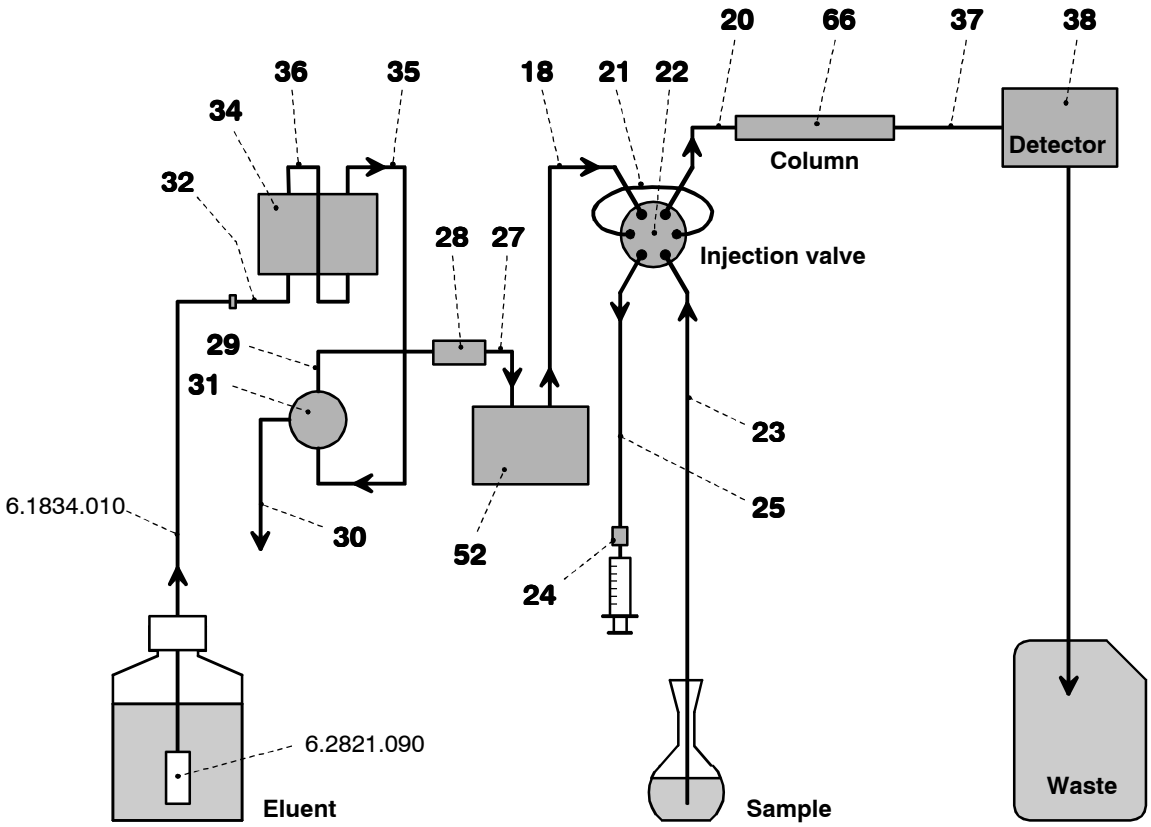


Fig. 4: Connecting diagram for 792 Basic IC without suppressor

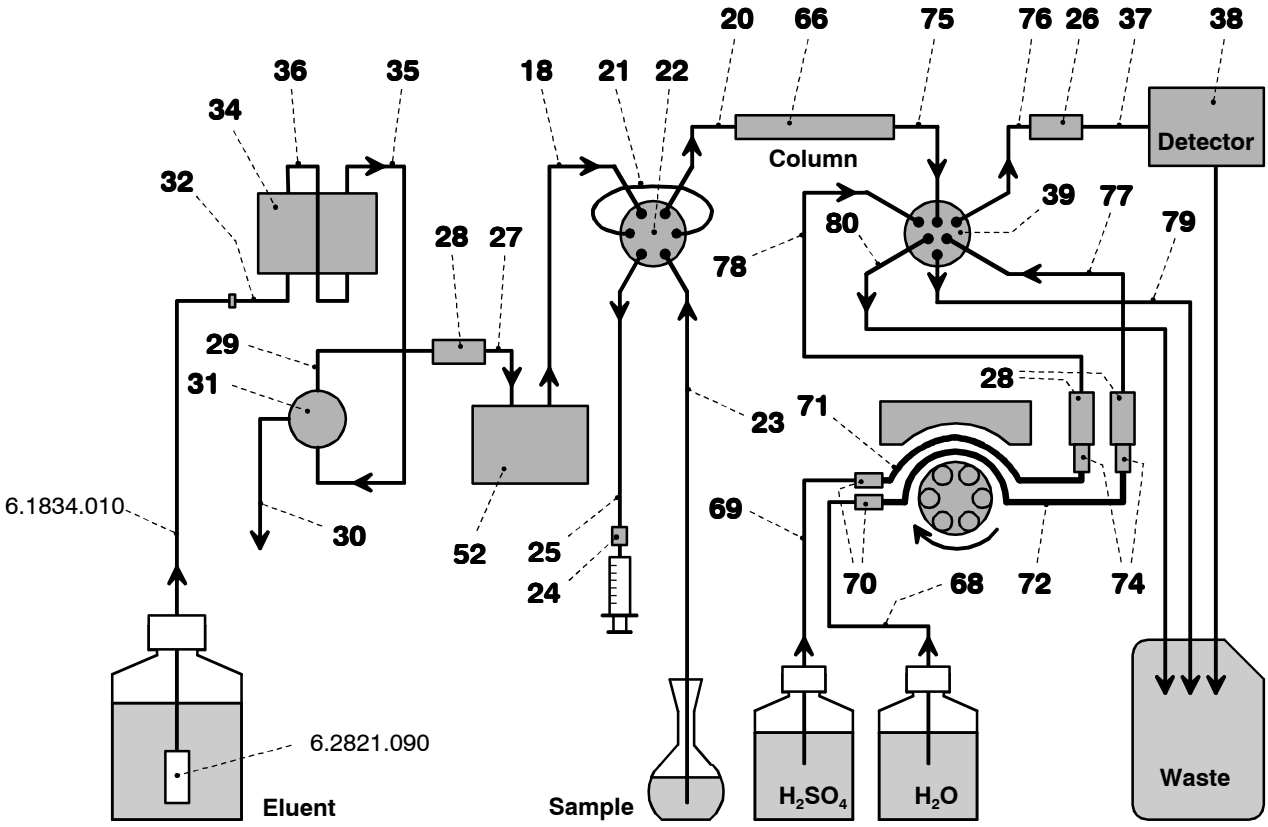


Fig. 5: Connecting diagram for 792 Basic IC with suppressor

2.2 Setting up the instrument

2.2.1 Packaging

The 792 Basic IC is supplied together with the separately packed accessories in special packagings containing shock-absorbing foam linings designed to provide excellent protection. The instrument itself is packed in an evacuated polyethylene bag to prevent the ingress of dust. Please store all these special packagings as only they assure transport of the instrument free from damage.

2.2.2 Check

After receipt, immediately check whether the shipment is complete and has arrived without damage (compare with delivery note and list of accessories in *section 6.2*). In the case of transport damage, see instructions in *section 6.4.1* "Warranty".

2.2.3 Location

Position the instrument in the laboratory at a location convenient for operation, free from vibrations and protected against a corrosive atmosphere and contamination by chemicals.

To avoid disturbing temperature influences on the insulated column compartment, the instrument must be protected against direct sunlight.

2.3 Attaching the accessories

2.3.1 Connection of detector block

The metal-free **1.732.0110 Detector block** belongs to the scope of delivery of the 792 Basic IC; it must be inserted in the instrument and connected up. Proceed as follows:

1 Note the cell constant

- The cell constant **c = XX,X /cm** is printed on the rear of the detector block. Note this value; it must subsequently be entered in the software in order to ensure that an exact display of the conductivity is obtained (see *section 2.5.3*).

2 Install detector block

- Unscrew the four knurled screws **8** from the top rear panel **9** of the 792 Basic IC and remove rear panel (see *Fig. 2*).
- Position detector block **38** from the back in the space provided in the 792 Basic IC and push fully to the front (see *Fig. 3*).

- Insert the cable permanently attached to the detector block **38** in one of the openings **5** and the outlet capillary in one of the openings **7** of the rear panel **9**.
- Replace rear panel **9** and screw to the 792 Basic IC using the four knurled screws **8**.

3 Connect detector block

- Plug the gray connecting cable permanently attached to the detector block **38** into connection **15** "Detector Block" of the 792 Basic IC and fasten to the instrument by tightening the screws in the cable connector (see *Fig. 2*).

4 Connect waste container

- Lead the outlet capillary of the detector block **38** to a sufficiently large waste container and fix in place.

2.3.2 Connection of syringe and aspirating tubing

For manual filling of the sample loop **22** mounted on the injection valve, the 6.2816.020 Syringe, the syringe tubing **25** with coupling **24** and the PTFE aspirating tubing **23** are needed. These accessories are mounted as follows:

1 Connect syringe to syringe tubing

- Pull syringe tubing **25** connected to injection valve **22** by hand out of feedthrough **3** as far as desired (see *Fig. 3*).
- Mount a PEEK compression fitting **46** (see *section 2.3.4*) to the end of the syringe tubing **25** and screw the coupling **24** (6.2744.120) to the compression fitting **46**.
- Push 6.2816.020 Syringe (without needle) as far as it will go into the connection of coupling **24**.

2 Install aspirating tubing

- Pull aspirating tubing **23** connected to injection valve **22** by hand out of feedthrough **4** as far as desired (see *Fig. 3*).

2.3.3 Connection of the 6.5324.000 Bottle rack (option)

The optional available 6.5324.000 Bottle rack for supply vessels can be placed on top of the 792 Basic IC. The accessories include the supply vessels for eluent (2 L), regeneration solution (1 L) and rinsing solution (1 L).

2.3.4 Connection of PEEK capillaries

For the connections between high-pressure pump and detector block **6.1831.010 PEEK capillaries** (i.d. = 0.25 mm, e.d. = 1/16") are used which are connected using either **6.2744.010 PEEK compression fittings (long)** or **6.2744.070 PEEK compression fittings (short)**. These PEEK connectors can also be used to connect 6.1822.010 PTFE microcapillaries (i.d. = 0.3 mm). Proceed as follows:

*Capillaries fitted with new connectors must have a perfectly flat cut surface. To cut PEEK or PTFE capillaries it is best to use the **6.2621.080 Capillary tubing cutter**.*

1 Mount compression fitting

Slide a compression fitting **46** (6.2744.010) or a compression fitting **47** (6.2744.070) over the end of the capillary **48** to be fastened as shown in *Fig. 6*.

2 Insert capillary in connection

Push capillary end in the corresponding connection as far as it will go (to avoid dead volume).

3 Tighten compression fitting

Tighten compression fitting **46** or **47** by hand (never use tools).

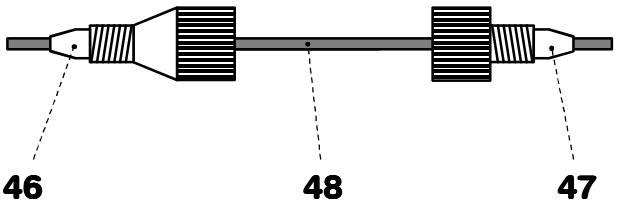


Fig. 6: Connectors for capillaries

46	**Compression fitting (6.2744.010)**
47	**Compression fitting (6.2744.070)**
48	**Capillary** 6.1831.010 PEEK capillary or 6.1822.010 PTFE microcapillary

2.3.5 Filter unit PEEK

One **6.2821.100 Filter unit PEEK** (see *Fig. 7*) is already installed between the high-pressure pump and the injection valve **22** at the 792 Basic IC. This filter unit serves to avoid contamination by abrasive particles of the piston seals.

The two other filter units PEEK supplied with the 792 Basic IC are installed between the pump tubings of the peristaltic pump and the inlet capillaries for regeneration and rinsing solution (see *section 2.8.2*). These filter units serve to protect the suppressor module from foreign particles and bacterial growth.

The Filter unit PEEK **28** consists of the housing **50** and the two connectors **49** (with filter) and **51** (without filter) screwed into the housing **50**. For the connection of capillaries **48**, PEEK compression fittings **46** (6.2744.010) or **47** (6.2744.070) must be used. New connectors **49** with filter are available as an option with the ordering number 6.2821.110 (set of 10).

For the connection of the filter unit, please note the flow direction arrow printed on the housing.

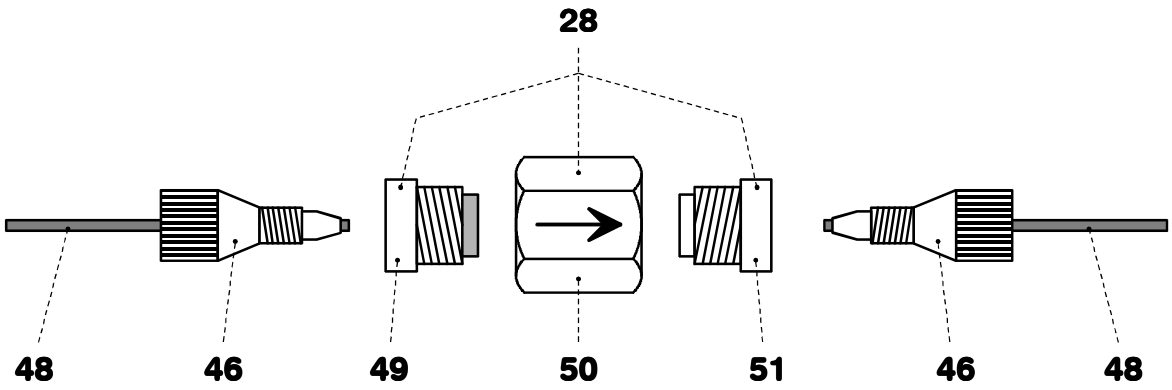


Fig. 7: 6.2821.100 Filter unit PEEK

28	**Filter unit PEEK (6.2821.100)**	**49**	**Connector with filter (6.2821.110)** Part of 6.2821.100 Filter unit
46	**Compression fitting (6.2744.010)**	**50**	**Housing for filter unit** Part of 6.2821.100 Filter unit
48	**Capillary** 6.1831.010 PEEK capillary or 6.1822.010 PTFE microcapillary	**51**	**Connector without filter** Part of 6.2821.100 Filter unit

2.4 Mains connection

Follow the instructions below for connecting to the power supply. If the instrument is operated with a mains voltage set wrongly and/or wrong mains fuse, there is a danger of fire!

2.4.1 Setting the mains voltage

Before switching on the 792 Basic IC for the first time, check that the mains voltage set on the instrument (see *Fig. 8*) matches the local mains voltage. If this is not the case, you must reset the mains voltage on the instrument as follows:

1 Disconnect mains cable

Disconnect mains cable from mains connection plug **12** of the 792 Basic IC.

2 Remove fuse holder

Using a screwdriver, loosen fuse holder **13** below the mains connection plug **12** and take out completely.

3 Check and change fuse if necessary

Carefully take the fuse installed for the desired mains voltage out of fuse holder **13** and check its specifications (the position of the fuse in the fuse holder is marked by the white arrow imprinted next to the mains voltage range):

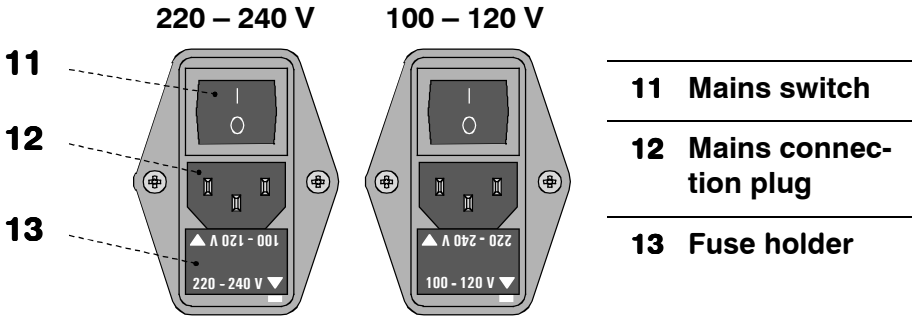
100…120 V	**1.0 A (slow-blow)**	Metrohm No. U.600.0016
220…240 V	**0.5 A (slow-blow)**	Metrohm No. U.600.0013

4 Insert fuse

Change fuse if necessary and reinsert in fuse holder **13**.

5 Install fuse holder

Depending on the desired mains voltage, insert fuse holder **13** in the 792 Basic IC so that the corresponding mains voltage range can be read normally and the adjacent white arrow points to the white bar imprinted below the fuse holder (see *Fig. 8*).



11	**Mains switch**
12	**Mains connection plug**
13	**Fuse holder**

Fig. 8: Setting the mains voltage

2.4.2 Fuses

One of the two fuses 1 A/slow-blow for 100…120 V or 0.5 A/slow-blow for 220…240 V is installed in fuse holder **13** of the 792 Basic IC as standard.

Ensure that the instrument is never put into operation with fuses of another type, otherwise there is danger of fire!

For checking or changing fuses, process as described in *section 2.4.1*.

2.4.3 Mains cable and mains connection

Mains cable

The instrument is supplied with one of three mains cables

- 6.2122.020 with plug SEV 12 (Switzerland, …)
- 6.2122.040 with plug CEE(7), VII (Germany, …)
- 6.2133.070 with plug NEMA 5-15 (USA, …)

which are three-cored and fitted with a plug with an earthing pin. If a different plug has to be fitted, the yellow/green lead (IEC standard) must be connected to protective earth (protection class 1).

Any break in the earthing inside or outside the instrument can make it a hazard!

Mains connection

Plug the mains cable into mains connection plug **12** of the 792 Basic IC (see *Fig. 8*).

2.4.4 On/off switching of the instrument

The 792 Basic IC is switched on and off using mains switch **11**. When the instrument is switched on, the mains pilot lamp **2** lights up.

2.5 Connection to the PC

2.5.1 Connecting cable

Always switch off 792 Basic IC and PC before you connect the two instruments with the 6.2134.100 Cable.

Connect the RS232 interface **14** at the 792 Basic IC to one of the serial COM ports at the PC using the 6.2134.100 Cable (9 pin/9 pin). If only a 25-pin COM interface is available on the PC then the optionally available 6.2125.110 Cable (9 pin/25 pin) or a commercially available adapter must be used.

2.5.2 Software installation

The PC program **«792 Basic IC 1.0»** is required for the operation of the 792 Basic IC; this is contained on the 6.6045.003 CD included in the accessories. This program runs under Windows 95, Windows 98, Windows NT and Windows 2000 operating systems and is installed as follows:

1 Install program

- Insert 6.6045.003 Installation CD into CD drive.
- Select **<Start>** and **Run**. Browse for the **setup.exe** file on the installation CD and click on **<OK>**.
- Click on "**792**" and follow the instructions given in the setup program.

  The software package will be installed in the desired directory. In addition to the program files, the following folders are installed:

Data	Folder for storage of chromatogram files (***.chw**) and batch reprocessing files (***.bar**)
Devices	Folder for storage of device files (***.dev**)
Methods	Folder for storage of method files (***.mtw**)
Reports	Folder for storage of report files (***.txt**) and graphic files (***.wmf**)
Systems	Folder with subfolders with system files (***.smt**).

2 Registrierung

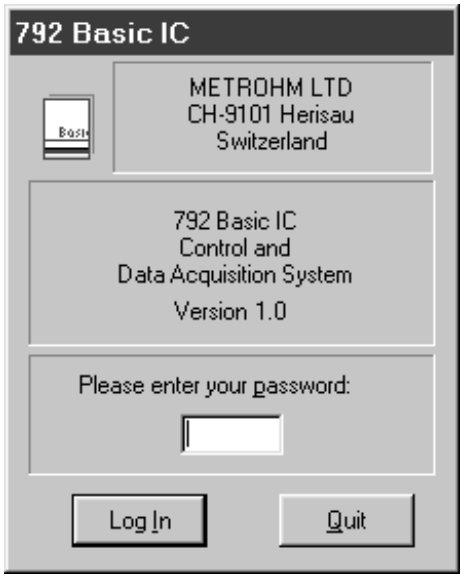
- Please send us your 8.792.8007 Registration card as soon as possible. Only registered users will get updated program versions at a special price.

2.5.3 Basic settings

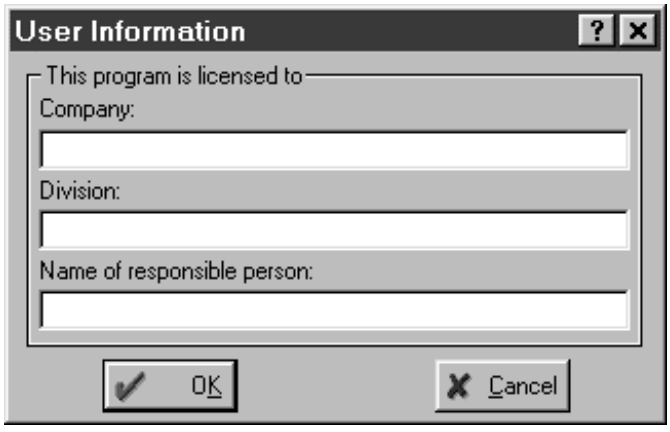
When the program is started for the first time several basic settings must be made for the 792 Basic IC. Proceed as follows:

1 Start program

- Double-click the software icon to start the program. The program window with the opening picture is opened and the Log In window appears on the screen:



- Do not enter any password here, just click on **<Log In>**. The following window appears:



- Enter company, division and name and click on **<OK>**. This window appears only one time after software installation.

2 COM port settings

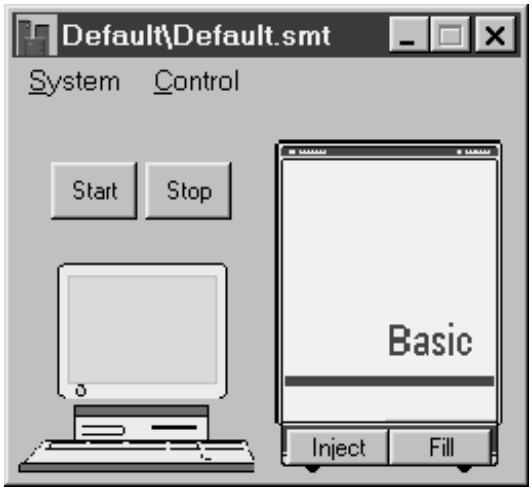
*This step must only be carried out if a different **COM interface from COM1** is used for connection to the 792 Basic IC.*

- Click on **Options** / **792 Basic IC:COM1** to open the **Links** window:

- Click on **COM1** using the right mouse button and select the **Change** menu item to open a window listing all available COM ports at the PC.
- Select the desired COM port to which the 792 Basic IC has been connected and click on **<OK>**. The window is closed.
- Close the **Links** window by clicking on **<OK>**.

3 Open a system

- Click on **File** / **Open** / **System** in the main window. Open the folder **Default**. Select the system file **Default.smt** and click on **<Open>**. The corresponding system window is opened:

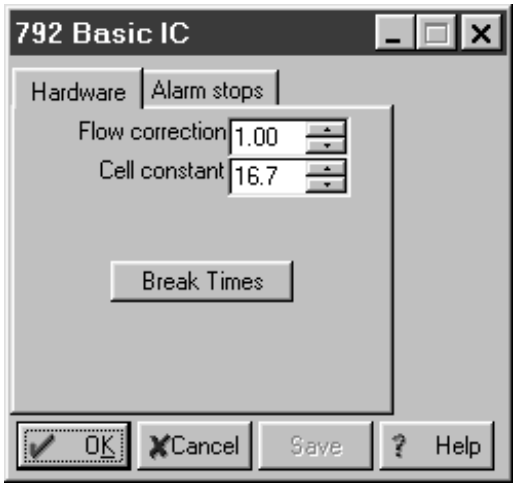


- If the connection between PC and 792 Basic IC is working the message **Hardware settings file for 792 unit with serial number '#####' not found! Create?** will appear. Click **<Yes>** in order to create the configuration file **#####.792** for this instrument.
- If the connection between PC and Personal IC does not work then the message **Detection of hardware failed[792 Basic IC [COM#]]** appears in the **SYSTEM STATE** window. In this case check whether the instrument has been switched on, whether the connection cable is connected up properly and whether the COM interface has been set correctly (see point **2**). Then repeat point **3**.

4 Hardware settings

Of the general hardware settings only the input of the cell constant is described. Standard settings can normally be used for all other parameters.

- Click the 792 icon using the right mouse button and select the **Hardware** item. The **Hardware settings** window is opened:



- In the **Cell constant** field enter the cell constant which is printed on the 1.732.0110 Detector block (see *section 2.3.1*).
- Click on **<OK>** to close the window and save the settings.

2.6 High-pressure pump

In order to avoid damage to the pump it must never be operated dry. Each time that the pump is switched on always first check that the eluent supply has been connected up correctly and that sufficient eluent is present in the eluent bottle.

2.6.1 Removing the transport security screws

In order to prevent the pump drive from being damaged during transport the pump head is fitted with three transport security screws **10** (see *Fig. 2*). These transport security screws must be removed before the high-pressure pump is started up. Also remove the red sticker attached to the pump head **34**.

In order to avoid damage to the pump head these three security screws should be attached to the pump head each time that it is to be transported.

2.6.2 Installing the pulsation dampener (option)

To protect the column material of sensitive separating columns (e.g. methacrylate-based columns) against pressure drops caused by the injector, the use of the optional **6.2620.150 Pulsation dampener MF** is recommended. It has to be installed between the high-pressure pump and the injection valve of the 792 Basic IC as follows (see *Fig. 9*):

1 Install pulsation dampener

- Position the pulsation dampener **52** in the interior of the 792 Basic IC on the base.

2 Connection to the pump

- Unscrew PEEK capillary **27** of coupling **26** and attach it to connection **54** of the pulsation dampener **52**.

3 Connection to injection valve

- Unscrew PEEK capillary **18** of coupling **26** and attach it to connection **53** of the pulsation dampener **52**.

The pulsation dampener is filled with isopropanol and must be rinsed with eluent before connection to a separating column (see section 2.6.4).

The 6.2620.150 Pulsation dampener can be operated in both directions.

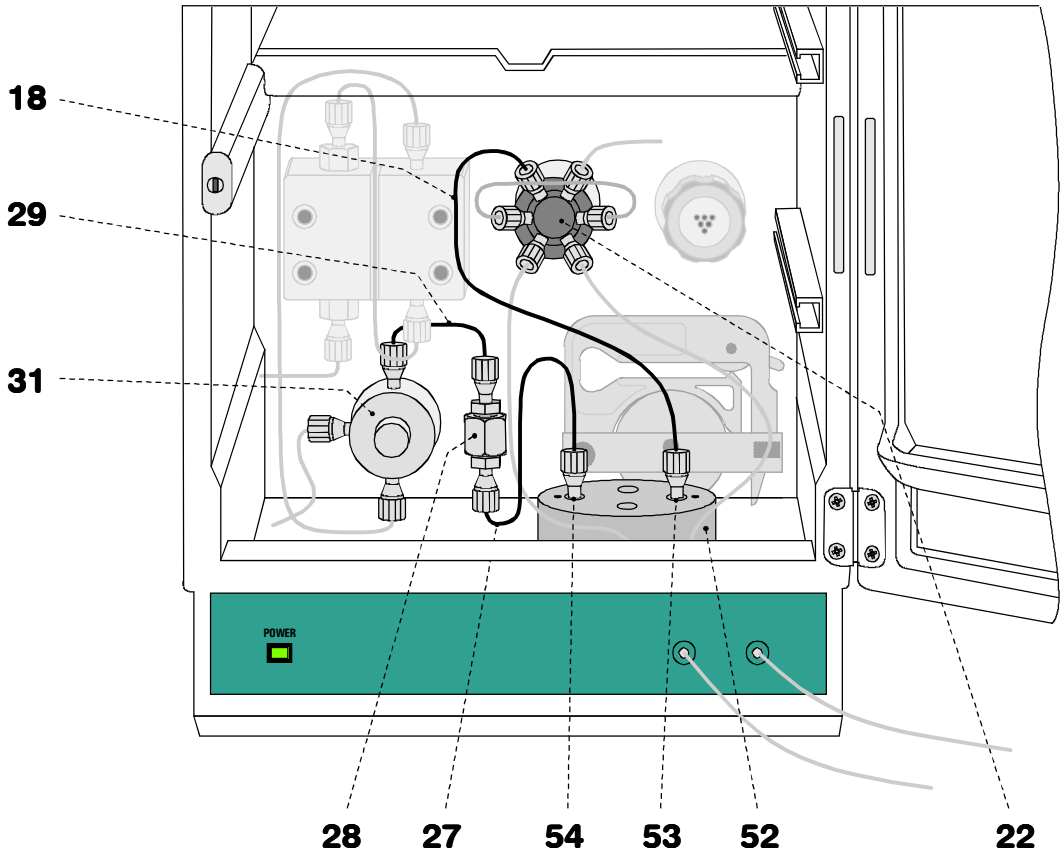


Fig. 9: Connection of the pulsation dampener (option)

18	**Inlet capillary for injector** PEEK capillary, length *L* = 24 cm	**31**	**Purge valve**
22	**Injection valve**	**52**	**Pulsation dampener (6.2620.150)**
27	**Connection capillary** PEEK capillary, length *L* = 13 cm	**53**	**Connection to injection valve**
28	**Filter unit PEEK (6.2821.100)**	**54**	**Connection to purge valve**
29	**Connection capillary** PEEK capillary, length *L* = 13 cm		

2.6.3 Connecting the eluent bottle

To connect the eluent bottle with the high-pressure pump, insert the supplied 6.1834.010 aspirating tubing (i.d. = 1.5 mm, e.d. = 2.5 mm, length = 2.5 m) into one of the openings **5** or **7** in the interior of the 792 Basic IC. Pull the aspirating tubing sufficiently far into the interior of the 792 Basic IC and push at least 5 mm of it onto aspirating capillary **32** (see *Fig. 3*) of the high-pressure pump (it may be necessary to use emery paper). Screw on the 6.2821.090 aspirating filter at the other end of the aspirating tubing and insert it into the eluent bottle.

*Only **degassed** (with N_2, He or vacuum) and **microfiltered** (0.45 µm filter) **eluents** should be used!*

*Care must be taken that the **eluent** used is **freely miscible** with any solvent remaining in the pump head (the pump head leaves the factory filled with either isopropanol or methanol/water). If this is not the case then the pump must first be rinsed with a solvent which is miscible with both the previous eluent and the following eluent (e.g. acetone).*

2.6.4 Deaerating the pump and rinsing the pulsation dampener

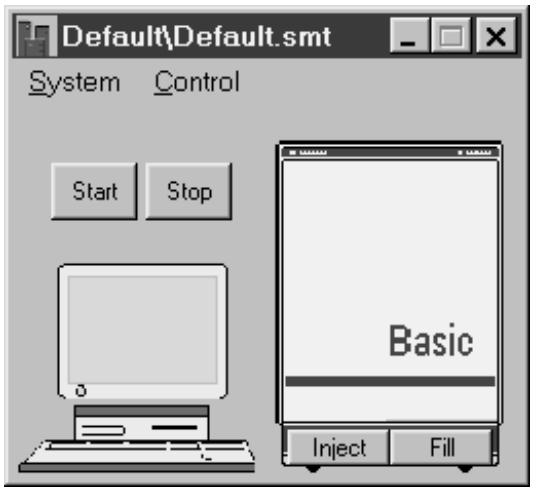
The first time that it is started up the high-pressure pump must be deaerated. Proceed as follows:

1 Prepare for deaeration

- Open the rotary knob on purge valve **31** by approx. ½ turn in the counterclockwise direction (see *Fig. 3*).
- Mount a PEEK compression fitting **46** (see *section 2.3.4*) to the end of capillary **30** and screw coupling **24** (6.2744.120) to the compression fitting **46**.
- Push 6.2816.020 Syringe (without needle) into the connection on coupling **24** until the stop is reached.

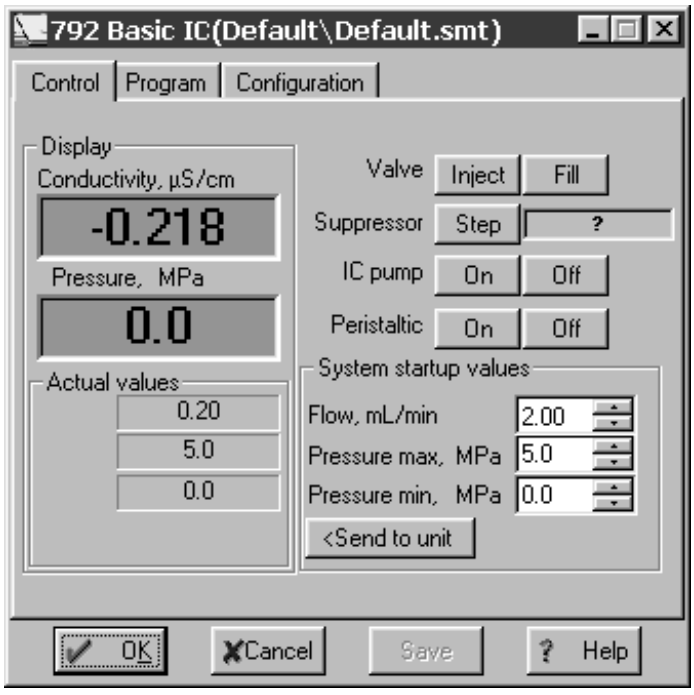
2 Open system

- Start the «792 Basic IC» PC program, if it has not been already been started (see *section 2.5.3*).
- Select **File** / **Open** / **System** in the main window and open the folder **Default**. Select the system file **Default.smt** and click on **<Open>**. The corresponding system window is opened:



3 Set flow rate to 2 mL/min

- Double-click the 792 icon in the system window to open the window for manual control of the 792 Basic IC (see below).
- Set the flow rate to **2 mL/min** in the **Flow** field.
- Click to **<Send to unit>** to send this value to the 792 Basic IC.



4 Deaerate pump

- Make sure that the 6.1834.010 aspirating tubing for the high-pressure pump has been immersed into the eluent.
- Click the **<On>** button for **IC pump** to switch on the high-pressure pump.
- Use the syringe connected to the purge valve **31** to aspirate air until eluent flows into the syringe.
- Click the **<Off>** button for **IC pump** to switch off the high-pressure pump.
- Close the rotary knob on purge valve **31** by turning it in a clockwise direction (see *Fig. 3*).
- Remove the syringe from coupling **24**.

5 Rinse pulsation dampener (if present)

- Place a beaker beneath the column connection capillary **20**.
- Click the **<On>** button for **IC pump** to switch on the high-pressure pump and rinse the pulsation dampener **52** filled with isopropanol for ca. 10 min with eluent.
- Click the **<Off>** button for **IC pump** to switch off the high-pressure pump.

6 Reduce flow rate

- Reset the original flow rate under **Flow** (e.g. **0.2 mL/min**).
- Click **<Send to unit>** to send this value to the 792 Basic IC.

2.7 Precolumns and separating columns

2.7.1 General information on precolumns

The use of easily exchangeable precolumns protects the separating columns and prolongs their lifetime. The precolumns available from Metrohm (see *section 6.3.2*) are either real precolumns or precolumn cartridges, which are used together with the 6.2821.050 Twin cartridge holder or the 6.2828.110 Precolumn cartridge holder.

New IC precolumns are normally filled with solution and sealed at both ends. Before the precolumn is installed in the system, it must be ensured that this solution is freely miscible with the eluent used (check manufacturer's specifications).

2.7.2 Precolumns with twin cartridge holder

The 6.1005.020, 6.1005.040, 6.1005.050, 6.1007.010 and 6.1010.010 Precolumn cartridges are installed in the 6.2821.050 Twin cartridge holder as follows (see *Fig. 10*):

1 Install cartridge

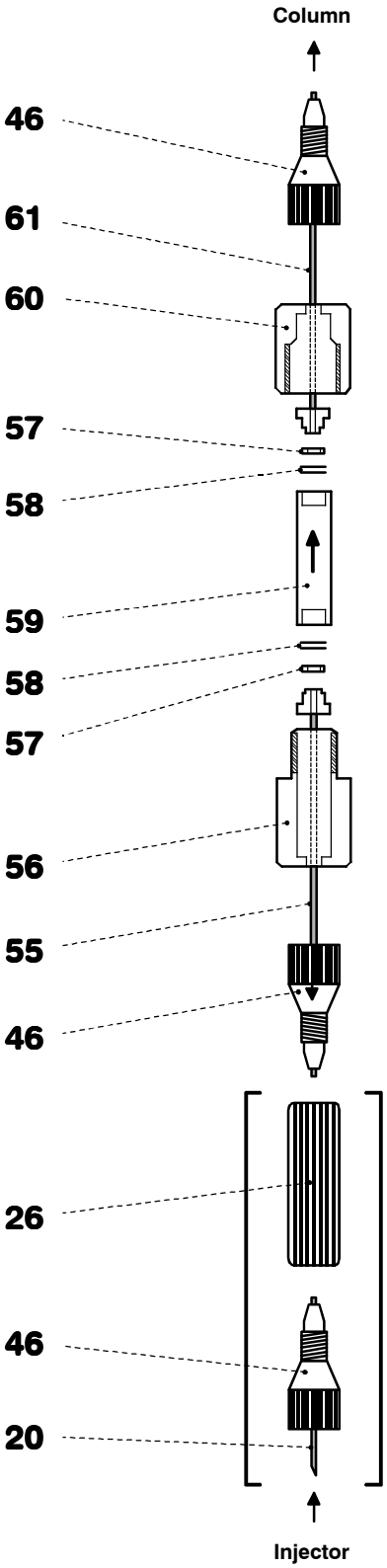
- Insert inlet capillary **55** with end piece for precolumn cartridge in Manufit housing **56**.
- Insert outlet capillary **61** with end piece for precolumn cartridge in Manufit pressure screw **60**.
- Remove end caps from the precolumn cartridge **59** (the steel mesh **58** and gaskets **57** are already inserted in the cartridge).
- Fit the two capillary end pieces onto the precolumn cartridge **59** (comply with the flow direction if specified on the column).
- Screw Manufit pressure screw **60** and Manufit housing **56** firmly together.

2 Connect precolumn

- Cut inlet capillary **55** of the assembled precolumn to the desired length and mount a compression fitting **46** (see *section 2.5*).
- Connect inlet capillary **55** either using the Coupling **26** to the column connection capillary **20** mounted on the injection valve or directly to connection "4" of injection valve A.
- Shorten outlet capillary **61** of the precolumn to ca. 5 cm and mount a compression fitting **46** (see *section 2.5*).

3 Rinse the precolumn

- Place a beaker beneath outlet capillary **61**.
- Switch on 709 IC Pump, rinse precolumn for ca. 10 min with eluent and then switch off 709 IC Pump.



20	**Column connection capillary of injector**
26	**PEEK coupling (6.2744.120)**
46	**Compression fitting (6.2620.000)**
55	**Inlet capillary**
56	**Manufit housing**
57	**PTFE gasket (6.2821.010)**
58	**2 Steel meshes (6.2821.020)**
59	**Precolumn cartridge**
60	**Manufit pressure screw**
61	**Outlet capillary**

Fig. 10: Installing precolumn cartridges

2.7.3 Precolumn glass cartridges with cartridge holder

The precolumn glass cartridge METROSEP Anion Dual 1 (6.1006.030) is inserted in the 6.2828.110 Precolumn cartridge holder as follows (see *Fig. 11*):

1 Insert cartridge

- Remove end fittings **62** from sleeve **63**.
- Insert precolumn cartridge **64** in sleeve **63** (mark flow direction of the column cartridge on sleeve, the column cartridge should always be operated in the same flow direction).
- Screw both end fittings **62** loosely to sleeve **63** by hand.
- Tighten both end fittings **62** first by hand, then firmly using a screwdriver (½ – ¼ turn).

2 Connect precolumn

- Provide the column connection capillary **20** mounted on the injection valve with a PEEK compression fitting **46** (see *section 2.3.4*) and screw it tightly onto end fitting **62** on the inlet side of the precolumn.
- Screw connection piece **65** to end fitting **62** on the other end of the precolumn.

3 Rinse precolumn

- Place a beaker beneath the outlet capillary of the precolumn.
- Open software window for manual system control.
- If necessary, modify **Flow rate** to the value suited for the inserted separating column and click on **<Send to unit>** to send this value to the 792 Basic IC.
- Switch on high-pressure pump (**IC pump**) by clicking **<On>** and rinse precolumn with eluent for ca. 10 min.
- Switch off high-pressure pump by clicking **<Off>**.

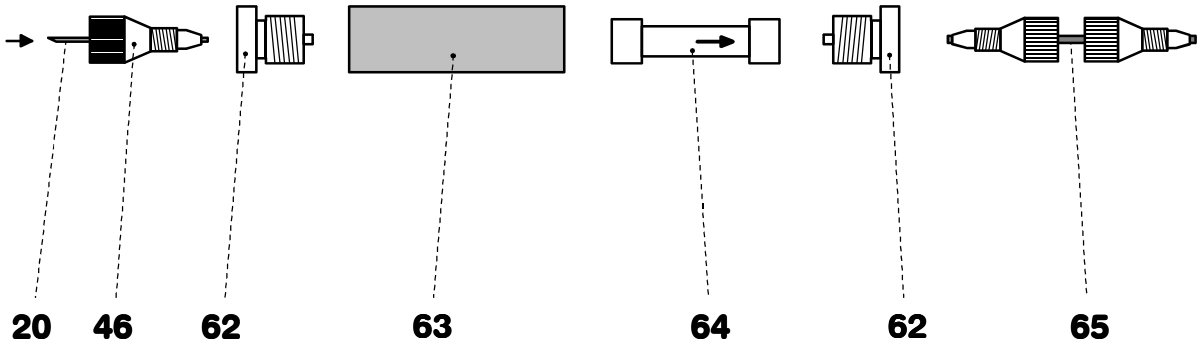


Fig. 11: Installation of precolumn glass cartridges with cartridge holder

20	**Column connection capillary from injector**	**63**	**Sleeve for precolumn cartridge**
46	**Compression fitting (6.2744.010)**	**64**	**Precolumn cartridge (6.1006.030)**
48	**PEEK capillary (6.1831.010)**	**65**	**Connection piece** for connection precolumn – column
62	**End fitting**		

2.7.4 IC anion precolumn SUPERSEP

The 6.1009.010 IC Anion Precolumn SUPERSEP has two connections for PEEK capillaries and is installed as follows:

1 Connect precolumn

- Remove end caps from the precolumn.
- Fit PEEK compression fitting **46** to column connection capillary **20** (see *section 2.3.4*).
- Screw precolumn to column connection capillary **20**.
- Cut a piece from the 6.1831.010 PEEK capillary as short as possible and fit with PEEK compression fittings **46** (see *section 2.3.4*).
- Fasten the prepared capillary to the other end of the precolumn.

2 Rinse precolumn

- Place a beaker beneath the outlet capillary of the precolumn.
- Open software window for manual system control.
- If necessary, modify **Flow rate** to the value suited for the inserted separating column and click on **<Send to unit>** to send this value to the 792 Basic IC.
- Switch on high-pressure pump (**IC pump**) by clicking **<On>** and rinse precolumn with eluent for ca. 10 min.
- Switch off high-pressure pump by clicking **<Off>**.

2.7.5 General information on separating columns

New IC separating columns are normally filled with solution and sealed at both ends. Before the column is installed in the system, it must be ensured that this solution is freely miscible with the eluent used (check manufacturer's specifications).

The IC separating columns and precolumns currently available from Metrohm are listed in *section 6.3.2*. A test chromatogram and an information leaflet is provided with each column. You will find additional information concerning these columns in the 8.732.2003 Metrohm Monograph «Ion chromatography» and in special «Application Bulletins», which are available on request free of charge from your local Metrohm agency.

When you install the column, always ensure that this is inserted correctly in accordance with the flow direction shown (arrow must point upwards).

2.7.6 Selection of the sample loop

Selection of the sample loop depends on the separating column used. Normally, the following sample loops are used:

Cation columns	10 µL
Anion columns with suppressor	20 µL
Anion columns without suppressor	100 µL

In the 792 Basic IC, the **6.1825.210 sample loop (20 µL, PEEK)** is installed. If desired, the built-in sample loop can be replaced by one of the sample loops available as an option (see *section 6.3.1*).

2.7.7 Installation of the separating column without suppressor

For operation of the 792 Basic IC 792 without suppressor module, the IC separating column is installed as follows (see *Fig. 12*):

1 Connect column to injector

- Remove end caps from column **66**.
- *without precolumn:*
  Screw inlet end of separating column **66** (note flow direction) to column connection capillary **20** mounted on the injector.
- *with precolumn in twin cartridge holder:*
  Screw inlet end of separating column **66** (note flow direction) to outlet capillary **61** of the twin cartridge holder as described in *section 2.7.2* (see *Fig. 10*).
- *with precolumn in cartridge holder:*
  Screw inlet end of separating column **66** (note flow direction) to the precolumn fixed in the cartridge holder as described in *section 2.7.3* (see *Fig. 11*).

- *with IC anion precolumn SUPERSEP:*
  Screw inlet end of separating column **66** (note flow direction) to the precolumn installed as described in *section 2.7.4*.

2 Rinse column

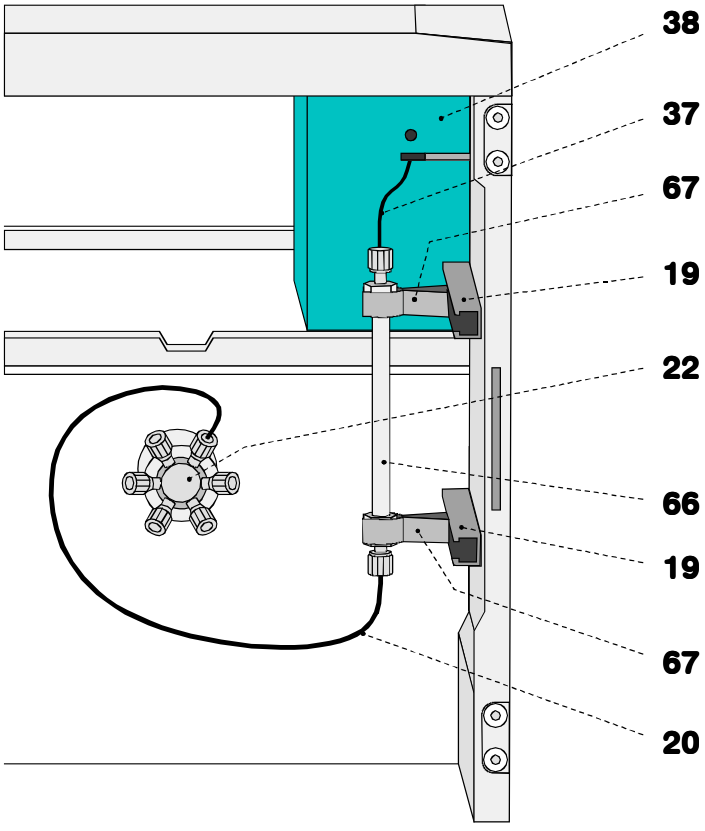
- Place a beaker beneath the column outlet.
- Open software window for manual system control.
- If necessary, modify **Flow rate** to the value suited for the inserted separating column and click on **<Send to unit>** to send this value to the 792 Basic IC.
- Switch on high-pressure pump (**IC pump**) by clicking **<On>** and rinse column with eluent for ca. 10 min.
- Switch off high-pressure pump by clicking **<Off>**.

3 Connect column to detector block

- Screw outlet end of separating column **66** to the inlet capillary **37** permanently mounted on the detector block **38**.

4 Fix column

- Insert one or two column holders **67** (6.2027.030, 6.2027.040 or 6.2027.050) in the mounting rails **19** and fasten separating column **66** in the column holder **67**.



19	**Mounting rail** for column holder **67**
20	**Column connection capillary** Connection injection valve **22** – separating column **66**
22	**Injection valve**
37	**Inlet capillary for detector block** PEEK capillary, fixed mounting
38	**Detector block (1.733.0110)**
66	**Separating column**
67	**Column holder (6.2027.0X0)**

Fig. 12: Installation of column without suppressor

2.7.8 Installation of the separating column with suppressor

For operation of the 792 Basic IC with suppressor module, the IC separating column is first connected to the injector or precolumn. The connection to the suppressor module and the detector block is described in *section 2.8*.

1 Connect column to injector

- Remove end caps from column **66**.
- Screw inlet end of separating column **66** (note flow direction) to column connection capillary **20** or to the already installed precolumn (procedure see *section 2.7.7*).

2 Rinse column

- Place a beaker beneath the column outlet.
- Open software window for manual system control.
- If necessary, modify **Flow rate** to the value suited for the inserted separating column and click on **<Send to unit>** to send this value to the 792 Basic IC.
- Switch on high-pressure pump (**IC pump**) by clicking **<On>** and rinse column with eluent for ca. 10 min.
- Switch off high-pressure pump by clicking **<Off>**..

3 Fix column

- Insert one or two column holders **67** (6.2027.030, 6.2027.040 or 6.2027.050) in the mounting rails **19** and fasten separating column **66** in the column holder **67**.

2.8 Suppressor module

2.8.1 General information on suppressor module

The **Metrohm Suppressor Module MSM** for chemical suppression installed in the 2.792.0020 Basic IC comprises a total of 3 suppressor units which are in turn used for suppression, regenerated with sulfuric acid and rinsed with water. To record every new chromatogram under comparable conditions, work is normally carried out with freshly regenerated suppressor. Switching is either automatic together with the valve switching or manual.

The suppressor units must never be regenerated with H_2SO_4 in the same flow direction used for the eluent. You should thus always install the inlet and outlet capillaries as described in section 2.8.4 according to the scheme shown in Fig. 15.

For operation of the suppressor module, the **two-channel peristaltic pump** built into the 2.792.0020 Basic IC is used which conveys the regeneration solution (normally **20 mmol/L H_2SO_4**) and the rinsing solution (normally **dist. H_2O**) to the suppressor units (flow rate of 0.5 mL/min).

The three inlets and outlets numbered 1...3 on the suppressor module each have 2 permanently mounted PTFE capillaries, which must be connected as described in *section 2.8.4* (see *Fig. 14* and *Fig. 15*).

To avoid contamination of the suppressor module by foreign particles or bacterial growth, the two **6.2821.100 Filter units PEEK** (see *section 2.3.5*) supplied with the 2.792.0020 Basic IC must be installed between the peristaltic pump and the inlet capillaries of the suppressor module.

The suppressor module must never be switched in the dry state as there is a danger of blocking. Before every switching operation of the suppressor module, the three suppressor units must have been rinsed for at least ½ h with eluent, regeneration and rinsing solution.

2.8.2 Preparation of the peristaltic pump

Before start-up the accessories for the 2-channel peristaltic pump built into the 792 Basic IC must be mounted according to *Fig. 13*. Proceed as follows:

1 Attach pump tubings

- Loosen both tubing cartridges **40** mounted above pump drive **44** from the holding clamp **42** by pressing down snap-action lever **43** and remove from mounting pin **45** (see *Fig. 14*).

- Press contact pressure lever **41** on both tubing cartridges down as far as it will go.
- Insert the pump tubings **71** and **72** (6.1826.060) into each of the tubing cartridges as shown in *Fig. 13*. The white-yellow stopper **73** must click into the corresponding holder on the left-hand side of the tubing cartridge.
- Place the tubing cartridges on mounting pin **45** and press down on the right-hand side until snap-action lever **43** clicks into position on holding clamp **42**. Take care that no kinks are formed in the pump tubing.

2 Install Filter units PEEK

- Mount a coupling **74** (6.2744.110) to the outlet end of the two pump tubings **71** and **72**.
- Attach a filter unit PEEK **28** (see *section 2.3.5*) to the other end of this coupling (note flow direction!).

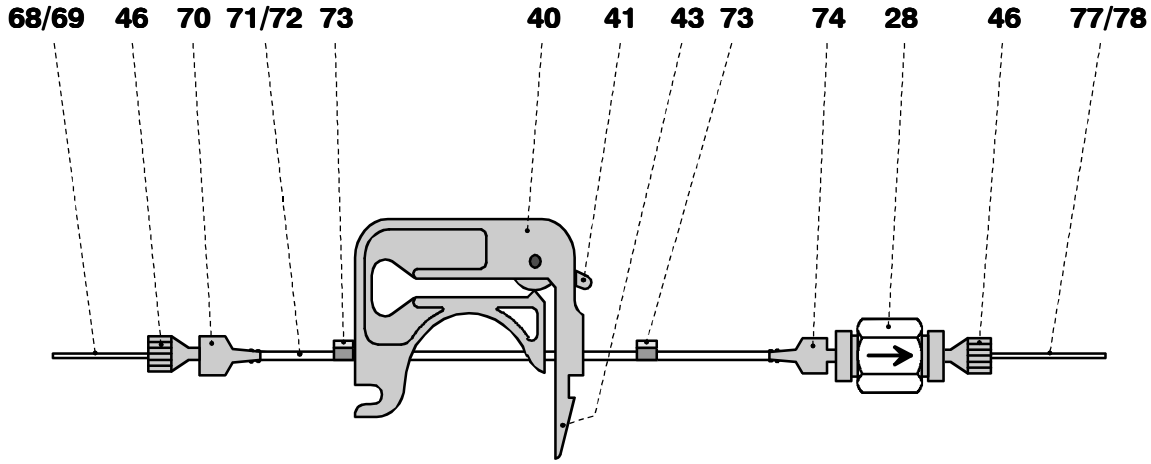


Fig. 13: Installing pump tubings

28	**Filter unit PEEK (6.2821.100)**	**70**	**Coupling (6.2744.030)**
40	**Tubing cartridge**	**71**	**Pump tubing (6.1826.060) for H_2SO_4**
41	**Contact pressure lever**	**72**	**Pump tubing (6.1826.060) for H_2O**
43	**Snap-action lever**	**73**	**Stopper (white-yellow)**
46	**PEEK compression fitting (6.2744.010)**	**74**	**Coupling (6.2744.110)**
68	**Aspirating tubing for H_2O**	**77**	**Suppressor inlet capillary for H_2O**
69	**Aspirating tubing for H_2SO_4**	**78**	**Suppressor inlet capillary for H_2SO_4**

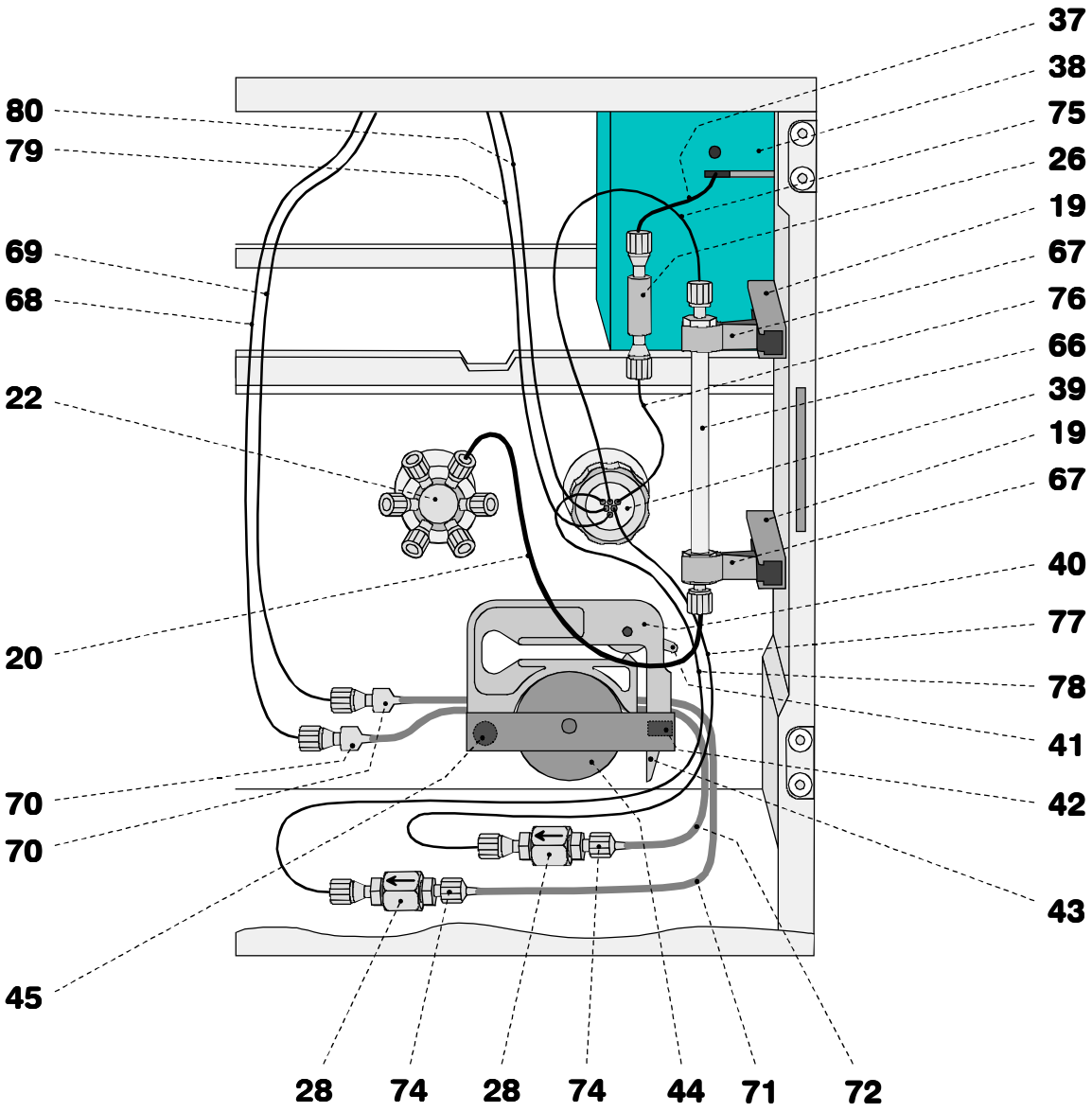


Fig. 14: Installation of column with suppressor

19	**Mounting rail** for column holder **67**	**66**	**Separating column**
20	**Column connection capillary** PEEK capillary (6.1831.010; 30 cm)	**67**	**Column holder (6.2027.0X0)**
22	**Injection valve**	**68**	**Aspirating tubing for H_2O** 6.1803.020 PTFE tubing
26	**PEEK coupling (6.2744.040)**	**69**	**Aspirating tubing for H_2SO_4** 6.1803.020 PTFE tubing
28	**Filter unit PEEK (6.2821.100)**	**70**	**Coupling (6.2744.030)**
37	**Inlet capillary to detector block** (fixed mounting)	**71**	**Pump tubing (6.1826.060) for H_2SO_4**
38	**Detector block (1.733.0110)**	**72**	**Pump tubing (6.1826.060) for H_2O**

39	**Suppressor module**	**74**	**Coupling (6.2744.110)**
40	**Tubing cartridge (6.2755.000)** for pump tubings **71/72**	**75**	**Suppressor inlet capillary for eluent**
41	**Contact pressure lever** for adjusting the contact pressure	**76**	**Suppressor outlet capillary for eluent**
42	**Holding clamp** for locking the tubing cartridge into place	**77**	**Suppressor inlet capillary for H_2O**
43	**Snap-action lever** for releasing the tubing cartridge	**78**	**Suppressor inlet capillary for H_2SO_4**
44	**Pump drive** Roller head with contact rollers	**79**	**Suppressor outlet capillary for H_2O**
45	**Mounting pin** for attaching the tubing cartridge	**80**	**Suppressor outlet capillary for H_2SO_4**

2.8.3 Connection of supply bottles

The supply lines for the regeneration and rinsing solution between the storage bottles and the peristaltic pump are installed as follows:

1 Prepare supply bottle for H_2SO_4

- Prepare regeneration solution suited for the desired application and separating column (normally 20 mmol/L H_2SO_4).
- Fill regeneration solution into supply bottle and label the bottle.

2 Connect aspirating tubing for H_2SO_4

- Prepare aspirating tubing **69**: Cut a piece of the 6.1803.020 PTFE tubing to the required length (normally ca. 120 cm).
- Insert one end of the aspirating tubing **69** into the regeneration solution storage bottle and tighten it so that the tubing is firmly held.
- Insert the free end of aspirating tubing **69** into one of the openings **5** of the 792 Basic IC (*see Fig. 2*) and pull it sufficiently far into the interior.
- Mount a coupling **70** (6.2744.030) to the inlet end of the rear pump tubing **71**.
- Mount a 6.2744.010 Compression fitting at the end of the aspirating tubing **69** and screw this compression fitting on to the coupling **70** (see *Fig. 14*).

3 Prepare supply bottle for H_2O

- Prepare rinsing solution suited for the desired application and separating column (normally dist. H_2O).
- Fill rinsing solution into a supply bottle and label the bottle.

4 Connect aspirating tubing for H_2O

- Prepare aspirating tubing **68**: Cut a piece of the 6.1803.020 PTFE tubing to the required length (normally ca. 120 cm).
- Insert one end of the aspirating tubing **68** into the rinsing solution storage bottle and tighten it so that the tubing is firmly held.
- Insert the free end of aspirating tubing **68** into one of the openings **5** of the 792 Basic IC (*see Fig. 2*) and pull it sufficiently far into the interior.
- Mount a coupling **70** (6.2744.030) to the inlet end of the front pump tubing **72**.
- Mount a 6.2744.010 Compression fitting at the end of the aspirating tubing **68** and screw this compression fitting on to the coupling **70** (see *Fig. 14*).

2.8.4 Connection of the suppressor module

The three inlets and outlets numbered 1...3 on the suppressor module **39** each have 2 permanently mounted PTFE capillaries, which must be connected as follows (see *Fig. 14* and *Fig. 15*):

1 Inlet capillary for eluent

- Screw inlet capillary **75** marked with "Eluent" of suppressor module **39** to outlet end of separating column **66** using a 6.2744.010 Compression fitting.

2 Outlet capillary for eluent

- Screw outlet capillary **76** marked with "Detector" of suppressor module **39** to coupling **26** using a 6.2744.010 Compression fitting.
- Screw inlet capillary **37** of detector block **38** to other end of coupling **26**.

3 Inlet capillary for H_2SO_4

- Attach inlet capillary **78** marked with "H_2SO_4" of suppressor module **39** using a 6.2744.010 Compression fitting to the filter unit PEEK **28** connected to the rear pump tubing **71**.

4 Outlet capillary for H_2SO_4

- Pull outlet capillary **80** marked with "Waste" of the suppressor module **39** from below through one of the openings **6** out of the inner compartment of the 792 Basic IC.
- Lead outlet capillary **80** to a sufficiently large waste container and fix it in place.

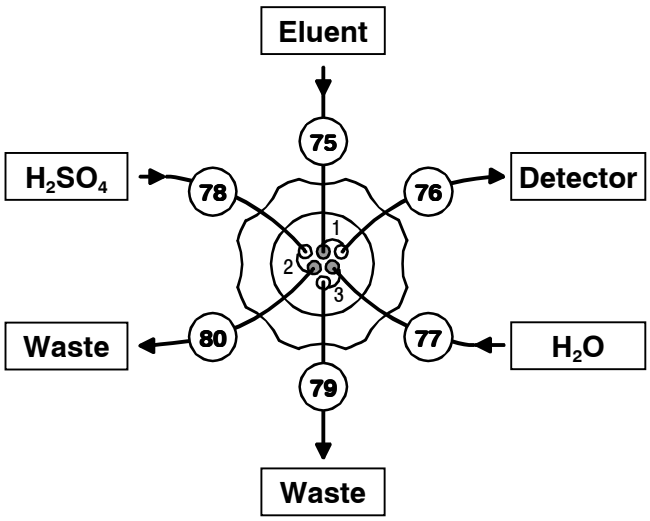


Fig. 15: Connections at suppressor module

75	**Suppressor inlet capillary for eluent**
76	**Suppressor outlet capillary for eluent**
77	**Suppressor inlet capillary for H_2O**
78	**Suppressor inlet capillary for H_2SO_4**
79	**Suppressor outlet capillary for H_2O**
80	**Suppressor outlet capillary for H_2SO_4**

5 Inlet capillary for H_2O

- Attach inlet capillary **77** marked with "H_2O" of suppressor module **39** using a 6.2744.010 Compression fitting to the filter unit PEEK **28** connected to the front pump tubing **72**.

6 Outlet capillary for H_2O

- Pull outlet capillary **79** marked with "Waste" of the suppressor module **39** from below through one of the openings **6** out of the inner compartment of the 792 Basic IC.
- Lead outlet capillary **79** to a sufficiently large waste container and fix it in place.

7 Fasten capillaries to the side walls

- If necessary, the two aspirating tubings **68** and **69** can be fixed in the required position in the interior with the help of a Y.107.0150 self-adhesive strap.
- If necessary, the two outlet capillaries **79** and **80** can be fixed in the required position in the interior with the help of a Y.107.0150 self-adhesive strap.

2.9 Putting into operation

2.9.1 Putting into operation without suppressor

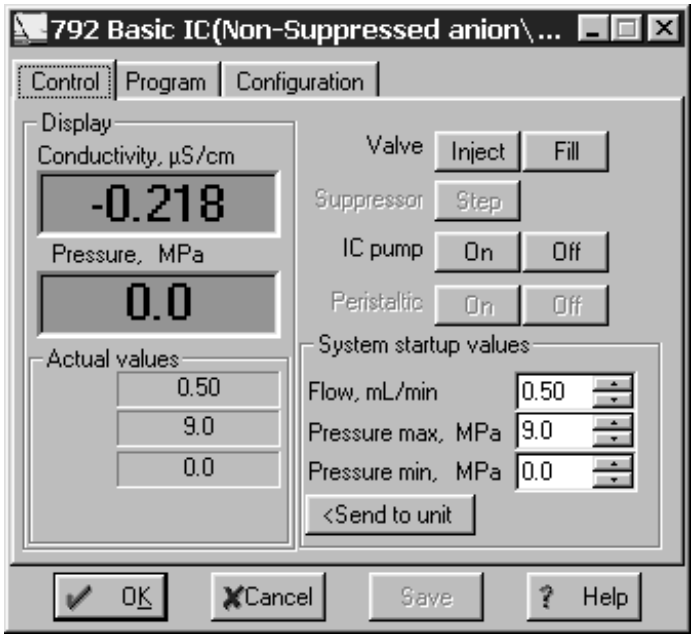
Before sample solutions can be injected at the **792 Basic IC** (without use of the suppressor), the entire system must be tested for leaks and then conditioned with eluent until the baseline is stable. Proceed as follows:

1 System öffnen

- Start the «792 Basic IC» PC program, if it has not already been started (see *section 2.5.3*).
- Select **File** / **Open** / **System** in the main window. Select the system file suited for the inserted column (e.g. **anionsupp.smt**) and click on **<Open>**.

2 Open control window

- Double-click the 792 icon in the system window. The control window for manual control of the 792 Basic IC appears, which indicates conductivity, pressure and current system parameters.



3 Start system

- Make sure, that the aspirating tubing 6.1834.010 for the high-pressure pump is immersed in the eluent.
- Select **Startup hardware (Measure baseline)** from the **Control** menu in the system window. The high-pressure pump is started, at the same time, a chromatogram window is opened where the baseline is recorded continuously.

4 Check for leaks

- Check all capillaries and their connections between the high-pressure pump and the detector block for escaping liquid. If eluent escapes anywhere, the appropriate compression fitting must be tightened further or changed.

5 Condition system

- Rinse the system with eluent until the desired stability of the baseline is reached (normally 30…60 min; if the eluent is changed, the establishment of the ion exchanger equilibrium on the separating column can take longer).
- The instrument is now ready for sample determinations using the selected system.

2.9.2 Putting into operation with suppressor

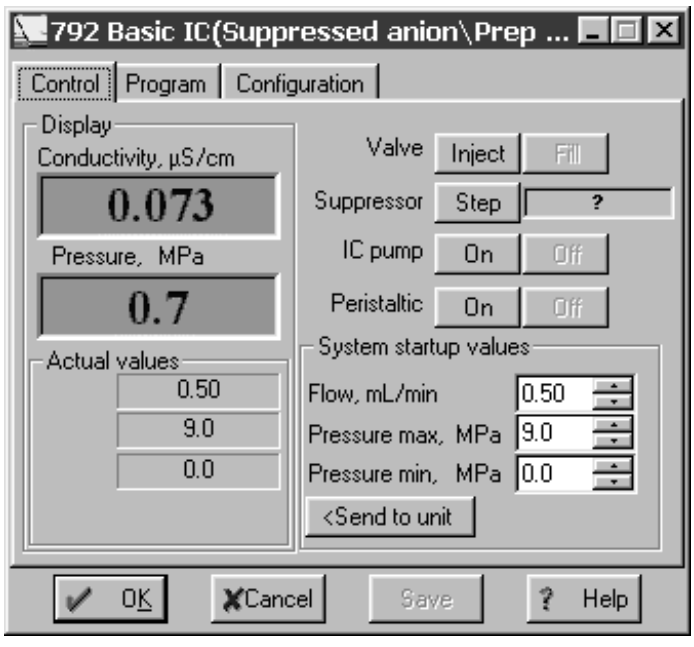
Before sample solutions can be injected at the **792 Basic IC** (with use of the suppressor), the entire system must be tested for leaks and then conditioned with eluent until the baseline is stable. At the same time, the suppressor module must be conditioned. Proceed as follows:

1 Open system "Prep MSM.smt"

- Start the «792 Basic IC» PC program, if it has not already been started (see *section 2.5.3*).
- Select **File** / **Open** / **System** in the main window. Open the folder **Suppressed anion** and select the system file **Prep MSM.smt**. Click on **<Open>**.

2 Open control window

- Double-click the 792 icon in the system window. The control window for manual control of the 792 Basic IC appears, which indicates conductivity, pressure and current system parameters.



3 Start system

- Make sure, that the aspirating tubing 6.1834.010 for the high-pressure pump is immersed in the eluent.
- Select **Startup determination** from the **Control** menu in the system window. The high-pressure pump and the peristaltic pump are started, at the same time, a chromatogram window is opened where the baseline is recorded continuously. The suppressor module is automatically switched to the next position every 20 min and conditioned in this way.

4 Set contact pressure for pump tubings

- Press contact pressure lever **41** on both tubing cartridges **40** upwards until regeneration and rinsing solution just start to be drawn in.
- Then press contact pressure lever **41** upwards until it clicks once more to obtain optimal contact pressure.

5 Check for leaks

- Check all capillaries and their connections in the 792 Basic IC for escaping liquid. If eluent escapes anywhere, the appropriate compression fitting must be tightened further or changed.

6 Condition system

- Rinse the system with eluent until the desired stability of the baseline is reached (normally 30…60 min; if the eluent is changed, the establishment of the ion exchanger equilibrium on the separating column can take longer). After this time the suppressor module is sufficiently conditioned too.
- The instrument is now ready for sample determinations using the selected system.

Pump tubings are consumable material with a lifetime, which depends on the contact pressure. This is why the tubing cartridges should be raised completely by loosening snap-action lever on the right-hand side if the pump is to remain switched off for a considerable length of time (the set contact pressure remains unchanged).

3 Operating tutorial

This section introduces you to the operation of the 792 Basic IC by means of a brief operating tutorial which describes the basic operating steps needed for the recording of an ion chromatogram using one of the system files supplied.

The determination of the anionic content of a drinking water sample with the METROSEP Anion Dual 1 column is used as an illustrative example. Please note that the steps and parameter settings described apply only to this example. If you use a different separating column and system file, the procedures described in the tutorial must be modified appropriately.

For further explanations of the operation, please refer to section 4.

3.1 Requirements

For the determination of anions in drinking water described in this tutorial, the following instruments, accessories and solutions are required:

- **2.792.0020 Basic IC**
  with suppressor module
- **6.1825.210 Sample loop (20 µL, PEEK)**
  already integrated in the 792 Basic IC
- **6.5325.000 Starter Kit**
  incl. the following accessories:
  - **6.1006.020 IC Column cartridge METROSEP Anion Dual 1 (150 mm)**
  - **6.2828.100 Glass cartridge holder (150 mm)**
  - **6.2620.150 Pulsation dampener**
- **Eluent**
  2.4 mmol/L $NaHCO_3$ / 2.5 mmol/L Na_2CO_3/ 2 % Acetone in dist. H_2O
  Flow: 0.5 mL/min
- **Standard**
  Standard solution with 0.5 mg/L fluoride, 5 mg/L chloride, 5 mg/L nitrite, 10 mg/L bromide, 10 mg/L nitrate, 10 mg/L phosphate and 10 mg/L sulfate (in dist. H_2O)

3.2 Preparations

Before you start this brief tutorial, the entire IC system must be correctly installed as described in *section 2.* In what follows, the most important points for the installation are described once again (for details, see the sections mentioned).

1 Install 792 Basic IC

⇒ Setting up instrument	*section 2.2*
⇒ Installing and connecting detector block	*section 2.3.1*
⇒ Mounting syringe and aspirating tubing	*section 2.3.2*
⇒ Mains connection	*section 2.4*
⇒ Connection to PC	*section 2.5*

2 Prepare eluent

⇒ Preparing eluent: 2.4 mmol/L $NaHCO_3$ / 2.5 mmol/L Na_2CO_3/ 2 % Acetone in dist. H_2O	
⇒ Microfiltering and degassing eluent	*section 5.1.3*

3 Install high-pressure pump

⇒ Removing transport security screws	*section 2.6.1*
⇒ Mounting pulsation dampener	*section 2.6.2*
⇒ Installing eluent supply	*section 2.6.3*
⇒ Degassing pump	*section 2.6.4*

4 Connecting separating column

⇒ Connecting IC cation column	*section 2.7.7*
⇒ Conditioning system	*section 2.9.1*

3.3 Calibration

After the complete IC system has been installed as described in *section 3.2*, the first calibration can be started. A standard solution is required for this; it should contain the substances to be determined in approximately the same concentrations in which they can be expected in the sample.

In our example of drinking water determination using the METROSEP Anion Dual 1 column a 20 µL sample loop is used; this is filled with the following standard solution:

0.5	mg/L	fluoride
5	mg/L	chloride and nitrite
10	mg/L	bromide, nitrate, phosphate and sulfate

Please note that all program displays refer to the condition in which the system **Asupp.smt** is loaded for the first time. If you want to work through this tutorial at a later date and the system **Asupp.smt** has been altered in the meantime then differences with respect to the program display and the parameter values may occur.

In the description of the calibration procedure, it is assumed that the PC and 792 Basic IC are not in operation and that the system must first be conditioned again. If this is not the case (e.g. if you start the tutorial immediately after conditioning) then you can skip steps **1** to **5**.

1 Switch on 792 Basic IC

⇒ Switch on 792 Basic IC with mains switch **11** on the rear of the instrument. After the instrument has been switched on the mains pilot lamp **2** lights up.

2 Switch on PC

⇒ Switch on PC and start «792 Basic IC» program.

3 Open system "Asupp.smt"

⇒ Select **File** / **Open** / **System** in the main window. Select the system file **Asupp.smt** in the folder **Suppressed anion** and click on **<Open>**.

4 Start system "Asupp.smt"

⇒ Select **Start determination** of the **Control** menu in the system window. The high-pressure pump is started, at the same time, a chromatogram window opens where the baseline is recorded continuously.

5 Condition system "Asupp.smt"

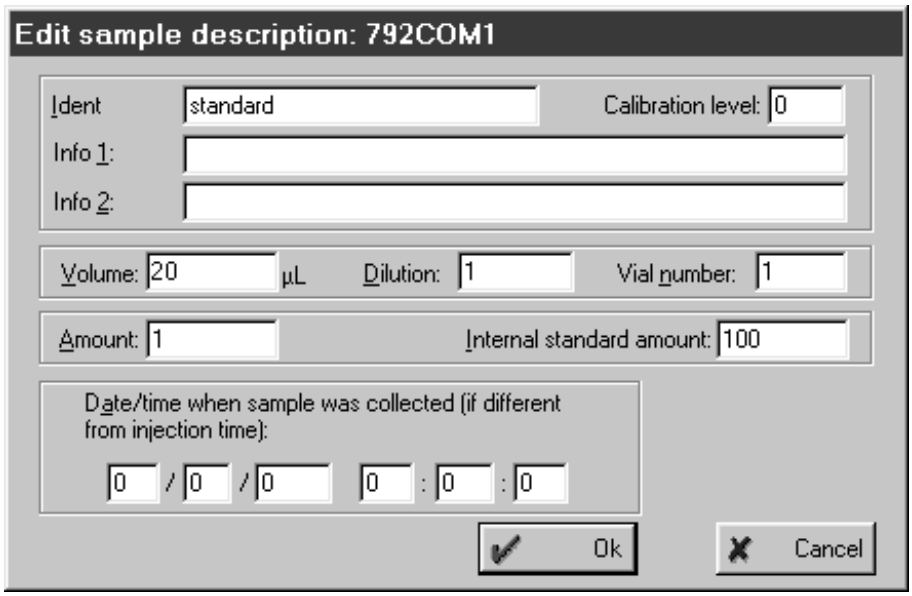
⇒ Rinse IC system with eluent until the desired stability of the baseline is achieved (at least 1 h).

6 Start determination

⇒ Click on **<Start>** in the system window or select **Start determination** of the **Control** menu. A chromatogram window opens where the baseline is recorded continuously. The status bar of this window shows the message **Measure(Baseline)**, beside this running time, analysis time, absolute conductivity and number of measuring points per second are displayed. The message **Waiting for INJECT [792COM#]** appears in the **SYSTEM STATE** window.

7 Enter information for determination

⇒ Enter the desired information concerning the sample in the automatically opened **Edit sample description** window. Set **Calibration level** to **0** and confirm with **<OK>**.



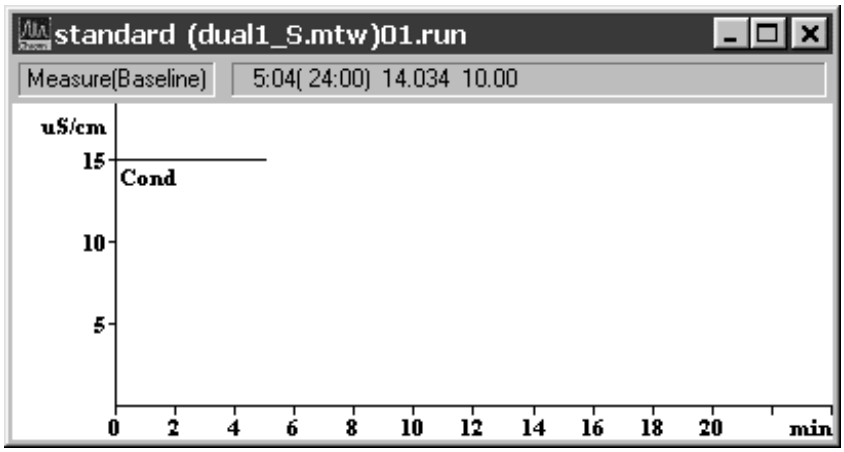
8 Condition system

⇒ Let the system run for several minutes. If the system has already been conditioned then a stable conductivity value of approx. 16 µS/cm will be obtained after a few minutes.

⇒ Double-click the chromatogram or select **View all** of the **View** menu. The sensitivity is set automatically so that all measuring points are visible.

This function is only available if the integration has been started. In the present example the integration only starts after a delay period **Delay = 3.3 min**.

⇒ Select the desired sensitivity using the cursor keys <↑> or <↓>. In the chromatogram window the following display is seen, for example:



9 Switch injection valve to "FILL" position

⇒ Click on the Fill button of the 792 icon in the system window to switch the injection valve to the "FILL" position. At the same time, the suppressor module is switched to the next position.

10 Fill sample loop

⇒ Immerse the aspirating tubing **23** in the standard solution.

⇒ Using the syringe fixed to syringe tubing **25**, siphon in ca. 1 mL standard solution.

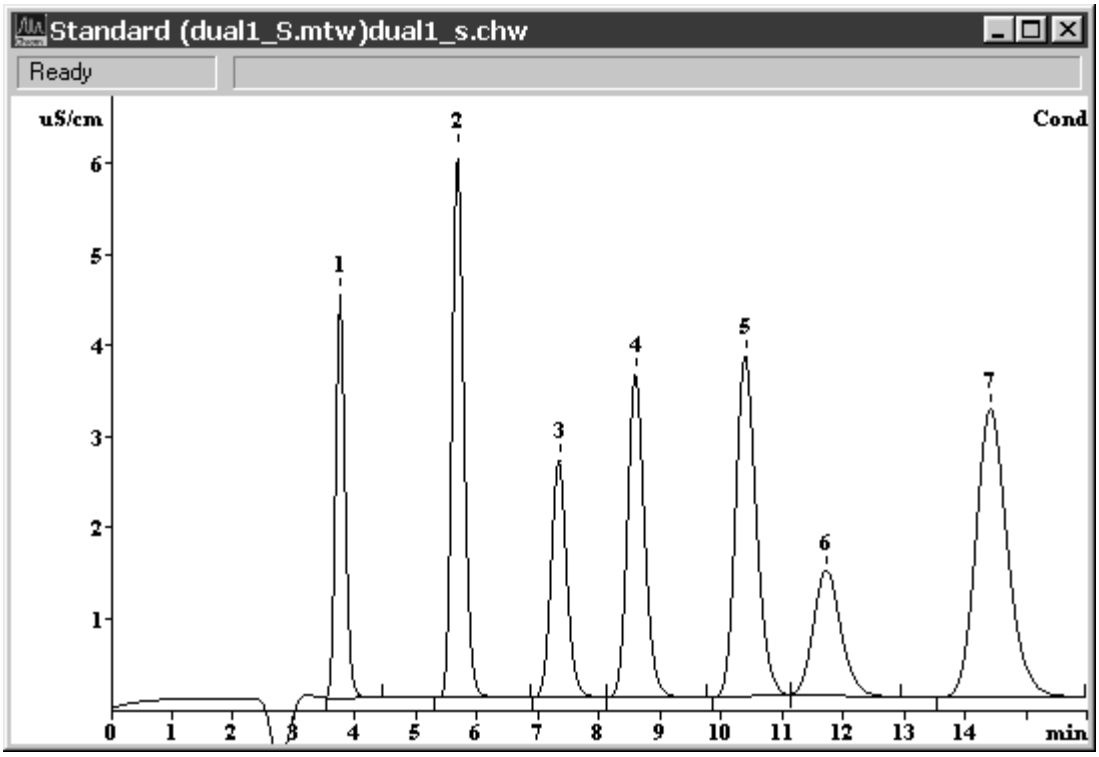
11 Switch injection valve to "INJECT" position

⇒ Click on the Inject button of the 792 icon in the system window to switch the injection valve to the "INJECT" position. At the same time, the data recording is started automatically. The status bar of the chromatogram window shows the message **Measure**, the **SYSTEM STATE** window shows the message **INJECT done [792COM#]**.

⇒ When the analysis time of 16 min set in the method has expired, the recorded chromatogram is automatically evaluated and stored. The chromatogram window then closes.

12 Open chromatogram

⇒ Click on  or **File** / **Open** / **Chromatogram** in the main window. Select the chromatogram file ***.chw** just recorded and click on **<OK>**. The chromatogram window is opened where the found peaks are numbered and the baselines are drawn in.

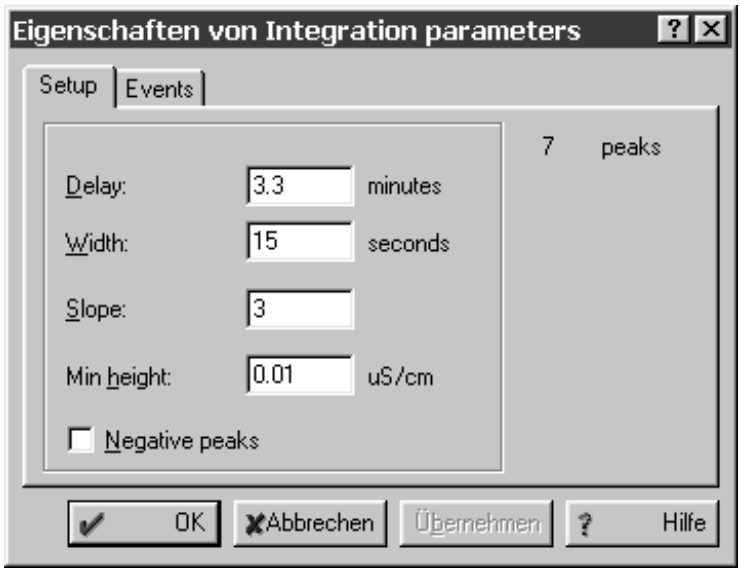


13 Modify integration parameters

⇒ Click on  or select **Integration** from the **Method** menu in the main window to open the integration parameters window.

⇒ If required (e.g. if the fluoride peak is not detected), change the time delay **Delay** before starting peak integration.

⇒ Click on **<Apply>**. The **Integration parameters** window is opened and the chromatogram is reintegrated.

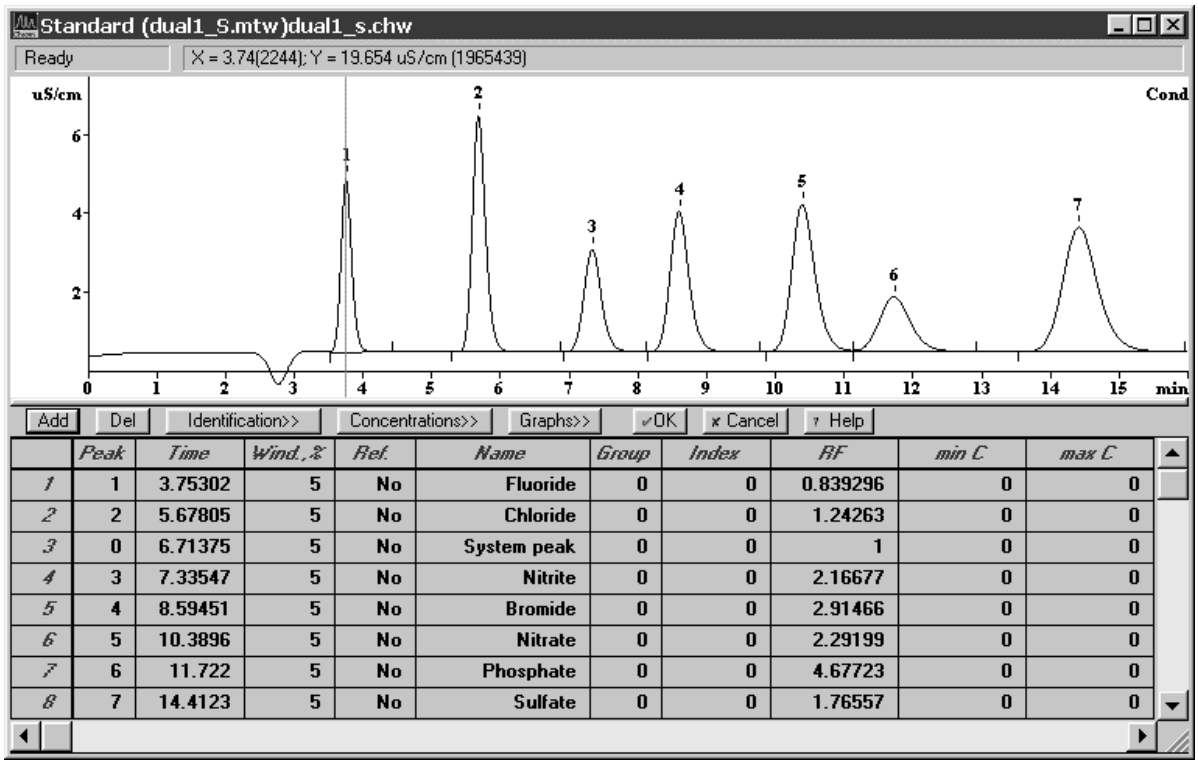


⇒ Repeat this procedure for all other integration parameters until the result satisfies your expectations. Click on **<Apply>** for each parameter change.

⇒ Close the **Integration parameters** window with **<OK>**.

14 Modify peak allocation

⇒ Click on  or select **Calibration** / **Components** from the **Method** menu. The prepared table for the components fluoride, chloride, nitrite, bromide, nitrate, phosphate and sulfate is displayed below the chromatogram. For all peaks, which could be allocated unambiguously to a component this table contains the peak number in the ***Peak*** column and the retention time in the ***Time*** column. In the chromatogram itself, this retention time is indicated by the cursor (vertical line).



	Peak	Time	Wind.,%	Ref.	Name	Group	Index	RF	min C	max C
1	1	3.75302	5	No	Fluoride	0	0	0.839296	0	0
2	2	5.67805	5	No	Chloride	0	0	1.24263	0	0
3	0	6.71375	5	No	System peak	0	0	1	0	0
4	3	7.33547	5	No	Nitrite	0	0	2.16677	0	0
5	4	8.59451	5	No	Bromide	0	0	2.91466	0	0
6	5	10.3896	5	No	Nitrate	0	0	2.29199	0	0
7	6	11.722	5	No	Phosphate	0	0	4.67723	0	0
8	7	14.4123	5	No	Sulfate	0	0	1.76557	0	0

⇒ If the ***Peak*** column contains a **0** the peak must be manually allocated to a component. In this case, insert the peak number from the chromatogram into the ***Peak*** column and click the ***Time*** field on this row with the mouse. The corresponding retention time is then inserted automatically as the new time for this component.

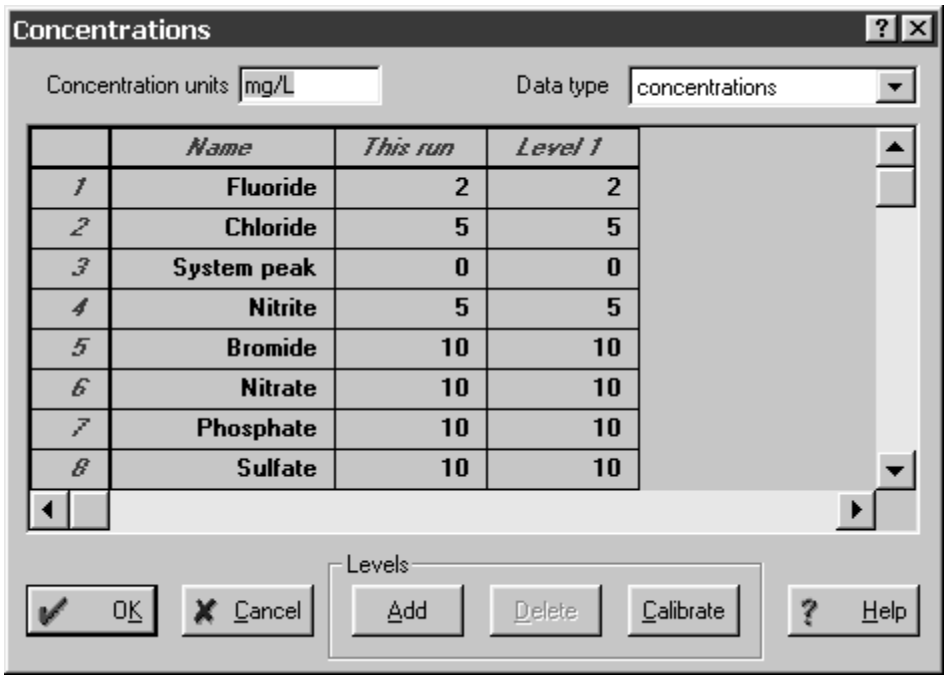
⇒ For each correctly allocated peak, click on the retention time in the ***Time*** column. This time is automatically shown in the chromatogram by the cursor. If the retention time is not located in the area of the middle of the peak, then the value in the ***Time*** column should be adapted accordingly. This is done by clicking on the chromatogram and moving the cursor with the aid of the cursor keys <🡐> and <🡒> to the middle of the peak and reading off the corresponding retention time in

the status line. Enter this value (rounded off if necessary) into the ***Time*** column. The optimized table could, for example, then appear as follows:

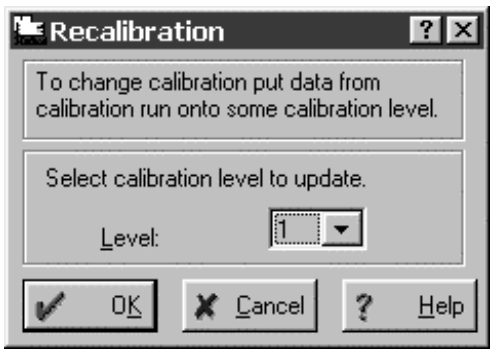
	Peak	Time	Wind./s	Ref.	Name	Group	Index	RF	min C	max C
1	1	3.8	5	No	Fluoride	0	0	0.839296	0	0
2	2	5.7	5	No	Chloride	0	0	1.24263	0	0
3	0	6.7	5	No	System peak	0	0	1	0	0
4	3	7.3	5	No	Nitrite	0	0	2.16677	0	0
5	4	8.6	5	No	Bromide	0	0	2.91466	0	0
6	5	10.4	5	No	Nitrate	0	0	2.29199	0	0
7	6	11.7	5	No	Phosphate	0	0	4.67723	0	0
8	7	14.4	5	No	Sulfate	0	0	1.76557	0	0

15 Start calibration

⇒ Click the **<Concentrations>** button in the component window.



⇒ Click on **<Calibrate>**. The following window appears:



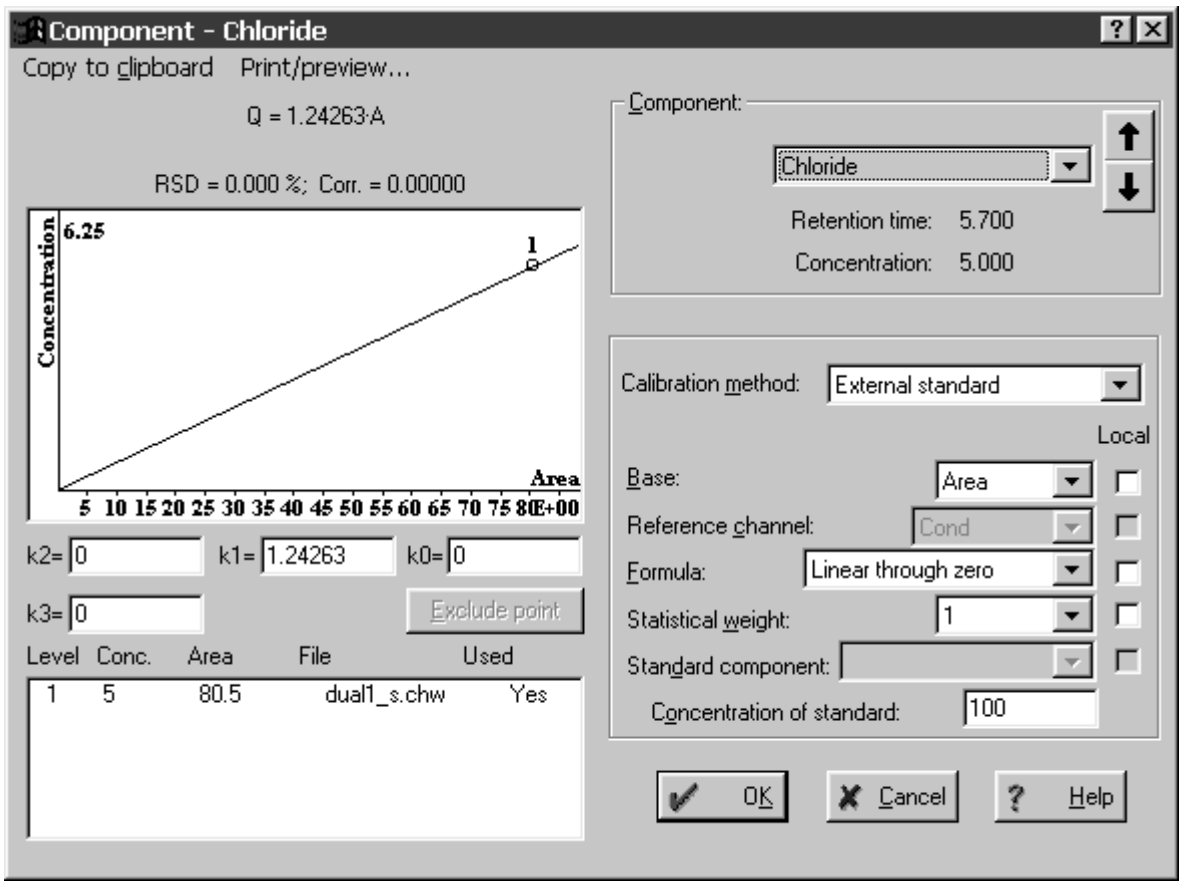
⇒ Confirm **Level 1** with **<OK>**.

⇒ Click on **<OK>** in the **Concentrations** window.

16 Display calibration curves

⇒ Click on **<Graphs>** in the **Components** window**.**

⇒ Select the desired component in the **Component** field for which the calibration curve should be displayed (e.g. for **chloride**).



⇒ Close the **Component - chloride** window with **<OK>**.

⇒ Close the **Components** window below the chromatogram by clicking on **<OK>**.

17 Save chromatogram and method

⇒ Close the chromatogram window. A window appears with the message **Changes in *.chw. Modified: Calibration. Save changes?**.

⇒ Click on **<Yes>**. A window appears with the message ***.chw already exists. Overwrite?**.

⇒ Click on **<Yes>**. A window appears with the message **Method dual1_S.mtw was modified. Save changes?**.

⇒ Click on **<Yes>**.

3.4 Sample determination

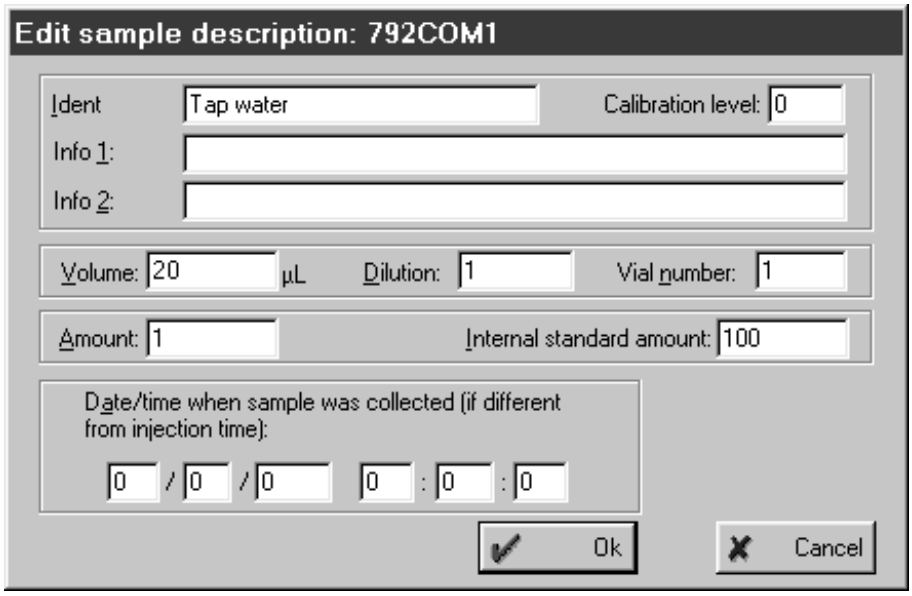
Following the calibration of the IC system as described in *section 3.3* the first sample solution can be injected.

1 Start determination

⇒ Click on **<Start>** or select **Start determination** of the **Control** menu in the system window. An empty chromatogram window opens where the baseline is recorded continuously. The message **Initialisation [792 COM#]** appears in the **SYSTEM STATE** window. Then the **Edit sample description** window is opened automatically.

2 Enter information for determination

⇒ Enter the desired information concerning the sample in the **Edit sample description** window and confirm with **<OK>**. Set **Calibration level** to **0** and confirm with **<OK>**.



3 Switch injection valve to "FILL" position

⇒ Click on the Fill button of the 792 icon in the system window to switch the injection valve to the "FILL" position. At the same time, the suppressor module is switched to the next position.

4 Fill sample loop

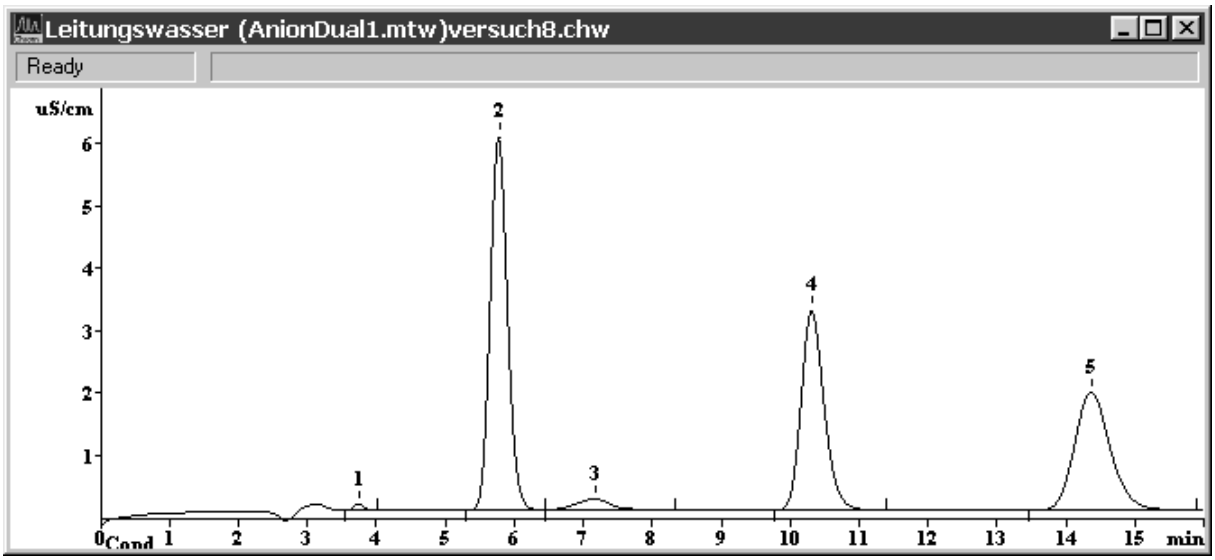
⇒ Immerse the aspirating tubing **23** in the vessel containing the drinking water sample.

⇒ Using the syringe fixed to the syringe tubing **25**, siphon in ca. 1 mL drinking water.

5 Switch injection valve to "INJECT" position

⇒ Click on the Inject button of the 792 icon in the system window to switch the injection valve to the "INJECT" position. At the same time, the data recording is started automatically. The status bar of the chromatogram window shows the message **Measure**, the **SYSTEM STATE** window shows the message **INJECT done [792COM#]**.

⇒ When the analysis time of 16 min set in the method has expired data recording is automatically stopped and the chromatogram is integrated and evaluated. In the chromatogram window the peaks which have been found are numbered and the baseline drawn. In the **SYSTEM STATE** window the message **Finished [792COM#]** appears. It is now possible to record further samples with the same system.



⇒ At the end of the determination, the chromatogram window is closed and the chromatogram is saved automatically. The file name is generated automatically and contains date and time in a coded form:

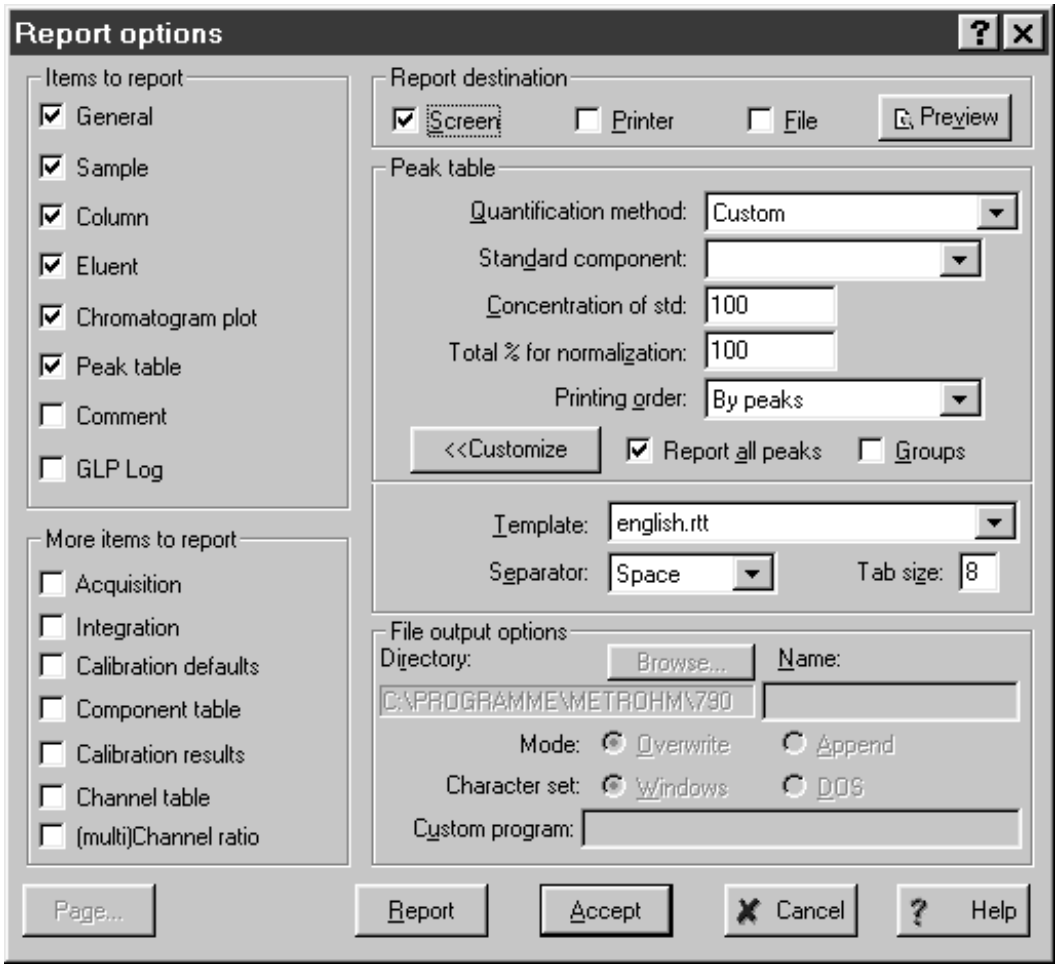
1st numeral:	Alphabetical code for year (e.g. j = 1999, k = 2000, l = 2001, etc.)
2nd numeral:	Code for month (1...9 = Jan....Sept., a...c = Oct....Dec.)
3rd+4th numeral:	Day (01 ... 31)
5th - 8th numeral:	Time (hh:mm)

6 Open chromatogram

⇒ Click on or **File** / **Open** / **Chromatogram** in the main window. Select the chromatogram file ***.chw** just recorded and click on **<OK>**. The chromatogram window is opened where the found peaks are numbered and the baselines are drawn in.

7 Report output

⇒ Click on  or select **Make report** of the **Process** menu in the main window. The **Report Options** window appears.



⇒ Under **Report destination**, switch on the desired target option for report output.

⇒ Under **Items to report** and **More items to report**, click all desired elements for the report output.

⇒ Click on **<Report>** to start the report output to the selected target.

8 Print report

⇒ Click on  or select **Print** of the **File** menu in the main window. The standard printing window is opened where printer, printing range and number of copies can be selected. After confirmation with **<OK>** the results including the chromatogram are printed out.

4 Operation

This section describes the most important points concerning the operation of the 792 Basic IC. For further details, please refer to the on-line help in the PC program, which can provide you with the required information rapidly and conveniently from any place in the program.

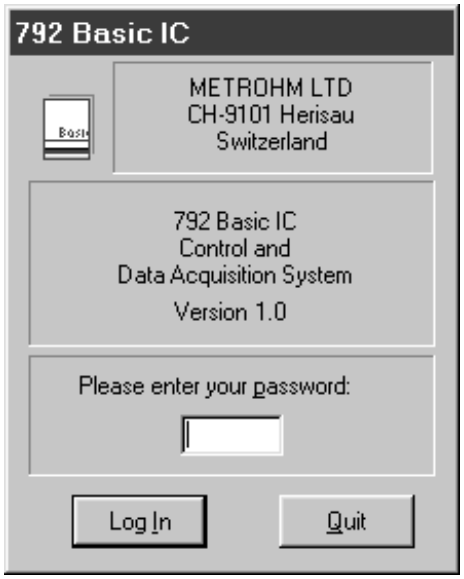
4.1 Fundamentals of the operation

4.1.1 Starting/closing the program

Start the «792 Basic IC» program

Metro792.exe

Start the program
Double-click this icon or the **Metro792.exe** file to start the «792 Basic IC 1.0» program. The Login window appears:



Enter your password and click on **<Log In>**.

After software installation, the program can be started without entering a **Password***. For the definition of users, see section 4.2.2.*

Close the «792 Basic IC» program

792 BASIC IC / File / Exit
Exit the «792 Basic IC» program.

The program is also quit by clicking on  in the upper right part of the main window **792 BASIC IC**.

4.1.2 Glossary

System

The term "system" is used to describe the combination of **instrument settings**, **time program** and **processing method**, which have been optimized for the specific separating column and the determination to be carried out with it. A system is used to start single determinations or determinations with the help of a sample queue.

Systems are stored as **system files** (***.smt**) in the **Systems** directory.

Method

A method contains all information necessary for **data acquisition**, **integration**, **peak evaluation** and **quantification**. It can be considered as the chromatogram template, i.e. chromatogram without raw data.

Methods are stored as **method files** (***.mtw**) in the **Methods** directory.

Each system is linked to a method. This method is called **processing method** and is opened automatically at the start of a new determination.

Chromatogram

A chromatogram is a graphic plot of the elution curve (signal vs. time) recorded following a chromatographic separation on a separating column.

Chromatograms are stored as **chromatogram files** (***.chw**) in the **Data** directory. As well as the measuring data, the chromatogram files also contain the method parameters and system settings, which have been used for data recording, data processing and remote control.

Determination

In order to carry out a determination a suitable **system** must be selected for the separating problem. The result of the determination is a **chromatogram**, in which the measuring data and results of the determination are stored.

Calibration

Calibration is used to describe the method of determining the relationship between the peak height or peak area found for one component and its concentration in the sample. The result of the calibration is a **calibration function** (calibration curve), which shows the relationship between the amount of sample and the evaluated quantity.

The determination of the calibration function with reference solutions can be carried out as a **one-point** or as a **multiple-point calibration**. The calibration method that is mainly used in ion chromatography is the **external standard calibration** (absolute calibration); calibrations with an **internal standard** (relative calibration) or **tabulated calibrations** are also possible.

Integration

Integration is to be understood as being the method for determining the peak area and peak height with the aid of approximate baselines. The integration algorithm included in the program is influenced by the **integration parameters** and the optionally programmable **integration events**, which are defined in the method. In addition, the integration can be manually corrected later with the aid of the **peak editor**.

Batch reprocessing

Batch reprocessing is understood to be the subsequent reprocessing of a series of chromatograms, which have been loaded in a batch reprocessing queue. During reprocessing with a selected method the settings for calibration, integration, passport, appearance and report can be altered at will.

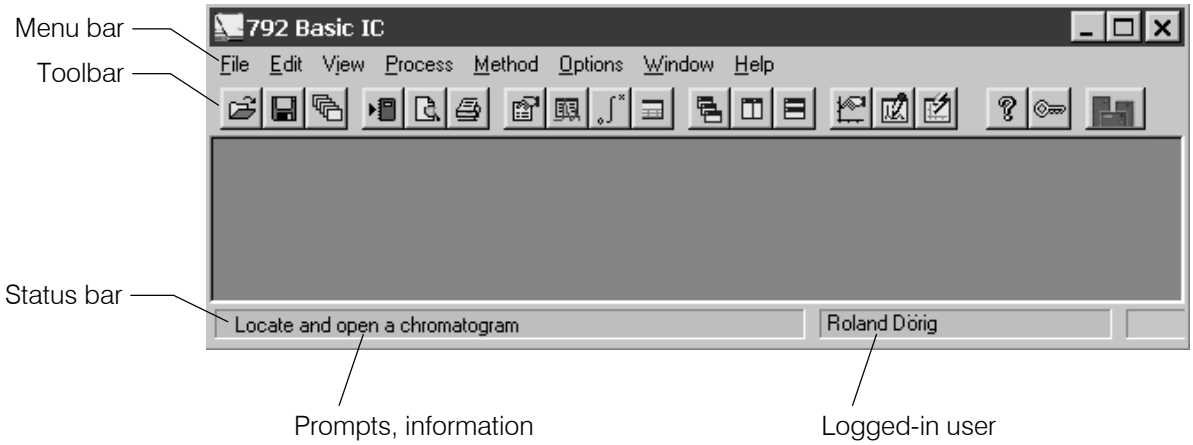
4.1.3 Overview of program windows

The «792 Basic IC» program consists of different windows whose functionality is linked together. The different windows are:

792 BASIC IC	Main program window for file administration, printing, opening of systems, methods and chromatograms, login and user rights, optional settings and window handling.
CHROMATOGRAM	Window for graphic plot of running or recorded chromatograms.
SYSTEM	Window for loaded system with possibility for manual control of the 792 Basic IC.
SYSTEM STATE	Window for display of status messages for the connected system.
WATCH WINDOW	Window for display of conductivity and pressure.
QUEUE EDITOR	Window for edition of batch reprocessing queues.

4.1.4 Main window elements

The elements of the main window **792 BASIC IC** are the menu bar, the tool bar and the status bar, indicating prompts and logged-in user.



4.1.5 Icons of the main window

The following icons are displayed in the **792 BASIC IC** main window:

 Open chromatogram

 Save chromatogram

 Open last batch reprocessing file

 Report settings

 Print preview

 Print report

 Passport

 General method settings

 Integration parameters

 Component table

 Cascade all opened chromatogram windows

 Vertical tiling of open chromatogram windows

 Horizontal tiling of open chromatogram windows

 Appearance of the chromatogram window

 Enable/disable peak editor mode

 View whole chromatogram

 Help

 Lock system

 Opened system

4.1.6 Overview of file types

The following file types are produced by the «792 Basic IC» software:

***.bar** **Batch reprocessing file**
This binary file contains data of the batch reprocessing queue. The ***.bar** file is stored automatically in the **Data** folder.

***.cal** **Calibration file**
This binary file contains calibration data, which can be exported with **792 BASIC IC** / **Method** / **Calibration** / **Export calibration**. The ***.cal** file is stored automatically in the **Methods** folder.

***.chw** **Chromatogram file**
This binary file contains chromatogram, system and method data of a determination. The ***.chw** file is stored automatically in the **Data** folder.

***.mtw** **Method**
This binary file contains the data acquisition method linked to a system. The ***.mtw** file is stored automatically in the **Methods** folder.

***.rtt** **Report template**
This ASCII file contains a report template. The ***.rtt** file is stored in the program folder.

***.smt** **System file**
This ASCII file contains the system settings. The ***.stm** file is stored automatically in the **Systems** folder.

***.dev** **Device file**
This ASCII file contains drivers for devices. The ***.dev** file is stored in the **Devices** folder.

4.1.7 Context sensitive menus

Some of the menu functions of the program windows are also accessible by clicking on the desired window or item and pressing the **right mouse button**. The pop up windows have different contents and functions depending on the selected active window or item type.

4.1.8 Keyboard and mouse functions

The **mouse** can be used to carry out the normal program operating functions such as the selection of menu items and fields. It can additionally be used for magnifying a section of a chromatogram (**zooming**). To **zoom** a portion of the plot it is necessary to place the mouse cursor to the upper left corner of the square to zoom, press the left mouse button and drag the cursor to the lower right corner of the rectangle. After releasing of the left mouse button the selected region will be zoomed full-screen. If the cursor is active in the peak editor mode then it can be moved by pressing down the right-hand mouse key.

The **keyboard** can also be used to scale a chromatogram in the window, as described below.

Keyboard quick reference

Cursor is inactive:

[up]	Increases sensitivity on the Y axis.
[down]	Reduces sensitivity on the Y axis.
[right]	Expands a chromatogram on the X axis.
[left]	Shrinks a chromatogram on the X axis.
[Ctrl] + [Home]	Autoscale procedure on the X axis (shows all on X).
[Ctrl] + [End]	Autoscale procedure on the Y axis (shows all on Y).
[PageUp]	Shifts a chromatogram on $^1/_{10}$ part of a screen upwards.
[PageDown]	Shifts a chromatogram on $^1/_{10}$ part of a screen downwards.
[Shift] + [up]	Increases a distance between channels of a chromatogram.
[Shift] + [down]	Reduces a distance between channels of a chromatogram.
[0 (Zero)]	Adjusts a zero on the last point of a chromatogram (running chromatogram) or its lowest level (finished run).

Only part of the chromatogram is on screen:

[Ctrl] + [right]	Moves one window right (without change of scale on X and Y axes).
[Ctrl] + [left]	Moves one window left (without change of scale on X and Y axes).
[Home]	Shows the beginning of a chromatogram (without change of scale on X and Y).
[End]	Shows the end of a chromatogram (without change of scale on X and Y).
[0 (Zero)]	Adjusts a zero on the lowest level in the window.

Cursor is active:

[0 (Zero)]	Adjust a zero in site of the cursor.
[right]	Moves cursor left to right.
[Shift] + [right]	Quickly moves cursor left to right.
[left]	Moves cursor right to left.
[Shift] + [left]	Quickly moves cursor right to left.
[Home]	Moves cursor to beginning of a window.
[End]	Moves cursor to end of a window.
[Shift] + [End]	Sets the beginning of a window in site of the cursor.
[Shift] + [Home]	Sets the end of a window in site of the cursor.

4.1.9 Help

By clicking on  , by clicking on  , by selecting the **Help** / **Contents** menu item, or by pressing the [F1] key you can get on-line help on the current topic anywhere in the program.

Green texts	can be clicked to jump to a different Help topic.
Violet texts	identify the dialog item, parameter or button in the corresponding window.
Blue texts	identify titles and important information.

4.2 Instrument and software settings

4.2.1 Fonts

792 BASIC IC / Options / Fonts

This option allows the selection of fonts used by the system.

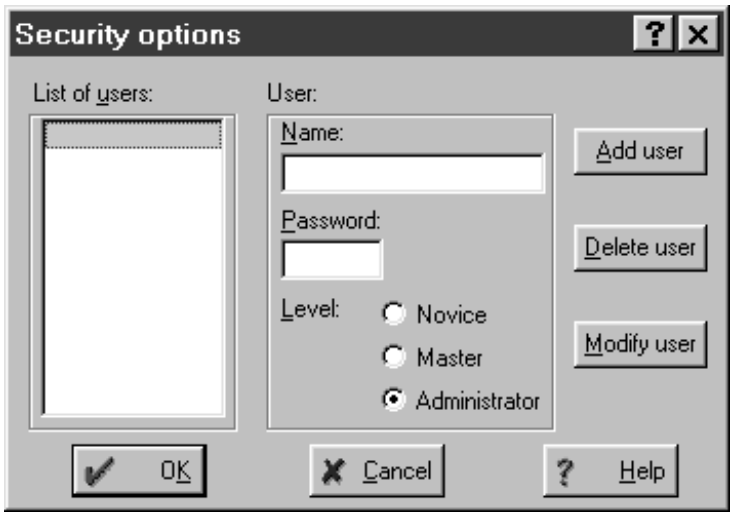
Font for dialog...	Selection of font used for dialog boxes. Default setting: **MS Sans Serif / Standard / 8 pt.**
Font for reports...	Selection of font used for report output to the screen or printer. Default setting: **Courier New / Standard / 10 pt.**
Font for tables...	Selection of font used for data presentation in tables on the screen. Default setting: **MS Sans Serif / Bold / 8 pt.**
Font for plots...	Selection of font used for labels on chromatogram plots and calibration curves. Default setting: **Times New Roman / Bold / 10 pt.**
Save fonts configuration	Save chosen font configuration.

4.2.2 Security system

The «792 Basic IC» program has a security system based on the list of users. Every user has his unique password and one of the following access levels:

Novice	Restricted access to program functions. Allows only start and stop of determinations using existing system and method files and manual control of the 792 Basic IC. Modifications of system, method and data files are not allowed.
Master	Access to all program functions with few exceptions: the user cannot set **Global preferences**, **Hardware settings** and security system.
Administrator	Access to all program functions.

It is recommended to make user lists and enter passwords as a first action after system installation. Therefore, select the menu item **792 BASIC IC / Options / Security** and click on **<Log In>** in the Log In window without entering a password. The **Security options** window appears:



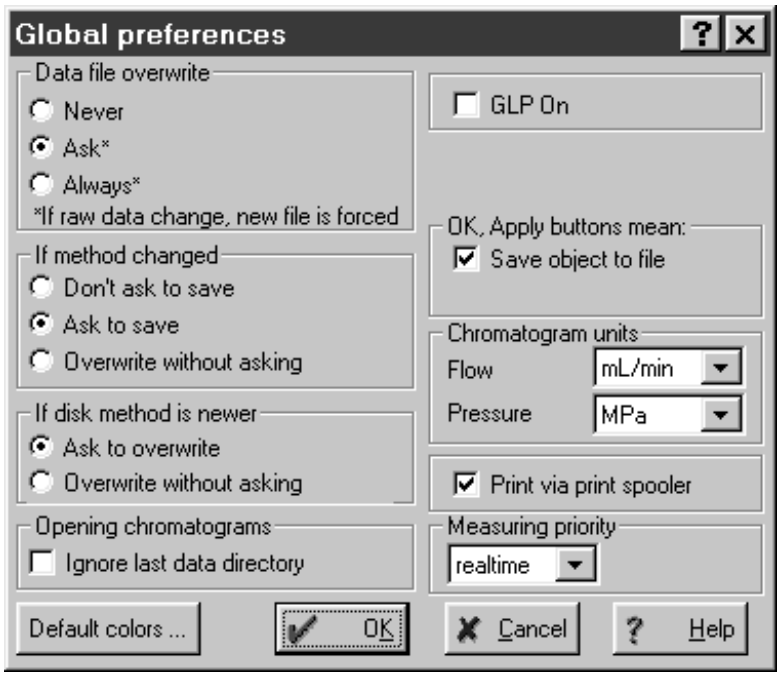
Enter user name, password and access level for all users. Don't forget to make one of the users an **Administrator**, otherwise this window will not open again. At the end, click on **<OK>**.

After configuration of the security system the program prompts for the password every time the system starts. This user name stamps all methods, chromatograms and reports. It is possible at any time to change the user with the menu item **792 BASIC IC** / **Options** / **Lock system**.

4.2.3 Global settings

792 BASIC IC / **Options** / **Global preferences**

This window is used for **global program settings**.



This window is only accessible for users with **Administrator** *access level.*

Data file overwrite Overwriting of chromatogram files:

- **Never** Chromatogram files cannot be overwritten. A modified chromatogram is saved as a new file with the file name number raised by 1.
- **Ask** The user is asked if the chromatogram should be overwritten.
- **Always** Chromatogram files are always overwritten without confirmation.

If method changed Saving of method files:

- **Don't ask to save** The method file is not saved automatically. It can be saved only with **File** / **Save** / **Method**.
- **Ask to save** The user is asked if the method should be saved.
- **Overwrite without asking** Method files are overwritten without confirmation.

If disk method is newer Overwriting of method files:

- **Ask to overwrite** The user is asked if the method should be overwritten.
- **Overwrite without asking** Method files are overwritten without confirmation.

Opening chromatograms Opening of chromatograms:

- **Ignore last data directory** If this option is enabled, the default data directory **Data** is opened.

GLP On If this option is enabled, the following parameters are automatically set:

Data file overwrite = Never
If method changed = Don't ask to save
If disk method is newer = Ask to overwrite

OK, Apply buttons mean

- **Save object to file** If this option is enabled, the **<Apply>** button in system settings windows is replaced by the **<Save>** button. The system settings are saved if the **<Save>** or **<OK>** button is clicked.

Chromatogram units Units for chromatograms:

- **Flow** Unit for flow rate: **µL/min**, **mL/min**
- **Pressure** Unit for pressure: **MPa**, **psi**, **bar**, **atm**

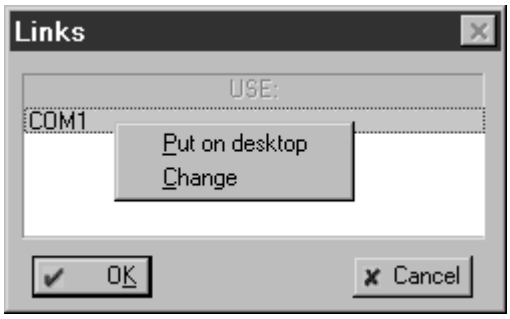
Print via print spooler Switch on/off printing via print spooler. Switch off this option if you use a GDI printer.

Measuring priority	Setting the priority of program execution. **real-time** means that the «792 Basic IC» program has the highest priority, **normal** means that all active programs have the same priority.
<Default colors>	Default colors for chromatographic windows (details see *section 4.5.3*).

4.2.4 COM port

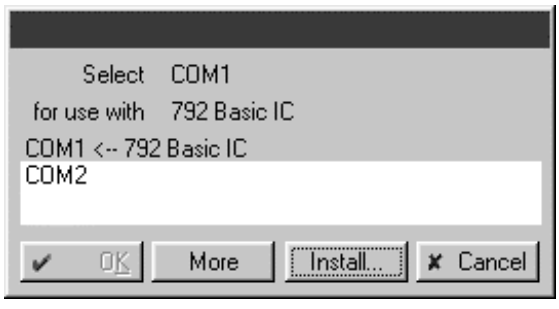
792 BASIC IC / Options / 792 Basic IC:COM1

This menu item opens the **Links** window for COM port (serial RS232 interface) selection and settings.



If **COM1** is clicked with the right mouse button, the following menu items appear:

Put on desktop	Possibility for setting COM port parameters for recording data transfer (details see on-line help).
Change	Possibility for changing the COM port (default setting: **COM1**). The following window is opened, where the interface can be changed by clicking on the desired COM port.

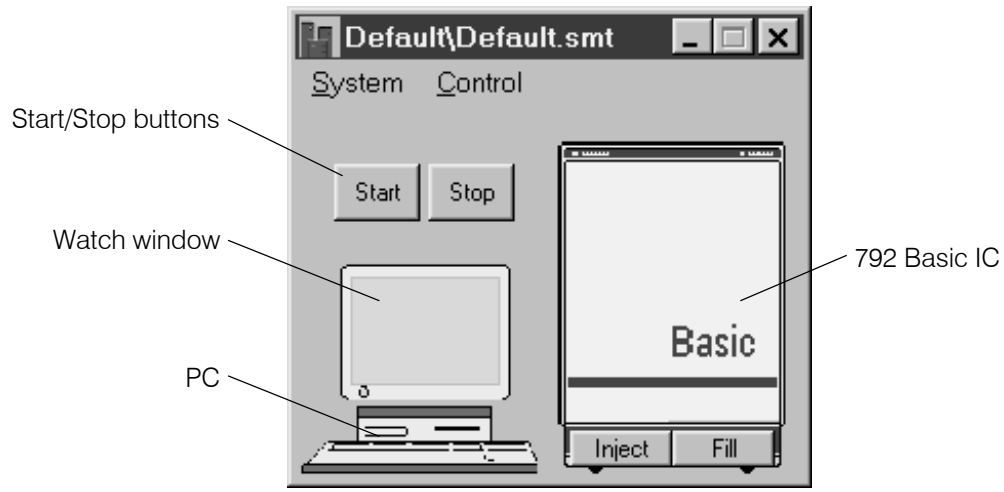


4.3 Systems

The term “System“ describes the combination of **instrument settings**, **time program** and **processing method** which has been optimized for a specific separating column and the determination to be carried out with it. A system is used to start single determinations. Systems are stored as **system files** (***.smt**) in the **Systems** directory.

4.3.1 System window

A system window is opened with **792 BASIC IC** / **File** / **Open** / **System** and the selection of the desired system file. It contains icons for **PC**, **Watch window** (screen) and **792 Basic IC**, and two buttons to **start** and **stop** a determination.



4.3.2 System file handling

The following menu items are used for opening, changing, saving and closing of systems:

792 BASIC IC / **File** / **Open** / **System**

Load an existing system file (***.smt**) from the **Systems** directory and open the corresponding system window.

The directory and name of the opened system file are displayed in the title bar of the system window. A star (*****) at the end of the name indicates that the system settings have been changed since the last saving.

SYSTEM / **System** / **Change**

Load a new system and open automatically the system window.

SYSTEM / **System** / **Save**

Save the current system settings in a system file (***.smt**) in the **Systems** directory.

SYSTEM / **System** / **Close**

Close the selected system.

4.3.3 System functions

Start/stop hardware and record baseline

SYSTEM / Control / Startup hardware (Measure Baseline)

Starting the hardware at the 792 Basic IC includes sending of **System startup values**, starting of the high-pressure pump and starting of the peristaltic pump.

At the same time, the **recording of the measurement signal** using the method defined for the system is started. Independently of the set chromatogram **Duration**, the measurement signal is recorded until a new determination is started. Alternatively the baseline recording can be stopped by clicking the icon of the chromatogram window. In this case, the user is asked if the recorded baseline should be saved or not.

SYSTEM / Control / Shutdown hardware

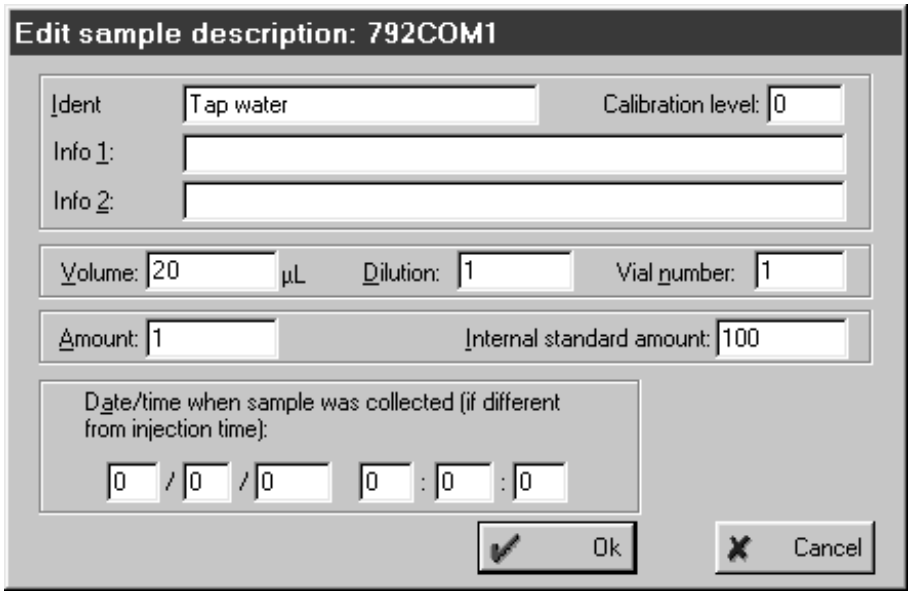
High-pressure pump and peristaltic pump at the 792 Basic IC are immediately stopped. A running determination is also stopped.

Start/stop determinations

SYSTEM / Control / Start determination

Start determination using the settings of the selected system. At this start command, the **System startup values** are set at the 792 Basic IC. The high-pressure pump and the peristaltic pump are started if they are not already running. The time program is started immediately; the data recording is started after switching the injection valve to the "Inject" position.

At each start of a determination, the **Edit sample description** window is opened automatically. This window can be used for entering information concerning the sample:



Ident	User defined identifier (title) for the chromatogram to be displayed in the title bar of the chromatogram window and in the **Chromatogram open** window.
Calibration level	Calibration level (0 = sample; 1…n = calibration solutions).
Info 1 / **Info 2**	Sample description.
Volume	Injected volume in µL.
Dilution	Dilution of the sample.
Vial number	Autosampler vial position to take sample from.
Amount	Sample amount. If this value is different for the calibration run (**c**) and the sample run (**s**), the component concentrations of the sample are calculated as follows: $C_s = C_c \cdot$ **Amount**$_s$ / **Amount**$_c$
Internal standard amount	Concentration of the internal standard component for relative concentration calculations.
Date/time when...	Date and time of sample collection (the default values are equal to the date and time when the chromatogram starts).

SYSTEM / **Control** / **Stop determination**

Stop running determination. Data acquisition and time program are terminated immediately. The recorded chromatogram is saved automatically if the **Save chromatogram after the run** option on the **Passport** / **Processing** tab is enabled.

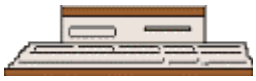
Alternatively the determination can be stopped by clicking the icon of the chromatogram window. In this case, the user is asked always if the determination should be saved or not.

Print system parameters

SYSTEM / **System** / **Print parameter**

A report of the system parameters including the time program is created and opened using the «Microsoft Word» program. The ***.rtf** file opened can be printed, saved and exported into other programs. The system report includes the name of the method linked to the system, the configuration settings for the 792 Basic IC, the system startup values and the time program (incl. **Remote configuration**), if such a program exists and is switched on (**ENABLED**).

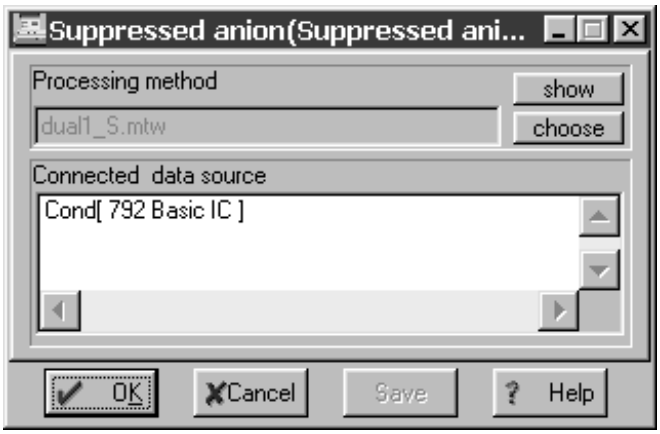
4.3.4 PC icon



The PC icon is one of the components of the system window. If the system is connected and this icon is clicked with the right mouse button, the following menu items appear:

Open Load the processing method linked to the system and open an empty chromatogram window.

Setup Open PC setup window for selection of processing method:



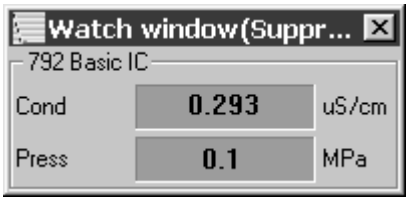
Processing method Directory and name of the method file (***.mtw**) linked to the system.
The method file can be selected with **<choose>** and opened with **<show>**.

Connected data source Display of data source for main measurement channel (read only).

4.3.5 Watch window

The watch window icon is one of the components of the **SYSTEM** window. If the system is connected and this icon is clicked with the right mouse button, the following menu item appears:

Open Open the **WATCH WINDOW** for live display of conductivity and pressure:



The colors of the watch window fields can be changed by clicking the fields with the right mouse button and selecting the menu item **Choose color / ...**.

4.3.6 Instrument icon

Menu options for instrument icon

System disconnected

System connected Injection valve in "**INJECT**" position

System connected Injection valve in "**FILL**" position

The instrument icon for the 792 Basic IC is one of the components of the **SYSTEM** window. If the system is connected, the icon contains two buttons for manual control of the injection valve:

<Inject> Switch injection valve to "INJECT" position.

<Fill> Switch injection valve to "FILL" position.

If the system is connected and the 792 icon is clicked with the right mouse button, the following menu appears:

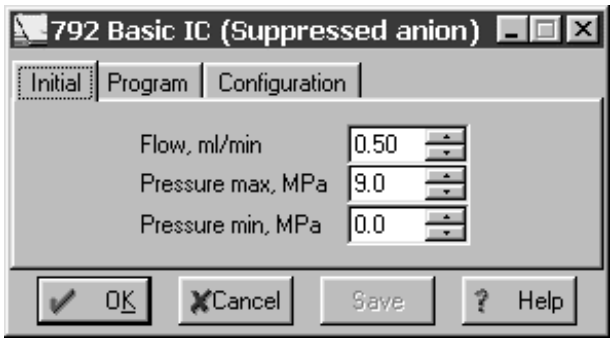
Open Open the **system settings** window.

Hardware Open the **hardware settings** window.

Diagnostics Open the **diagnostics** window.

System parameters for disconnected system

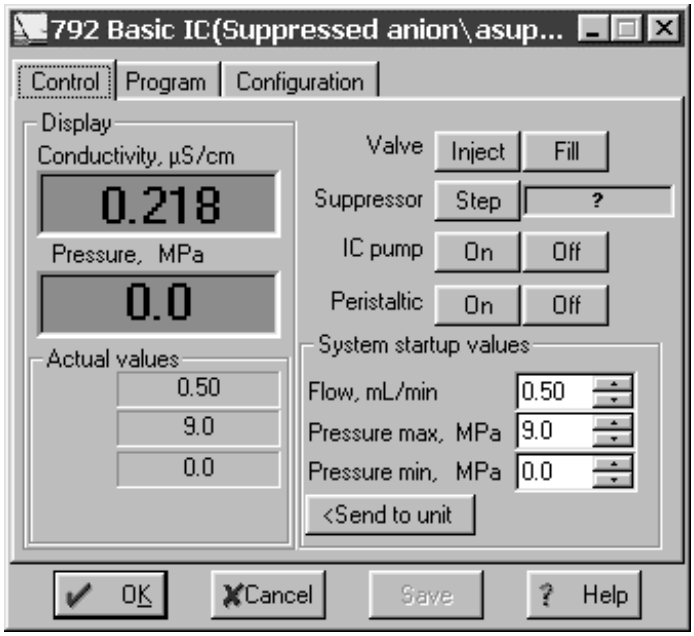
A double-click on the instrument icon or selection of the **Open** menu item using the right mouse button opens the system settings window. For a disconnected system, the **Initial** tab is displayed.



Flow, mL/min	Startup value for flow rate of the high-pressure pump. Entry range: **0.20** ... **2.50 mL/min**
Pressure max, MPa	Startup value for maximum pressure limit for high-pressure pump. Entry range: **0.0** ... **25.0 MPa**
Pressure min, MPa	Startup value for minimum pressure limit for high-pressure pump. Entry range: **0.0** ... **25.0 MPa**

Instrument control for connected system

A double-click on the instrument icon or selection of the **Open** menu item using the right mouse button opens the system settings window. For a connected system, the **Control** tab is displayed. It allows manual control of the 792 Basic IC functions and setting of startup values to be sent to the instrument. This tab shows the current measurement values for conductivity and pressure.



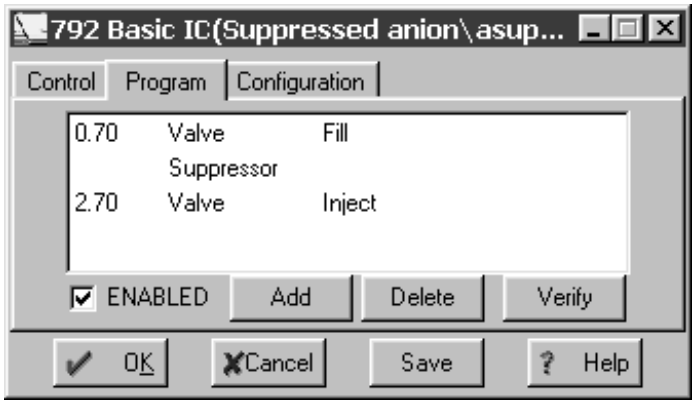
Conductivity, µS/cm	Live display of measured conductivity.
Pressure, MPa	Live display of measured pressure. The color settings for this two fields can be changed by clicking the fields with the right mouse button and selecting the menu item **Choose color** / **...** .

Actual values	Display of actual values
Flow, mL/min	Display of flow rate of the high-pressure pump.
Pressure max, MPa	Display of maximum pressure limit for high-pressure pump.
Pressure min, MPa	Display of minimum pressure limit for high-pressure pump.

Valve	Injection valve
<Inject>	Switch injection valve to "INJECT" position.
<Fill>	Switch injection valve to "FILL" position
Suppressor	Suppressor module
<Step>	Switch the suppressor module to the next position. The time since the last switching of the suppressor module is displayed in the field beside the **<Step>** button.
IC pump	High-pressure pump
<On>	Start high-pressure pump.
<Off>	Stop high-pressure pump.
Peristaltic	Peristaltic pump
<On>	Start peristaltic pump.
<Off>	Stop peristaltic pump.
System startup values	The system startup values are sent and applied to the 792 Basic IC each time the system is connected, a determination is started, or the values are sent manually with **<Send to unit>**.
Flow, mL/min	Startup value for flow rate of the high-pressure pump. Entry range: **0.20** ... **2.50 mL/min**
Pressure max, MPa	Startup value for maximum pressure limit for high-pressure pump. This limit is controlled even without connection to the PC. Entry range: **0.0** ... **25.0 MPa**
Pressure min, MPa	Startup value for minimum pressure limit for high-pressure pump. This limit is controlled even without connection to the PC. Entry range: **0.0** ... **25.0 MPa**

Time program

On the **Program** tab of the system settings window a user-defined time program for instrument control can be entered. This program is started automatically at the moment the determination is started. The time program contains program steps including time, program instruction and parameter.



Time (1st column)	Time at which program instruction is applied. Entry range: **0.0 ... 999.9 min** If no time is entered, the program instruction is applied together with the last instruction with time entry.
Command (2nd column)	Program instruction (see *List of program instructions*).
Parameter (3rd column)	Parameter for program instruction (see *List of program instructions*).
ENABLED	Enable program start (a disabled program is not started).
<Add>	Add new program instruction.
<Delete>	Delete selected program instruction.
<Verify>	Test the time program (error messages are displayed if program is faulty).

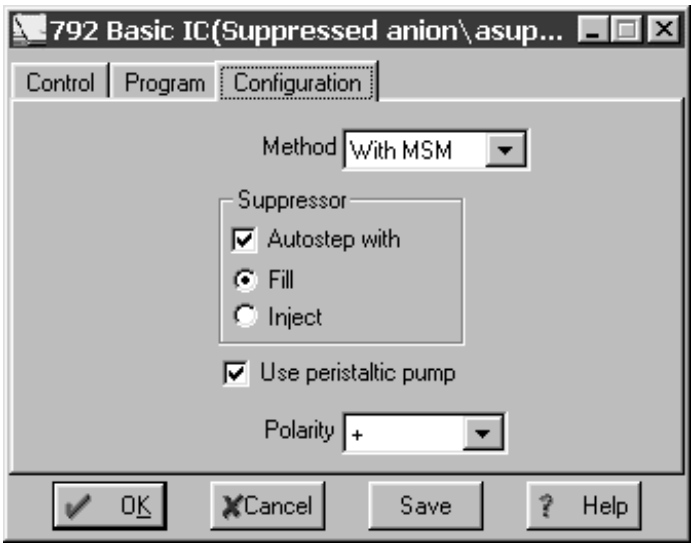
List of program instructions

The following program instructions can be added to the time program on the **Program** subpage:

Instruction	*Parameter entry*	*Meaning*
Valve	**Inject, Fill**	Switch **injection valve** to "INJECT" or "FILL" position.
ICPump	**on, off**	Switch **on** or **off** the **high-pressure pump**.
Flow	**0.2 ... 2.5 mL/min**	Set **flow rate** of the high-pressure pump to the desired value.
Pmax	**0.0 ... 25.0 MPa**	Set **maximum pressure limit** for the high-pressure pump to the desired value.
Pmin	**0.0 ... 25.0 MPa**	Set **minimum pressure limit** for the high-pressure pump to the desired value.
Program	**END, RESET**	The **END** flag can be used to end a program, especially if the program time should be longer than the chromatogram duration. Additional steps after this flag are not allowed. The **RESET** flag is used to reset the parameters to the system startup values.
Suppressor		Switch **suppressor module** to the next position**.**
Peristaltic	**on, off**	Switch **on** or **off** the **peristaltic pump**.

Configuration

The **Configuration** tab in the system settings window contains configuration settings for the 792 Basic IC.



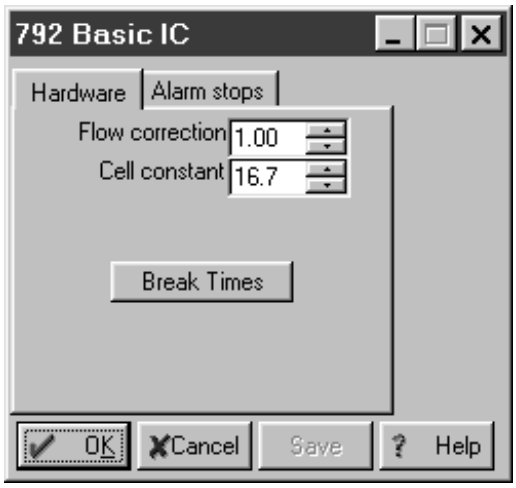
Method	Selection of the method with or without suppressor: **With MSM** method with suppressor **Without MSM** method without suppressor
Suppressor	Suppressor module:
Autostep with	Automatic switching to the next position each time the injection valve is switched either to the **Fill** or to the **Inject** position.
Use peristaltic pump	If this option is disabled, the peristaltic pump is not switched on automatically at the start of a determination or with **Startup hardware**.
Polarity	Selection of the polarity of the output signal: **+** positive polarity (for anions) **–** negative polarity (for cations)

Hardware settings

Selection of the **Hardware** menu item using the right mouse button opens the hardware settings window consisting of the two tabs **Hardware** and **Alarm stops**.

Hardware

This tab of the hardware settings window defines general parameters which are set automatically at power on of the instrument.



Flow correction

Factor for correction of the difference between displayed and actual flow rate of the high-pressure pump.
Range: **0.9** ... **1.09**

The flow correction is determined by measurement of the actual flow rate with the aid of a measuring cylinder as follows:

$$\textbf{Flow correction} = \frac{\textit{Displayed flow rate}}{\textit{Measured flow rate}}$$

Cell constant

Cell constant of the conductivity cell for correct display of the absolute conductivity. Enter the cell constant printed on the detector block into this field.
Range: **0.1** ... **99.9 /cm**

For a precise determination of the cell constant, pump a calibration solution of known conductivity through the IC system, observe the displayed conductivity and change the cell constant until the correct conductivity value is displayed.

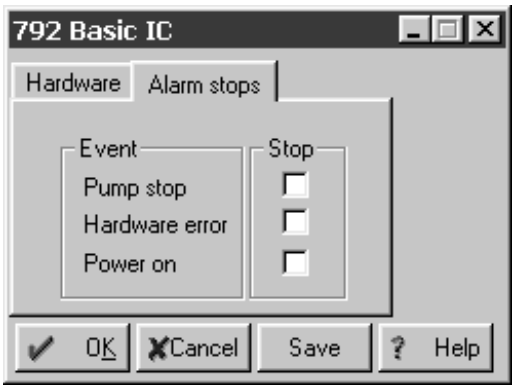
<Break times>

Possibility for changing the break times for injection valve **Valve** and suppressor module **Suppressor**.

These values should only be changed after consulting the Metrohm Service.

Alarm stops

The **Alarm stops** tab of the hardware settings window defines the events for which the 792 Basic IC is stopped immediately. At an alarm stop, high-pressure pump and peristaltic pump are stopped immediately; the running determination and the active sample queue are also stopped.



Event Events for alarm stop:

- **Pump stop** Pump stopped because pressure limits are exceeded.
- **Hardware error** Hardware error detected at the 792 Basic IC (high-pressure pump, injection valve, or suppressor not working correctly).
- **Power on** Temporary power failure at the 792 Basic IC.

4.3.7 System state window

The **SYSTEM STATE** window is automatically opened if a system is opened. It shows status and error messages for this system. Messages concerning the 792 Basic IC hardware are followed by **[792 Basic IC]**, messages concerning the loaded system are followed by **["folder"]** (name of subfolder containing the system file).

Status messages

Checking on-line	Checking connection between PC and 792 Basic IC.
On-line	Connection between PC and 792 Basic IC ok.
UploadStartupValues	System startup values have been loaded to the 792 Basic IC.
Initialization	Hardware or system initialization.
Ready	System is ready for starting a new determination.
Starting	Starting program or chromatogram data acquisition.
Running	Running program or chromatogram data acquisition.
Running program (xxx min left)	Running time program (in brackets: time left).
Waiting for INJECT	Waiting for "INJECT" to start program and/or chromatogram data acquisition.
INJECT done	Injection valve has been switched to the "INJECT" position.
Finished	Determination has been finished.
SHUTDOWN	792 Basic IC hardware is shutdown

Error messages

Detection of hardware failed	Bad connection between PC and 792 Basic IC or instrument switched off (check connecting cable or switch on instrument).
E1	Program checksum wrong (call Metrohm service).
E2	RAM faulty (call Metrohm service).
E200	Invalid instrument adjustment (call Metrohm service).
E237	Storage of configuration values failed (repeat last action; if error reappears, call Metrohm service).
E238	Storage of instrument number failed (repeat last action; if error reappears, call Metrohm service).
E240	EEPROM faulty (call Metrohm service).
E258	Storage of setup values failed (repeat last action; if error reappears, call Metrohm service).
E295	Storage of memory values failed (repeat last action; if error reappears, call Metrohm service).
E296	Instrument stopped (restart instrument; if error reappears, call Metrohm service).
E298	Storage of flow correction value failed (repeat last action; if error reappears, call Metrohm service).
E299	Storage of break time values failed (repeat last action; if error reappears, call Metrohm service).
E300	High-pressure pump faulty (restart pump; if error reappears, call Metrohm service).
E301	Injection valve blocked (check injection valve; if error reappears, call Metrohm service).
E302	Suppressor module blocked (check suppressor; if error reappears, call Metrohm service).
E303	Storage of maintenance information failed (repeat last action; if error reappears, call Metrohm service).

4.4 Methods

A method contains all information necessary for **data acquisition**, **integration**, **peak evaluation** and **quantification**. It can be considered as the chromatogram template, i.e. chromatogram without raw data.

Methods are stored as **method files** (***.mtw**) in the **Methods** directory. 35 prepared, write-protected methods are copied to this directory at program installation.

Each system is linked to a method. This method is called **processing method** and is opened automatically at the start of a new determination.

4.4.1 Method file handling

The following menu items are used for opening and saving of methods:

SYSTEM / PC icon / Open

By clicking this menu item or by double-clicking the PC icon in the system window, the method file (***.mtw**) belonging to the system is loaded from the **Methods** directory. At the same time, an empty chromatogram window is opened.

The name of the method is displayed in the title bar of the system window. A star (*****) at the end of the name indicates that the method has been changed since the last saving.

792 BASIC IC / File / Save / Method

Save the method of the current chromatogram in a method file (***.mtw**) in the **Methods** directory.

4.4.2 Passport

792 BASIC IC / Method / Passport

This menu item opens the **Passport** window that includes a detailed textual description of the chromatographic run and consists of the following tabs:

General	General information on determination.
Sample	Sample information.
Column	Column information.
Eluent	Eluent information.
Comment	User comments on chromatogram.
Method Log	GLP log with date/time stamp for method.
Data Log	GLP log with date/time stamp for chromatogram.

General

Tab **General** of the passport with general description of the method and determination.

Ident — User defined identifier (title) for the chromatogram to be displayed in the title bar of the chromatogram window and in the **Chromatogram open** window.

Duration — Duration of the chromatogram in minutes. You can modify this value when the chromatogram is running.

METHOD — Path and file name of the **method** used for data acquisition (read-only).

DATA — Path and file name of the current **chromatogram** (read-only).

Date/time — Date and time of the chromatogram start (read-only).

Last update — Date and time of the last chromatogram modification and saving (read-only).

Calibration level — If the current run is used for calibration, the calibration level is a positive integer, otherwise it equals zero. You can modify this value when the chromatogram is running.

User — Name of the current user. It is taken from the list of users, in accordance with the password entered at the program starting.

Detector — Name of the detector (read-only).

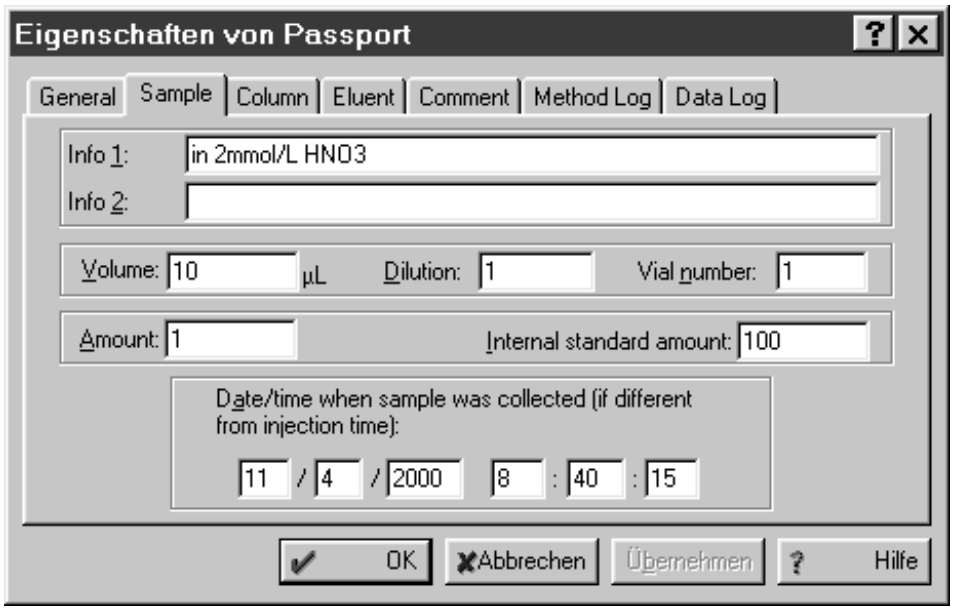
Run — Number of the current run starting from the very first one. All runs are automatically numbered by the system.

To reset the **Run** *number press [Ctrl] [F8]. The* **Analysis number** *window is opened where the run number for the next run can be modified to the desired value.*

Batch X/Y: total number of started sample queues / current analysis number in the sample queue (read-only).

Sample

Tab **Sample** of the passport with sample information.



Info 1 First sample description (max. 256 characters).

Info 2 Second sample description (max. 256 characters).

Volume Injected volume in µL.

Dilution Dilution of the sample.

Vial number Autosampler vial position to take sample from.

Amount Sample amount. If this value is different for the calibration run (**c**) and the sample run (**s**), the component concentrations of the sample are calculated as follows:

$$C_s = C_c \cdot \text{Amount}_s / \text{Amount}_c$$

Internal standard amount Concentration of the internal standard component for relative concentration calculations.

Date/time when... Date and time of sample collection (the default values are equal to the date and time when the chromatogram starts).

Column

Tab **Column** of passport with column information.

Number	Serial number of column (max. 256 characters).
ID	Internal diameter of the column in mm.
Length	Length of the column in mm. This parameter is used to calculate **Linear flow**.

Packing material

Column	Column description (max. 256 characters).
Particle size	Particle size of the column in µm. This value is used for the calculation of reduced theoretical plate height **Reduced TP height**.
Void volume	Void volume for the column in %. Used to calculate **Logarithmic index**, **Capacity factor** and **Linear flow**. It is calculated by the system in accordance with the settings defined on **Method setup / Math**.

Precolumn

ID	Internal diameter of the precolumn in mm.
Length	Length of the precolumn in mm (set length to 0 if no precolumn is used).

Eluent

Tab **Eluent** of passport with eluent information.

Eluent A — Description of eluent composition (max. 256 characters).

Eluent B — Description of eluent composition (max. 256 characters).

Eluent C — Description of eluent composition (max. 256 characters).

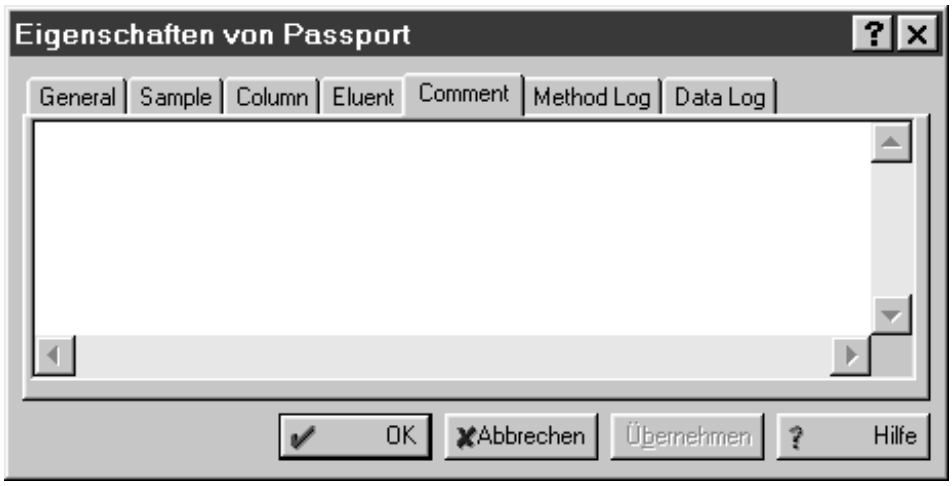
Flow — Flow rate of the high-pressure pump in mL/min. The flow rate is used to recalculate the time axis into volumetric units. The system startup value for the flow rate is entered automatically into this field at the start of a determination.

Pressure — Pressure in MPa. The measured value for the pressure is entered automatically into this field at the start of a determination.

Temp. — Temperature in °C. Here you can enter the temperature of the column's thermostat or the ambient temperature.

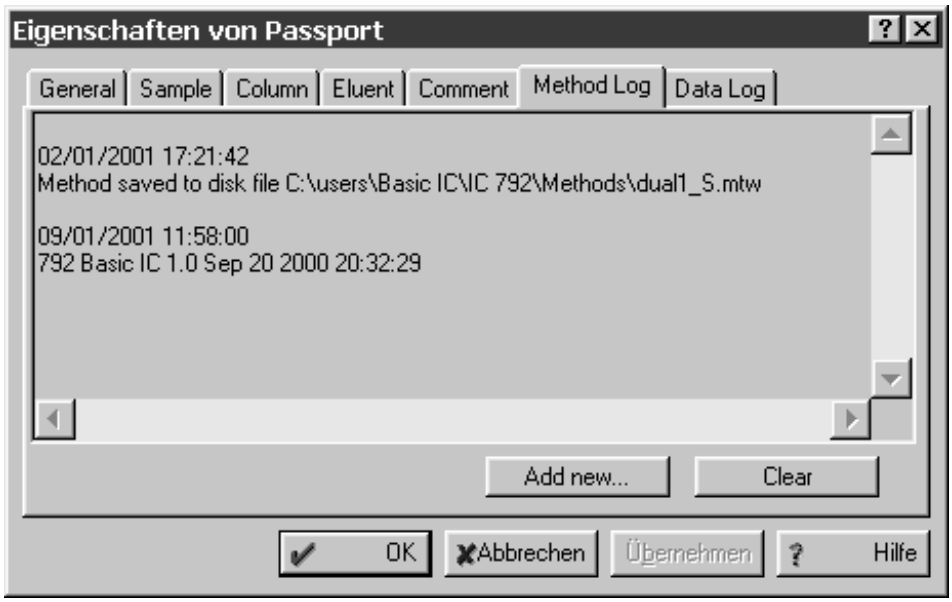
Comment

Tab **Comment** of passport for entry of free-text user comments into the chromatogram description. Use this feature to enter any additional information about the chromatogram not included in other sections of the method.



Method Log

Tab **Method Log** of passport with GLP Log for the method. The **Method Log** displays all automatically produced GLP messages concerning modifications made on a method. In addition to these messages, free-text user comments can be entered. All this entries are stamped automatically with date and time of the entry.

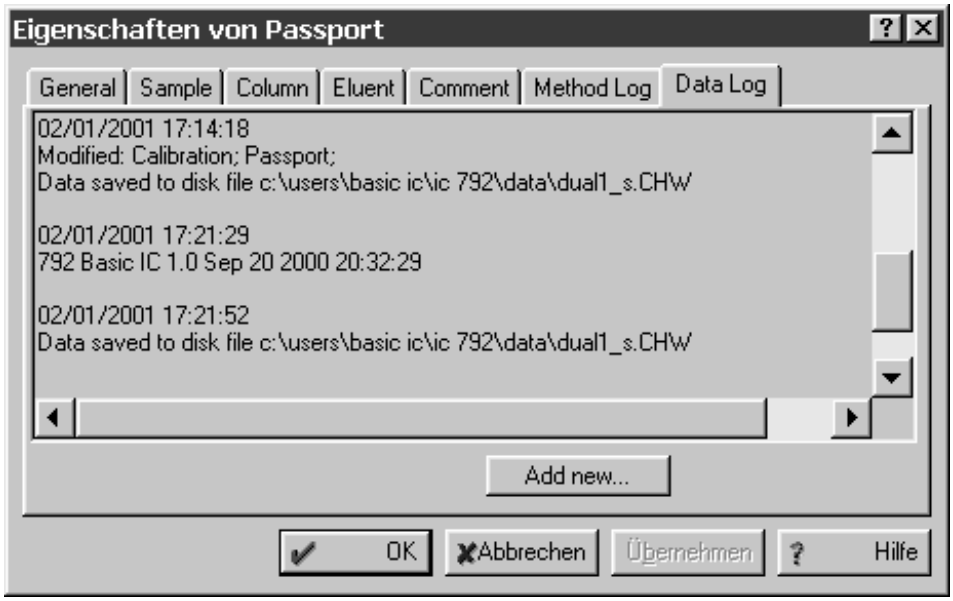


<Add new> Add a new GLP comment. Text can be entered in the **New comment** window, date/time and logged-in user are automatically added.

<Clear> Clear all GLP messages and add a new GLP comment. Text can be entered in the **New comment** window, date/time and logged-in user are automatically added.

Data Log

Tab **Data Log** of passport with GLP Log for the recorded chromatogram. Here a GLP message is automatically produced for every modification made on a recorded chromatogram. In addition to these messages, free-text user comments can be entered. All this entries are stamped automatically with date and time of the entry and cannot be cleared.



<Add new> Add a new GLP comment. Text can be entered in the **New comment** window, date/time and logged-in user are automatically added.

4.4.3 Method setup

792 BASIC IC / Method / Method setup

This menu item opens the **Method setup** window that includes the most common parameters for data acquisition and evaluation of the method and consists of the following tabs:

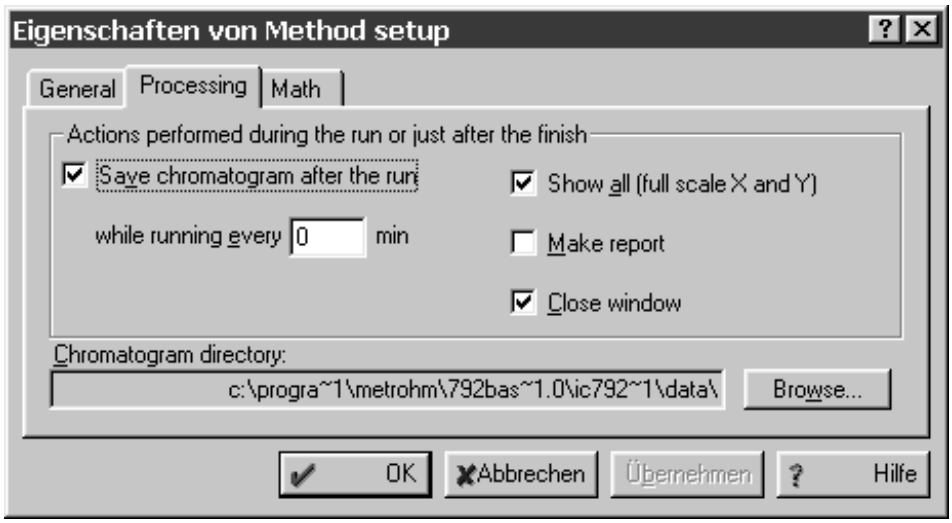
General	General information on determination.
Processing	Set actions that are performed when the chromatogram finishes.
Math	Parameters that are used for various types of calculations.

General

Tab **General** of **Method setup** window with general description of the method and determination. This tab is identical to the **General** tab called with **Method / Passport** (see *section 4.4.2*).

Processing

Tab **Processing** of **Method setup** window for definition of actions that are performed during the run or when the chromatogram finishes. Automatic post-run data processing is especially useful for chromatographic systems that include an autosampler.



Save chromatogram after the run

If checked, autosaving of the chromatogram will be performed on data acquisition ending.

while running every ... min

Save the chromatogram during the run for data safety at the time interval set (if **0** is set, the chromatogram is not saved during the run).

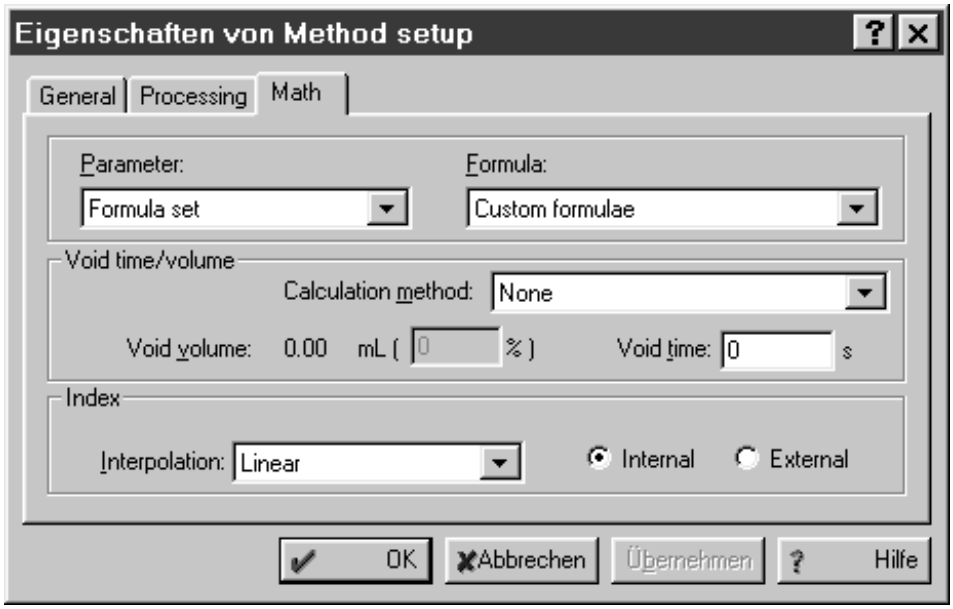
Show all

If checked, scales on X and Y axes will be automatically chosen so that the recorded chromatogram fits the window.

Make report	If checked, report auto-printing will be performed on data acquisition ending.
Close window	If checked, the window is closed automatically after the run (or sample queue) is finished.
Chromatogram directory	Directory where the current chromatogram is saved. Use the **<Browse>** button to select a new directory.

Math

Tab **Math** of **Method setup** window with parameters that are used for various types of calculations.



Parameter	Selection of **calculation parameter**:
Formula set	Formula setting by customer (**Custom formulae**) or according either to **European Pharmacopoeia** or **US Pharmacopoeia**.
Theoretical plates	Selection of calculation formula for number of theoretical plates if **Formula set** = **Custom formulae** is set.
Resolution	Selection of calculation formula for resolution if **Formula set** = **Custom formulae** is set.
Asymmetry	Selection of calculation formula for asymmetry if **Formula set** = **Custom formulae** is set.
Formula	Selection of **calculation formula** for the calculation parameter selected for **Parameter**. With **Parameter = Formula set** the following settings are possible:
Custom formulae	Formula setting by customer.

European Pharmacopoeia
Formula setting according to European Pharmacopoeia.

US Pharmacopoeia Formula setting according to US Pharmacopoeia.

Void time/volume Calculation of **void time/void volume**:

Calculation method Selection of the method for void time calculation:

None Manual entry in the **Void time** field.

1st component The peak corresponding to the first component is selected as a void time marker and its retention time replaces the previous value of the void time. If the first component is not identified, the expected retention time is used.

1st peak The first detected peak is used as a void time marker for the run and its retention time is stored in the **Void time** field.

From void volume %
For the calculation of the void time, the % value entered in the **Void volume** field is multiplied by the ratio of empty column volume and eluent flow rate.

Void volume Void volume in mL and % of column volume. The % value can be entered manually if **Calculation method = From void volume %** is set.

Void time Void time in s. This value can be entered manually if **Calculation method = None** is set.

Index Calculation of **Retention index**:

Interpolation Use of linear or logarithmic interpolation scale for retention index calculation.

Internal The index scale is constructed on the basis of the current chromatogram. All components used for index scale calibration should be present in the current sample.

External The index scale is constructed based on another standard chromatogram.

4.4.4 Integration

792 BASIC IC / Method / Integration

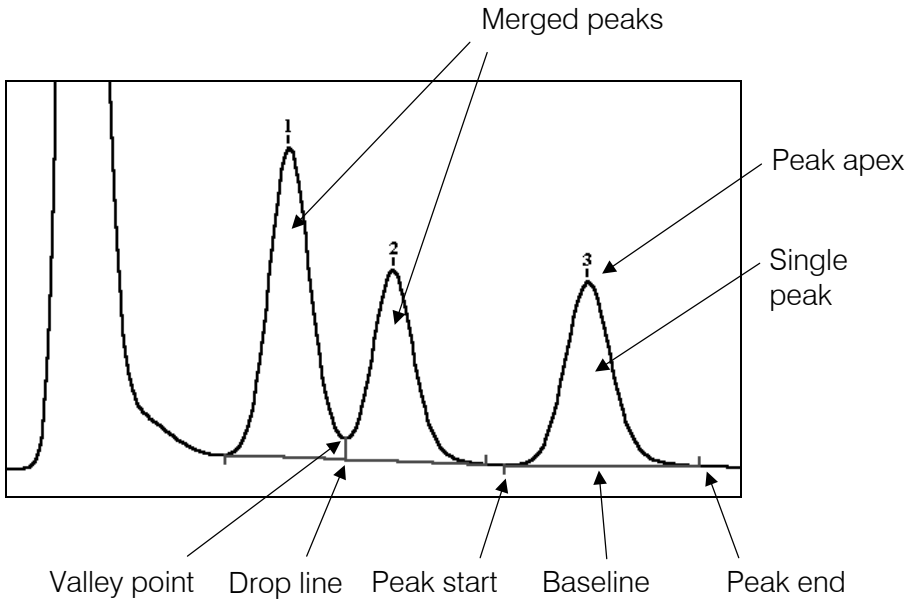
This menu item opens the **Integration parameters** window that contains parameters and events for peak integration and consists of the following two tabs:

Setup	Integration parameters.
Events	Integration events.

The «792 Basic IC» software includes a built-in automatic integration algorithm to detect peaks on the chromatographic curve and to evaluate them using calculated baselines. The integration procedure is tuned by the integration parameters on the **Setup** tab and the integration events on the **Events** tab. Integration events have higher priority than integration parameters. The integration can be modified manually using the peak editor (see *section 4.5.4*).

The built-in integrator algorithm is based on the use of the first derivative (slope). In order to decide whether the slope at some point is significant, the first derivative value is divided by the baseline noise and the result is compared with a threshold value called "**Slope**". The threshold values for the upslope and down slope differ.

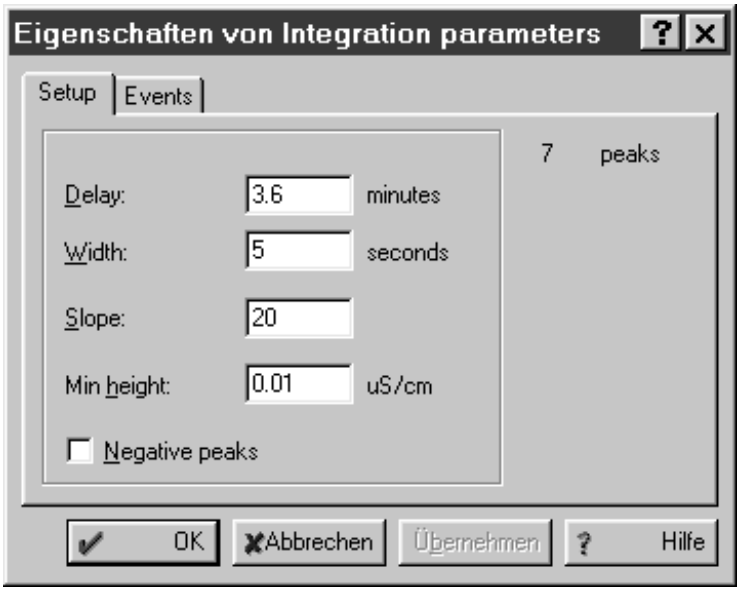
The baseline and the start and end points are determined for each peak. For separated peaks, the baseline consists of a straight line between the start point and the end point. For overlapping neighboring peaks, a common baseline is normally constructed; this connects the start point of the first peak with the end point of the last peak. The peaks are separated from one another by dropping a perpendicular line from the lowest point (valley) between the peaks to the common baseline. Alternatively, the baseline can also be drawn directly between the valleys of the peaks with the event **Enable valley-to-valley** (see integration events for baseline).



Setup

Tab **Setup** of **Integration parameters** window with integration parameters. The two most important of these parameters for peak recognition are **Width** and **Slope**.

If the signal-to-noise ratio of the chromatogram is high enough (e.g. 100:1 or higher), the integration algorithm is not too sensitive to changes in integration parameters. On the contrary, if the baseline noise is high, careful tuning of these parameters may be needed.



Number of peaks — Number of peaks detected (read-only).

Delay — Time delay before starting peak detection (in min).
Entry range: **0…1440 min**

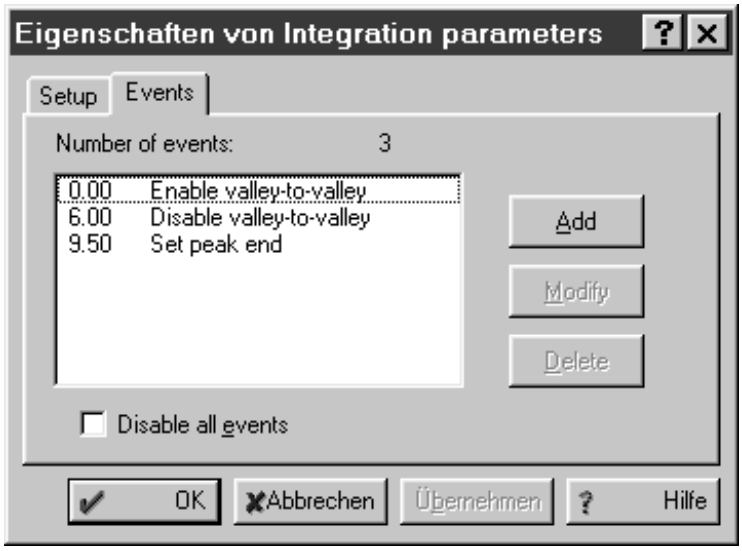
Width — **Peak width** (at the baseline, in s).
This parameter is used for setting baseline start and end points. If this value is too low, excessive narrow peaks are detected from the baseline noise. If it is too large, several adjacent peaks or baseline drift can be integrated as a single peak. For an optimal evaluation, it is recommended to enter the width of the narrowest peak on the chromatogram (normally 2…10 s).
Entry range: **0.1…480 s**

Slope — **Threshold for peak recognition**.
The value of the first derivation (slope) of the curve is divided by the baseline noise (which is estimated using a special algorithm) and the result is compared with the **Slope** threshold value. Reasonable range of **Slope** parameter is 0.5...25.
Entry range: **0.1…400**

Min height	Minimum height of peaks to be detected.
Negative peaks	If this option is enabled, negative peaks are also detected.

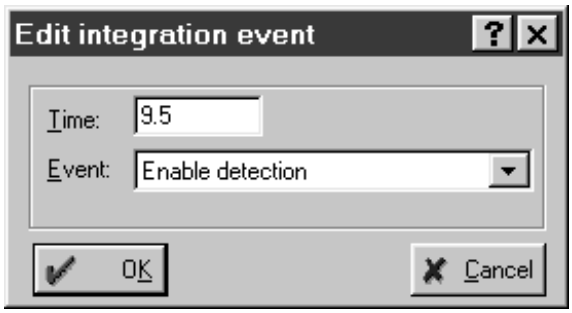
Events

Tab **Events** of **Integration parameters** window for definition of integration events. Integration events have a higher priority than integration parameters and are used for fine-tuning of the integration process. They should be used only in the case when problems cannot be solved by tuning a set of parameters from the integration parameters window.



Number of events	Number of integration events (read-only).
<Add>	Add event to the list.
<Modify>	Edit the selected event.
<Delete>	Delete the selected event.
<Apply>	Accept integration parameters and perform re-integration.

If an integration event is added or modified, the **Edit integration event** window is opened where the following parameters can be set:



Time Start time for integration event in min.

Event List box with integration events to be selected (see below).

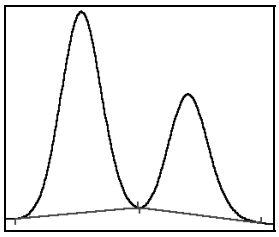
Integration events

Disable detection Set this mode to stop detection of new peaks. If a peak is available at the moment of the event it is either terminated (down slope peaks) or rejected (upslope peaks).

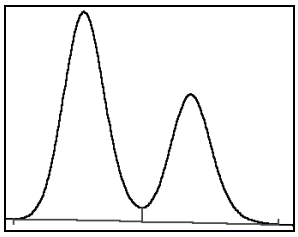
Enable detection Clear **Disable detection** mode.

Set peak start Force the beginning of a new peak. If a peak is available at the moment of the event it is either rejected (upslope) or terminated (down slope).

Set peak end Force peak end at the time of the event. Upslope peaks are rejected (except those born by **Set peak start** event), down slope peaks are terminated.



Enable valley-to-valley



Disable valley-to-valley

Enable valley-to-valley Disable perpendicular drop peak separation. All peaks are considered to be baseline-separated. The bottom of the valley becomes the baseline point.

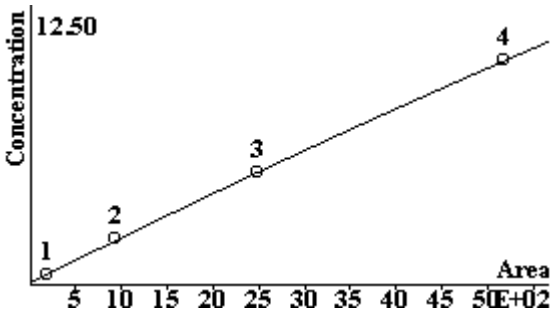
Disable valley-to-valley Enable perpendicular drop peak separation (default setting).

4.4.5 Calibration and quantification

General information

The aim of any chromatographic analysis is to answer the question "What components are present in the sample and what are their concentrations?". Two procedures are used to achieve this goal: the first step is called **calibration**, the second step includes **quantification**.

Calibration has two aims: to get retention characteristics for all components of interest (these data are stored in the component table) and to establish a relation between injected amounts and corresponding instrumental responses for all components of interest (stored in the concentration table). Calibration is performed by running one or several chromatograms of samples with known composition and known concentration of components (standards). For each calibrated component a **calibration curve** is constructed as a result.



With the 792 Basic IC three different procedures can be used for the construction of the calibration curve. By far the most important method for ion chromatography is the **external standard calibration** (absolute calibration) that is described in detail in this section. The other methods of **internal standard calibration** (relative calibration) and **tabulated calibration** (relative gradient factor, a modified method for external standard calibration) are of lesser importance and are not described in detail here (for details please refer to on-line help).

Identification is a procedure that enables to decide what peaks on the chromatogram correspond to what components. The identification is performed based on the **Component table** created for calibration.

Quantification is a calculation procedure that determines components concentrations, based on instrumental response (peak height or area), using the calibration curves obtained earlier for each component.

Notations

R	Stands for response value, either **area** or **height**, depending on setting selected in the **Calibration graphs** window.
V	Sample **Volume** injected.
D	**Dilution** coefficient, shows number of times to which the initial solution is dissolved before injection.
V' = V / D	**Adjusted volume** of injected sample. A correction is made for the dilution coefficient.
C	Concentration of the component in the initial solution (before dilution).
Q = C • V'	**Quantity** of component, used for calibration curve construction.
t	**Retention time**. Time needed by the mobile phase to flow through the separation system.
$\mathbf{t_0}$	**Void time**. Dead time needed by the mobile phase to flow through the separation system.
$\mathbf{t' = t - t_0}$	**Corrected retention time**, called also net retention time.
L	Column length.
$\mathbf{v = L / t_0}$	Linear **Flow rate**.
$\mathbf{W(R) = k_2R^2 + k_1R + k_0}$	Calibration function (component quantity **W** vs. detector response **R**). In the case of the most common linear calibration curve $\mathbf{Q = W(R) = k_1R}$ it comes through the origin. The concentration of the component in the analyzed mixture is calculated by the formula $\mathbf{C = W(R) / V'}$.
RSD(Q, R)	Procedure, used for computation of regression coefficients ($\mathbf{k_0}$, $\mathbf{k_1}$ and $\mathbf{k_2}$) of the calibration function **W(R)** using RSD (Residual Standard Deviation). The procedure gets input as a set of calibration points (quantity **Q** vs. response **R**) and outputs the calibration function **W(R)** used for prediction of the component quantity $\mathbf{Q_i = W(R_i)}$.

Subscript values used:

j	Stands for j-th calibration level run.
s	Stands for standard component.
i	Stands for component number.

External standard calibration

External standard calibration (absolute calibration) is a key way of calibration. Basically this procedure calculates the dependence of injected component's quantity versus area (or height) of the corresponding peak. This dependence is showed as a calibration plot with injected quantity along the Y axis and peak area (or height) along the X axis. The injected quantity $\mathbf{Q_i}$ is calculated as product of component's concentration $\mathbf{C_i}$ to the reduced injected sample volume $\mathbf{V'}$:

$$\mathbf{Q_i = C_i \cdot V'}$$

The calibration function $\mathbf{W_i(R)}$ for each component is calculated using the RSD method.

$$\mathbf{W_i(R) = RSD(Q_{ij}, R_{ij}) = RSD((C_i \cdot V'), R_{ij})}$$

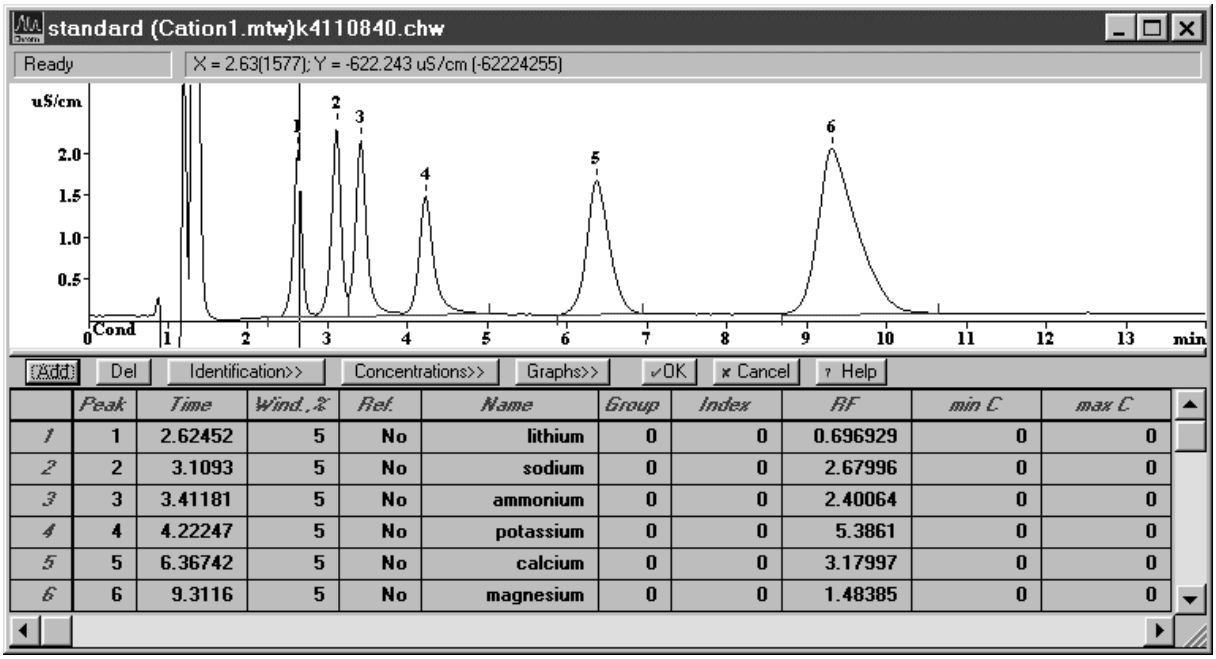
When quantification procedure is performed, a concentration $\mathbf{C_i}$ (absolute concentration of a component in the sample) is determined as a ratio of the computed quantity $\mathbf{W_i(R_i)}$ to the corrected volume of sample injected $\mathbf{V'}$:

$$\mathbf{C_i = W_i(R_i) / V'}$$

Component table

792 BASIC IC / Method / Calibration / Components

If the component table is opened, the chromatogram window is split into two parts. The upper one shows the chromatogram, the component table appears in the bottom part of the screen. When moving into the component table, a special cursor in the upper part of the window jumps to the peak corresponding to the current component.



	Peak	Time	Wind./%	Ref.	Name	Group	Index	RF	min C	max C
1	1	2.62452	5	No	lithium	0	0	0.696929	0	0
2	2	3.1093	5	No	sodium	0	0	2.67996	0	0
3	3	3.41181	5	No	ammonium	0	0	2.40064	0	0
4	4	4.22247	5	No	potassium	0	0	5.3861	0	0
5	5	6.36742	5	No	calcium	0	0	3.17997	0	0
6	6	9.3116	5	No	magnesium	0	0	1.48385	0	0

The **Components table** stores the following information on the components to be analyzed:

Number	**Row number** (read-only).
Peak	Number of the peak in the chromatogram that corresponds to the given component. If this field contains a **0**, the **peak number** must be entered manually.
Time	**Expected retention time** of the component in the calibration run. After a new entry of the peak number the corresponding retention time is entered automatically as soon as this field is clicked on with the mouse.
Wind.%	**Identification window** of the component. This value is the maximum allowed difference of the actual retention time of the component and its expected retention time, measured as % of expected retention time. The component will be identified within its identification window only.
Ref.	**Reference component**. The entry **Yes** defines components as reference components; these ensure improved peak identification of the other **Ordinary components** (details see on-line help).
Name	**Component's name** (cannot include spaces). Rows with empty names are excluded from the table of components when you leave the component table editor.
Group	Number of the **group** to which the components are allocated. If group numbers ≥ 1 are entered here then a group report can be outputted for each group; this also contains the intermediate totals for this group. This group report is produced after the main report table.
Index	**Retention index** for components with known index. In the case of an unknown index this value should be equal to **0**. For index calculation the user must define index values for at least two peaks, and all other values will be calculated by the software using linear or logarithmic approximation (details see on-line help).
RF	**Response factor**. This value corresponds to the slope of the calibration curve (coefficient $\mathbf{k_1}$ of the calibration formula).
min C (max C)	**Minimum (Maximum) concentration** value for the component. Components whose concentration leaves the range **min C…max C** are marked in the peak table by the sign " **!** ".

Additionally, the **Components table** contains the following buttons:

<Add>	Add a new component (an empty column) to the component table.
<Del>	Delete the current component from the component table.
<Identification>	Open the **Peak identification** window (see *Identification*).
<Concentrations>	Open the **Concentration table** (see *Concentration table*).
<Graphs>	Open the component window with display of calibration curve and calibration parameters.
<OK>	Accept all changes and close the **Component table**.
<Cancel>	Reject all changes and close the **Component table**.

The standard method **Default.mtw** supplied with the «792 Basic IC» program has an empty component table. All other methods contain a component table with pre-defined components with entries for the names and retention times.

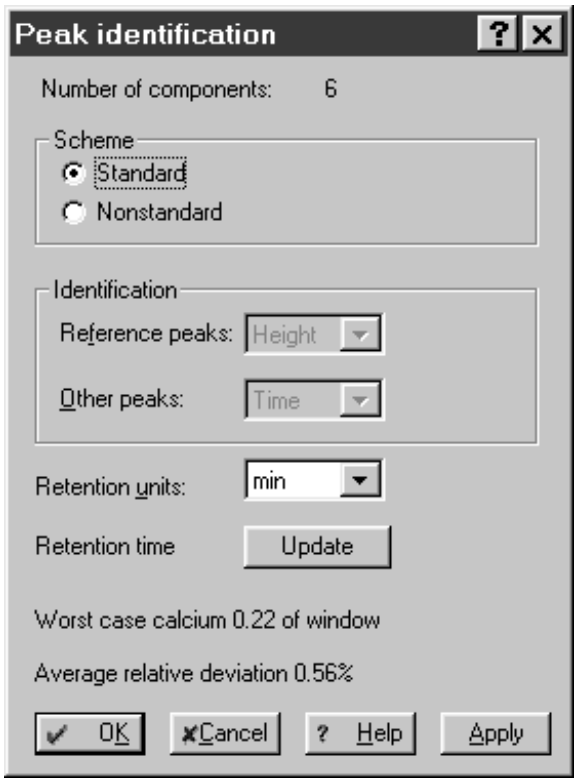
If the output of all peaks is required in the result report then a so-called universal component can be defined in the component table for this purpose; this receives the value **0** *in the* **Time** *field and no peak is allocated to it. The name entered under* **Name** *(e.g.* **unknown***) is then used for all peaks for which no component can be allocated.*

Peak identification

792 BASIC IC / Method / Calibration / Identification

Selecting this menu item or clicking on **<Identification>** in the component table opens the **Peak identification** window with parameters for tuning the peak identification procedure.

Number of components	Number of components in the component table (read-only).
Scheme	Quick choice of identification parameters scheme.
Standard	Set default meanings of identification parameters: **Height** for reference components, **Time** for all other components (ordinary components).
Nonstandard	Set custom meanings of identification parameters.

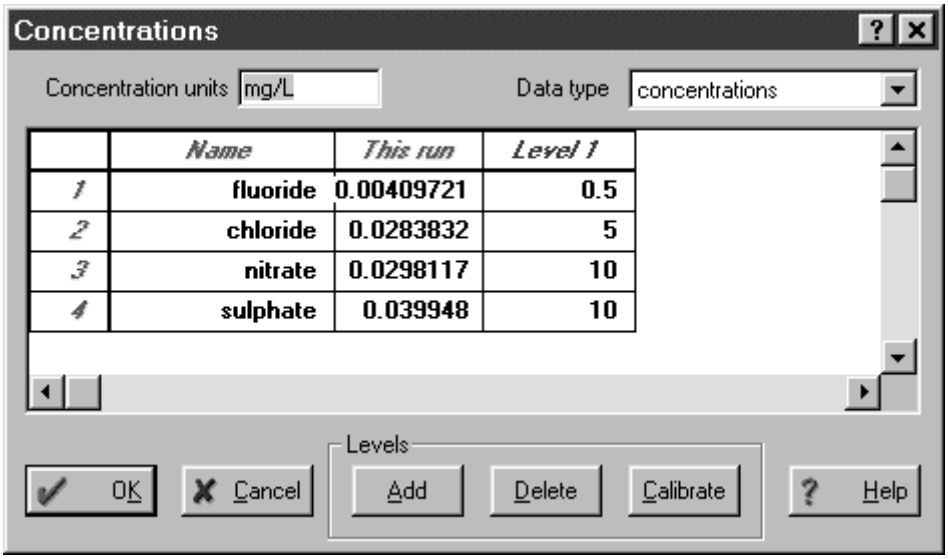


Identification	Identification parameters.
Reference peaks	Identification parameter for reference components. Default is **Height**.
Other peaks	Identification parameter for ordinary components. Default is **Time**.
Retention units	Choice of retention units. Default is **min**.
Retention time	Retention time.
<Update>	Updates expected retention times of components according to the current chromatogram.
Worst case...	Information on the component with the worst (largest) deviation of actual and expected retention time. Deviation is given as a part of component's identification window.
Average relative deviation	Relative deviation averaged for all components.

Concentration table

792 BASIC IC / Method / Calibration / Concentrations

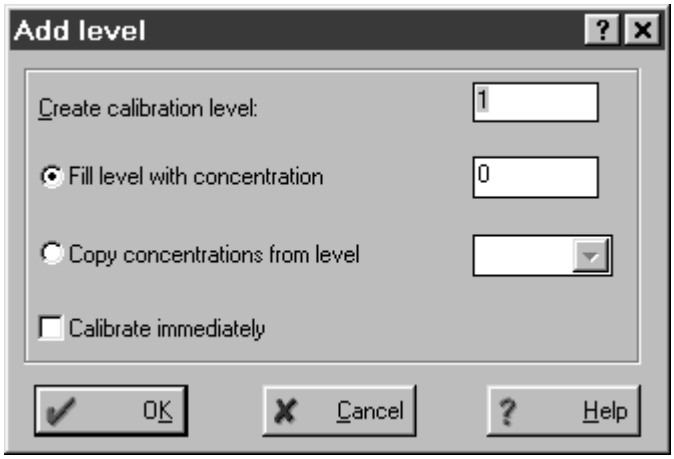
Selecting this menu item or clicking on **<Concentrations>** in the component table opens the **Concentrations** window with the concentration table containing concentrations of all components for all **Calibration levels**. Each calibration level corresponds to a sample used for calibration and to a point on the calibration curve.



Concentration units	User defined units of concentration that will appear in the report. Nevertheless, entry of new concentration units does not cause recalculation of concentrations.
Data type	Choice of the data type that will be shown in the concentration table: **concentrations** (default setting), peak **heights**, peak **areas**, **volumes**.
Number	Number of the component (read-only).
Name	Name of the component taken from the component table (read-only).
This run	Contains concentrations (or other chosen values) obtained in the current run (read-only, except for universal component).
Level 1...Level N	Contains concentrations (or other chosen values) of components for corresponding **Calibration level**.

<Add>

Add a new **Calibration level** to the concentration table. The following window appears:



Create calibration level

Number of calibration level to add.

Fill level with concentration

Concentration to be filled in for all components.

Copy concentrations from level

Number of calibration level from which concentrations are copied.

Calibrate immediately

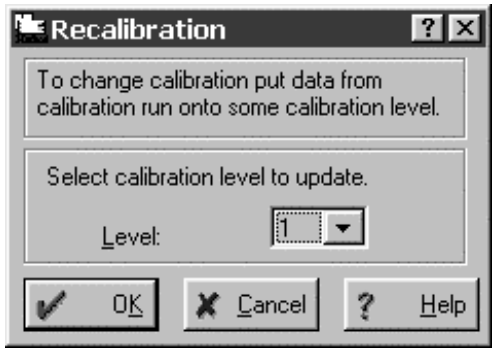
Recalibration with new calibration levels.

<Delete>

Delete the current calibration level (where cursor is situated) from the concentration table.

<Calibrate>

Calibrate the current chromatogram with the selected calibration level. The following window appears:



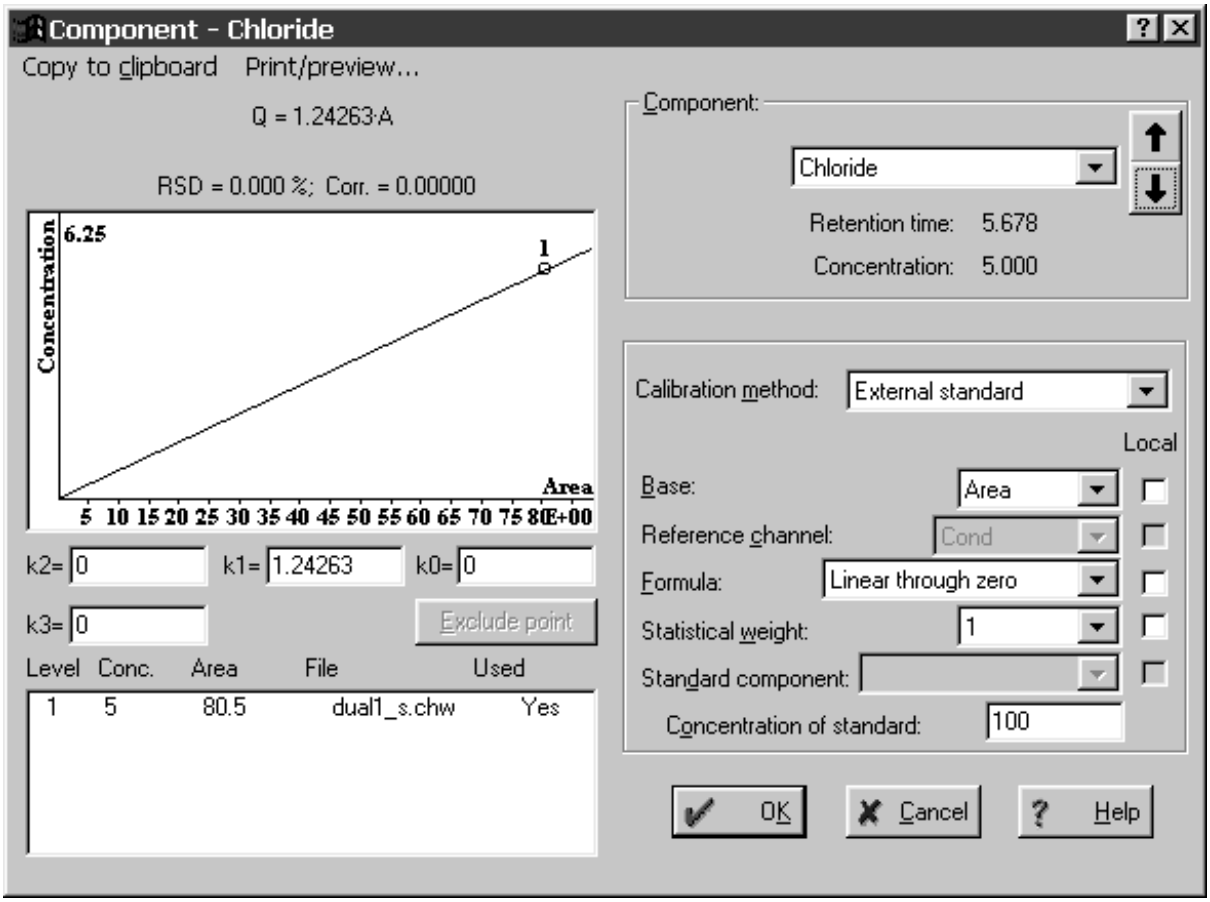
Level

Calibration level to be used for recalibration.

Calibration curve

792 BASIC IC / Method / Calibration / Graphs

Selecting this menu item or clicking on **<Graphs>** in the component table opens the **Component** window.



In this window the results of the calibration are shown for each component together with the calibration curve. The parameters for calculating the calibration curve can also be entered here.

Calibration results and curve

Analytical expression — A line above the calibration curve looking like $Q = k_3 \cdot A^3 + k_2 \cdot A^2 + k_1 \cdot A + k_0$.
This formula is used for approximation of the calibration curve.

RSD — RSD (Residual Standard Deviation) value to evaluate the error of calibration curve approximation.

Corr. — Correlation coefficient value is available only in the case of linear calibrations without weighting of data points.

Calibration curve — Plot of measured calibration points and calculated calibration curve.

k0, k1, k2, k3 — Calibration coefficients k_0, k_1, k_2 and k_3 (coefficients of the calibration formula).

Calibration points table

This table contains the basic information used to construct the calibration curve:

Level Number of **Calibration level**.

Conc. Concentration of the current component in the calibration sample. It is taken from the concentration table.

Area (or Height) Peak height or area of the current component, depending on calibration base.

File File name of calibration chromatogram that stores data on the given calibration level.

Used Information whether the calibration level is used for calculation of the calibration curve or not.

<Exclude point> Exclude the selected calibration point from the list and recalculate calibration coefficients for the current component. Repeated pressing includes the point again. You can exclude points that drop out of the calibration curve watching for RSD values.

Component information

Component Allows to select the current component from the list. It is possible also to scroll the list of components by mouse, using the special arrow buttons on the right.

Retention time Retention time of the selected component (read-only).

Concentration Concentration of the selected component (read-only).

Calibration parameters

Calibration method Method that is used for calibration procedure. There are three basic methods of calibration:

External standard calibration
Absolute calibration. It is the basic calibration procedure in ion chromatography.

Internal standard calibration
Relative calibration.

Tabulated calibration Relative response factor calibration. It is a simplified method of external standard calibration.

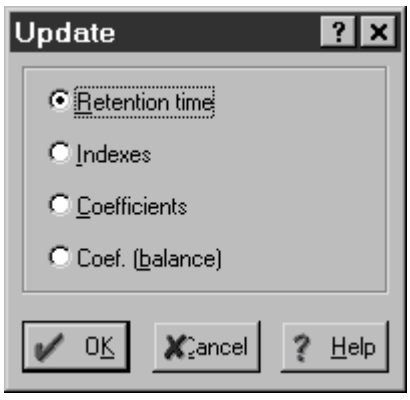
Local If this checkbox is marked then the corresponding parameter is valid for the current component only. Otherwise, this parameter is global (i.e. default for all other components).

Base	Base for calculations (**Area** or **Height**) in quantification and calibration procedures. Indicates, which parameter is to be used as a peak response.
Reference channel	Channel which is used to measure area or height (read-only).
Formula	Formula for calibration function. There are six possible calibration dependencies for linear and nonlinear calibration curves.
Linear through zero	function $Y = \mathbf{k_1} X$
Linear	function $Y = \mathbf{k_1} X + \mathbf{k_0}$
Quadratic through zero	function $Y = \mathbf{k_1} X + \mathbf{k_2} X^2$
Quadratic	function $Y = \mathbf{k_1} X + \mathbf{k_2} X^2 + \mathbf{k_0}$
Cubic through zero	function $Y = \mathbf{k_1} X + \mathbf{k_2} X^2 + \mathbf{k_3} X^3$
Cubic	function $Y = \mathbf{k_1} X + \mathbf{k_2} X^2 + \mathbf{k_3} X^3 + \mathbf{k_0}$
Statistical weight	Weighting parameter used to weight calibration points deviations on calculating coefficients of the calibration formula. Apart from the uniform weighting **1** the values **1/x**, **1/x²**, **1/y** and **1/y²** are also possible.
Standard component	Name of the standard component in the case of **Internal standard calibration** or **Tabulated calibration** method (details see on-line help).
Concentration of standard	Concentration of the standard component in the case of **Internal standard calibration** or **Tabulated calibration** method (details see on-line help).

Update calibration

792 BASIC IC / Method / Calibration / Update

Selection of this menu item opens the **Update** window.



Retention time	Replace the expected retention times of the components with the retention times of the corresponding peaks obtained in the current run.

Indexes	Fill **Index** field for components with zero index.
Coefficients	Recalculate all calibration coefficients for all components (performs re-calibration).
Coef. (balance)	Recalculate coefficient of the universal component. The aim of this action is to adjust the response factor of this component so, that the total amount of the injected components becomes equal to the declared value. This declared summary amount is entered into the **Concentration** field of the universal component for **This run** level.

Load and save calibration data

792 BASIC IC / Method / Calibration / Load from method

Load the calibration from the method. This option is used to update the calibration for the current run by the one taken from the method used for acquisition.

792 BASIC IC / Method / Calibration / Save to method

Save the current calibration to the method. This option is used to transfer the updated calibration from the run to the current method (i.e. the method associated with the current chromatogram window).

Import and export calibration data

792 BASIC IC / Method / Calibration / Import calibration

This option imports a calibration from a calibration file ***.cal** to the current method or chromatogram. It is used to transfer the updated calibration from chromatogram-to-chromatogram or from method-to-method. Different methods can be processed in this case using the same calibration.

792 BASIC IC / Method / Calibration / Export calibration

This option exports a calibration to a in calibration file ***.cal**. It is useful to transfer a calibration from chromatogram-to-chromatogram for chromatograms that were obtained by different methods.

Put out calibration curves

COMPONENT / Copy to clipboard

This option allows to copy the calibration curve of the selected component to the clipboard so that it is available for other Windows applications, such as WinWord, Excel, etc.

COMPONENT / Print/Preview / Preview this

Display calibration curve print preview of the selected component.

COMPONENT / Print/Preview / Preview all

Display calibration curve print preview of all components.

COMPONENT / Print/Preview / Print this

Print selected calibration curve of the selected component.

COMPONENT / Print/Preview / Print all

Print calibration curves of all components.

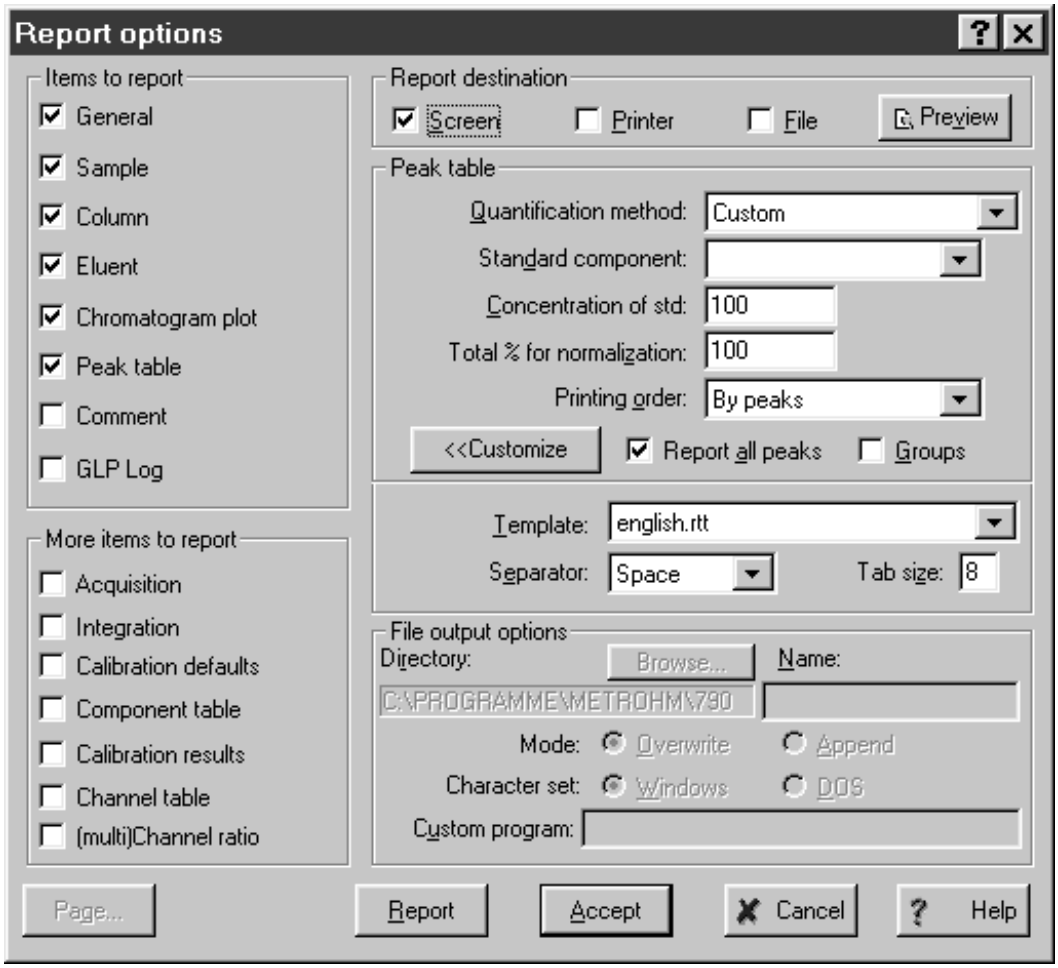
4.4.6 Report output

Report options

792 BASIC IC / Method / Report options

792 BASIC IC / Process / Make report

The **Report options** window is divided into several regions that combine parameters for report output on their functionality and includes several different areas. The report output is started by clicking on **<Report>**.



Items to report

This part of the **Report options** window contains a list of important report items that can be included into the report on the user's choice:

General General description on the analysis from the Passport. The **Report date** and the logged-in user **Printed by** are also put out.

```
Report date:          05/04/2000 12:34:00
Printed by:           Roland Dörig

Ident:                tap water
Analysis from:        11/04/2000 17:45:46
File:                 k4111745.chw      Last save: 13/04/2000 06:33:12

Method:                 Anion1.mtw      Last save: 11/04/2000 15:13:10
Run operator:         Urs Waldburger
Analysis number:      29
```

Sample Sample information from the **Sample** tab of the passport.

```
SAMPLE Info 1:      Tap water from Application Laboratory
       Info 2:      Herisau, Switzerland
Vial number:        2
Volume:             20.0 µl
Dilution:           1.00
Amount:             1.0000
```

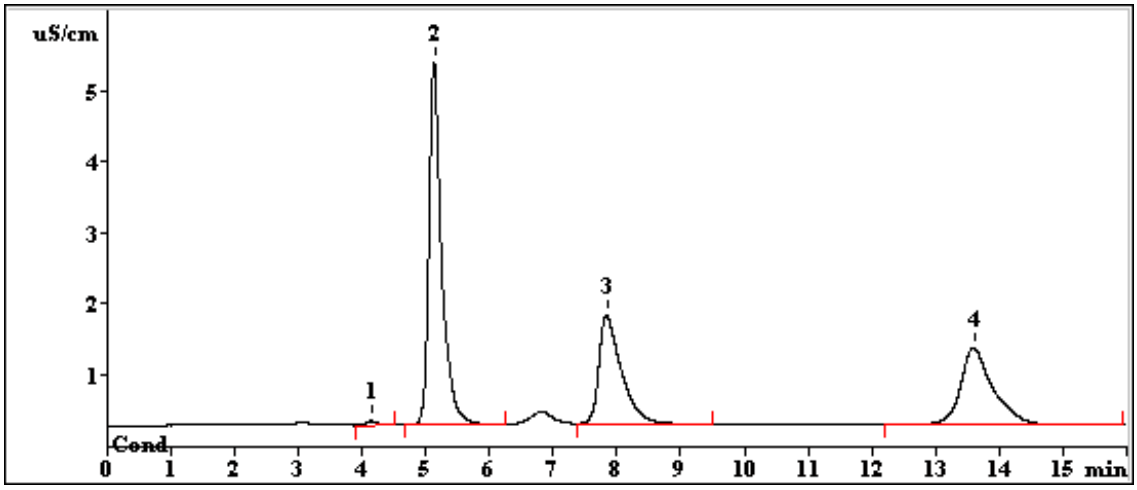
Column Column information from the **Column** tab of the passport.

```
COLUMN:             6.1005.320 Metrosep A Supp3
Size:               4.6 x 250 mm
Number:             A106
Part.size:          9.0 µm
```

Eluent Eluent information from the **Eluent** tab of the passport.

```
ELUENT A:           1.7 mM NaHCO3 / 1.8 mM Na2CO3
       B:
       C:
Flow:               1.00 mL/min
Temperature:        20.0°C
Pressure:           8.0 MPa
```

Chromatogram plot Plot of the chromatogram (only for **Printer** or **File** destination).



Peak table Peak table with results. The structure of the peak table depends on the selected **Quantification method**. The following report is put out as default:

```
PEAK TABLE
Quantification method:   Custom

 No  Retention   Height      Area       Conc.   Name
           min    uS/cm uS/cm*sec        ppm
  1       4.15     0.06      0.688      0.057   fluoride
  2       5.13     5.10     70.561      9.092   chloride
  3       7.84     1.53     37.506      8.743   nitrate
  4      13.59     1.09     38.682      6.584   sulfate
_____________________________________________________
  4      16.01     7.77    147.437     24.477
```

Comment User defined comment from the **Comment** tab of the passport.

```
COMMENT
Beispielmethode zur Wasserbestimmung.
```

GLP Log Method and Data GLP messages from the **Method Log** and **Data Log** tabs of the passport.

```
METHOD GLP LOG
13/04/2000 08:32:49 W. Terzer

04/05/2000 10:45:23
792 Basic IC 1.0 Apr 27 2000 14:05:01

DATA GLP LOG
Analysing data of channel :Cond
Time constant, ms: 100.00
Sigma: 0.0
Rejection difference: 1.0

11/04/2000 18:01:45
Status: Processing
Data saved to disk file c:\programme\ic 792\data\K4111745.CHW
```

More items to report

This part of the **Report options** window contains a list of rarely used report items that can be included into the report on the user's choice:

Acquisition Parameters used for data acquisition.

```
ACQUISITION PARAMETERS
Method duration:        16.00 min
Run duration:           16.01 min
Measurements (method): 9606
Measurements (run):     9606
Freq.divisor:           1
Sampling:               10.00 pts/sec
Device:                 792 Basic IC
```

Integration Integration parameters and integration events.

```
INTEGRATION DEFAULTS
Delay:                  3.60 min
Width:                  5.00 sec
Slope:                  20.00
MinHeight:              0.01

No.   min
1  0.00 Enable valley-to-valley
2  6.00 Disable valley-to-valley
3  9.50 Set peak end
```

Calibration defaults Calibration parameters defined in the component window and on the **Math** tab of the **Method setup** window.

```
CALIBRATION
Method:                External standard
Response:              Area
Standard:              No

IDENTIFICATION
Reference peaks:       Height
Other peaks:           Time
Retention units:       min
```

Component table Component table.

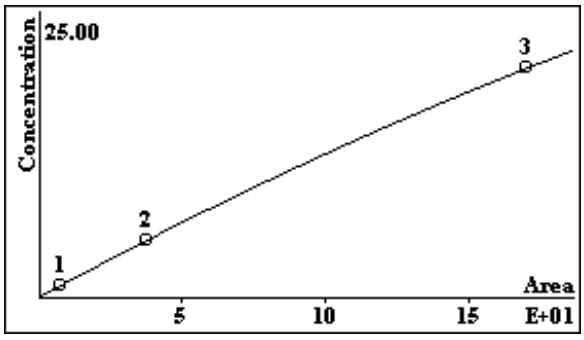
```
COMPONENT TABLE
 No Retention Window%        RF   Conc.   Index Type Group Name

  1     4.05     5.0  1.660e+00    0.06   0.000          0 fluoride
  2     5.01     5.0  2.735e+00    9.09   0.000    S     0 chloride
  3     5.82     5.0  4.137e+00    0.00   0.000          0 nitrite
  4     6.63     5.0  6.027e+00    0.00   0.000          0 bromide
  5     7.74     5.0  4.763e+00    8.74   0.000          0 nitrate
  6    11.67     5.0  9.164e+00    0.00   0.000          0 phosphate
  7    13.20     5.0  3.449e+00    6.58   0.000          0 sulfate
```

Calibration results Calibration results of the component window. For each component a new page with calibration results and calibration curve is put out.

```
CALIBRATION OF COMPONENT  chloride

Method:                   Anion1.mtw
Equation:                 Q = - 0.0022434·A^2 + 2.73542·A
RSD:                      0.072 %
Correlation coefficient:  0.999709
```




```
K3 = 0     K2 = -0.0022434     K1 = 2.73542     K0 = 0
Base:         Area
Ref.channel: Cond
ISTD:
Formula:      Y=K2·X^2+K1·X
Weight:       1

Level  Height   Area    Conc.  Vol/Dil  Retention  Used File
  1    0.6004  7.311       1     20         5.013   Yes k4101634.chw
  2    3.092   37.74       5     20         5.013   Yes k4101653.chw
  3    14.64   169.9      20     20         5.013   Yes k4101712.chw
```

Channel table Parameters of the data acquisition channel used.

```
CHANNELS TABLE
 No      Name     Units Input  Minimum      Zero  Maximum      Range Coefficient  Noise Shift

  1      Cond     uS/cm     1 -8388607         0  8388607 8.389e+01   1.000e-05   1.52     0

 # Name/Units      Noise          RMS   PeakToPeak  Drift/hour
  1 Cond             1.5      52871.6    512493.0    4232.464
    uS/cm        1.52e-05        0.529        5.12      0.0423
```

Name Channel's name. This text appears as **Channel label** in the chromatogram.

Units Units of detector response (µS/cm).

Input Number of data acquisition channel.

Minimum Minimum value of the linear range of the AD converter (in ADC conversion units). This parameter is used to detect an underflow condition.

Zero A signal level on a baseline (in ADC conversion units). This parameter is a result of the ADC calibration.

Maximum Maximum value of the linear range of the AD interface (in ADC conversion units). This parameter is used to detect overflow condition.

Range An input signal value in maximum in µS/cm.
Range = (**Maximum** - **Zero**) • **Coef**

Coef ADC sensitivity coefficient (weight of ADC bit in µS/cm).

Noise Estimated baseline noise value of the channel in ADC conversion units (bits).

Shift *Not used for 792 Basic IC*.

Report destination

The following output devices can be selected simultaneously in any combination as targets for report output:

Screen Output report (without curves) to screen.

Printer Output report to printer.

File Output report to file (see *File output options*).

Peak table

The following parameters can be selected for peak table output with determination results:

Quantification method Selection of the method to calculate concentrations of components:

Response normalization

The method normalizes the sum of responses for all peaks of the chromatogram to the **NORM** factor entered in the **Total % for normalization** field:

$$R_i\% = NORM \cdot R_i / \sum R_i.$$

All peaks are calculated and reported no matter whether they have been recognized or not.

The peak table includes the following columns: **number**, **retention time**, **area + area%** or **height + height%**, **name**

Normalized concentration

The method normalizes the sum of absolute concentrations for all peaks of the chromatogram to the **NORM** factor entered in the **Total % for normalization** field:

$$C_i\% = NORM \cdot W_i(R_i) / \sum W_i(R_i)$$

As long as no universal component is defined, only peaks with non-zero concentrations are listed.

The peak table includes the following columns: **number**, **retention time**, **height**, **area**, **response factor**, **concentration%**, **name**

Absolute concentration

This quantification method reports raw quantity (absolute concentration) of the component that is calculated directly from the calibration formula:

$$Q_i = W_i(R_i) / V'$$

As long as no universal component is defined, only peaks with non-zero concentrations are listed.

The peak table includes the following columns: **number**, **retention time**, **height**, **area**, **response factor**, **concentration**, **concentration%**, **name**

Relative concentration

This quantification method uses the internal standard method to calculate the relative concentrations of the components. For this procedure, a **Standard component** must be selected and the concentration of this internal standard must be entered in the **Concentration of std** field.

	As long as no universal component is defined, only peaks with non-zero concentrations are listed. The peak table includes the following columns: **number**, **retention time**, **height**, **area**, **response factor**, **relative concentration**, **relative concentration%**, **name**
Index	This column reports retention indexes of identified components. The peak table includes the following columns: **number**, **retention time**, **width/2**, **height**, **index**, **name**
Column test	Column test quantification method calculates multiple values that are necessary to evaluate column performance. The peak table includes the following columns: **number**, **retention time**, **K'** (capacity factor), **TP** (number of theoretical plates per column), **TP/m** (number of theoretical plates per m), **HETP/dp** (reduced height equivalent to theoretical plate), **asym.** (peak asymmetry), **name**
Custom	This quantification method enables to customize the peak table on the user's choice using the **<Customize>** button. The peak table for the methods supplied contains the following columns as standard: **number**, **retention time**, **height**, **area**, **response factor**, **raw concentration**, **name**
Standard component	Internal standard component for quantification procedure.
Concentration of std	Concentration of the internal standard component for relative concentration calculations. This value is stored in **This run** column of the concentration table.
Total % for normalization	A value to which the sum of concentrations is normalized. It is used for **Response normalization** and **Normalized concentrations** quantification methods. The default value is 100.
Printing order	Determines the order of the components in the peak table.
By peaks	Lists run results for all peaks detected. Unidentified peaks (corresponding to the universal component) are included, but missing components are not listed.
By components	Missing components are always included into the report, even those with concentration equal to zero. In the case of presence of universal

	component the summary for all unidentified peaks is presented as a single line.
<Customize>	Calls up a box with a list of columns that can be included into the report (see *Report elements*). It is available only if **Quantification method = Custom** has been selected.
Report all peaks	Checkbox that includes all peaks irrespective of the concentration of the substance. Otherwise the report generator excludes lines with zero concentration of the component. It is available only if **Quantification method = Custom** has been selected.
Groups	If this checkbox is checked, a separate peak table report is put out for every group specified in the component table.

Template options

For report output using a report template the following parameters can be modified:

Template	Selection of the report template file ***.rtt**. Several templates for different languages and applications are available.
Separator	Defines which character separates report columns in tables. A separator other than **Space** is useful when the report is printed to a file and this file is imported into a spreadsheet software.
Tab size	Sets tab stop value for the screen window. Important only when **Separator = Tabulation** has been selected or there are tab characters in the template file ***.rtt**.

File output options

If **File** has been selected for the report destination, the following parameters can be modified:

Directory	Directory for report output. For creation of a new directory, use the **<Browse>** button.
Name	File name to save report to. The report is saved in text form in the ANSI or ASCII format. So add an extension like ***.txt** to the file name. If the chromatogram plot checkbox is checked, the plot is saved in a separate file ***.wmf** in the WMF format under the same name.
Mode	The two options **Overwrite** (overwrite the file) or **Append** (append to existing file) are available.

Character set The two options **Windows** (ANSI) or **DOS** (ASCII) are available. These settings are essential for printing of non-English symbols (e.g. ö, ä, ü).

Custom program Path and name of the program to be started after report output. This option enables to transfer the report to a database, an electronic table or another application for further processing.

Report elements

If **Quantification method = Custom** has been selected, the peak table can be customized on the user's choice. After clicking the **<Customize>** button, the following columns can be included in the peak table.

number Peak number.

retention time Retention time of the component (in minutes, irrespective of the chosen retention units on the chromatogram graph axes). The total value in the column is equal to the chromatogram duration.

halfwidth Width of the peak at half height (in minutes).

height Height of the peak (in µS/cm). The total value in this column is the sum of heights for all identified peaks.

height% Normalization of peak heights for all peaks using the **NORM** value entered in the **Total % for normalization** field (default setting 100%):

$$H_i\% = NORM \cdot H_i / \Sigma H_i$$

area Area of the peak. Depends on the units on the X and Y axes of the chromatogram. The total value in this column is the sum of areas for all identified peaks (including universal component).

area% Normalization of peak areas for all peaks using the **NORM** value entered in the **Total % for normalization** field (default setting 100%):

$$A_i\% = NORM \cdot A_i / \Sigma A_i$$

capacity factor The capacity factor k'_i of the component is equal to the ratio of its corrected retention time $(t - t_0)$ to the void time of the system t_0:

$$k'_i = (t_i - t_0) / t_0$$

Total for this column is equal to the capacity factor of the last peak of the chromatogram.

resolution

Resolution **R** for two neighboring peaks is calculated as:

$$R = (t_{i+1} - t_i) / (w_{0.607i} + w_{0.607(i+1)})$$

where **i** and **i+1** indexes refer to the neighboring peaks, and $w_{0.607}$ stands for the peak width at 60.7 % of the peak height.

effectivity, TP

Effectivity for the peak in number of theoretical plates. The number of theoretical plates N_i per column for a chosen peak is calculated for a chromatographic peak by one of two formulas:

$$N_i = 2\ PI\ (t_i \cdot\ H_i / A_i)^2,$$

where **PI** = 3.1415926..., t_i = retention time, H_i = height, A_i = area of the peak. The more commonly used formula is:

$$N_i = 5.54\ (t_i / w_i)^2,$$

where w_i is the width on the half-height of the peak. The first formula offers better estimates for fused or unresolved peaks, because the half-width errors for those peaks are much greater than height or area errors.

Total for this column includes average value for the peaks listed.

effectivity, TP/m

Effectivity for the peak in number of theoretical plates per meter. The number of theoretical plates per meter **N'** for the given component is calculated as:

$$N' = N_i \cdot\ 1000 / L,$$

where **L** is length of the column in mm and N_i is effectivity of the column for i-th component.

Total for this column includes average value for the peaks listed.

reduced TP height, HETP/dp

The height of theoretical plate divided by particle size, called also reduced height, is calculated by formula:

$$H_i = 1000 \cdot\ L / (N_i\ dp).$$

where **L** is length of the column in mm, **dp** is particle diameter in µm.

asymmetry

Peak asymmetry A_s is calculated at $^1/_{10}$ of the peak height as a ratio of width after the top of the peak w_2 to the width before the top w_1.

$$A_s = w_2 / w_1$$

response factor

Coefficient k_1 of the calibration curve.

raw concentration

Absolute concentrations (raw quantity) of the components, calculated as

$$C_i = W_i(R_i) / V'$$

Total value for the column is the sum of concentrations for all components.

concentration%

Normalization of concentrations for all peaks using the **NORM** value entered in the **Total % for normalization** field (default setting 100%):

$$C_i\% = NORM \cdot W_i(R_i) / \sum W_i(R_i)$$

Total value for the column equals **NORM** for the main table, and the sum of concentrations in the group for the group table.

rel. concentration

Relative concentration of the component relative to the standard component, assumes concentration of one of the components to be known in advance. The concentration of the component is calculated by the formula:

$$C'_i = W_i(R_i) / V' = W_i(R_i) \cdot C_s / W_s(R_s),$$

where $V' = W_s(R_s) / C_s$ is the effective (reduced) volume of injected sample. The standard component concentration C_s is entered by the user.

Total value for relative concentration column does not include the concentration of the standard component.

rel. concentration%

Relative concentration percent differs from **concentration%** by exclusion of standard component(s) from summation, so that sum of all concentrations (excluding standard) equals **NORM**.

Total value for the column equals **NORM** value for main peak table, and the sum of concentrations in the group for Group table.

index

Linear or logarithmic retention index for identified components.

Total value for the column is a weighted index average with absolute concentration as weight.

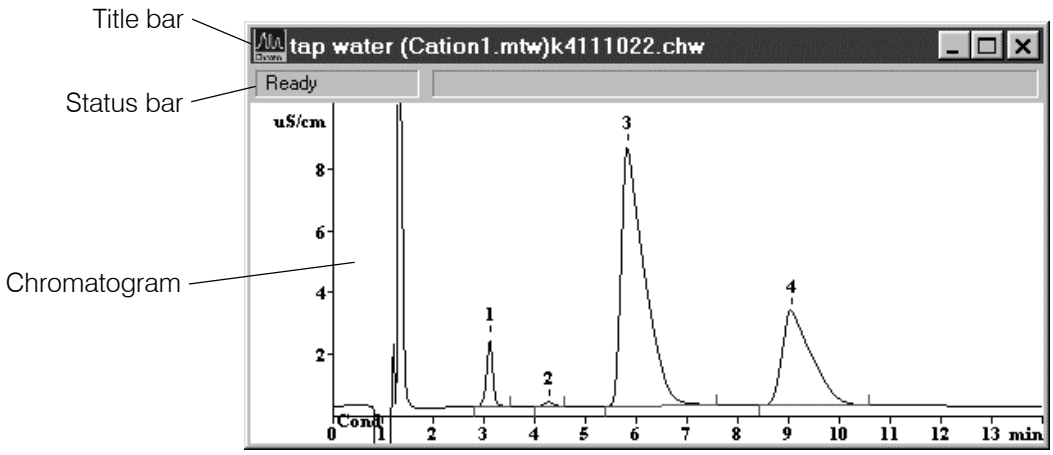
$$I = \sum (I_i C_i) / \sum C_i.$$

type		The types of components are designated by a one-letter code:
	R	Reference component (used for peak identification).
	S	Standard component.
	C	Calibration standard in the case it is different from the quantification standard.
	?	Some points of corresponding peak are out of ADC or detector range – suspicious result.
	!	Component concentration is outside of minimum (**min C**) and maximum limits (**max C**), set in the component table.
	p	Special component (it has one of the special flags checked on in the **COMPONENT** window).
	N	The component response is outside of calibrated region.
		In the case of peaks additional letters precede the component type information, indicating, how peaks are separated from other peaks, for example:
	BD_	Peak that starts on the baseline (**B**) and ends on the drop line (**D**) that separates it from another adjacent peak.
	BBR	Special case of a rider (**R**) peak that is tangentially separated from the main one. A main peak will have a third letter **H** (horse) in this case.
		The complete component type may look like: **BBD : !R**.
group		Number of the group for the component.
spectral ratio		*Not used for 792 Basic IC.*
name		Name of the component.
file name		File name of chromatogram. This column is very useful for processing of exported data.
ident		Title (identifier) for the chromatogram. This column is useful for the processing of exported data.

4.5 Chromatograms

4.5.1 Chromatogram window

The **CHROMATOGRAM** window is used to show a running or recorded chromatogram.



The **title bar** of the chromatogram window contains buttons for minimizing, maximizing and closing the window. The window name consists of the elements "**Ident (method name) chromatogram name**". A star (*****) at the end of the name indicates that the chromatogram has been changed since the last saving.

The **status bar** contains two fields. The first field indicates the current measurement status, one of the listed below:

Ready	Chromatogram is ready to start.
Waiting	Chromatogram is waiting for the first measuring points.
Measure	Chromatogram is being measured.
Measure(Baseline)	Recording of baseline.
Finished	Measurement finished, but the chromatogram is not processed.
Processing	Chromatogram is being processed after finishing.
Failure	Failure, e.g. unexpected pump stop, etc.
COM error	Error on COM port interface.

During active data acquisition the elapsed time, the duration of the chromatogram or program and the current X and Y values are shown in the second field of the status bar. If the peak editor is switched on then the position of the cursor will be shown.

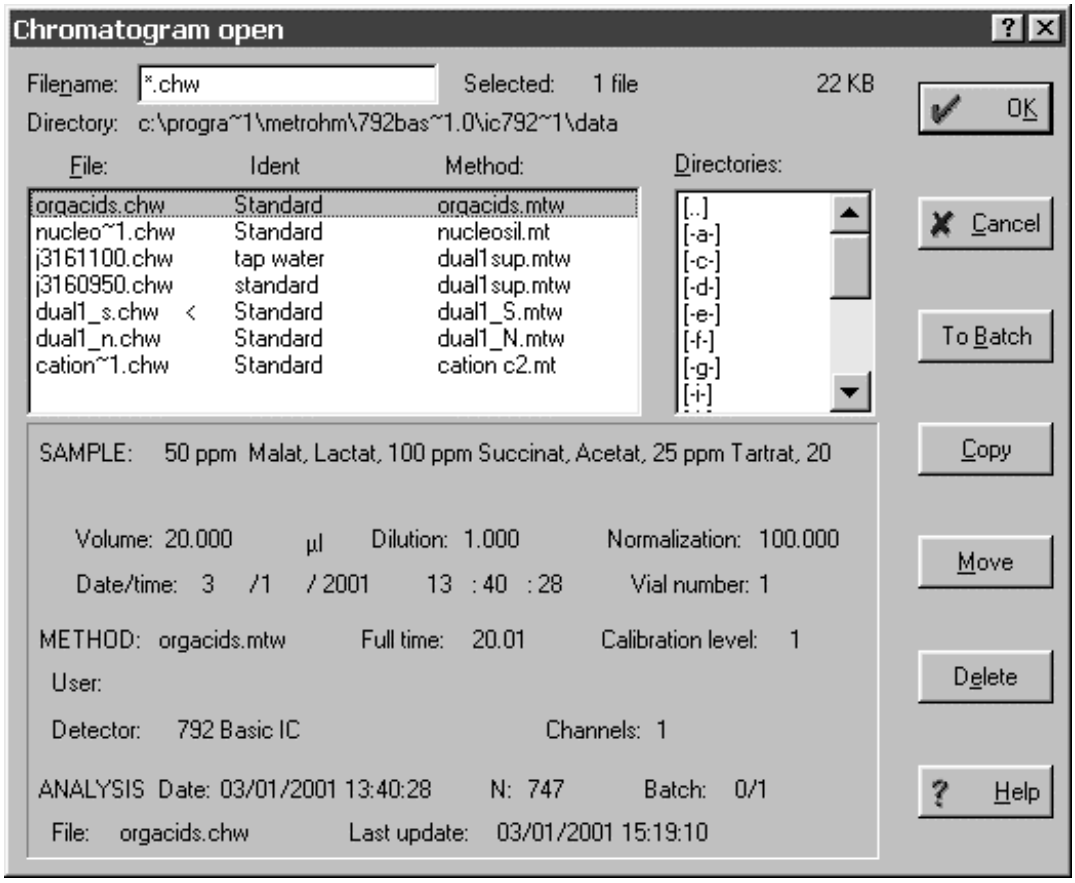
A chromatogram can be scaled with the help of keyboard or mouse functions or through the **Chromatogram axes** window opened with **792 BASIC IC** / **View** / **Appearance** / **Chromatogram axes**. Some of the window control functions are collected in the **Window** menu.

4.5.2 Chromatogram file handling

Open chromatogram

792 BASIC IC / File / Open / Chromatogram

Load an existing chromatogram file (***.chw**) from the **Data** directory and open the chromatogram window. The following window appears:



Filename	Filename (common wildcards as ***** and **?** are possible).
Selected	Number of selected chromatograms and their total size.
Directory	Path name of the working directory.
File window	Box with the list of files residing in the working directory sorted by time (the last recorded chromatogram is at the top of the list). As additional short information on the chromatogram the two parameters **Ident** and **Method** are also displayed. Files in this box can be selected by moving the selection bar to the desired chromatogram and pressing the [Space] key or by a single mouse click.
	It is possible to select several chromatograms at once. Press [Shift] and the left mouse button to select all chromatograms up to last item clicked, press [Ctrl] and the left mouse button

	to add a single chromatogram to the selection already made. All selected items are painted.
Directories	Box with the list of directories. Allows to change the working directory defined in the method, if necessary.
Chromatogram description	A set of fields with the description of the current chromatogram. Selected fields from the passport are listed here.
<OK>	Load all selected chromatogram files (***.chw**) and open each in its own window.
<Cancel>	Close this window without any action.
<To Batch>	Add selected chromatograms to the specified batch reprocessing file.
<Copy>	Copy selected chromatograms to the specified location.
<Move>	Move selected chromatograms to the specified location.
<Delete>	Delete selected chromatograms and move them to the Windows wastebasket.

Save chromatogram

792 BASIC IC / File / Save / Chromatogram

Save the selected chromatogram in a chromatogram file (***.chw**) in the working directory. If this chromatogram has been already stored in this directory, the message **File ... exists. Overwrite?** appears. If it is preferable to overwrite the previous copy (for example, after the reprocessing), press the **<OK>** button. Pressing **<No>** saves the chromatogram into the new file (a new copy of the chromatogram is created).

Close chromatogram

792 BASIC IC / File / Close

Close the selected chromatogram window. If the data were not saved or the method was modified, a warning appears. Usually it is more convenient to close the window by clicking the  button at the top corner area of the window.

Delete chromatogram

792 BASIC IC / File / Delete

Delete the selected chromatogram window. A warning will be generated by the software in any case.

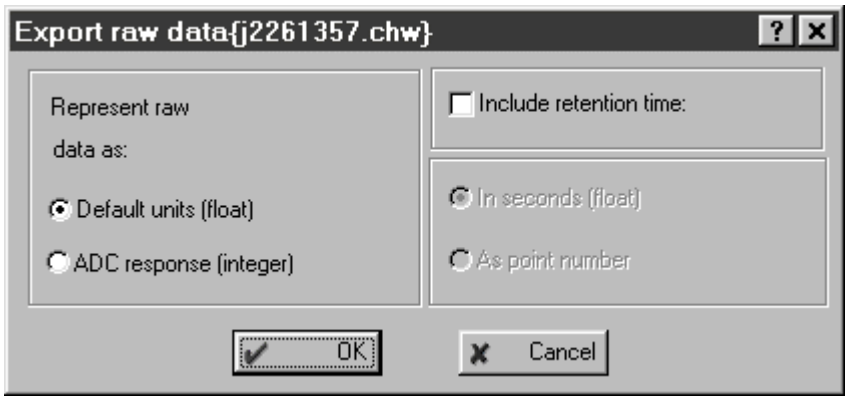
Export chromatogram

792 BASIC IC / File / Export / AIA file

Export the selected chromatogram in the AIA format (Analytical Instrument Association) as CDF file (***.cdf**).

792 BASIC IC / File / Export / Raw data to txt

Export chromatographic raw data into an ASCII text file (***.txt**). The following window appears:



Represent raw data as Output of raw data:

Default units (float) Y values are exported in default units for the channel (µS/cm).

ADC response (integer) Y values are exported in bits.

Include retention time

In seconds (float) X values are exported in seconds.

As point number X values are exported as point number.

4.5.3 Graphical representation

Appearance

792 BASIC IC / View / Appearance

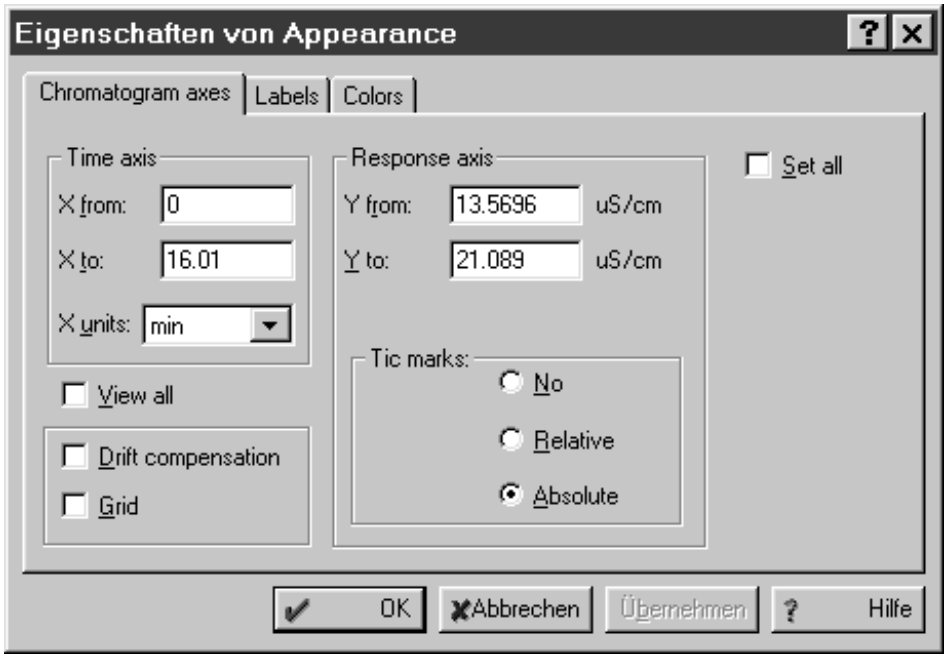
This menu item opens the **Appearance** window. It determines the appearance of the chromatogram and consists of four tabs:

Chromatogram axes	Scaling of chromatogram axes.
Labels	Settings for peak labels and baseline drawing.
Select channel	Select channels to be displayed (only available for multi-channel chromatograms).
Colors	Color settings for chromatogram elements.

The appearance settings for a chromatogram are not saved automatically on closing the chromatogram. In order to have the same appearance after reopening the chromatogram, it must be saved explicitly after modification of these parameters with **792 BASIC IC** / **File** / **Save** / **Chromatogram**.

Chromatogram axes

Tab **Chromatogram axes** of the **Appearance** window with parameters for scaling of the chromatogram axes.



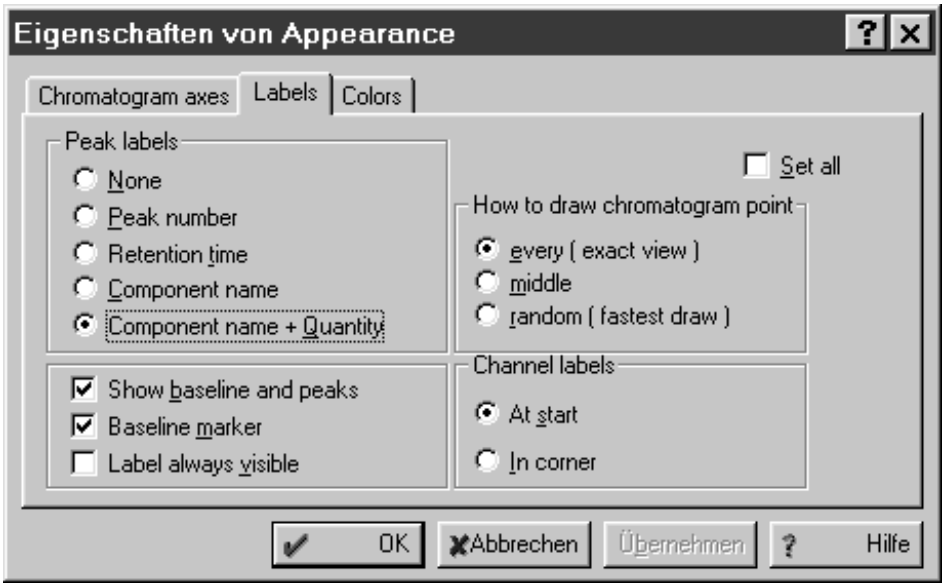
Time axis

X from	Beginning of the window on X axis.
X to	End of the window on X axis.
X units	Selection of unit (**Retention unit**) for X axis.

Response axis	
Y from	Beginning of the window on Y axis.
Y to	End of the window on Y axis.
Tic marks	Plot axes labels and tic marks on Y axis with **no**, **relative** or **absolute** scaling.
View all	Set scales on X and Y axes so that the whole chromatogram is visible.
Drift compensation	Turns the chromatogram screen image so that the last and first points of the chromatogram are on the same level. This option is useful for gradient chromatograms. Drift compensation has no effect while a chromatogram is running.
Grid	Plot dotted grid lines in the selected chromatogram window.
Set all	Set scales on X and Y axes of all opened chromatograms automatically to the settings in the selected chromatogram window.

Labels

Tab **Labels** of the **Appearance** window with parameters for peak labeling and baseline drawing.



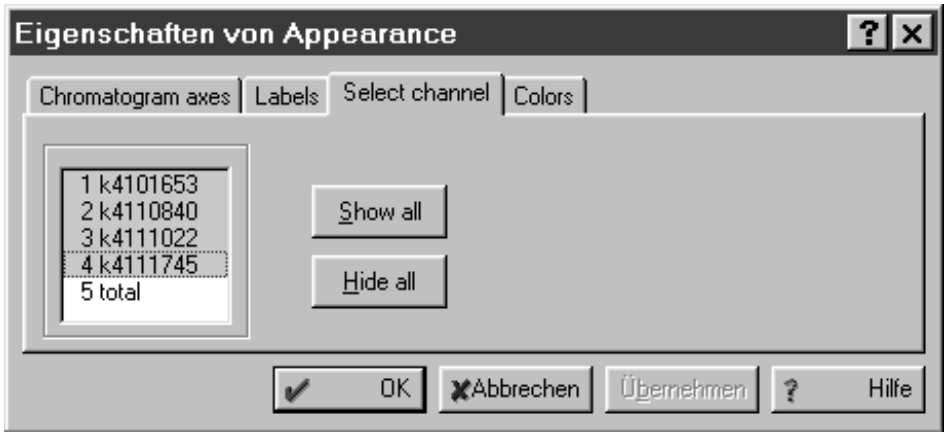
Peak labels

None	No peak labels.
Peak number	Peak number.
Retention time	Retention time.
Component name	Name of the component.
Component name + Quantity	Name and quantity of the component.

Show baseline and peaks	Baselines are shown.
Baseline marker	Start and end of baselines are marked.
Label always visible	Label is shown always with zooming.
How to draw chromatogram point	
every	Normal chromatogram drawing with all raw data points.
middle	Chromatogram drawing with additional smoothing of raw data points.
random	Fast chromatogram draw for slow PCs.
Channel labels	Label for data acquisition channel.
At start	Channel label is shown at the start of the chromatogram.
In corner	Channel label is shown in the upper right corner of the chromatogram.
Set all	Set peak labeling of all opened chromatograms automatically to the settings in the selected chromatogram window.

Select channel

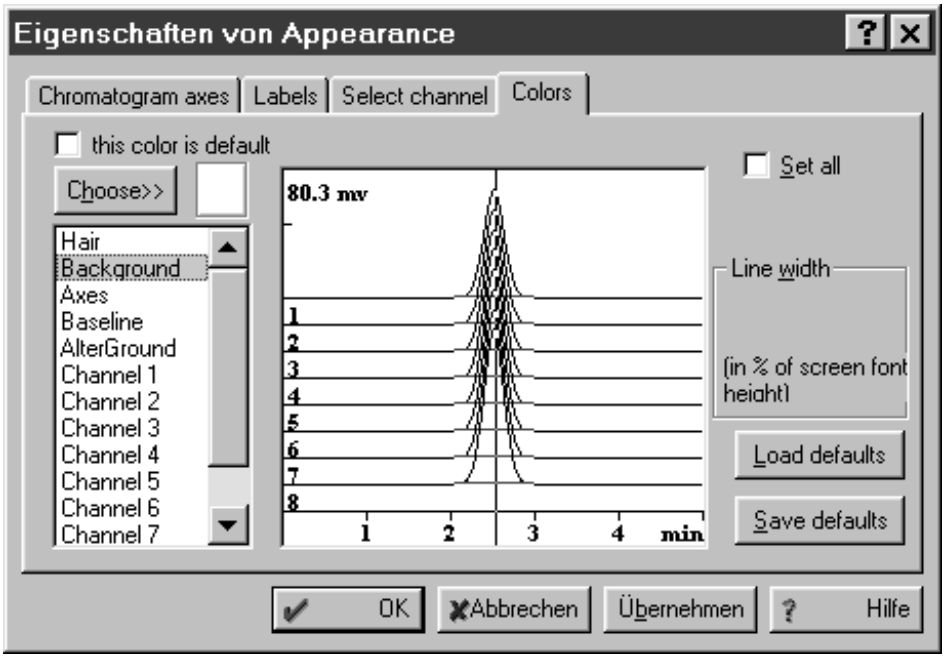
Tab **Select channel** of the **Appearance** window for selection of channels for multi-channel chromatograms.



Selection window	The selection window shows all chromatograms of the batch reprocessing queue which can be selected for display. If **total** is selected, all chromatograms are added and the resulting addition curve is shown.
<Show all>	Select all chromatograms in the selection window.
<Hide all>	Deselect all chromatograms in the selection window.

Colors

Tab **Colors** of the **Appearance** window with color settings parameters for chromatograms.



this color is default	Reset the selected element to the default color.
<Choose>	Choose a new color for the selected element. An example of the chosen color is shown beside the button.
Hair	Cursor's color.
Background	Background color.
Axes	Axes and axes labels color.
Baseline	Baseline color.
AlterGround	Alternative background color for **Measure baseline** option.
Channel 1...8	Color of the selected channel. Each channel can be of a unique color.
Line width	Line width for the selected element (**Axes** or **Channel 1...8**) in % of selected plot font height. Range: **0** ... **232**
Set all	Set colors of all opened chromatograms automatically to the settings in the selected chromatogram window.
<Load defaults>	Set colors in the selected chromatogram window to the set defaults colors.
<Save defaults>	Save color settings in the selected chromatogram window as default colors.

Other graphical functions

792 BASIC IC / View / X full scale

By selecting this menu item or pressing [Ctrl] + [Home] the X axis is scaled so that the chromatogram perfectly fits the window horizontally.

792 BASIC IC / View / Y full scale

By selecting this menu item or pressing [Ctrl] + [End] the Y axis is scaled so that the chromatogram perfectly fits the window vertically.

792 BASIC IC / View / View all

By selecting this menu item or pressing [Alt] + [V] the X and Y axes are scaled so that the chromatogram perfectly fits the window horizontally and vertically.

792 BASIC IC / View / Recorder autoscale

This option allows to look at the chromatogram so that the last point is always visible on the screen while data are acquired.

If the **Recorder autoscale** option is switched on, the following autoscaling rules apply:

- If the last acquired point comes out of the window down, autozero is performed.
- If the last point is too high, the recorder scale shrinks twice until the point comes to screen.
- If the last point comes outside of the plotting area to the right, the window is shifted half-screen right.

If the **Recorder autoscale** option is switched off, the window scale does not change automatically during data acquisition.

4.5.4 Peak editor

Switching on/off the peak editor

792 BASIC IC / Process / Peak editor

The peak editor mode is used for subsequent manual correction of the automatic integration for chromatogram peaks (see *section 4.4.4*). It can be used to select the most important points for the peak evaluation (start, end and top of peak, valley between peaks) and move them to the required position.

If the peak editor mode is enabled, the vertical bar cursor appears in the chromatogram window. At the same time, the **Peak** menu appears in the menu bar and the peak editor icons appear in the icon bar of the main window.

The peak editor mode is switched on or off by clicking on  or by pressing [Alt] + [C]. It is also possible to click the right mouse button somewhere in the chromatogram window and to select the **Peak editor** item.

You cannot edit the peak pattern while the component table is active and vice versa, when the peak editor mode is switched on the component table option is disabled.

Peak editor functions

The functions of the peak editor can be triggered with the corresponding menu items of the **Peak** menu, by the peak editor symbols in the symbol bar or with key combinations.

792 BASIC IC / Peak / Undo

Undo the last action.

792 BASIC IC / Peak / Insert peak [Insert]

Add a peak to the chromatogram.

792 BASIC IC / Peak / Delete peak [Delete]

Delete selected peak.

792 BASIC IC / Peak / Select nearest point

Move the cursor to the nearest start, top, end, or valley point and select the peak.

792 BASIC IC / Peak / Select start point

Move the cursor to the beginning of the nearest peak and select the peak.

792 BASIC IC / Peak / Select top point

Move the cursor to the top of the nearest peak and select the peak.

792 BASIC IC / Peak / Select end point

Move the cursor to the end of the nearest peak and select the peak.

792 BASIC IC / Peak / Select valley point

Move the cursor to the valley of the two nearest peaks.

792 BASIC IC / Peak / Unselect peak

Delete the selection.

792 BASIC IC / Peak / Move selected point [–]

Move a selected point (start, top, end, valley) to the cursor position.

792 BASIC IC / Peak / Merge peaks [+]

Merge two neighboring peaks into a single peak.

792 BASIC IC / Peak / Fuse peaks [*]

Fuse the beginning of the previous and the end of the next peak at the cursor position.

792 BASIC IC / Peak / Split peaks [/]

Split a single peak into two peaks at the cursor position.

792 BASIC IC / Peak / Delete all left

Delete all peaks to the left of the selected point.

792 BASIC IC / Peak / Delete all right

Delete all peaks to the right of the selected point.

Moving the cursor

The cursor can be dragged by the **mouse** when the right mouse button is pressed. Releasing the button will leave the cursor at the new position. The position of the cursor is displayed in the status bar of the chromatogram window.

The cursor can also be moved using the **keyboard**:

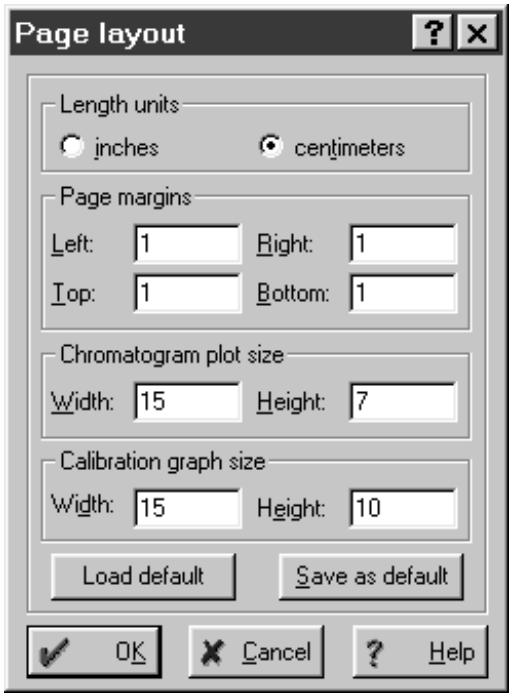
[←]	Move cursor left.
[Shift] + [←]	Move cursor left quickly.
[→]	Move cursor right.
[Shift] + [→]	Move cursor right quickly.
[Home]	Move cursor to the beginning of the window.
[End]	Move cursor to the end of window.

4.5.5 Printing

Page layout for printing

792 BASIC IC / File / Page layout

The selection of this menu item or clicking on **<Page...>** in the **Report options** window opens the **Page layout** window for page layout parameters.



Length units	Selection of length units.
inches	Inches.
centimeters	Centimeters.
Page margins	Selection of page margins.
Left	Left margin.
Right	Right margin.
Top	Top margin.
Bottom	Bottom margin.
Chromatogram plot size	Selection of plot area for chromatograms.
Width	Width of plot area.
Height	Height of plot area.
Calibration graph size	Selection of plot area for calibration curves.
Width	Width of plot area.
Height	Height of plot area.
<Load default>	Load default values for page layout parameters.
<Save as default>	Save set page layout parameters as default values.

Printer settings

792 BASIC IC / File / Printer setup

By selecting this menu item the **PRINT SETUP** window is opened where printer, paper size and format can be defined.

Print preview

792 BASIC IC / File / Preview

By selecting this menu item the **Preview** window appears on the screen where the report is shown in the appearance formatted for the desired printer as defined in the **Report options** window.

Printing

792 BASIC IC / File / Print

By selecting this menu item the **Printing** window is opened where printer, printing range and number of copies can be defined. All settings defined in the **Report options** window will be active except the destination of the printout.

In order for the chromatogram to be printed, the option **Chromatogram plot** must be switched on in the **Report options** window under **Items to report**.

792 BASIC IC / Process / Make report

Selection of this menu item opens the **Report options** window for report output to screen, printer or file (details see *section 4.4.6*).

4.5.6 Miscellaneous functions

Reintegration

792 BASIC IC / Process / Reintegrate

This menu item opens the **Integration parameters** window where the reintegration of the chromatogram can be started (details see *section 4.4.4*).

Recalibration

792 BASIC IC / Process / Calibrate

This menu item opens the **Recalibration** window for entry of the calibration level and recalibration of the chromatogram using this level (details see *section 4.4.5*).

Subtraction of a chromatogram

792 BASIC IC / Process / More / Subtract

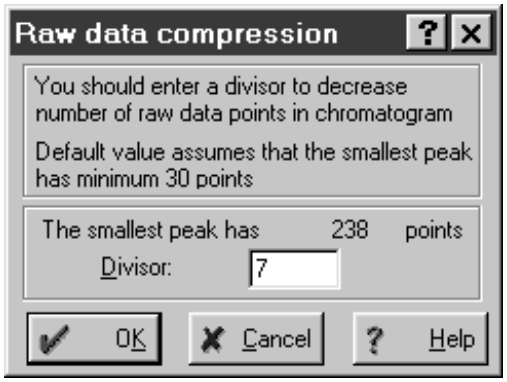
This menu item opens the **Subtract chromatogram** window allowing the subtraction of any opened chromatogram from the active, selected chromatogram.

Select the chromatogram that should be subtracted, click on **<Subtract>** and then on **792 BASIC IC / View / View all**. The result is shown in the active chromatogram window, which is considered as a new chromatogram and will be stored under a new name to avoid overwriting of old data.

Data compression

792 BASIC IC / Process / More / Compress

Selection of this menu item opens the **Raw data compression** window for compression of the raw data of the active chromatogram by summing up several neighboring points.



Divisor Coefficient of compression (the number of data points is reduced by this value). The default value of the compression coefficient is calculated so that the width at half-height of the narrowest peak will be digitized by at least 30 points. If the user enters a coefficient of compression that exceeds the value offered by the software, integration precision may decrease.

Invert chromatogram

792 BASIC IC / Process / More / Invert!

This menu item inverts the response curves for all channels of the chromatogram so that negative peaks become positive and vice versa (useful for chromatograms with wrong input polarity).

4.6 Batch reprocessing

Reprocessing is understood to be the subsequent reprocessing of a series of chromatograms which have been loaded in a **queue (Batch reprocessing queue)**. For reprocessing according to a selected method the settings for calibration, integration, passport, appearance and report can be altered at will.

A batch reprocessing queue is stored in a batch reprocessing queue file ***.bar** in the **Data** directory.

4.6.1 Batch reprocessing queue file handling

Open batch reprocessing queue

792 BASIC IC / File / Open / Batch reprocessing

Load an existing batch reprocessing file (***.bar**) from the **Data** directory and open the **Reprocess** window.

792 BASIC IC / File / Open / Last batch

Load the last opened batch reprocessing file (***.bar**) from the **Data** directory and open the **Reprocess** window.

Create new batch reprocessing queue

792 BASIC IC / File / Open / Chromatogram

For creation of a new batch reprocessing queue, open the **Chromatogram open** window. Select the desired chromatograms (***.chw**) and click the **<To Batch>** button. Enter the name of the new batch reprocessing file and press **<OK>**. The selected chromatograms are then added to this batch reprocessing queue.

If the reprocessing includes reintegration and/or recalibration, only chromatograms recorded with the same method should be loaded into the batch reprocessing queue.

Save batch reprocessing queue

QUEUE EDITOR / File / Save

Save the batch reprocessing queue in a batch reprocessing queue file (***.bar**) in the working directory. The batch reprocessing queue editor window remains open.

QUEUE EDITOR / File / Save & exit

Save the batch reprocessing queue in a batch reprocessing queue file (***.bar**) in the working directory and close the batch reprocessing editor window.

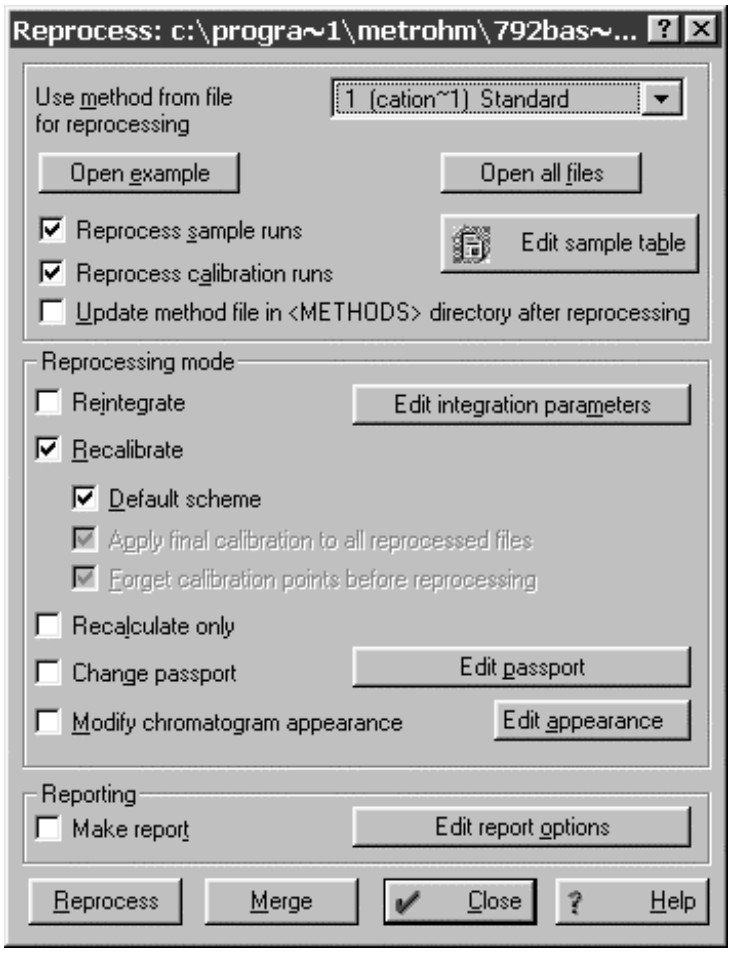
4.6.2 Perform batch reprocessing

Reprocess options window

792 BASIC IC / File / Open / Batch reprocessing

792 BASIC IC / File / Open / Last batch

These two menu items are used to open the **Reprocess** window, in which the various options for reprocessing are set and can then be triggered.



Use method from file for reprocessing

Selection of the desired chromatogram file whose method should be used for reprocessing.

If the reprocessing includes reintegration and/or recalibration, only chromatograms recorded with the same method should be loaded into the batch reprocessing queue.

<Open example>	Open the chromatogram selected above in the **Use method...** field.
<Open all files>	Open all chromatograms of the batch reprocessing queue.

<Edit sample table>	Open the batch reprocessing editor program for editing the batch reprocessing table (see *section 4.7.3*).
Reprocess sample runs	Reprocess all sample chromatograms (**calibration level = 0**).
Reprocess calibration runs	Reprocess all calibration chromatograms (**calibration level > 0**).
Update method file in <METHODS> directory after reprocessing	Save the method file ***.mtw** after reprocessing if the method is changed.
Reintegrate	Reintegrate chromatograms according to the current settings of the integration parameters and integration events.
<Edit integration parameters>	Open the **Integration parameters** window for modification of integration parameters and integration events.
Recalibrate	Reprocess all calibration chromatograms (if **Reprocess calibration runs** is switched on) and apply new calibration to all sample chromatograms (if **Reprocess sample runs** is switched on) by updating the concentration table.
Default scheme	Default setting for recalibration reprocessing. The two options **Apply final calibration...** and **Forget calibration points...** are switched on. A new calibration is performed with the calibration runs and the resulting new calibration parameters (component table, concentration table and calibration curve) are applied to all sample runs.
Apply final calibration to all reprocessed files	Apply the updated calibration to all calibration and sample runs. If this option is switched off, the calibration stored in the first chromatogram is used for all other chromatograms.
Forget calibration points before reprocessing	Forget old calibration points of the calibration curve and perform a new calibration using all calibration runs of the batch reprocessing queue. In this case, each calibration chromatogram adds a new point to the calibration curve. If this option is switched off, the calibration curve stored in the first chromatogram remains active. Each further calibration chromatogram in the batch reprocessing queue adds a new point to this calibration curve.

Recalculate only

Enable recalculation of chromatograms with values for **Volume**, **Dilution**, **Amount** and **Internal standard amount** entered in the batch reprocessing table.

The recalculation is done automatically if the **Reintegrate** *and/or* **Recalculate** *options are enabled. If the* **Recalculate only** *option is enabled, the* **Reintegrate** *and* **Recalculate** *options are disabled automatically.*

Change passport

If this option is enabled, those parameters of the passport which have been changed after clicking the **<Edit passport>** button are applied to all chromatograms.

<Edit passport>

Open the **Passport** window for modification of the passport parameters.

Only some of the passport parameters can be modified. The passport parameters **Ident**, **Sample Info 1** *and* **Sample Info 2** *entered in the batch reprocessing table are overwritten if these values are modified in the* **Passport** *window.*

Modify chromatogram appearance

If this option is enabled, the chromatogram **Appearance** parameters which have been changed after clicking the **<Edit appearance>** button are applied to all chromatograms.

<Edit appearance>

Open the **Appearance** window for modification of the settings for chromatogram axes, labels and colors.

Make report

Print report for all chromatograms using the current report settings of the selected chromatogram in the **Use method...** field.

<Edit report options>

Open the **Report options** window for modification of the report settings.

<Reprocess>

Start reprocessing.

<Merge>

Combine all chromatograms of the batch reprocessing queue into a single multi-channel chromatogram.

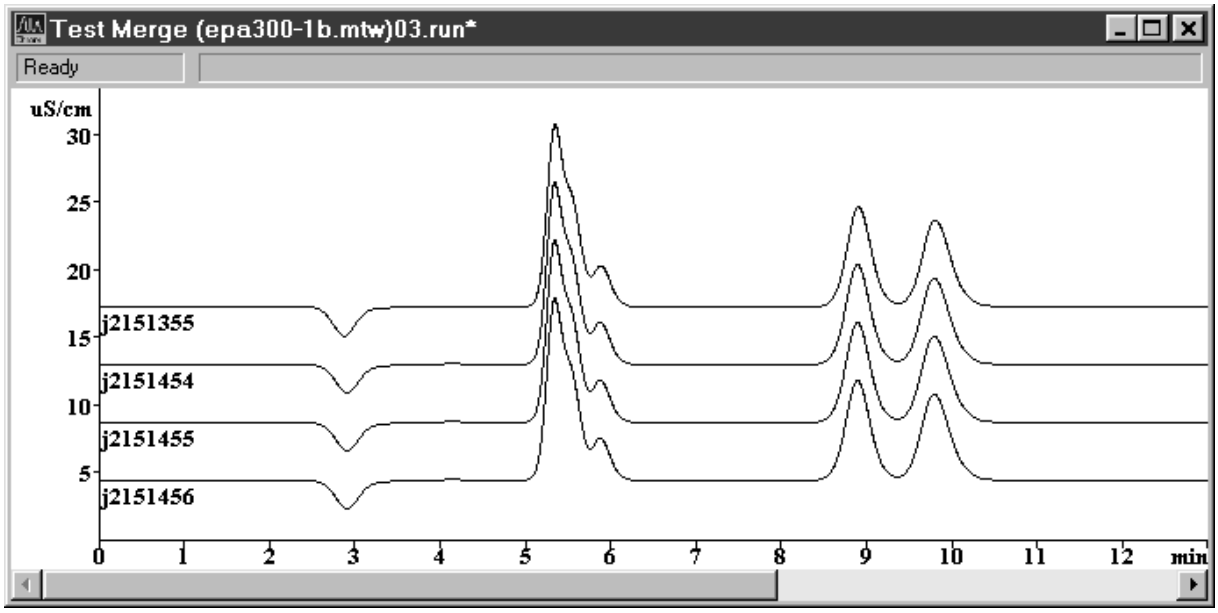
<Close>

Close the **Reprocess** window.

Merge chromatograms

REPROCESS / <Merge>

Combine all chromatograms of the batch reprocessing queue into a single multi-channel chromatogram.



The chromatograms are displayed in the same order as in the batch reprocessing table slightly displaced one upon the other. The distance between the curves can be increased by pressing [Shift] + [↑] and decreased by pressing [Shift] + [↓].

The chromatogram axes, labels and colors can be set in the **Appearance** window.

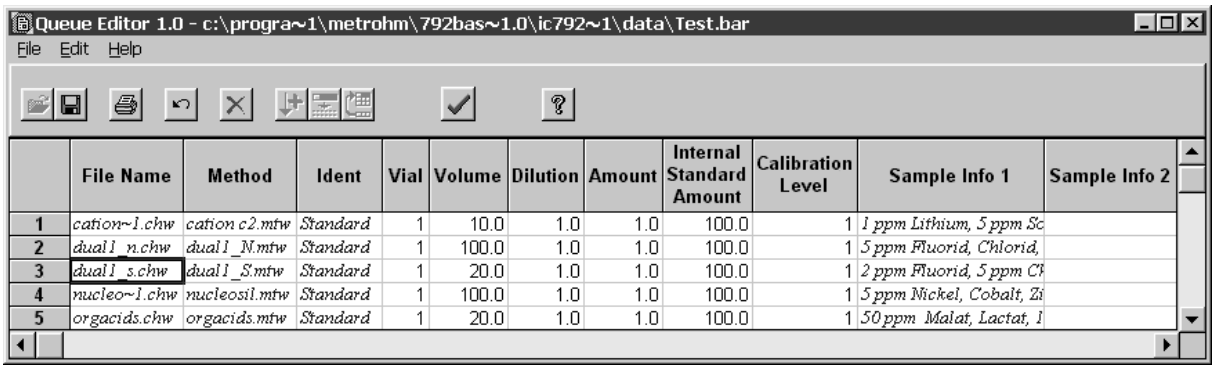
The multi-channel chromatogram can be saved with **File** / **Save** / **Chromatogram**.

4.6.3 Batch reprocessing queue editor

Open batch reprocessing queue editor window

REPROCESS / <Edit sample table>

This menu item opens the batch reprocessing editor program for editing the batch reprocessing table.



	File Name	Method	Ident	Vial	Volume	Dilution	Amount	Internal Standard Amount	Calibration Level	Sample Info 1	Sample Info 2
1	cation~1.chw	cation c2.mtw	Standard	1	10.0	1.0	1.0	100.0	1	1 ppm Lithium, 5 ppm Sc	
2	dual1_n.chw	dual1_N.mtw	Standard	1	100.0	1.0	1.0	100.0	1	5 ppm Fluorid, Chlorid,	
3	dual1_s.chw	dual1_S.mtw	Standard	1	20.0	1.0	1.0	100.0	1	2 ppm Fluorid, 5 ppm Cl	
4	nucleo~1.chw	nucleosil.mtw	Standard	1	100.0	1.0	1.0	100.0	1	5 ppm Nickel, Cobalt, Zi	
5	orgacids.chw	orgacids.mtw	Standard	1	20.0	1.0	1.0	100.0	1	50 ppm Malat, Lactat, I	

No	Row number.
File name	Name of the chromatogram file (read-only).
Method	Name of the method file ***.mtw** used for recording the chromatogram (read-only).
Ident	User defined identifier for chromatogram. Will be placed into appropriate passport field when starting the chromatogram.
Vial	Autosampler vial position to take sample from. Will be placed into appropriate passport field.
Volume	Injected volume of sample in µL. Will be placed into appropriate passport field.
Dilution	Sample dilution prior to injection. Will be placed into appropriate passport field.
Amount	Sample amount. If this value is different for the calibration run (**c**) and the sample run (**s**), the component concentrations of the sample are calculated as follows: $C_s = C_c \cdot Amount_s / Amount_c$ Will be placed into appropriate passport field.
Internal standard amount	Concentration of the internal standard component for relative concentration calculations. Will be placed into appropriate passport field.
Calibration level	Calibration level (see *section 4.4.5*) for the sample: Level **0** stays for normal analysis, levels **1** and greater for calibration runs. Correct filling of this column enables to calculate calibration coefficients automatically.

Sample Info 1	First sample description. Will be placed into appropriate passport field.
Sample Info 2	Second sample description. Will be placed into appropriate passport field.

Batch reprocessing queue editor functions

The functions in the editor window for the batch reprocessing queues can be triggered with the corresponding menu items of the **Edit** menu or with the corresponding symbols in the symbol bar.

QUEUE EDITOR / Edit / Undo

Undo the last modification of the batch reprocessing queue.

QUEUE EDITOR / Edit / Delete row(s)

Delete the selected rows from the batch reprocessing queue.

QUEUE EDITOR / Edit / Increment

Fill selected column fields with values automatically incremented by 1. The last character of the first selected field must be a number. This function is available for the fields **Ident**, **Vial**, **Calibration level**, **Sample Info 1** and **Sample Info 2**.

QUEUE EDITOR / Edit / Propagate

Fill selected column fields with the same value as the first field.

QUEUE EDITOR / Edit / Rotate rows

Rotate selected rows by one position (the bottom line is moved to the first position; all other lines are moved down by 1 position).

Print batch reprocessing queue

QUEUE EDITOR / File / Print

Print the batch reprocessing table in landscape format.

Close batch reprocessing queue editor

QUEUE EDITOR / File / Save & Exit

Save the modified batch reprocessing queue and close the **QUEUE EDITOR** window.

QUEUE EDITOR / File / Exit

Close the batch reprocessing **QUEUE EDITOR** window without saving the modified batch reprocessing table.

5 Notes – Maintenance – Faults

5.1 Practical notes on ion chromatography

5.1.1 Separating columns

Separation efficiency

The attainable quality of analyses with the 792 Basic IC depends to a large extent on the separation efficiency of the column used. When purchasing an IC column you should ensure that the separation efficiency suffices for the analysis problems at hand. Ascertain the **characteristic data of the IC column** on the standard chromatogram enclosed with the column such as capacity factors, selectivity, plate number and resolution and check these data with your own measurements. If any difficulties arise, you should always first check the quality of the column by recording a **standard chromatogram**.

You will find additional general tips on handling IC separating columns in the **8.732.2003 Metrohm Monograph "Ion chromatography"** and in the **8.792.2003 Metrohm Monograph "Practical ion chromatography"**, as well as detailed information on the separating columns available from Metrohm (see *section 6.3.2*) in the leaflets supplied and in the **8.732.2013 "IC Application Notes"** folder.

Protection

To protect the column against foreign particles which could have an adverse influence on the separation efficiency, we advise you to subject both the eluents and all samples to **microfiltration** (0.45 µm filter) and to siphon the eluent through the **6.2821.090 Aspirating filter**.

To avoid contamination by abrasive particles arising from piston seals of the high-pressure pump, it is advantageous to install an **in-line filter** between the pump and the injection valve. In the 792 Basic IC a **6.2821.100 Filter unit PEEK** is already mounted for this purpose (see *section 2.6.2*).

The use of readily interchangeable **precolumns** serves to protect the actual separating columns and increase their service life appreciably. The precolumns available from Metrohm (see *section 6.3.2*) are either actual precolumns or so-called precolumn cartridges that are used together with the 6.2821.050 Twin cartridge holder or the 6.2828.110 Precolumn cartridge holder (see *section 2.7*).

Storage

Always store the separating columns closed when not in use and filled in accordance with the manufacturer's specifications.

Dead volume

Dead volume at the end of a column can be the cause of extreme peak broadening or splitting (appearance of double peaks). Filling the column with glass beads (∅ ≤ 100 µm) frequently improves the separation efficiency.

Regeneration

If the separation properties of the column have deteriorated, it can be regenerated in accordance with the column manufacturer's specifications. With the separating columns available from Metrohm (see *section 6.3.2*), the instructions for regeneration can be found on the leaflet enclosed with every column.

In the case of separating columns with carrier material based on silica, ***only solutions with pH 2…7*** *may be used for regeneration, otherwise the columns could be damaged.*

5.1.2 High-pressure pump

Pulsation dampener

The use of the optional **6.2620.150 Pulsation dampener MF** is recommended to protect sensitive separating columns (e.g. methacrylate based columns). It is used to reduce interfering pulsation in highly sensitive measurements and also protects the column material against pressure shocks caused by the injection. Its installation is described in *section 2.6.2*.

Maintenance

To protect the pump against foreign particles, we advise you to subject the eluent to **microfiltration** (0.45 µm filter) and siphon the eluent through the **6.2821.090 Aspirating filter**.

In many cases, an unstable baseline (pulsation, flow fluctuations) can be traced to contaminated valves or faulty, leaky piston seals.

Contaminated valves are cleaned by rinsing with water, RBS solution or acetone (see *section 5.2.6*). When the cleaned valves are reinstalled, you must ensure that the flow direction is correct.

The **replacement of piston seals** is described in *section 5.2.6*.

Salt crystals between the piston and the seal are the cause of abrasive particles, which can enter the eluent. These lead to contaminated valves, pressure rise and in extreme cases to scratched pistons. It is thus essential to ensure that **no precipitates** can appear (see also *section 5.1.3*).

5.1.3 Eluents

Treatment

For the preparation of the eluents, only chemicals of a purity degree of at least "**p.a.**" should be used. For diluting, please use only **high purity water**.

Fresh eluents should always be **microfiltered** (0.45 µm filter) and **degassed** (with N_2, He or vacuum). For alkaline eluents and eluents with low buffering capacity one should preferably use a **CO_2 absorber**.

The supply vessel containing the eluent must be closed as tightly as possible to avoid excessive evaporation. This is primarily important with eluents containing organic solvents (e.g. acetone), the evaporation of which can lead to drifts in the long term. If work is performed in a very sensitive range, even if one drop of condensate falls back in the eluent this can cause a noticeable change in the background conductivity.

Influence of various parameters on anion columns

- *Concentration:* An increase in the concentration usually leads to shorter retention times and quicker separation, but also to a higher background conductivity.
- *pH:* pH alterations lead to shifts in the dissociation equilibrium and thus to changes in the retention times.
- *Organic modifiers:* Addition of an organic solvent (e.g. methanol, acetone, acetonitrile) to aqueous eluents generally accelerates lipophilic ions.

Eluent change

When the eluent is changed, it must be ensured that **no precipitates** can be formed. Solutions used in direct succession must therefore be miscible. If the system has to be rinsed with an organic solution, several solvents with increasing or decreasing lipophilic character may possibly have to be used (e.g. water ↔ acetone ↔ chloroform).

5.1.4 Peristaltic pump

The 6.1826.060 pump tubings used by the peristaltic pump are consumable material with a limited lifetime and should be exchanged at regular intervals (approx. every 4 weeks under continuous use; see *section 5.2.10*).

The working life of pump tubing depends to a considerable extent on the contact pressure. This is why the contact pressure must be correctly set as described in *section 2.9.2*. If the pump is to remain switched off for a lengthy period of time the tubing cartridges **40** should be raised completely by loosening the snap-action lever **43** on the right-hand side (the set contact pressure remains unchanged).

5.1.5 Suppressor module

Protection

To avoid contamination of the suppressor module by foreign particles or bacterial growth, the two **6.2821.100 Filter units PEEK** (see *section 2.3.5*) supplied must be installed between peristaltic pump and inlet capillaries of the suppressor module (see *section 2.8.2*).

Operation

The **Metrohm Suppressor Module MSM** comprises a total of 3 suppressor units which are in turn used for suppression, regenerated with sulfuric acid and rinsed with water. To record every new chromatogram under comparable conditions, work is normally carried out with freshly regenerated suppressor. Switching takes place automatically together with the valve switching.

For operation of the suppressor module, a **two-channel peristaltic pump** is needed which conveys the regeneration solution (normally **20 mmol/L H_2SO_4**) and the rinsing solution (normally **dist. H_2O**) to the suppressor units (flow rate of 0.5 mL/min).

The suppressor units must never be regenerated with H_2SO_4 in the same flow direction used for the eluent. You should thus always install the inlet and outlet capillaries as described in section 2.8.4 according to the scheme shown in Fig. 15.

The suppressor module must <u>never</u> be switched in the dry state as there is a danger of blocking. Before every switching operation of the suppressor module, the three suppressor units must have been rinsed for at least ½ h with eluent, regeneration and rinsing solution.

The capacity of the suppressor units is exhausted after approx. 2 h. With longer interruptions between the individual measurements, it is recommended that the **Prep MSM.smt** system is started during the pauses; this automatically switches the suppressor module further every 20 min.

Maintenance

In the event of reduced capacity or high counter-pressure the suppressor module must be regenerated (*section 5.2.7*), cleaned (*section 5.2.8*) or exchanged (*section 5.2.9*).

5.1.6 Connections

All connections between injector, column and detector must be as short as possible, have a low dead volume and be absolutely tight. The PEEK capillary after the detector block must be free from constriction (the measuring cell is tested to 5 MPa = 50 bar back pressure).

5.2 Maintenance and servicing

5.2.1 General information

Care

The 792 Basic IC requires proper care and attention. Excessive contamination of the instrument could possibly lead to malfunctions and a shorter service life of the inherently rugged mechanical and electronic parts.

Spilled chemicals and solvents should be wiped up immediately. It is especially important to protect the plug connections at the rear of the instrument (particular the mains plug) against contamination.

Although constructional measures have been designed to virtually eliminate such a situation, should corrosive media penetrate the interior of the instruments the mains plug of the 792 Basic IC must be immediately disconnected to prevent extensive damage to the instrument electronics. Inform Metrohm service if your instrument(s) have been damaged in such a way.

The instrument must not be opened by untrained personnel. Please comply with the safety notes in section 1.4.1.

Maintenance by Metrohm service

Maintenance of the 792 Basic IC is best done as part of an annual service performed by specialists from the Metrohm company. If work is frequently performed with caustic and corrosive chemicals, it may be necessary to shorten the interval between servicing.

The Metrohm service department is always willing to offer expert advice on the maintenance and servicing of all Metrohm instruments.

5.2.2 Passivation

Passivation of the complete IC System (without column) by rinsing with 20...50 mL 0.2 mol/L HNO_3 is only required when unusual alterations to the measuring properties of the cell are observed. For passivation, the separating column **66** is removed from the 792 Basic IC. The two capillaries **20** and **37** (see *Fig. 12* and *Fig. 14*) are directly connected to each other using the Coupling **26** (6.2620.060).

5.2.3 Recycling

To keep the eluent consumption between injections to a minimum when the system is at rest (e.g. overnight), the so-called recycling procedure can be used. In recycling the eluent exiting the outlet capillary of the detector block is led back directly to the eluent supply vessel. The IC system is thus quickly ready for new injections without a long conditioning period.

*The recycling procedure must **not** be used*

- *in operation with the suppressor module,*
- *with alkaline eluents,*
- *with the 6.1010.000 IC Cation column METROSEP Cation 1-2.*

5.2.4 Shutdown

If the 792 Basic IC is shut down for a considerable length of time, the entire IC system (**without** column and suppressor) must be **rinsed free from salt** with methanol/water (1:4) to avoid crystallization of eluent salts with the corresponding subsequent damage.

For rinsing, the connections to the separating column and the suppressor module are removed; the two capillaries **20** and **37** (see *Fig. 12* and *Fig. 14*) are directly connected to each other using coupling **26** (6.2620.060). Rinse with methanol/water (1:4) until the conductivity drops below 10 µS/cm.

5.2.5 Changing separating columns

Identical separation system

If you wish to replace an IC separating column by a column of the same type, proceed as follows (see *Fig. 12* and *Fig. 14*):

1 Remove old column

- Switch off high-pressure pump and wait for pressure to drop.
- Unscrew column **66** from inlet capillary **37** of the detector block or from suppressor inlet capillary **75**.
- Unscrew column **66** from column connection capillary **20** or the precolumn.

2 Connect new column to injector

- Remove end caps from column **66**.
- Screw inlet end of separating column **66** (note flow direction) to column connection capillary **20** or to the precolumn (see *section 2.7.7*/*section 2.7.8*).

3 Rinse column

- Place beaker beneath the column outlet.
- Switch on high-pressure pump and rinse column with eluent for ca. 10 min, then switch off pump.

4 Connect column to detector block

- Screw outlet end of separating column **66** to inlet capillary **37** or suppressor inlet capillary **75**.

Changing the separation system

If you wish to replace an IC separating column by a column of a different type, proceed as follows (see *Fig. 12* and *Fig. 14*):

1 Remove old column

- Switch off high-pressure pump and wait for pressure to drop.
- Unscrew column **66** from inlet capillary **37** of the detector block or from the suppressor inlet capillary **75**.
- Unscrew column **66** from column connection capillary **20** or the precolumn.

2 Rinse with eluent

- Place beaker beneath the column connection capillary **20**.
- Rinse IC system with eluent used for the separating column (flow rate 1 mL/min) for ca. 15 min.

3 Connect new column to injector

- Remove end caps from column **66**.
- Screw inlet end of separating column **66** (note flow direction) to column connection capillary **20** or to the precolumn (see *section 2.7.7*/*section 2.7.8*).

4 Rinse column

- Place beaker beneath the column outlet.
- Set flow rate for new separating column.
- Switch on high-pressure pump and rinse column with eluent for ca. 10 min, then switch off pump.

5 Connect column to detector block

- Screw outlet end of separating column **66** to inlet capillary **37** or suppressor inlet capillary **75**.

5.2.6 Maintenance work at the pump head

In many cases, an unstable baseline (pulsation, flow fluctuations) can be traced to contaminated valves or faulty, leaky piston seals at the high-pressure pump. For cleaning contaminated valves and/or replacement of wear parts such as pistons, piston seals and valves, proceed as follows:

1 Detach pump head

- Disconnect aspirating tubing from aspirating capillary **32** at the pump head **34** (see *Fig. 3*).
- Unscrew connection capillary **35** from the pump head **34**.
- Remove pump head **34** by loosening the 4 hexagon screws **33** using the 6.2621.030 Hexagon key. The main piston is on the left (when viewed from front), the auxiliary piston on the right.

2 Disassemble pump head

- Strip down pump head **34** in accordance with *Fig. 16*. Main and auxiliary pistons are identical with the following exceptions:

– The spring **84** of the auxiliary piston (right piston) is more powerful (longer) than that of the main piston (left piston).

– Inlet and outlet valve are not present in the secondary cylinder.

*To prevent the piston **82** suddenly jumping out of the piston cartridge **85**, the screw **81** must be undone very carefully by hand.*

3 Cleaning/replacement of piston 82

- Pistons contaminated by abrasive particles or deposits are cleaned with scouring powder and rinsed free of any particles with dist. water.
- Relatively badly contaminated or scratched pistons must be replaced (spare part: 6.2824.070 Zircon piston).

4 Replacement of piston seal 89

- To remove damaged piston seals **89** the special tool **93** is used. This is screwed into the seal **89**, which can then be pulled out (see *Fig. 17A*).

*When the special tool **93** is screwed into the piston seal **89** the latter is completely destroyed!*

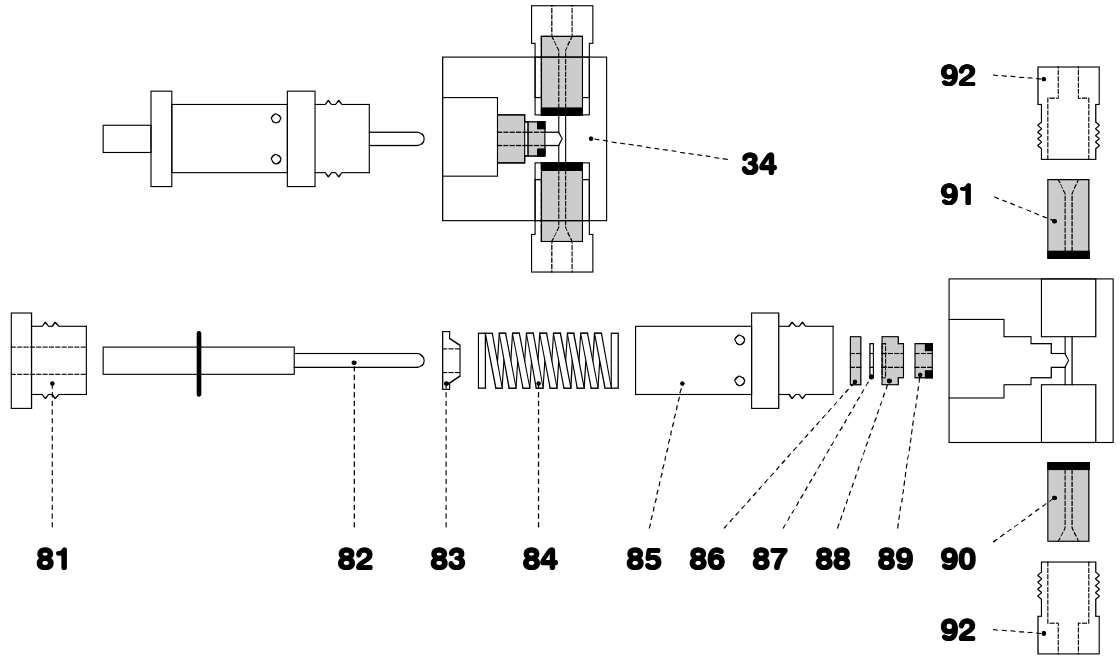


Fig. 16: Components of the pump head

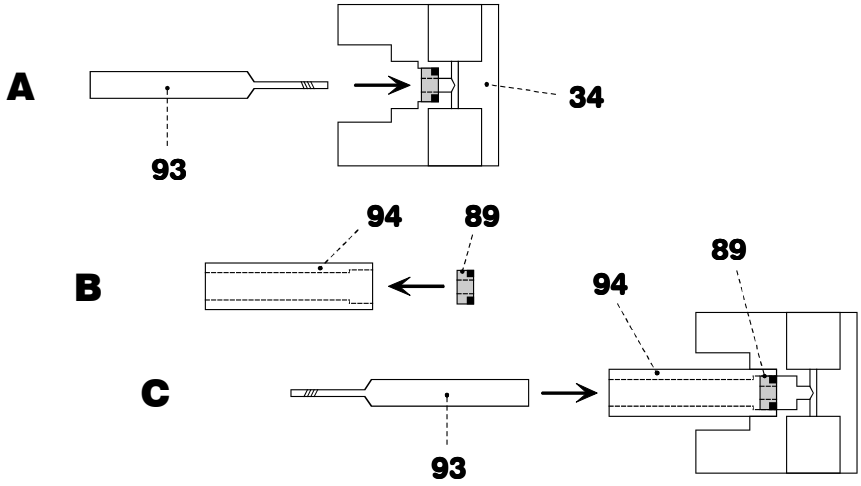


Fig. 17: Replacement of the piston seal 89

34	**Pump head (6.2824.100)**	**88**	**Piston guide sleeve (4.709.4370)**
81	**Screw (3.709.1100)** for piston cartridge **85**	**89**	**Piston seal (6.2741.020)**
82	**Zircon piston (6.2824.070)** with piston shaft	**90**	**Inlet valve (6.2824.090)**
83	**Spring retainer 4.709.0730**	**91**	**Outlet valve (6.2824.080)**
84	**Spring (6.2824.050)** for main piston or **Spring (6.2824.060)** for auxiliary piston	**92**	**Screw holder** for valve
85	**Piston cartridge (4.709.0760)**	**93**	**Special tool (6.2617.010)** to remove the piston seal **89**
86	**Piston guide sleeve (4.709.4380)**	**94**	**Special tool (6.2617.010)** to install the piston seal **89**
87	**Sapphire supporting ring (6.2824.030)**		

- To install a new piston seal **89** the special tool **94** is used.
- First the new seal is inserted firmly in the recess of tool **94** by hand (see *Fig. 17B*). The seal spring must be located on the outside.
- The tool **94** together with the seal is then inserted in the pump head **34** and the seal pressed into the pump head recess with the aid of tool **93** (see *Fig. 17C*).

*The seal surface in the pump head **34** must not be damaged (avoid contact with tool)!*

5 Cleaning/replacement of inlet valve 90 and outlet valve 91

- Contaminated or blocked valves are cleaned by rinsing with dist. water, RBS solution or acetone. The rinsing effect can be reinforced by brief treatment in an ultrasonic bath (max. 20 s; if longer the sapphire sphere of the valve can be damaged).
- If this does not have the desired effect, the valves can be disassembled as shown in *Fig. 18*. The valve components are pushed out with the aid of a syringe needle inserted through the upper opening in the valve housing **95**. The individual components are rinsed with dist. water and/or acetone, and the sapphire sphere cleaned with a paper towel. The valve is then reassembled in accordance with *Fig. 18*. The components of the inlet and outlet valves are identical, they are distinguished only by the positioning of the sapphire sleeve **98** and the ceramic holder **100** (see *Fig. 18*).
- Valves that fail to function faultlessly after such cleaning must be replaced.
- In the reinstallation of the inlet valve **90** or the outlet valve **91** on no account must the two outwardly identical valves be interchanged. To determine which valve is which, note that the liquid flows through the pump head from the bottom up. The flow direction of the valves can be checked simply by blowing through the clean valve. Both valves are installed with the black face in the direction of the pump head (see *Fig. 18*).

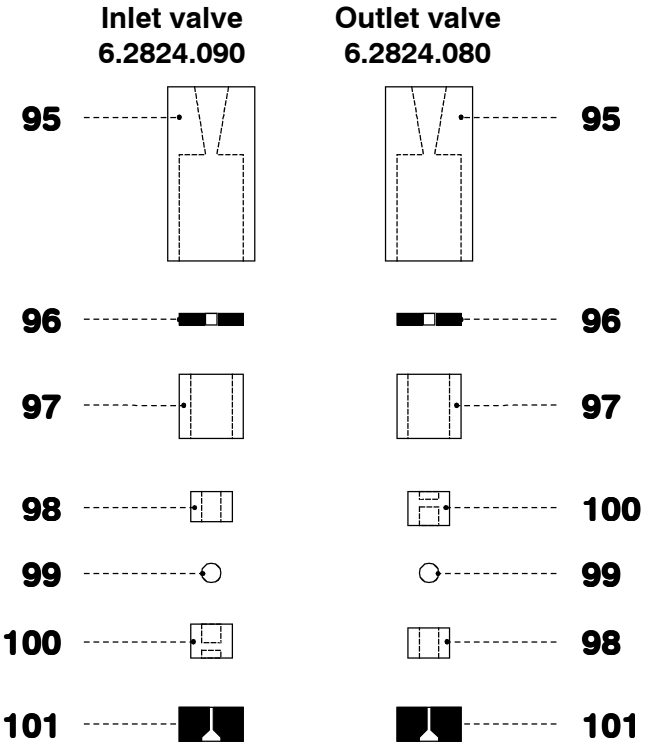
*If by mistake an inlet valve **90** is installed instead of the outlet valve **91**, an extreme pressure buildup occurs within the working cylinder, which is not detected by the pressure transducer and will destroy the piston seal **89**!*

6 Mounting the pump head

- Reassemble the components of the pump head **34** as shown in *Fig. 16*. Tighten the screw **81** by hand. First screw in piston cartridge **85** manually until the stop is reached and then use a wrench to turn it through a further 15°. Firmly tighten the two valve screw holders **92** with a wrench.
- Reattach pump head **34** to the pump with the help of the 4 fixing screws **33**. Firmly tighten them with the 6.2621.030 Allen key.

To ensure that the pump head is not positioned wrongly, the holes at the rear for the clamping bolts have different depths, i.e. 1 clamping bolt is longer than the rest. The deepest hole must naturally accommodate the longest bolt. If this is not the case, the pump will not function properly.

- Screw connection capillary **35** to pump head **34** (see *Fig. 3*).
- Connect aspirating tubing to aspirating capillary **32** at the pump head **34**.



95	**Valve housing**
96	**Sealing ring** (black)
97	**Sleeve**
98	**Sapphire sleeve** The bright side must point towards the sapphire sphere
99	**Sapphire sphere**
100	**Ceramic holder for sapphire sphere** The large recess must point in the direction of the sapphire sphere
101	**Seal** The larger opening must point outwards

Fig. 18: Components of inlet valve 90 and outlet valve 91

5.2.7 Regeneration of the suppressor module

Regenerating a suppressor operating at reduced capacity

If the suppressor units are exposed to certain heavy metals (e.g. iron) or organic contaminants for long periods, these can no longer be completely removed by the regeneration solution normally used (20 mmol/L H_2SO_4). This diminishes the capacity of the suppressor units, which, in milder cases, results in a reduced sensitivity to phosphates and, in severe cases, in a strong increase in the baseline. If such capacity problems occur at one or several positions, the suppressor units must be treated as follows:

1 Disconnect suppressor from IC system

- Disconnect suppressor from separating column and detector.

2 Regenerate suppressor

- Rinse each suppressor unit for about 15 min with one of the following solutions:

  Contamination with heavy metals
  1 mol/L H_2SO_4

  Contamination with organic cationic complexing agents
  0.1 mol/L H_2SO_4 / 0.1 mol/L oxalic acid / acetone 5%

  Severe contamination with organic substances
  0.2 mol/L H_2SO_4 / acetone ≥ 20%

The 6.1826.060 pump tubing is made of PP and must not be used for rinsing with solutions that contain organic solvents. In such cases, rinse with different pump tubing or a different pump.

3 Connect suppressor to IC system

- Reconnect suppressor to the IC system. If capacity problems persist, replace the suppressor rotor (see *section 5.2.9*).

Regenerating the suppressor in case of high counter pressure

If excessive counter pressure is observed in one or several suppressor units, treat the units as follows:

1 Disconnect suppressor from IC system

- Disconnect suppressor from separating column and detector.

2 Regenerate suppressor

- Connect the inlet capillary **78** marked "H_2SO_4" to the inlet capillary **18** using coupling **26** (see *Fig. 9* and *Fig. 14*). This connects the suppressor module directly to the high-pressure pump.

- Set the flow at the high-pressure pump to 0.5 mL/min and rinse the suppressor unit with 1 mol/L H_2SO_4 for 5 to 10 min.
- As the pressure falls, slowly increase the flow at the high-pressure pump to 2 mL/min. Do not exceed a maximum pressure of 2 MPa (20 bar).
- Switch off high-pressure pump.
- Switch suppressor to the next position using the Step button.
- Connect the inlet capillary **77** marked "H_2O" to the inlet capillary **18** using coupling **26** (see *Fig. 9* and *Fig. 14*).
- Set the flow at the high-pressure pump to 0.5 mL/min and rinse the suppressor unit with 1 mol/L H_2SO_4 for 5 to 10 min.
- As the pressure falls, slowly increase the flow at the high-pressure pump to 2 mL/min. Do not exceed a maximum pressure of 2 MPa (20 bar).
- Switch off high-pressure pump.

3 Connect suppressor to IC system

- Connect inlet capillaries **77** and **78** to the peristaltic pump (see *section 2.8.4*).
- If the pressure problems persist, replace the suppressor rotor (see *section 5.2.9*).

5.2.8 Cleaning the suppressor

It may be necessary to clean the suppressor in the following cases:

- High counter pressure on the suppressor connection tubing
- Irremediable blockage of the suppressor (the suppressor can no longer deliver solutions)
- Irremediable obstruction of the suppressor (the suppressor can no longer be switched to next position)

To clean the connection piece and the rotor, proceed as follows (see *Fig. 19*):

1 Disconnect suppressor from IC system

- Disconnect input capillary **75** of the suppressor module **39** from the separating column **66** (see *Fig. 14*).
- Disconnect output capillary **76** from inlet capillary **37**.
- Disconnect inlet capillaries **77** and **78** from the filter units **28** (supply from peristaltic pump).

2 Dismantle suppressor

- Unscrew nut **102** from suppressor holder **105**.
- Pull out connection piece **103** and suppressor rotor **104** from suppressor holder **105** (the connection piece and the rotor normally stick together).
- Loosen connection piece **103** from suppressor rotor **104**.

3 Clean input and output leads

- Connect each of the 6 capillary tubings attached to connection piece **103** to the high-pressure pump one after another, and pump through ultrapure water.
- Check whether solution emerges from connection piece **103**. If one of the input or output leads remains blocked, replace the connection piece **103** (order number 6.2832.010).

4 Clean suppressor rotor

- Clean the sealing surface of suppressor rotor **104** using a lint-free cloth and ethanol.

5 Insert suppressor rotor

- Insert suppressor rotor **104** in suppressor holder **105** in such a way that the tubing connections at the rear of the rotor fit in the corresponding openings inside the rotor, and that one of the three holes in the rotor can be seen from below in one of the openings of the holder.
- If the rotor has been inserted correctly, its sealing surface will be about 4 mm inside the holder. If this is not the case, bring the rotor into the correct position from below with the aid of a sharp object (e.g. a screwdriver).

6 Clean connection piece

- Clean the sealing surface of connection piece **103** using a lint-free cloth and ethanol.

7 Insert connection piece

- Insert connection piece **103** in suppressor holder **105** in such a way that connection "1" is at the top, and that the three lugs on the connection piece fit in the corresponding openings of the holder.
- Screw nut **102** onto the thread of suppressor holder **105** manually (do not use tools).

8 Connect and condition the suppressor

- Reconnect the suppressor to the IC system.
- Before switching the suppressor to the next position for the first time, rinse all 3 suppressor units with solution for 5 min.

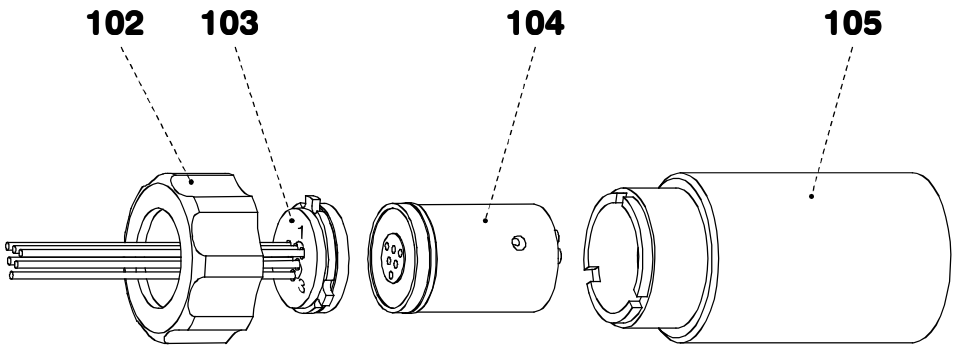


***Fig. 19*: Assembling the suppressor**

102	**Screw nut**	**104**	**Suppressor rotor (6.2832.000)**
103	**Connection piece (6.2832.010) with input and output leads**	**105**	**Suppressor holder**

5.2.9 Replacing the suppressor

The suppressor in the suppressor block may have to be replaced in the following cases:

- Irremediable loss of suppressor capacity (reduced phosphate sensitivity and/or strong rise in baseline)
- Irremediable blockage of the suppressor (the suppressor can no longer deliver solutions)

Both the 6.2832.000 Suppressor rotor and the 6.2832.010 Connection piece with the input and output leads can be replaced. To replace these components proceed as follows (see *Fig. 19*):

1 Disconnect suppressor from IC system

- Disconnect all input and output leads of the suppressor from IC system and peristaltic pump.

2 Dismantle suppressor

- Unscrew nut **102** from suppressor holder **105**.
- Pull out connection piece **103** and suppressor rotor **104** from suppressor holder **105** (the connection piece and the rotor normally stick together).
- Loosen connection piece **103** from suppressor rotor **104**.

3 Clean suppressor rotor

- Clean the sealing surface of new suppressor rotor **104** (6.2832.000) using a lint-free cloth and ethanol.

4 Insert suppressor rotor

- Insert new suppressor rotor **104** in suppressor holder **105** in such a way that the tubing connections at the rear of the rotor fit in the corresponding openings inside the rotor and that one of the three holes in the rotor can be seen from below in one of the openings of the holder.
- If the rotor has been inserted correctly, its sealing surface will be about 4 mm inside the holder. If this is not the case, bring the rotor into the correct position from below with the aid of a sharp object (e.g. a screwdriver).

5 Clean connection piece

- Clean the sealing surface of new connection piece **103** (6.2832.010) with the aid of a lint-free cloth and ethanol.

6 Insert connection piece

- Insert new connection piece **103** in suppressor holder **105** in such a way that connection "1" is at the top and that the three lugs on the connection piece fit in the corresponding openings of the holder.
- Screw nut **102** onto the thread of suppressor holder **105** manually (do not use tools).

7 Connect and condition the suppressor

- Reconnect the suppressor to the IC system.
- Before switching the suppressor to the next position for the first time, rinse all 3 suppressor units with solution for 5 min.

5.2.10 Exchanging the pump tubing

The pump tubings used by the peristaltic pump are consumable material with a limited lifetime and should be exchanged at regular intervals (approx. every 4 weeks under continuous use).

The working life of pump tubing depends to a considerable extent on the contact pressure. This is why the contact pressure must be correctly set as described in *section 2.9.2*. If the pump is to remain switched off for a lengthy period of time the tubing cartridges **40** should be raised completely by loosening the snap-action lever **43** on the right-hand side (the set contact pressure remains unchanged).

As the pump is always operated on the same side, the 6.1826.060 Pump tubings supplied can be used on both sides. To exchange a pump tubing proceed as follows:

1 Remove old pump tubing

- Press contact pressure lever **41** on the tubing cartridge **40** down as far as it will go.
- Release tubing cartridge **40** from holding clamp **42** by pressing down snap-action lever **43** and remove from mounting pin **45** (see *Fig. 14*).
- Remove old pump tubing **71** or **72**.

2 Insert new pump tubing

- Insert the new pump tubing **71** or **72** in the tubing cartridge **40** as shown in *Fig. 13*. The white-yellow stopper **73** must click into the corresponding holder on the left-hand side of the tubing cartridge.
- Place the tubing cartridge **40** on mounting pin **45** and press down on the right-hand side until snap-action lever **43** clicks into position on holding clamp **42**. Take care that no kinks are formed in the pump tubing.

3 Set contact pressure

- Switch on peristaltic pump.
- Press contact pressure lever **41** upwards until the solution just starts to be drawn in. Then press contact pressure lever upwards until it clicks once more to obtain optimal contact pressure.
- Switch off peristaltic pump.

5.3 Faults and malfunctions

5.3.1 Error messages

If any type of malfunction occurs during operation of the 792 Basic IC, this is shown by error messages in the PC program, which appear either in an **error window** or in the **SYSTEM STATE** window.

Follow the instructions given in the **error window** and close this window with **<OK>**.

You will find further details of the error messages of the **SYSTEM STATE** window, their possible causes and the procedure for their rectification in *section 4.3.7*.

5.3.2 Malfunctions and their rectification

If difficulties appear with the 792 Basic IC during analyses, their causes are best investigated in the order **separating column → high-pressure pump → eluent → connections**. Several of the malfunctions which may appear are listed in the following table with details of possible causes and countermeasures.

Malfunction	*Cause*	*Rectification*
Baseline with high noise level, pulsation	• Contaminated pump valves • Faulty piston seals	• Clean the valves (see *section 5.1.5*) • Replace the piston seals (see *section 5.1.5*)
Drift of the baseline	• Thermal equilibrium not yet reached • Leak in system • Evaporation of organic solvent in eluent	• Condition system with heating switched on • Check connections and make leakproof • Ensure better closure of eluent supply vessel
Considerable pressure drop	• Leak in system	• Check connections and make leakproof
Considerable pressure rise	• Contamination of the filter in the 6.2821.100 Filter unit PEEK • Contamination of the column inlet filter • Change of column packing by injection of contaminated samples	• Replace the 6.2821.110 Filter (see *section 2.3.5*) • Clean or replace 6.2821.020 Steel mesh(es) • Regenerate column (see *section 5.1.1*) or replace column *Note:* *Samples should always be microfiltered.*

Malfunction	*Cause*	*Rectification*
Chromatograms with poor resolution, change in the retention times	• Deterioration in separation efficiency of the IC column	• Regenerate column (see *section 5.1.1*) or replace column
Extreme peak broadening, splitting (double peaks)	• Dead volume at the column ends	• Fill column with glass beads (∅ ≤ 100 µm) or replace column
No feed of regeneration or rinsing solution for suppressor	• Contact pressure too low	• Adjust contact pressure (see *section 2.9.2*)
	• Leak in system	• Check connections and make leakproof
	• Defective pump tubing	• Replace pump tubing (see *section 5.2.9*)
	• Contamination of the filter in the 6.2821.100 Filter unit PEEK	• Replace the 6.2821.110 Filter (see *section 2.3.5*)
	• Counterpressure at suppressor module too high	• Clean or replace suppressor (see *section 5.2.6…5.2.8*)

5.4 Diagnostic tests / Validation / GLP

The requirements of **GLP** (**G**ood **L**aboratory **P**ractice) include a periodic check of analytical measuring instruments with regard to their reproducibility and accuracy using **S**tandard **O**perating **P**rocedures, **SOP**. Under the title **«Application Bulletin No. 277 – Validation of Metrohm Ion Chromatography Systems by using Standard Operating Procedures (SOP)»** an example of such a standard operating procedure is available from Metrohm; it can be adapted and used with the 792 Basic IC.

Further information on the subjects of QA, GLP and validation can also be found in the brochure «**Quality management with Metrohm**», which is available from your local Metrohm agency.

Testing of the electronic and mechanical function groups of Metrohm instruments can and should be performed as part of a regular service by trained personnel of the manufacturing company (see *section 5.2.1*). All Metrohm instruments are equipped with start-up-test routines that check for perfect functioning of the relevant assemblies when the instrument is switched on. If no error message is displayed, it may be assumed the instrument is operating without faults.

The 792 Basic IC has an integrated diagnostic program which, in the case of possible malfunctions or faulty behavior, allows the service technician to check the functioning of certain assemblies and localize the fault.

6 Appendix

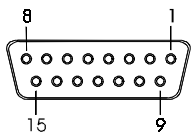
6.1 Technical data

6.1.1 Conductivity measurement

Measurement range	0…1000 µS/cm (resolution: 0.56 nS/cm)
Maximum error	± 10 µS/cm and ± 1 % of measurement value (k = 16.7/cm)
Linearity	Deviations < ± 5 µS/cm
Noise	typ. 3 nS/cm
Drift (electronic)	typ. < 10 nS/cm / h
Temperature dependence	typ. < 40 nS/cm / °C
Reserve range	> 33 % (k = 16.7/cm)
Sampling rate	10 measurements/s (fixed)

6.1.2 Conductivity detector

Construction	Thermostatted conductivity detector with 2 ring-shaped steel electrodes
Measurement principle	Alternating current measurement with 1 kHz frequency and ca. 1.7 V amplitude (peak to peak).
Cell volume	1.5 µL
Cell constant	approx. 17 /cm (the exact value is printed on the detector)
Maximum back pressure for measuring cell	5.0 MPa (50 bar)
Thermostatting	Connectable dynamic control to operating temperature
Operating temperature	40 °C
Max. temperature deviation	± 2.5°C
Heating time	≥ 30 min
Temperature stability	≤ 0.01°C at constant ambient temperature
Connection for detector block	Dsub 15 pin (female)



6.1.3 Injection valve

Actuator switching duration	100…150 ms
Pressure resistance	25 MPa (250 bar)

6.1.4 High-pressure pump

Type	Serial dual piston pump with two valves	
Pump capacity		
Flow range	0.20...2.5 mL/min	
Maximum error	< ± 2 % of set value	
Flow constancy	< 0.5 % of set value	
Reproducibility of eluent flow	typ. better than ± 0.1 %	
Pressure measurement		
Pressure range	0...25.0 MPa (0...250 bar)	
Residual pulsation	< 10 % (at 1 mL/min water and 10 MPa pressure, without pulsation dampener)	
Measurement principle	Piezoresistive measurement Response time: 3 ms Measurement volume: ca. 50 µL	
Maximum error	± 3 % of set value	
Resolution	0.1 MPa (conductivity measurements)	
Sampling rate	1 measurement/piston stroke (pump running) 1 measurement/s (pump not running)	
Safety shutdown		
Function	Automatic shutdown when upper and lower pressure limits violated	
Maximum pressure limit	adjustable between 0.1...25.0 MPa (1...250 bar) Response time: 1 pump cycle	
Minimum pressure limit	adjustable between 0.1 ... 25.0 MPa (1...250 bar), inactive at 0 MPa Response time: 5 pump cycles	
Pump head		
Pump head volumes	Main piston: Priming piston:	40 µL 20 µL
Pump displacement volumes	Main piston: Priming piston:	28.5 µL 14.25 µL
Length of stroke	Main piston: Priming piston:	3.6 mm 1.8 mm

6.1.5 Peristaltic pump

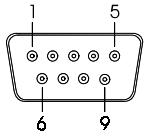
Type	2-channel peristaltic pump
Pump capacity	
Rotational speed	20 U/min at 50 Hz 24 U/min at 60 Hz
Flow range	0.5…0.6 mL/min with 6.1826.060 Pump tubing
Maximum error	± 5 %
Maximum pressure	0.4 MPa (4 bar)
Pumpable liquids	Clear liquids with no solid contents
Pump tubing material	PP (polypropylene)

6.1.6 Suppressor module

Switching duration	140 ms
Pressure resistance	2.5 MPa (25 bar)

6.1.7 RS232 interface

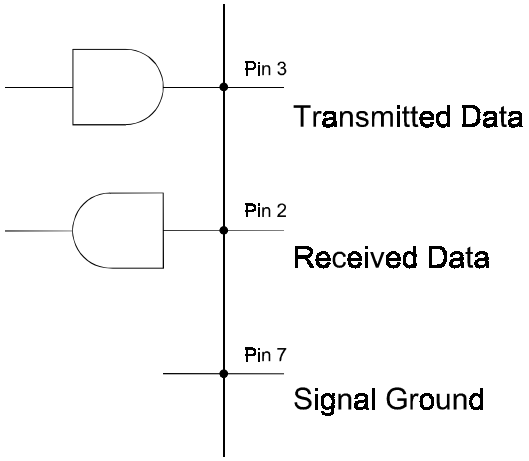
Connector Dsub 9 pin (male)



Function TxD and RxD signal for connection with software handshake

Default settings 9600 baud, 8 bit, 1 stop bit, no parity, XON/XOFF

Pin assignment



6.1.8 Mains connection

Voltage	115 V: 100...120 V ± 10 % 230 V: 220...240 V ± 10 %
Frequency	50...60 Hz
Power consumption	100 VA
Fuse	5 mm dia., 20 mm length 100…120 V: 1.0 A (slow-blow) 220…240 V: 0.5 A (slow-blow)

6.1.9 Safety specifications

Construction/testing	According to IEC 1010 / EN 61010 / UL 3101-1, protection class 1, degree of protection IP20
Safety directions	The Instructions for Use include information and warnings that must be heeded by the user to assure safe operation of the instrument.

6.1.10 Electromagnetic compatibility (EMC)

Emitted interference	Standards met: EN55011 (class B), EN55022 (class B), EN50081-1, IEC61326 (class B)
Immunity to interference	Standards met: IEC801-2/IEC1000-4-2 (class 3), IEC801-3/ IEC1000-4-3 (class 2), IEC801-4/IEC1000-4-4 (class 4), IEC801-5/IEC1000-4-5 (class 2/3), IEC801-6/IEC1000-4-6 (class 2), EN50082-1, EN61000-3-2/IEC1000-3-2, EN61000-3-3/ IEC1000-3-3, EN61000-4-11/IEC1000-4-11, IEC61326

6.1.11 Ambient temperature

Nominal operating range	+5…+45°C (at 20…80 % atmospheric humidity)
Storage	–20…+70°C
Transport	–40…+70°C

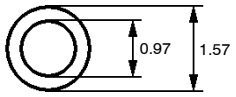
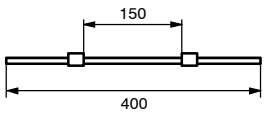
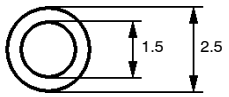
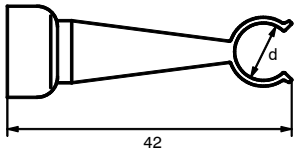
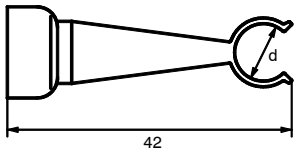
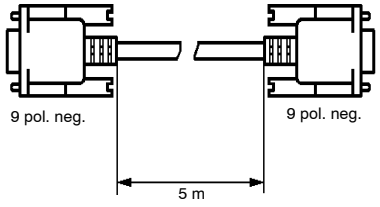
6.1.12 Housing

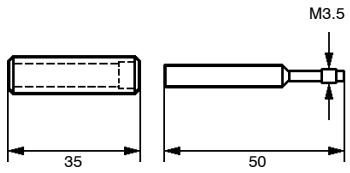
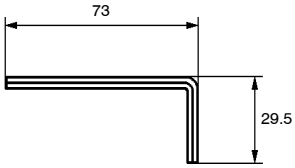
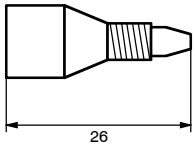
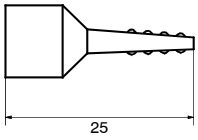
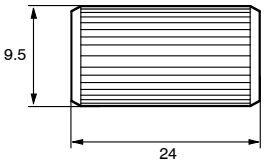
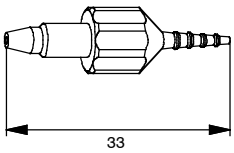
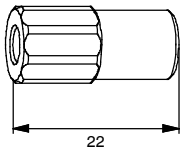
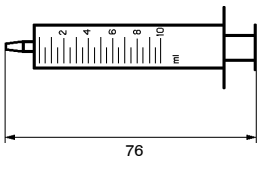
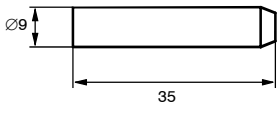
Material of cover	Polyurethane rigid foam (PUR) with fire protection for fire class UL94VO, CFC-free
Material of base	Steel, enameled
Width	255 mm
Height	385 mm
Depth	343 mm
Weight (incl. accessories)	15.8 kg

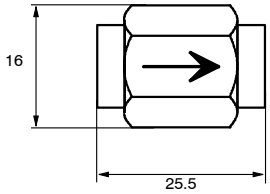
6.2 Standard equipment

Subject to changes !
All dimensions are given in mm.

The **2.792.0020 Basic IC** includes the following parts:

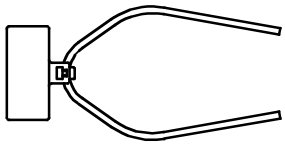
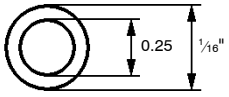
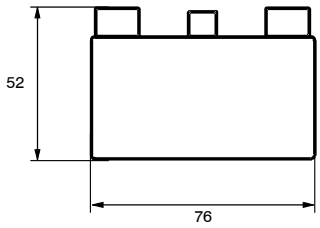
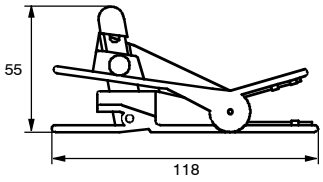
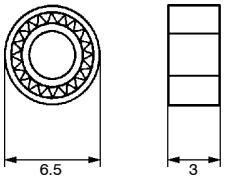
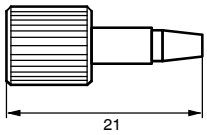
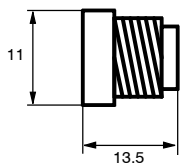
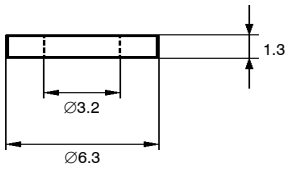
Quant.	*Order No.*	*Description*
1	**1.732.0110**	**Detector block (metal-free)** with permanently attached connecting cable to 792 Basic IC
1	**6.1803.020**	**PTFE capillary** Length = 5 m 
2	**6.1826.060**	**Pump tubing** made of PP (polypropylene) with 2 firmly attached white-yellow stoppers; in.d. = 0.51 mm, ex.d. = 2.31 mm 
1	**6.1834.010**	**Aspirating tubing** made of PTFE, with connector for 6.2821.090 aspirating filter Length = 2.5 m For the connection high-pressure pump – eluent bottle 
1	**6.2027.030**	**Column holder** Diameter d = 8.5 mm 
1	**6.2027.040**	**Column holder** Diameter d = 11.3 mm 
1	**6.2122.0X0**	**Mains cable** to customer's specifications: Cable socket / Cable connector Type IEC 320/C 13 — Type SEV 12 (CH…) .....6.2122.020 Type IEC 320/C 13 — Type CEE (7), VII (D…) .....6.2122.040 Type CEE (22), V — Type NEMA 5-15 (USA…).....6.2122.070
1	**6.2134.100**	**Connecting cable** Connecting cable 792 Basic IC (RS232) – PC 

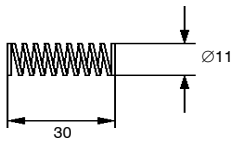
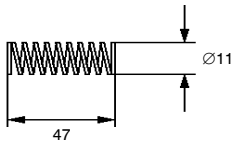
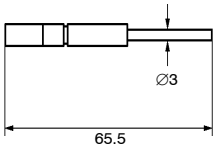
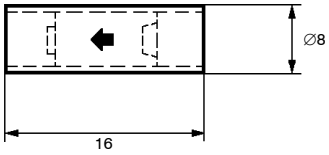
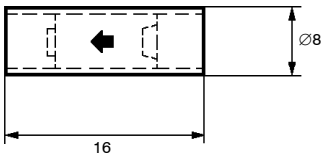
Quant.	Order No.	Description
1	6.2617.010	**Special tool** For removing the piston seal of the pump head 
1	6.2621.030	**Hexagon key 4 mm** For mounting the pump head of the high-pressure pump. 
2	6.2744.010	**PEEK compression fitting** For the connection of 6.1831.010 PEEK capillaries or 6.1822.010 PTFE microcapillaries, set of 5 
1	6.2744.030	**PEEK coupling** Connection between 6.2744.010 PEEK compression fitting and 6.1826.060 Pump tubing; set of 4 
1	6.2744.040	**PEEK coupling** For connection of 1/16" capillaries 
2	6.2744.110	**PEEK coupling** Connection between 6.2821.100 Filter unit PEEK and 6.1826.060 Pump tubing 
1	6.2744.120	**Coupling1/16" – Luer** Connection between 6.2744.010 PEEK compression fitting and 6.2816.020 Syringe 
1	6.2816.020	**Syringe** made of PP, volume = 10 mL; for manual filling of the sample loop 
1	6.2821.090	**Aspirating filter** Pore dimension 20 µm For 6.1834.000 Aspirating tubing. Set of 5. 

Quant.	Order No.	Description
2	6.2821.100	**Filter unit PEEK 2 µm** To avoid contamination due to abrasive particles of piston seals. Spare part: 6.2821.110 Filter 
1	6.6045.003	**Software-CD «792 Basic IC 1.0»**
1	Y.107.0150	**Cable strap**
1	8.732.2003	**Metrohm Monograph «Ion chromatography» (English)**
1	8.732.2013	**«IC Application Notes» (English)**
1	8.792.1003	**Instructions for Use (English)** for 792 Basic IC
1	8.792.2003	**Metrohm Monograph «Practical ion chromatography» (English)**
1	8.792.8007	**Registration card (German/English)** for PC program «Metrodata 792 PC Software 1.0»

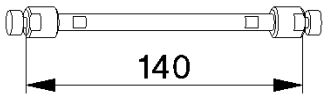
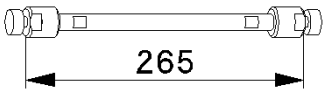
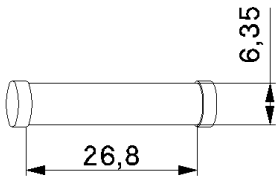
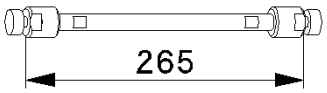
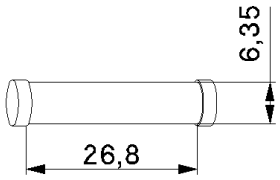
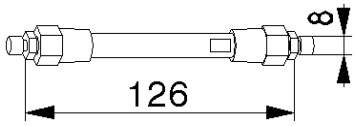
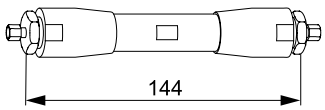
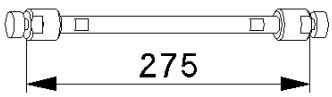
6.3 Optional accessories

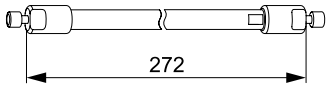
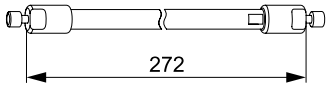
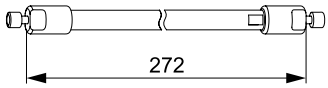
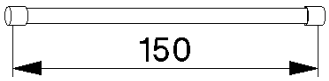
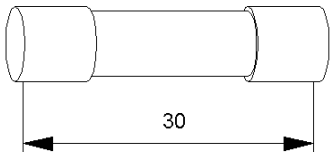
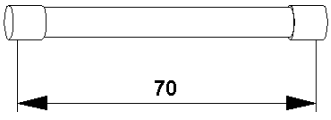
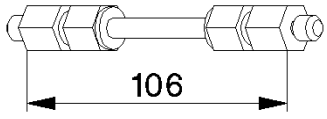
6.3.1 Accessories for 792 Basic IC

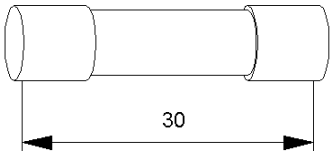
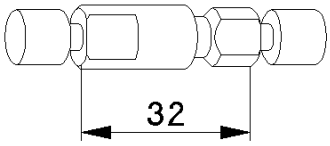
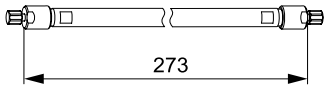
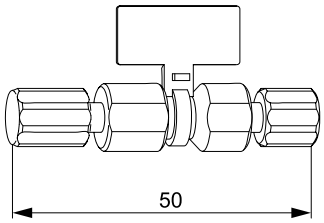
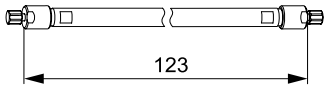
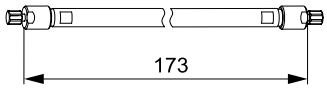
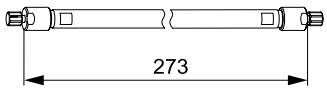
Order No.	Description	
6.1825.XXX	**Sample loop, made of PEEK** For injection valve; incl. two 6.2744.010 PEEK compression fittings 6.1825.230: Volume = 10 µL 6.1825.210: Volume = 20 µL 6.1825.220: Volume = 100 µL	
6.1831.010	**PEEK capillary** Length = 3 m	
6.2620.150	**Pulsation dampener MF** Metal-free pulsation dampener to reduce pulsation and prolong the life of separating columns.	
6.2621.080	**Capillary tubing cutter for plastic capillaries** For 6.1831.010 PEEK capillaries and 6.1822.010 PTFE microcapillaries incl. 5 additional blades	
6.2741.020	**Piston seal (orange)** Spare part for 6.2824.100 Pump head	
6.2744.070	**PEEK compression fitting short** Spare part for 6.2824.100 Pump head Set of 5	
6.2821.110	**Filter for filter unit PEEK 2 µm** Spare part for 6.2821.100 Filter unit PEEK. Set of 10	
6.2824.030	**Sapphire supporting ring** Spare part for 6.2824.100 Pump head	

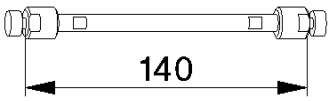
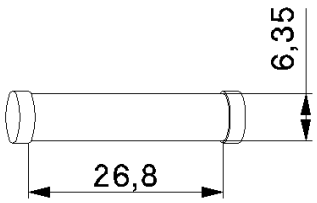
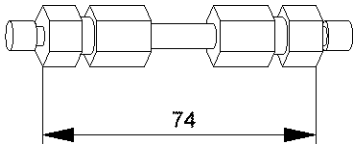
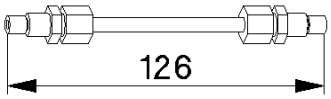
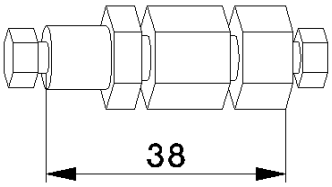
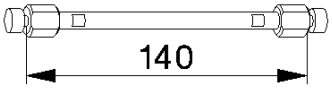
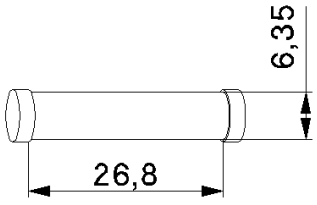
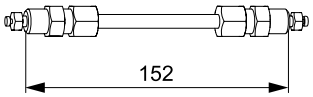
Order No.	Description
6.2824.050	**Spring for main piston** Spare part for 6.2824.100 Pump head 
6.2824.060	**Spring for auxiliary piston** Spare part for 6.2824.100 Pump head 
6.2824.070	**Zircon piston** Spare part for 6.2824.100 Pump head 
6.2824.080	**Outlet valve (metal-free)** Spare part for 6.2824.100 Pump head 
6.2824.090	**Inlet valve (metal-free)** Spare part for 6.2824.100 Pump head 
6.2824.100	**Pump head (metal-free)** Complete, with fixations screws
6.5324.000	**Bottle rack** Complete, incl. supply vessels for eluent (2 L), regeneration solution (1 L) rinsing solution (1 L)
6.5325.000	**Basic IC Starter Kit** incl. the following accessories: 6.1006.020 Metrosep Anion Dual 1 (150 mm) 6.2620.150 Pulsation dampener MF 6.2828.100 Glass cartridge holder (150 mm)

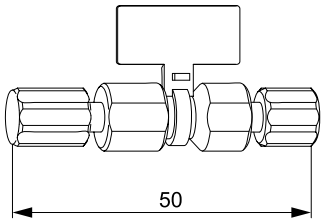
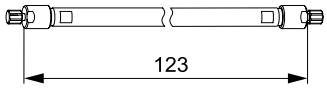
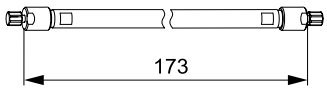
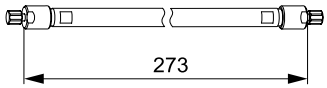
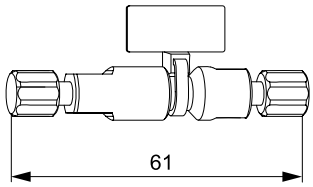
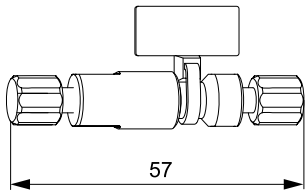
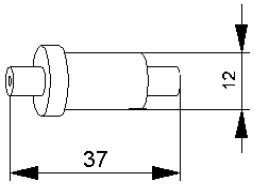
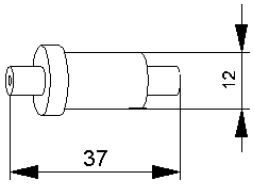
6.3.2 Separating columns and precolumns

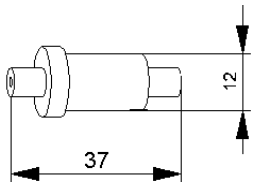
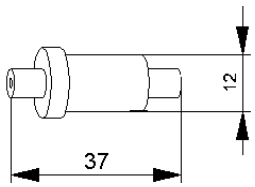
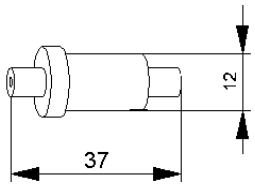
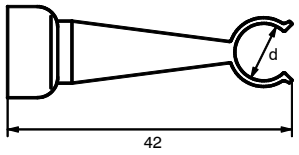
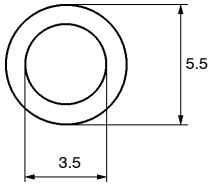
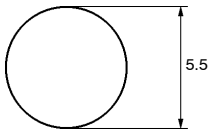
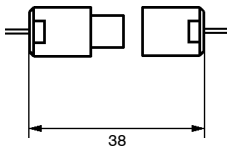
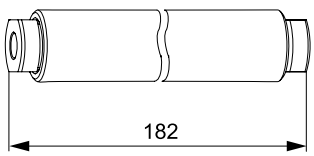
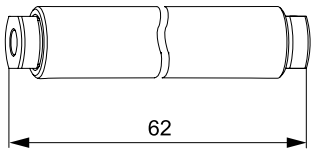
Order No.	Description	
6.1005.000	**IC anion column PRP-X100 (125 mm)** For the determination of anions without chemical suppression. Column dimensions: 125 × 4.0 mm Precolumn: 6.1005.020	
6.1005.010	**IC anion column PRP-X100 (250 mm)** For the determination of anions without chemical suppression. Column dimensions: 250 × 4.0 mm Precolumn: 6.1005.020	
6.1005.020	**IC precolumn cartridge PRP-X100** To prolong the service life of 6.1005.000 and 6.1005.010 IC anion columns PRP-X100. Column dimensions: 20 × 4.0 mm Installation using 6.2821.050 Twin cartridge holder.	
6.1005.030	**IC exclusion column PRP-X300** For the determination of organic acids without chemical suppression. Column dimensions: 250 × 4.0 mm Precolumn: 6.1005.040	
6.1005.040	**IC precolumn cartridge PRP-X300** To prolong the service life of the 6.1005.030 IC exclusion column PRP-X300. Column dimensions: 20 × 4.0 mm Installation using 6.2821.050 Twin cartridge holder.	
6.1005.100	**IC anion column Star-Ion A300** For the determination of anions with chemical suppression. Column dimensions: 100 × 4.6 mm Precolumn: 6.1011.020	
6.1005.110	**IC anion column Star-Ion A300HC** High-capacity anion column for determination of anions with chemical suppression. Column dimensions: 100 × 10 mm Precolumn: 6.1011.020	
6.1005.200	**IC anion column Organic Acids** For the determination of organic acids. Column dimensions: 250 × 7.8 mm	

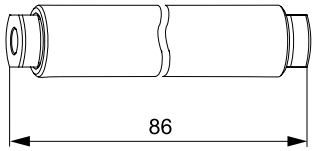
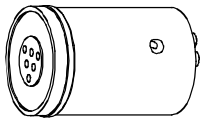
Order No.	Description	
6.1005.300	**IC anion column METROSEP A SUPP 1** For the determination of anions with chemical suppression. Column dimensions: 250 × 4.6 mm Precolumn: 6.1011.020	
6.1005.310	**IC anion column METROSEP A SUPP 2** For the determination of anions with chemical suppression. Column dimensions: 250 × 4.6 mm Precolumn: 6.1011.020	
6.1005.320	**IC anion column METROSEP A SUPP 3** For the determination of anions with chemical suppression. Column dimensions: 250 × 4.6 mm Precolumn: 6.1011.020	
6.1006.020	**IC column cartridge METROSEP Anion Dual 1** For the determination of anions with and without chemical suppression. Column dimensions: 150 × 3.0 mm Installation using 6.2828.100 Glass cartridge holder. Precolumn: 6.1006.030 + 6.2828.110 ***Note**: The 6.2620.150 Pulsation dampener must be used for operation of this column!*	
6.1006.030	**IC precolumn cartridge METROSEP Anion Dual 1** Set of 3 To prolong the service life of the 6.1006.020 IC column cartridge METROSEP Anion Dual 1. Column dimensions: 30 × 3.1 mm Installation using 6.2828.110 Precolumn cartridge holder.	
6.1006.040	**IC column cartridge METROSEP Anion Dual 1** For the determination of anions with and without chemical suppression. Column dimensions: 70 × 3.1 mm Installation using 6.2828.120 Glass cartridge holder. Precolumn: 6.1006.030 + 6.2828.110 ***Note**: The 6.2620.150 Pulsation dampener must be used for operation of this column!*	
6.1006.100	**IC anion column METROSEP Anion Dual 2** For the determination of anions with and without chemical suppression. Column dimensions: 75 × 4.6 mm Precolumn: 6.1011.020	

Order No.	Description	
6.1006.200	**Preconcentration cartridge METROSEP Anion** For anion preconcentration. Column dimensions: 30 × 3.1 mm Installation using 6.2828.110 Precolumn cartridge holder.	
6.1006.300	**Preconcentration column METROSEP Anion** For anion preconcentration.	
6.1006.430	**IC anion column METROSEP A SUPP 4** For the determination of anions with chemical suppression. Column dimensions: 250 × 4.0 mm Precolumn: 6.1006.500 ***Note**: The 6.2620.150 Pulsation dampener must be used for operation of this column!*	
6.1006.500	**IC precolumn METROSEP A SUPP 4/5 Guard** To prolong the service life of the METROSEP A SUPP 4/5 anion columns.	
6.1006.510	**IC anion column METROSEP A SUPP 5 100** For the determination of anions with chemical suppression. Column dimensions: 100 × 4.0 mm Precolumn: 6.1006.500 ***Note**: The 6.2620.150 Pulsation dampener must be used for operation of this column!*	
6.1006.520	**IC anion column METROSEP A SUPP 5 150** For the determination of anions with chemical suppression. Column dimensions: 150 × 4.0 mm Precolumn: 6.1006.500 ***Note**: The 6.2620.150 Pulsation dampener must be used for operation of this column!*	
6.1006.530	**IC anion column METROSEP A SUPP 5 250** For the determination of anions with chemical suppression. Column dimensions: 250 × 4.0 mm Precolumn: 6.1006.500 ***Note**: The 6.2620.150 Pulsation dampener must be used for operation of this column!*	

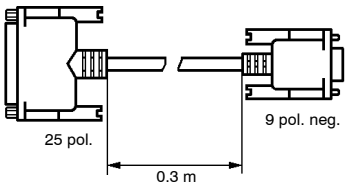
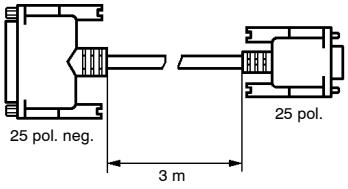
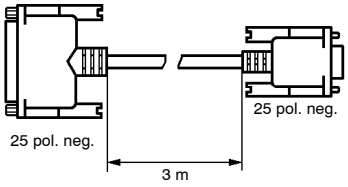
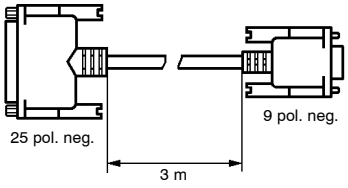
Order No.	Description	
6.1007.000	**IC cation column Nucleosil 5SA** For the determination of divalent cations without chemical suppression. Column dimensions: 125 × 4.0 mm Precolumn: 6.1007.010	
6.1007.010	**IC precolumn cartridge Nucleosil 5SA** To prolong the service life of the 6.1007.000 IC cation column Nucleosil 5SA. Column dimensions: 20 × 4.0 mm Installation using 6.2821.050 Twin cartridge holder.	
6.1008.010	**IC cation column Hyperrez Monovalent** For the determination of monovalent cations without chemical suppression. Column dimensions: 50 × 4.6 mm	
6.1009.000	**IC anion column SUPERSEP** For the determination of anions without chemical suppression. Column dimensions: 100 × 4.6 mm Precolumns: 6.1009.010 IC anion column SUPERSEP or 6.1005.010 IC precolumn cartridge.	
6.1009.010	**IC anion precolumn SUPERSEP** To prolong the service life of the 6.1009.000 IC anion column SUPERSEP.	
6.1010.000	**IC cation column METROSEP Cation 1-2** For the determination of monovalent and divalent cations without chemical suppression. Column dimensions: 125 × 4.0 mm Precolumn: 6.1010.010	
6.1010.010	**IC precolumn cartridge METROSEP Cation 1-2** To prolong the service life of the 6.1010.000 IC cation column METROSEP Cation 1-2. Column dimensions: 20 × 4.0 mm Installation using 6.2821.050 Twin cartridge holder.	
6.1010.100	**IC cation column METROSEP C 1** For the determination of monovalent and divalent cations without chemical suppression. Column dimensions: 125 × 4.6 mm Precolumn: 6.1010.200	

Order No.	Description
6.1010.200	**IC precolumn METROSEP C 2 Guard** To prolong the service life of the METROSEP C 1 and C 2 cation columns. 
6.1010.210	**IC cation column METROSEP C 2 100** For the determination of monovalent and divalent cations without chemical suppression. Column dimensions: 100 × 4.0 mm Precolumn: 6.1010.200 
6.1010.220	**IC cation column METROSEP C 2 150** For the determination of monovalent and divalent cations without chemical suppression. Column dimensions: 150 × 4.0 mm Precolumn: 6.1010.200 
6.1010.230	**IC cation column METROSEP C 2 250** For the determination of monovalent and divalent cations without chemical suppression. Column dimensions: 250 × 4.0 mm Precolumn: 6.1010.200 
6.1010.300	**Preconcentration column METROSEP C PCC 1** For cation preconcentration. 
6.1011.020	**IC precolumn METROSEP RP Guard** To prolong the service life of the METROSEP C 1 and C 2 cation columns. 
6.1012.X00	**Sample pretreatment cartridge IC-RP** For non-polar solid phase extraction. Removes organic substances; for the enrichment of heavy metals. With Luer connection. 6.1012.000: set of 50 6.1012.100: set of 10 
6.1012.X10	**Sample pretreatment cartridge IC-H** Cation exchanger in H^+ form. Removes interfering cations, CO_3^{2-}, HCO_3^- or for alkaline samples. With Luer connection. 6.1012.010: set of 50 6.1012.110: set of 10 

Order No.	Description	
6.1012.X20	**Sample pretreatment cartridge IC-Ag** Cation exchanger in Ag^+ form. Removes halides. With Luer connection. 6.1012.020: set of 50 6.1012.120: set of 10	
6.1012.X30	**Sample pretreatment cartridge IC-OH** Cation exchanger in OH^- form. For highly acidic samples. With Luer connection. 6.1012.030: set of 50 6.1012.130: set of 10	
6.1012.200	**Sample pretreatment cartridge Chromafix C18** Removes organic substances (not suitable for fluoride determinations). With Luer connection. 6.1012.200: set of 50	
6.2027.050	**Column holder** Diameter d = 15.0 mm	
6.2821.010	**PTFE gasket** Spare part for 6.1005.000, 6.1005.010, 6.1005.030, 6.1007.000 and 6.1010.000 separating columns; set of 4.	
6.2821.020	**Steel mesh** Spare part for 6.1005.000, 6.1005.010, 6.1005.030, 6.1007.000 and 6.1010.000 separating columns; set of 4.	
6.2821.050	**Twin cartridge holder** To hold precolumn cartridges; installed in the inlet capillary of the separating column.	
6.2828.100	**Glass cartridge holder** To hold the 6.1006.0020 Column cartridge METROSEP Anion Dual 1.	
6.2828.110	**Precolumn cartridge holder** To hold the 6.1006.0030 Precolumn cartridge METROSEP Anion Dual 1.	

Order No.	Description
6.2828.120	**Glass cartridge holder** To hold the 6.1006.0040 Column cartridge METROSEP Anion Dual 1. 
6.2832.000	**Suppressor rotor** Replacement cartridge for Metrohm suppressor module. 
6.2832.010	**Connection piece for suppressor rotor** with input and output leads 

6.3.3 Additional devices and cables

Order No.	Description
6.2125.010	**Cable** Connecting cable 792 Basic IC (RS232 interface) – PC Adapter cable 25-pin to 9-pin. 
6.2125.020	**Cable** RS232 extension cable 
6.2125.060	**Cable** Connecting cable 792 Basic IC (RS232 interface) – PC 
6.2125.110	**Cable** Connecting cable 792 Basic IC (RS232 interface) – PC 

6.4 Warranty and conformity

6.4.1 Warranty

The warranty on our products is limited to defects that are traceable to material, construction or manufacturing error that occur within 12 months from the day of delivery. In this case, the defects will be rectified in our workshops free of charge. Transport costs are to be paid by the customer.

For day and night operation, the warranty is limited to 6 months.

Glass breakage in the case of electrodes or other parts is not covered by the warranty. Checks, which are not a result of material or manufacturing faults, are also charged during the warranty period. For parts of outside manufacture insofar as these constitute an appreciable part of our instrument, the warranty stipulations of the manufacturer in question apply.

With the regard to the guarantee of accuracy, the technical specifications in the instruction manual are authoritative.

Concerning defects in material, construction or design as well as the absence of guaranteed features, the orderer has no rights or claims except those mentioned above.

If damage of the packaging is evident on receipt of a consignment or if the goods show signs of transport damage after unpacking, the carrier must be informed immediately and a written damage report demanded. Lack of an official damage report releases Metrohm from any liability to pay compensation.

If any instruments and parts have to be returned, the original packaging should be used if at all possible. This applies above all to instruments, electrodes, burette cylinders and PTFE pistons. Before embedment in wood shavings or similar material, the parts must be packed in a dust-proof package (for instruments, use of a plastic bag is imperative). If open assemblies are enclosed in the scope of delivery that are sensitive to electromagnetic voltages (e.g. data interfaces etc.) these must be returned in the associated original protective packaging (e.g. conductive protective bag). (Exception: assemblies with built-in voltage source belong in a non-conductive protective packaging). For damage, which arises as a result of non-compliance with these instructions, no warranty responsibility whatsoever will be accepted by Metrohm.

6.4.2 EU Declaration of conformity

CE

EU Declaration of Conformity

The METROHM AG company, Herisau, Switzerland hereby certifies, that the instrument:

792 Basic IC

meets the requirements of EC Directives 89/336/EEC and 73/23/EEC.

Source of the specifications:

EN 50081-1	Electromagnetic compatibility, basic specification; Emitted Interference
EN 50082-1	Electromagnetic compatibility, basic specification; Interference Immunity
EN 61010	Safety requirements for electrical laboratory measurement and control equipment

Description of the instrument:

Instrument for recording ion chromatograms with electronic or chemical suppression.

Herisau, April 15, 2001

Dr. J. Frank	Ch. Buchmann
Development Manager	Production and Quality Assurance Manager

6.4.3 Certificate of conformity and system validation

Certificate of Conformity and System Validation

This is to certify the conformity to the standard specifications for electrical appliances and accessories, as well as to the standard specifications for security and to system validation issued by the manufacturing company.

Name of commodity:	792 Basic IC
System software:	Stored in ROMs
Name of manufacturer:	Metrohm Ltd., Herisau, Switzerland
Principal technical information:	Voltages: 100…120, 220…240 V Frequency: 50…60 Hz

This Metrohm instrument has been built and has undergone final type testing according to the standards:

IEC801-2/IEC1000-4-2 (class 3), IEC801-3/ IEC1000-4-3 (class 2), IEC801-4/IEC1000-4-4 (class 4), IEC801-5/IEC1000-4-5 (class 2/3), IEC801-6/IEC1000-4-6 (class 2), EN50082-1, EN61000-3-2/3/IEC1000-3-2/3, EN61000-4-11/IEC1000-4-11, IEC61326 (class B), EN55011 (class B), EN55022 (class B), EN50081-1 — *Electromagnetic compatibility*

IEC1010, EN61010, UL3101-1 — *Security specifications*

It has also been certified by the Swiss Electrotechnical Association (SEV), which is member of the International Certification Body (CB/IEC).

The technical specifications are documented in the instruction manual.

The system software, stored in Read Only Memories (ROMs) has been validated in connection with standard operating procedures in respect to functionality and performance. The features of the system software are documented in the instruction manual.

Metrohm Ltd. is holder of the SQS-certificate of the quality system ISO 9001 for quality assurance in design/development, production, installation and servicing.

Herisau, April 15, 2001

Dr. J. Frank	Ch. Buchmann
Development Manager	Production and Quality Assurance Manager

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