*S*EDI*G*RAPH™ III *P*LUS

PARTICLE SIZE ANALYZER

*O*PERATOR *M*ANUAL

512-42835-01
Sep 2022
(Rev B)

mi micromeritics®

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MICROMERITICS INSTRUMENT CORPORATION warrants for one year from the date of shipment each instrument it manufactures to be free from defects in material and workmanship impairing its usefulness under normal use and service conditions except as noted herein.

Our liability under this warranty is limited to repair, servicing and adjustment, free of charge at our plant, of any instrument or defective parts when returned prepaid to us and which our examination discloses to have been defective. The purchaser is responsible for all transportation charges involving the shipment of materials for warranty repairs. Failure of any instrument or product due to operator error, improper installation, unauthorized repair or alteration, failure of utilities, or environmental contamination will not constitute a warranty claim. The materials of construction used in MICROMERITICS instruments and other products were chosen after extensive testing and experience for their reliability and durability. However, these materials cannot be totally guaranteed against wear and/or decomposition by chemical action (corrosion) as a result of normal use.

Repair parts are warranted to be free from defects in material and workmanship for 90 days from the date of shipment.

No instrument or product shall be returned to MICROMERITICS prior to notification of alleged defect and authorization to return the instrument or product. All repairs or replacements are made subject to factory inspection of returned parts.

MICROMERITICS shall be released from all obligations under its warranty in the event repairs or modifications are made by persons other than its own authorized service personnel unless such work is authorized in writing by MICROMERITICS.

The obligations of this warranty will be limited under the following conditions:

1. Certain products sold by MICROMERITICS are the products of reputable manufacturers, sold under their respective brand names or trade names. We, therefore, make no express or implied warranty as to such products. We shall use our best efforts to obtain from the manufacturer, in accordance with his customary prac-tice, the repair or replacement of such of his products that may prove defective in workmanship or materials. Ser-vice charges made by such manufacturer are the responsibility of the ultimate purchaser. This states our entire liability in respect to such products, except as an authorized person of MICROMERITICS may otherwise agree to in writing.
2. If an instrument or product is found defective during the warranty period, replacement parts may, at the dis-cretion of MICROMERITICS, be sent to be installed by the purchaser, e.g., printed circuit boards, check valves, seals, etc.
3. Expendable items, e.g., sample tubes, detector source lamps, indicator lamps, fuses, valve plugs (rotor) and stems, seals and O-rings, ferrules, etc., are excluded from this warranty except for manufacturing defects. Such items which perform satisfactorily during the first 45 days after the date of shipment are assumed to be free of manufacturing defects.

Purchaser agrees to hold MICROMERITICS harmless from any patent infringement action brought against MICROMERITICS if, at the request of the purchaser, MICROMERITICS modifies a standard product or manufactures a special product to the purchaser's specifications.

MICROMERITICS shall not be liable for consequential or other type damages resulting from the use of any of its products other than the liability stated above. This warranty is in lieu of all other warranties, express or implied, including but not limited to, the implied warranties of merchantability or fitness for use.

CORPORATE PROFILE

Micromeritics Instrument Corporation is the world's leading supplier of high-performance systems to characterize particles, powders and porous materials with a focus on physical properties, chemical activity, and flow properties. Our technology portfolio includes: pycnometry, adsorption, dynamic chemisorption, particle size, intrusion porosimetry, powder rheology, and activity testing of catalysts. The company has R&D and manufacturing sites in the USA, UK, and Spain, and direct sales and service operations throughout the Americas, Europe, and Asia. Micromeritics systems are the instruments-of-choice in more than 10,000 laboratories of the world's most innovative companies and prestigious government and academic institutions. Our world-class scientists and responsive support teams enable customer success by applying Micromeritics technology to the most demanding applications. For more information, please visit www.Micromeritics.com.

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    Support@Micromeritics.com

ABOUT THIS MANUAL

The following can be found on the Micromeritics web page (www.Micromeritics.com).

- Error Messages document (PDF)
- Parts and Accessories

The following symbols or icons indicate safety precautions and/or supplemental information and may appear in this manual:

NOTE — Notes contain important information applicable to the topic.

CAUTION — Cautions contain information to help prevent actions that may damage the analyzer or components.

WARNING — Warnings contain information to help prevent actions that may cause personal injury.

GENERAL SAFETY

C A U T I O N   X - R A Y S

THIS EQUIPMENT PRODUCES X-RAYS WHEN ENERGIZED

> ⚠ Do not modify this instrument without the authorization of Micromeritics Service Personnel.

Any piece of laboratory equipment can become dangerous to personnel when improperly operated or poorly maintained. All employees operating and maintaining Micromeritics instruments should be familiar with its operation and should be thoroughly trained and instructed on safety.

- Read the operator manual for any special operational instructions for the instrument.
- Know how the instrument functions and understand the operating processes.

> ⚠
> - Wear the appropriate personal protective equipment when operating this instrument — such as eye protection, lab coat, protective gloves, etc.
> - When lifting or relocating the instrument, use proper lifting and transporting devices for heavy instruments. Ensure that sufficient personnel are available to assist in moving the instrument. The 5125 SediGraph II Plus weighs approximately 43 kg (95 lb). The MasterTech weighs approximately 18 kg (40 lb).
> - Always pay attention to the safety instructions provided on each label affixed to the instrument and do not alter or remove the labels. When inspecting the instrument, ensure that the safety labels have not become worn or damaged.
> - Proper maintenance is critical to personnel safety and smooth instrument operation and performance. Instruments require regular maintenance to help promote safety, provide an optimum end test result, and to prevent costly down time. Failure to practice proper maintenance procedures can lead to unsafe conditions and shorten the life of the instrument.
> - Improper handling, disposing of, or transporting potentially hazardous materials can cause serious bodily harm or damage to the instrument. Always refer to the MSDS when handling hazardous materials. Safe operation and handling of the instrument, supplies, and accessories is the responsibility of the operator.

INTENDED USE

The SediGraph III Plus determines particle size by using the highly accurate and reproducible sedimentation technique which measures the gravity-induced settling rates of different size particles in a liquid with known properties. This is a simple yet extremely effective technique for providing particle size information for a wide variety of materials.

> ⚠️ The instrument is intended to be operated by trained personnel familiar with the proper operation of the equipment recommended by the manufacturer and as well as relevant hazards involved and prevention methods. Other than what is described in this manual, all use is seen as unintended use and can cause a safety hazard.

> ✏️ The instrument is intended to be used as per applicable local and national regulations.

TRAINING

It is the customer's responsibility to ensure that all personnel operating or maintaining the equipment participate in training and instruction sessions. All personnel operating, inspecting, servicing, or cleaning this instrument must be properly trained in operation and machine safety before operating this instrument.

ENVIRONMENTALLY FRIENDLY USE PERIOD

SediGraph III Hazardous Substances Table

Part Name	Hazardous Substances					
	Lead (Pb)	Mer-cury (Hg)	Cad-mium (Cd)	Hexa-valent Chromium (Cr (VI))	Poly-brominated biphenyls (PBB)	Poly-brominated diphenyl eth-ers (PBDE)
Cover	x	o	o	o	o	o
Power Supplies	x	o	o	o	o	o
Printed Circuit Boards	x	o	o	o	o	o
Cables, Connectors & Trans-ducers	x	o	o	o	o	o

MasterTech Hazardous Substances Table

Part Name	Hazardous Substances					
	Lead (Pb)	Mercury (Hg)	Cadmium (Cd)	Hexavalent Chromium (Cr (VI))	Polybrominated biphenyls (PBB)	Polybrominated diphenyl ethers (PBDE)
Cover	o	o	o	o	o	o
Power Supplies	o	o	o	o	o	o
Printed Circuit Boards	x	o	o	o	o	o
Ultrasonic Driver and Probe	x	o	o	o	o	o
Cables & Connectors	x	o	o	o	o	o

o   Hazardous substance is below the specified limits as described in SJ/T11363-2006.

x   Hazardous substance is above the specified limits as described in SJ/T11363-2006.

The Environmentally Friendly Use Period (EFUP) for all enclosed products and their parts are per the symbol shown here unless otherwise marked. Certain parts may have a different EFUP (for example, battery modules) and are marked to reflect such. The Environmentally Friendly Use Period is valid only when the product is operated under the conditions defined in the product manual.

Symbols that may appear on your instrument

The following symbols or icons indicate safety precautions and/or supplemental information and may appear on your instrument:

Use extreme caution when working on the instrument where one of these symbols may be displayed. These symbols indicate the part may be hot and cause serious burns.

Use the cotton gloves provided in the accessory when handling heated surfaces. These cotton gloves are not intended to protect hands when heated surfaces are above 60 °C.

When working on the instrument where this symbol is displayed, refer to your Micromeritics' instruction manual for additional information.

When this symbol is displayed, toxic or flammable gases require proper venting of exhaust.

This symbol can also indicate the instrument uses mercury which is an extremely toxic substance. Read the Material Safety Data Sheet (MSDS) and be aware of the hazards of mercury and know what to do in the event of a spill or an exposure incident

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SediGraph III Plus Operator Manual
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1 ANALYZER COMPONENTS FOR SEDIGRAPH III PLUS

Parts and accessories are located on the Micromeritics web page.

> ✏️ The SediGraph was surveyed for radiation leakage prior to shipping. The radiation detected was well below the government limits. See *SediGraph Safety on page 1 - 4*.

FRONT COMPONENTS
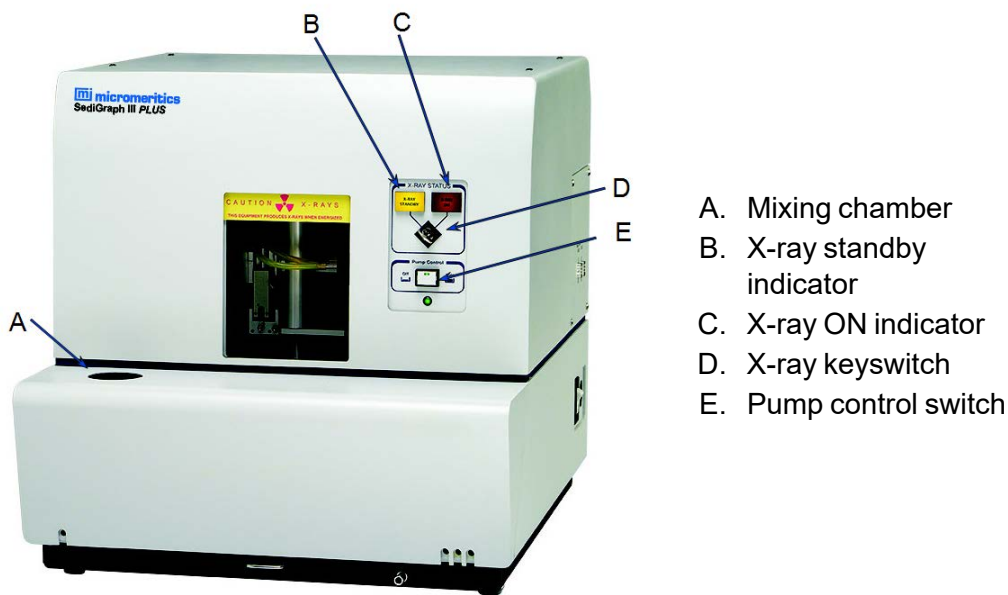
A. Mixing chamber
B. X-ray standby indicator
C. X-ray ON indicator
D. X-ray keyswitch
E. Pump control switch

Front Components

Component	Description
Mixing chamber	Contains the sample during an analysis and maintains sample dispersion throughout the analysis with a built-in stirrer.
Pump control Off/Auto switch	Selects the operational mode of the mixing and cell pumps. The OFF position turns off power to the pumps. The Auto position places the pumps in automatic mode.

Front Components (continued)

Component	Description
X-ray keyswitch	Sets the X-ray to either the ON or STANDBY position.
X-ray ON indicator	Illuminates when X-rays are being generated. The X-ray keyswitch must be turned to the X-RAY ON position.
X-ray standby indicator	Illuminates when the analyzer is ON and the X-ray keyswitch is turned to the standby position, when the door to the analysis compartment is open, or any interlock is disengaged.

SIDE PANEL COMPONENTS
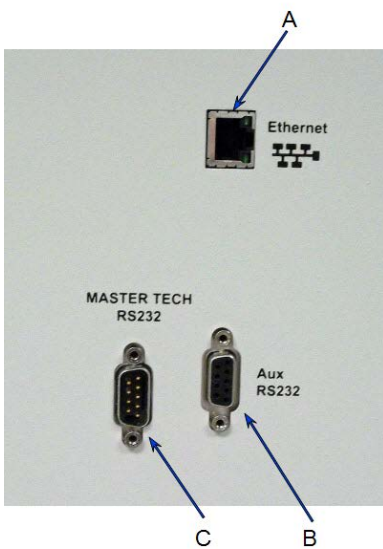
A. Ethernet port
B. Aux RS-232
C. MasterTech RS-232
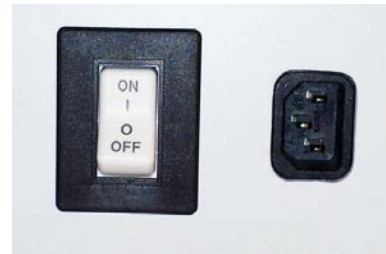
Power switch and electrical inlet

Side Panel Components

Component	Description
Aux RS-232 port	For Micromeritics use only.
Ethernet Port	Port for a shielded Ethernet cable allowing communication between the analyzer and the computer.
MasterTech RS-232 port	For connecting the MasterTech to the analyzer.

EQUIPMENT OPTIONS AND UPGRADES

Parts and accessories are located on the Micromeritics web page.

Option	Description
MasterTech	An automatic sampling device that operates in conjunction with the SediGraph.

The MasterTech allows up to 18 predispersed samples to be "queued up" and run consecutively and unattended. It allows samples to be redispersed either by stirring only or by stirring and disruption with an ultrasonic probe. The MasterTech transfers each sample to the SediGraph, then after analysis is complete, rinses the mixing chamber, the connecting tubing, and the stirrer.

The MasterTech 052 consists of three main components: the arm assembly, the body, and the beaker tray. The arm assembly controls the movement of the stirring rotor, the ultrasonic probe, and the transfer tube. The body houses the electronics, the transfer pump, the front panel controls, and supports the beaker tray, which holds up to 18 sample beakers.

During operation, the beaker tray is loaded with beakers containing 60 to 80 mL of predispersed sample.

When the SediGraph is ready for a sample, the tray rotates until the correct sample is underneath the head of the arm assembly. The head then lowers until it rests on top of the beaker. Stirring action begins and continues for a user-specified length of time. The ultrasonic probe can be activated to aid in redispersion.

When redispersion is complete, the pump transfers most of the sample to the SediGraph, where it is loaded into the mixing chamber. Analysis now proceeds as if the mixing chamber was filled manually with predispersed sample. When analysis is complete, the contents of the mixing chamber are disposed to the waste container, and a small amount of rinsing fluid is back-flushed to the MasterTech to rinse the tubing. The arm rises so that the rinse liquid removes the sample residue from the stirrer blades and transfer tube. Once rinsing is complete, the arm rises to the Up position. The MasterTech is now ready to proceed to the next sample.

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SEDIGRAPH SAFETY

In a continuing effort to provide maximum safety to operators of Micromeritics equipment, and to ensure full compliance with all known government safety regulations regarding X-rays, Micromeritics provides a high level of X-ray safety on its SediGraph line.

GENERAL

The SediGraph Particle Size Analysis System employs soft X-rays to detect relative particle concentration because X-ray absorption is directly proportional to particle mass. This X-ray beam is inaccessible to the operator at all times due to cabinet construction, a door enclosing the cell compartment, a mechanical shutter that blocks the beam's entry into the cell compartment when that door is opened more than 12 mm (0.5 in.), and electrical interlocks that interrupt power to the X-ray tube when the cell compartment door or top panel is opened.

X-RAY SOURCE

X-rays are generated by a small, air-cooled tube having a tungsten target inclined at 55° to a thin beryllium window. It is operated at a potential of 13,600 VDC with a power input of less than 41 watts. The greatest value the anode voltage can attain in a malfunction is 15,000 VDC. Only the tungsten L-lines are excited, of which the L is primary. This primary radiation has an energy of approximately 10,000 eV and a corresponding wavelength of 0.125 nm (1.25 angstroms). The integrated radiation density of the direct, unattentuated beam over a 25 mm circular aperture is between 300 and 400 milliroentgens per hour. The X-ray beam is, for example, 60% blocked by a 51 µm (0.002 in.) thick film of the plastic polyvinyl chloride and essentially completely blocked by 130 µm (0.005 in.) thick steel. Nevertheless, the shutter mechanism should never be defeated.

Radiation levels outside the instrument or in the cell compartment when the compartment door is open are well below 0.5 milliroentgen per hour. Most jurisdictions require the registration of radiation producing devices regardless of kind or intensity level. Check with the appropriate authority in your area[1].

Since a potential of 13,600 VDC and a current of up to 3 mA generate the X-rays, the instrument should be unplugged from the power source before any panel is removed for any purpose. This ensures that X-ray generation ceases and high voltages are eliminated.

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[1] Based on the above information, SediGraph users in the State of Georgia have regularly been granted waivers to the State of Georgia "Rules and Regulations for X-ray" by the Radiological Health Section of the Georgia Department of Human Resources.

WARNING AND INDICATOR LIGHTS

The SediGraph control switches and indicators are located on the front panel of the analytical unit and include a keyswitch to turn the X-ray tube on. The key is held captive when the keyswitch is on. There are two warning lights: An amber X-RAY STANDBY light and a red X-RAY ON light. With the analytical unit connected to the electric mains and the power switch on, the amber X-RAY STANDBY light is lit. Turning the keyswitch to the ON position causes the red X-RAY ON light to illuminate signaling that power is applied to the X-ray tube. When the X-RAY ON light is illuminated, power is applied to both the filament and anode of the X-ray tube. If the X-RAY ON lamp filament burns out, then power is interrupted to both the filament and anode of the X-ray tube. In order for power to be supplied to the X-ray tube filament and anode when a failure (open circuit) occurs in the X-RAY ON light, concurrent failures must occur in two independent circuits such that these circuits continue to supply power to the X-ray tube.

The SediGraph has magnetically actuated reed switches. These switches are in series with the X-RAY ON lamp filament. Whenever the top or rear panel of the SediGraph is removed, the cell-compartment door is opened, the fluid module is removed, or the X-RAY ON lamp filament burns out (opens), both filament and anode power to the X-ray tube are interrupted.

These switches are in addition to the mechanical shutter which operates when the cell compartment door is opened, blocking X-rays and removes filament power when the top cover is removed. During the last 12 mm (0.5 in.) of travel of the cell compartment door to the fully closed position, the sliding pin actuates the gravity-operated, spring-assisted shutter so that the shutter is opened to allow X-rays to enter the cell compartment. When the cell compartment door is opened from the fully closed position, the shutter is actuated during the first 12 mm (0.5 in.) of travel to close and block x-rays from entering the cell compartment. As long as the cell compartment door remains open, the shutter blocks X-rays from entering the cell compartment and the X-ray Detection Indicator remains off.

Now, when the cell compartment door is opened, not only does the shutter block the X-ray beam but the power to the X-ray tube also is interrupted.

SEDIGRAPH X-RAY CERTIFICATION

X-radiation in the Micromeritics SediGraph III Plus is electronically generated by a tungsten target x-ray tube operated at 13,600 volts of regulated DC. X-ray tube current is nominally 1.0 mA and cannot exceed 3.5 mA in the event of any failure of circuit components . The x-rays are derived from excitation of the L electron shell (primarily L*a*). The operating wavelength corresponds to approximately 8.3KeV of photon energy. The integrated radiation density of the direct, unattenuated beam over a 25 mm circular aperture is between 300 and 400 milliroentege ns per hour. By definition, all x-rays consist of ionizing radiation. **There is no emission of x-radiation unless the x-ray tube is supplied with electrical power. When power is removed from the x-ray tube, there is no generation of x-rays and there is no residual x-ray radiation nor any other type of radiation.**

The SediGraph III Plus is designed to prevent x-radiation exposure of personnel through the use of interlocks and shielding. All SediGraph III Pius instruments are tested for x-radiation leakage. Maximum allowable external levels are 0.02 mrem/hr (200 nSv/hr) at 0.05 m (5 cm). Typical value is 0.002 mrem/hr (20 nSv/hr).

Primary electrical power to the x-ray tube is controlled by a master key switch. The key is removable to prevent unauthorized personnel from operating the instrument.

The SediGraph III Plus has three types of safety interlocks used to prevent x-radiation exposure. Three interlock switches are located under the top panel of the SediGraph III Plus and a magnetic switch is mounted on the sample compartment door. When any of the switches are actuated, electrical power to the x-ray tube is removed and the emission of x-radiation ceases. Top panel removal and replacement subsequently requires that the key switch be cycled to restore x-ray generation.

Redundancy is built into the sample compartment door interlocks. In addition to the electrical door interlock, the SediGraph III Plus also has a gravity-operated mechanical shutter which blocks the x-ray beam from entering the sample compartment when the sample compartment door begins to open. Both of these door interlocks function before the door moves out of the frame grooves.

Two warning lights on the front of the SediGraph III Plus indicate the status of the x-ray tube. The X-RAY STANDBY light indicates that the potential of emitting x-rays exists but that x-rays are not now present. X-ray emission from standby status could require only a single switch operation. The X-RAY ON light indicates that x-rays are being produced. If the X- RAY ON light bums out, this is detected by the electronics, which will not allow x-rays to be produced until filament continuity is re-established.

The SediGraph III Plus cabinet, analysis compartment , x-ray compartment cover, and base plate are designed as x-ray shields . In additional , extra shield panels are mounted inside the SediGraph III Plus to further minimize the likelihood of any x-ray exposure if other shields are removed (e.g., in servicing).

SPECIFICATIONS FOR THE SEDIGRAPH III PLUS

Particle Diameter Range	300 to 0.1 micrometers Equivalent Spherical Diameter
Wetted Materials	Stainless steel, Teflon impregnated anodized aluminum, nickel plated aluminum, nylon, polypropylene, polystyrene, Tygon and Pharmed tubing, tungsten carbide, Ertalyte, Viton, Buna-N, and epoxy.
Sample Size	50 mL of dispersed sample. Precise concentration is not required.
Suspending Liquids	Any liquid compatible with sample cell materials and not highly absorptive of X-rays. Typical liquids are water, glycols, mineral oils, SediSperse, and alcohols.

Electrical

Voltage	100-240 VAC
Power	450VA, maximum
Frequency	50/60Hz
Overvoltage category	II

Physical

Height	52 cm (21 in.)
Width	51 cm (20 in.)
Depth	58 cm (23 in.)
Weight	43 kg (95 lbs)

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Environment

Temperature	10 to 40 °C (50 to 104 °F), operating -10 to 55 °C (14 to 131 °F), non-operating
Humidity	20 to 80% relative, non-condensing
Indoor or outdoor use	Indoor only (not suitable for wet locations) Altitude: 2000 m max (6500 ft) Pollution degree of the intended environment: 2
Degree of Ingress Protection	IPX0

Computer Requirements

Operating System	Windows 10 or higher operating system is required.
Desktop Installation Required	The application should not be installed on a network drive with shared access. Multiple users cannot operate the application at the same time. **CAUTION** Ensure the "Sleep" setting on the desktop is set to "Never" to avoid interruption while running an analysis. If this occurs, the application loses network connectivity with the instrument and a communications error will be reported. A restart of the Windows application may be required if automatic reconnection is not successful.
10 Base T or 100 Base T Ethernet Port	If the computer is to be connected to a network, two Ethernet ports are required. If more than one Ethernet-based unit is connected to the same computer, an Ethernet switch will also be required.
Read/Write Permissions	All application users will need Read/Write permission to all directories and subdirectories where the application is installed.
Drives	USB port

Due to continuous improvements, specifications are subject to change without notice.

MASTERTECH COMPONENTS (OPTIONAL ACCESSORY)

Parts and accessories are located on the [Micromeritics](link) web page.
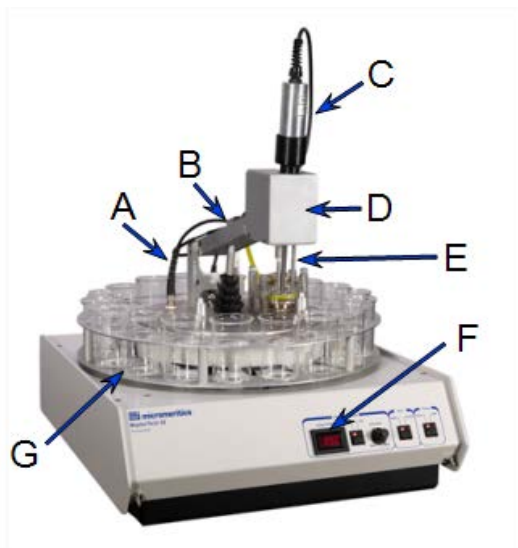
A. Probe cable
B. Arm assembly
C. Ultrasonic probe
D. Arm
E. Cylinder Slots (one on each side)
F. Ultrasonic power display
G. Tray

The MasterTech is an optional accessory that features an ultrasonic probe with a 1/4 in. probe tip to supply more dispersion power to the sample. Power to the probe tip is adjustable and the driving circuit is self-tuning for maintaining efficient and consistent sonic energy from the input power. A digital readout on the front panel assures that the desired power is reached for dispersing each sample and that the same power is applied each time the method is repeated.

When the instrument is ready to analyze a sample, the tray rotates until the selected sample is underneath the arm assembly. The arm assembly lowers and stirring begins. Stirring continues until the sample is thoroughly resuspended. At a predetermined time (specified through the software), the ultrasonic probe can be activated to aid in dispersion. After redispersion is complete, the MasterTech transfers the sample to the mixing chamber of the SediGraph for analysis.

![micromeritics logo]
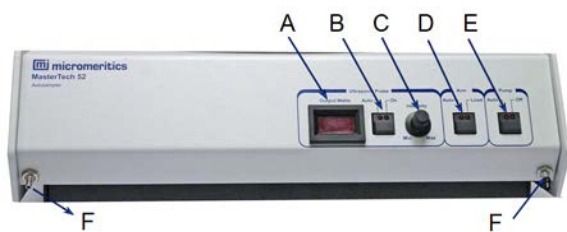
FRONT COMPONENTS

A. Intensity display
B. Ultrasonic probe AUTO/ON switch
C. Intensity control
D. Arm AUTO/LOAD switch
E. Pump AUTO/OFF switch
F. Transfer tube connector

Front Components

Component	Description
Arm AUTO/LOAD switch	The LEDs on the switch indicate the mode of operation. **CAUTION** — Do not press the ARM AUTO/LOAD switch while an automatic operation is in progress. ■ **AUTO**. Places the arm under automatic control. ■ **LOAD**. Raises the arm to remove or load the tray. This switch will not work unless the computer is installed and the analyzer software is operating. Ensure the LOAD switch has been released when finished removing or loading the beaker tray. The MasterTech will not operate if the arm is in the Load position.
Intensity control	■ Turn clockwise to increase the intensity of the probe. ■ Turn counterclockwise to decrease the intensity.
Power Display	Displays the power being generated by the ultrasonic probe.
Pump AUTO/OFF switch	The LEDs on the switch indicate the mode of operation. ■ **AUTO**. Places the pump under automatic control. ■ **OFF**. Powers off the pump.
Transfer tubing connectors	Attach the tubing to the side that coordinates with the one used on the MasterTech pump during installation of the MasterTech.

Front Components (continued)

Component	Description
Ultrasonic probe AUTO/ON switch	LEDs on the switch indicate the mode of operation. ■ **AUTO** position. Places the probe under automatic control. ■ **ON** position. Turns on the probe. Remove the probe from its holder and place it in the liquid before turning on the probe. ⚠ **CAUTION** Never turn the probe on unless the tip is submerged in liquid. After using the probe, press the switch again to place the probe in automatic mode. Then replace it in its holder.

REAR COMPONENTS
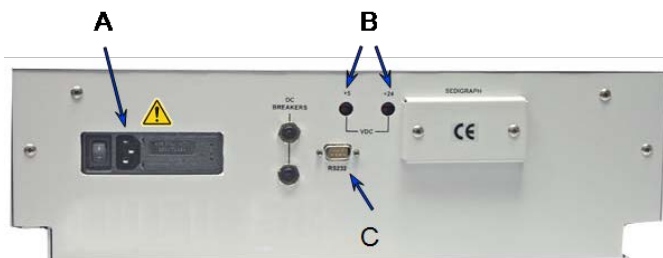
A. Power switch, power connector, and voltage selector card
B. +5 and +24 VDC indicators
C. RS-232 connector

Rear Panel Components

Component	Description
+5 and +24 VDC Indicators	Illuminates when appropriate power is present in the MasterTech.
Power switch, power connector, voltage selector card	Powers the MasterTech on and off.
RS-232 Connector	Connects the MasterTech to the analyzer.

SPECIFICATIONS FOR THE MASTERTECH

Sample Capacity	18 per tray; continues indefinitely if tray is replenished
Sample Size	0.5 to 4 g of powder in 60 to 80 mL of liquid
Sample Type	Any suitable for SediGraph 5100 analysis
Suspending liquids	Any liquid compatible with sample cell materials and not highly absorptive of X-rays. Typical liquids are water, glycols, kerosene, mineral oils, alcohols, Sedisperse, and mineral spirits.
Wetted Materials	Glass, stainless steel, Viton, Tygon, Silicone rubber, Polypropylene

Electrical

Voltage	100/120/220/240VAC ± 10%
Frequency	50/60 Hz
Power	180 VA maximum
Current	1.25 A (100/120VAC) 0.75 A (220/240VAC)

Environment

Temperature	10 to 40 °C (50 to 104 °F), operating -10 to 55 °C (14 to 131 °F), non-operating
Humidity	20 to 80% relative, non-condensing
Indoor or outdoor use	Indoor only (not suitable for wet locations) Altitude: 2000 m max (6500 ft) Pollution degree of the intended environment: 2
Degree of Ingress Protection	IPX0

Physical

Height	69 cm (27.25 in.) maximum at load position
Width	46 cm (18.25 in.)
Depth	54 cm (21.25 in.)
Weight	18 kg (40 lbs)

Due to continuous improvements, specifications are subject to change without notice.

2 ABOUT THE SOFTWARE

The analyzer allows other computer programs to run while an automatic operation is in progress. The *Help* menu provides access to the online operator manual.

Report options can be specified when creating the sample file. When running an analysis, data gathered during the analysis process are compiled into predefined reports. Reports can also be defined and generated after an analysis has been run. Each selected report is displayed on its own tab and reflects data collected during the analysis.

MENU STRUCTURE

All program functions use standard Windows menu functionality.

Main Menu Bar Options

Selections	Description
File	Use to manage files used by the application — such as sample files, analysis conditions files, report options files, etc.
Unit [*n*]	Use to perform analyses, calibrations, and other analyzer operations. Up to two analyzers can be installed on the same computer.
Reports	Use to start or initiate reports and view the results.
Options	Use to change presentation options, set the method and active metals defaults, configure signal calibration, manage libraries, select units, and create report styles.
Window	Use to manage open windows and display a list of open windows. A checkmark appears to the left of the active window.
Help	Use to access the embedded operator manual, Micromeritics web page, and information about the application.

COMMON FIELDS AND BUTTONS

The fields and buttons in the following table are located in multiple windows throughout the analyzer application and have the same description or function. Fields and button descriptions not listed in this table are found in tables in their respective sections. All entry fields will accept information when using a bar code reader.

Common Fields and Buttons

Selections	Description
Add	Adds an item to the list.
Add Log Entry	Use to enter information that will display in the sample log report that cannot be recorded automatically through the application. Click the button again to enter multiple log entries.
Append	Use to insert one row at the end of a table.
Autoscale	When enabled on report parameters windows, allows the x- and y-axes to be scaled automatically. *Autoscale* means that the x- and y- ranges will be set to show all the data. If *Autoscale* is not selected, the entered range is used.
Axis Range	On report parameters windows, the *From* / *To* fields are enabled when *Autoscale* options are not selected. Enter the starting and ending values for the x- and/or y-axes.
Bar Code *(default field label name)*	Use to enter additional information about the sample, such as a sample lot number, sample ID, etc.
Browse	Searches for a file.
Cancel	Discards any changes or cancels the current process.
Clear	Use to clear the table entries and display only one default value.
Close	Closes the active window and displays a prompt to either accept or reject changes.
Close All	Closes all active windows. If changes were made and not yet saved, a prompt displays for each changed file providing the option to save the file.
Comments	Enter comments to display in the report header about the sample or analysis.
Copies	Selects the number of copies to print. This field is only enabled when *Print* is selected.
Delete	When working with tables, deletes the selected information.
Destination	Selects the report destination.

Common Fields and Buttons (continued)

Selections	Description
Edit	When working with report parameters, highlight the item in the *Selected Reports* list box and click **Edit** to modify the report details.
Exit	Exits the application. If a file is open with unsaved changes, a prompt displays the option to save the changes and exit or exit the application without saving the changes. If an analyzer is currently operating, an additional prompt displays to confirm exiting from the software.
Export	Exports data in a sample file as a .TXT, .XML or .XLS file. When saved to a file, the data can be imported into other applications.
File	Selects the destination directory. Enter a new file name in the *File name* field or accept the default. Select to save the file as a spreadsheet (.XLS), a portable document format (.PDF), or an ASCII text (.TXT) file format.
File name	Selects a file name from the list shown or enter a file name. If the required file type is not shown, select the type of file from the list.
From / To	Indicates the *From* and *To* range for x- and/or y-axes when working with report parameters windows.
Insert	Inserts one row above the selected row in the table.
List	Creates a list of samples or other types of files. The list will contain the file name, date/time the file was created or last edited, file identification, and file status.
Name	Contains a list of files in the selected directory or library.
Next	Moves to the next window or next step.
OK	Saves and closes the active window.
Open	Opens the selected file. Alternatively, double-click the file name in the Name column to open the file.
Prev	Moves to the previous window.
Preview	Previews predefined reports. Click the tabs at the top of the window to preview each selected report. When an analysis has not been run on a sample, this button is disabled.
Print	Sends the report to the selected destination (screen, printer, or file).
Remove	Removes the selected file or files from the list.
Replace	Selects another file where the values will replace the current file's values.

Common Fields and Buttons (continued)

Selections	Description
Replace All	Selects another .SMP file where the values will replace all values for the active sample file. The original file will remain unchanged. No analysis data is added to the file. The only information added is sample information, material properties, liquid properties, analysis, and reporting parameters.
Report	Displays a window to specify report output options.
Save	Saves changes.
Save As	Saves a file in the active window under a different file name. A portion can be saved as a separate, stand-alone file, such as Analysis Conditions or Report Options, when saving sample information.
Start	Starts the report, test, analysis, or operation.
Start Date	Displays a calendar to select the start date for the report.
View	**Operation**. Displays the data from the current analysis. **Instrument Log**. Displays recent analyses, calibrations, errors, or messages. Enabled only in Service Test Mode. **Instrument Schematic**. Displays a schematic of the analyzer system.

FILE STATUS

In the *File Selector* window, the *Mic Description* column and the *Mic Status* column display the file description and file status. The *File Selector* incorporates standard Windows features for resizing windows, reordering and repositioning columns, and right-clicking an entry to display a menu of standard Windows functions.

File Status

File Status	Description
Analyzing	Sample files that are currently used for analysis.
Complete	Sample files used in an analysis that is completed.
Entered	Sample files containing manually entered data.
No Analysis	Sample files that have not been used to perform an analysis.

File Type and File Name Extension

File Type	File Name Extension
Analysis Conditions	.ANC
Export to Disk (Text)	.TXT
Liquid Properties	.LIQ
Report Options	.RPO
Report to Disk	.RPT
Sample Information	.SMP

KEYBOARD SHORTCUTS

Shortcut keys can be used to activate some menu commands. Shortcut keys or key combinations (when applicable) are listed to the right of the menu item.

Certain menus or functions can also be accessed using the **Alt** key plus the underlined letter in the menu command. For example, to access the *File* menu, press **Alt + F**, then press the underlined letter on the submenu (such as pressing **Alt + F**) then pressing **O** to open the *File Selector*).

> If the underscore does not display beneath the letter on the menu or window, press the **Alt** key on the keyboard.

Keyboard Shortcuts

Selections	Description
Alt + F4	Exits the program. If files are open with unsaved changes, a prompt to save changes displays.
F1	Opens the online help operator manual.
F2	Opens the *File Selector* window.
F6	Cascades open windows.
F7	Tiles all open application windows.
F8	Opens the *File Selector* to start a report from a selected .SMP file.
F9	Closes all open reports.

OPTION PRESENTATION

Options > Option Presentation

Use to change the way sample files and parameter files display: *Advanced*, *Basic*, or *Restricted*. Each display option shows sample information and options differently.

Option Presentation Display

Presentation Display	Description
Advanced	Displays all parts of sample and parameter files. Navigate to parameter windows by selecting the tabs across the top of the window.
Basic	Displays sample information in a single window. This display option is used after the parameter files have been created. The previously entered or default parameter files are then accessible using drop-down lists.
Restricted	Displays the sample file in a single window like the *Basic* display option with certain functions disabled. A password is set when the *Restricted* option is selected. That same password must be entered to change to the *Basic* or *Advanced* display option. This display type is typically used in laboratories — such as the pharmaceutical industry — where analysis conditions must remain constant. The *Advanced* option is not available in the view selector at the bottom of the window when using the *Restricted* display option.
Always Open Edit View	Opens files with a *Complete* status in the tabbed file editor rather than in the Peak Editor view.
Show Splash Screen	Enables (or disables) the splash screen upon application startup.

> To change the view for the selected window, use the drop-down list at the bottom of the sample file editor.

The following examples show the same sample file in *Advanced* and *Basic* display. *Basic* and *Restricted* displays will look the same. A password is required if using *Restricted* format.
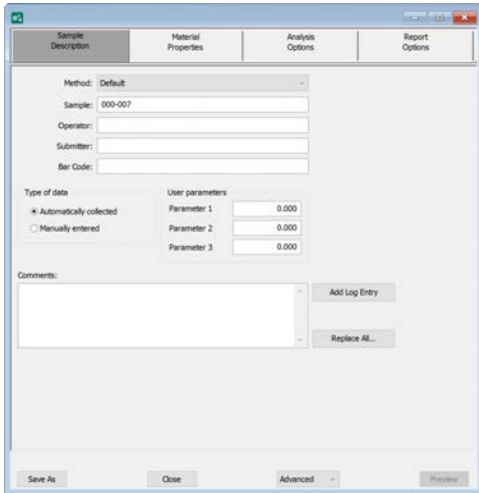
Advanced view
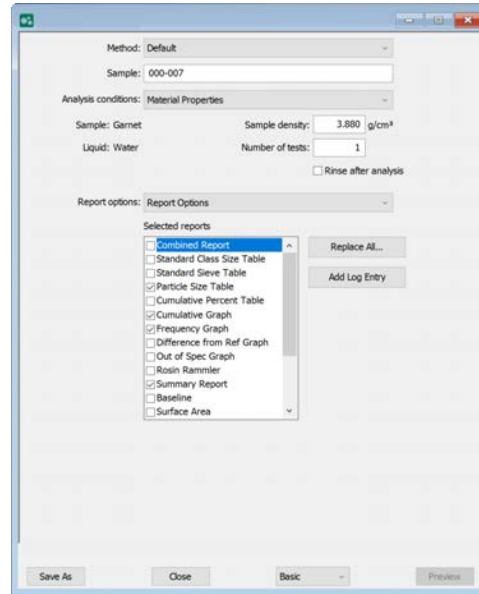
Basic or Restricted view

A sample file must be created for each analysis. The file can be created prior to or at the time of analysis. The sample file identifies the sample, guides the analysis, and specifies report options.

LIBRARIES

Options > Manage Libraries

> This feature is not available when using *Restricted* option presentation.

Manage Libraries

Adsorptive Properties   Manage

Close
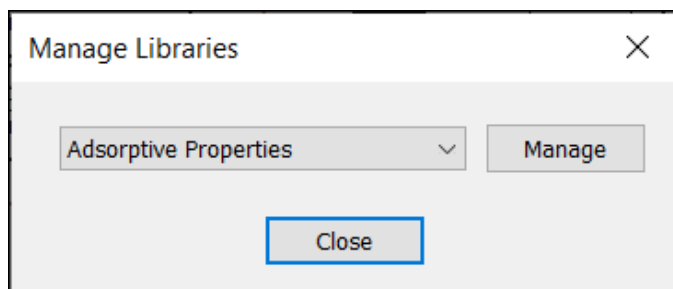
The library provides an easy way to locate and open specific analyzer files. Libraries are located within the *File Selector* window and can be viewed only within the application.

The library gathers sample and parameter files stored in multiple locations, such as folders on a C: drive, a network location, a connected external hard drive, or a connected USB flash drive, and provides access to all files. Even though libraries do not store actual sample and parameter files, folders can be added or removed within each library.

One library can include up to 50 folders. Other items, such as saved searches and search connectors, cannot be included.

When *removing* a folder from a library, the folder and its contents are not deleted from the original file storage location. However, when *deleting* files or folders from within a library, they are deleted from their original file storage location. Deleted files and folders can be recovered from the Recycle Bin located on the Windows desktop.

METHODS

Options > Default Method
File > Open > [.MTH File]

A *Method* determines the default sample identification format and sequence number. A *Method* is a template of specifications that go into a newly created sample file. It allows for the definition of complete sets of parameters for each type of sample commonly analyzed. Only a single selection is required for each new sample file created.

The *Method* drop-down list displays only those methods applicable to the open sample file type.
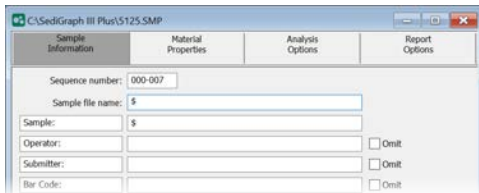
Default Method Example
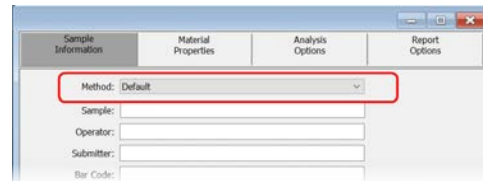
Sample Information File Example

Default Methods

Selections	Description
Sample file name [*text box*]	Enter a format for the sample identification. The entry in this field becomes a part of the saved sample file name. Include the $ symbol to have the sample file number included as part of the identification.
Sample Operator Submitter Bar Code [*text box*]	These field labels may be renamed, and the new label becomes a part of all new sample files.
Sequence Number [*text box*]	Specify a default numeric string to use as a prefix in the *Sample* field when a new sample file is created. This number increments with each sample file created.

CONFIGURE THE ANALYZER

UNIT CONFIGURATION

Unit [n] > Unit Configuration

Use to display and confirm hardware and software configurations and calibrations of the analyzer.
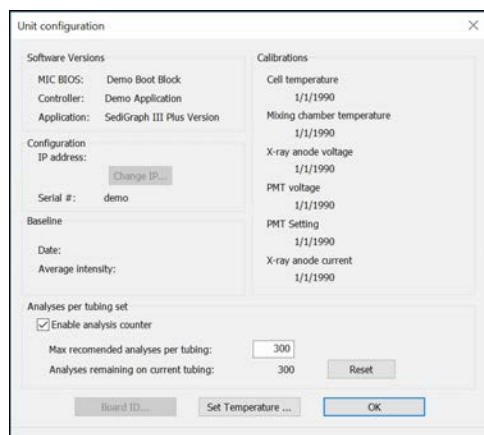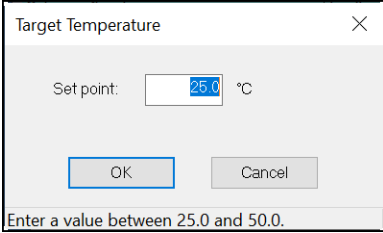
Unit Configuration

Selections	Description
Analyses per tubing set [*group box*]	**Enable analysis counter**. Enables or disables the analyses counter. The analysis program keeps a counter of the number of analyses remaining before the next recommended tubing change. For every sample information file for which an analysis is started (excluding service tests or baseline measurements) this counter is decremented.
	Max recommended analyses per tubing set. Maximum number of analyses to be performed before the application displays this message:
	The maximum number of analyses for this tubing has been reached. It is time to change the tubing. When the tubing has been replaced, reset the counter in the unit configuration dialog.
	Analyses remaining on current tubing. Number of analyses remaining before the maximum recommended number is reached.
	Reset button. Resets the counter to the recommended maximum number.

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Unit Configuration (continued)

Selections	Description
Baseline [*group box***]**	Displays the *Date* and the *Average Intensity* of the last baseline performed.
Board ID [*button***]**	Displays the IP address used by the analysis program, serial number, and type of analyzer. **IP address.** Displays the IP address of the analyzer. **Change IP.** Displays the Board ID dialog, which describes the circuit boards in the analyzer. Use the Board drop-down list to select a board to view. **Board ID.** Click to display information from the circuit boards in the analyzer. Use the drop-down list to select a board to view. The parameters shown cannot be edited.
Calibration [*group box***]**	Displays calibration information for analyzer components.
Configuration [*group box***]**	Displays the IP address used by the analysis program, serial number, and type of analyzer. **IP address.** Displays the IP address of the analyzer. **Change IP.** Displays the Board ID dialog, which describes the circuit boards in the analyzer. Use the Board drop-down list to select a board to view. **Board ID.** Click to display information from the circuit boards in the analyzer. Use the drop-down list to select a board to view. The parameters shown cannot be edited.
Reset [*button***]**	Resets the analysis counter to the recommended maximum number.

Unit Configuration (continued)

Selections	Description
Set Temperature [*button*]	Enter the target temperature in the *Set Point* field. Target Temperature ✕ Set point: 25.0 ℃ OK Cancel Enter a value between 25.0 and 50.0.
Software Versions [*group box*]	Version of the installed software application.

For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.

SIEVE TABLE

Options > Sieves

Sieves specifies the default sieve sizes to use when sieve data are presented. The sieve sizes follow the technical specifications per ASTM Specification E-11.

Aperture Diameter (µm)	Sieve Name
☑ 20	No. 635
☐ 25	No. 500
☐ 32	No. 450
☐ 38	No. 400
☐ 45	No. 325
☑ 53	No. 270
☐ 63	No. 230
☐ 75	No. 200
☐ 90	No. 170
☐ 106	No. 140
☑ 125	No. 120
☐ 150	No. 100
☐ 180	No. 80
☐ 212	No. 70

Sieve Table (ASTM Specification E-11)

OK   Cancel
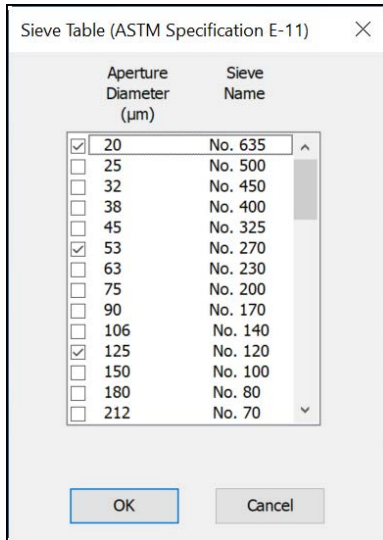
REYNOLDS NUMBER

Options > Reynolds Number
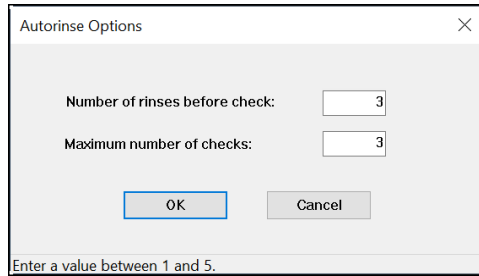
Specifies the Reynolds number to be used in estimating the maximum measurable diameter displayed on the *Material Properties* window.

Default Reynolds Number

Specify the Reynolds number to be used in estimating the "Maximum Diameter" on the Material Properties dialog.

Reynolds number: 0.30

OK   Cancel

Enter a value between 0.01 and 10.00.
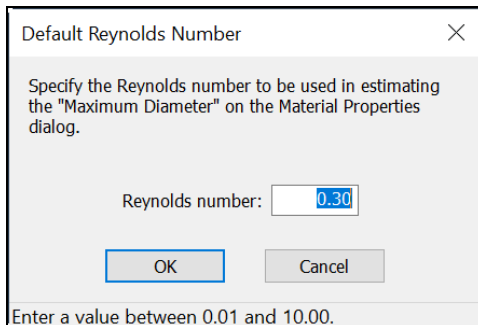
AUTORINSE

Options > Autorinse

Use to specify autorinse options. The system default for Autorinse is 3 cycles of 3 rinses per cycle. The analyzer will rinse a maximum of 9 times in an attempt to reestablish baseline conditions before displaying an error message.

```
Autorinse Options                              ×

      Number of rinses before check:        [      3]

      Maximum number of checks:             [      3]


                [   OK   ]          [  Cancel  ]

Enter a value between 1 and 5.
```

Autorinse

Selections	Description
Number of rinses before check [*text box***]**	Number of rinses per cycle to be performed after each analysis before baseline conditions are checked.
Maximum number of checks [*text box***]**	Maximum number of baseline checks to be performed before notification that baseline conditions have not been met.

🖉	**For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.**

INVERT SIZE AXIS

Options > Invert Size Axis

Use to invert the size axis.

UNIT SELECTION

Options > Units

Use to specify how data should appear on the application windows and reports. This menu option is not available if using *Restricted* option presentation in a standard installation environment.

![Micromeritics logo]
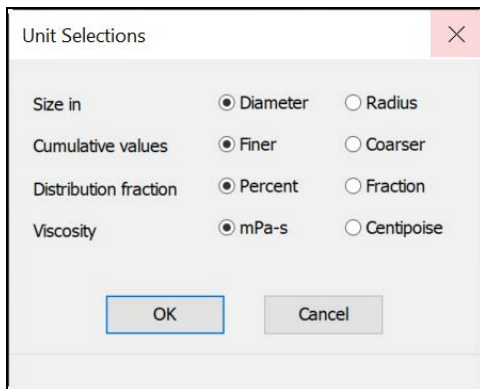
REPORT STYLE

Options > Report Style

A report style can also be configured from an analysis with a *Completed* status.
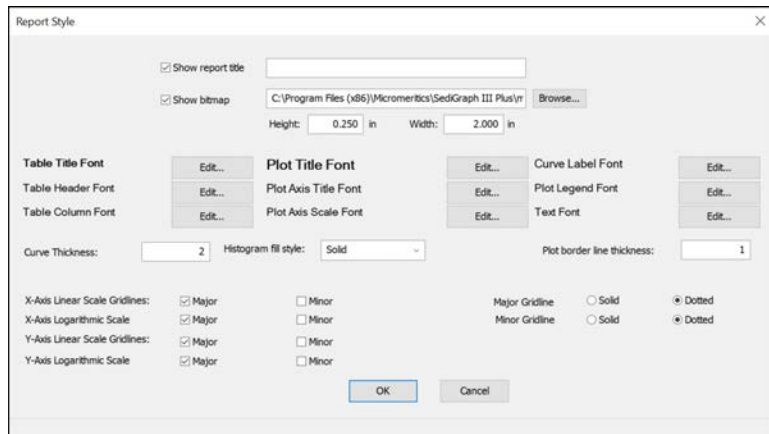
Report Style

Selections	Description
Curve Thickness [*text box*]	Enter a value to indicate the thickness of the curve on reports.
Font Options	Click **Edit** to select font type, font style, and font size.
Histogram fill style [*drop-down box*]	Select how histograms are to appear on the report.
Linear Scale Logarithmic Scale [*check box*]	Select major and/or minor lines to display in reports for the logarithmic and linear scales. Deselect this option to remove the grid lines.
Major Gridline Minor Gridline [*button*]	Select if the major and/or minor grid lines should appear as solid or dotted lines.
Plot border line thickness [*text box*]	Enter a value to indicate the thickness of the plot borders on reports.
Show bitmap [*text box*]	Use to show a graphic on the report header. **Height/Width.** Enter the height and width of the selected graphic. These values determine the graphic's appearance on the generated report.

Report Style (continued)

Selections	Description
Show report title [*text box*]	Select then enter a report title to appear on the report header.

> **For fields and buttons not listed in this table; see _Common Fields and Buttons on page 2 - 2_.**

INSTRUMENT STATUS

SHOW INSTRUMENT LOG

Unit [n] > Show Instrument Log

Use to display a log of recent analyses, calibrations, errors, or messages. The information is logged for a 7-day period for analyses and a 30-day period for messages and calibrations.
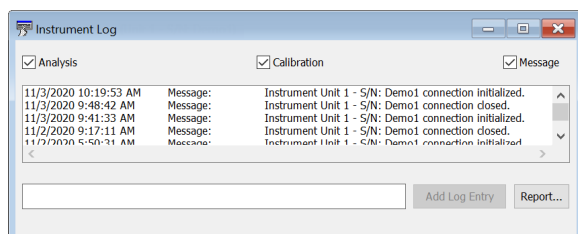
Instrument Log

Selections	Description
Add Log Entry [*button*]	Use to enter information to appear in the sample log report that cannot be recorded automatically through the application. Click the button again to enter multiple log entries.
Analysis/ Calibration/ Message [*check box*]	Select the logs to display.
Report [*button*]	Click to select the print destination and the report start date.

For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.

SHOW INSTRUMENT SCHEMATIC

Unit [n] > Show Instrument Schematic

Select this option to display a schematic of the analyzer and the MasterTech (if one is being used).

To operate the valves from this window, manual control must be enabled (**Unit [n] > Enable Manual Control**).
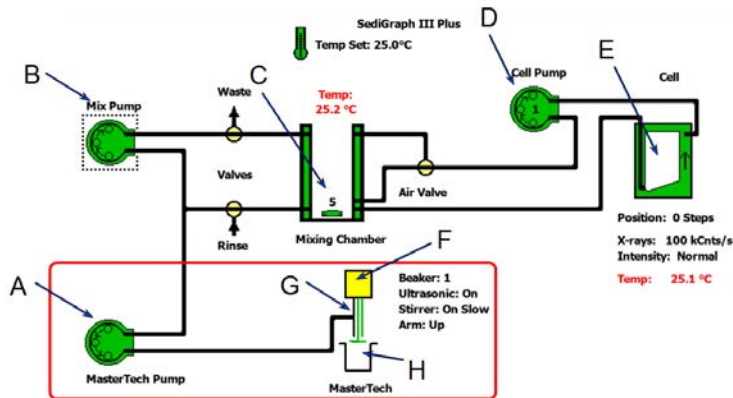
A. MasterTech pump
B. Mixing pump
C. Mixing chamber
D. Cell pump
E. Analysis cell
F. MasterTech arm
G. MasterTech stirrer
H. MasterTech Beaker
Items in the red box show only if MasterTech is installed

The colors of the valves and pumps indicate their state:

Valves
- White: Closed or Off (when manual control is disabled)
- Yellow: Closed or Off (when manual control is enabled)
- Green: Opened

Pumps
- White: Off (when manual control is disabled)
- Yellow: Off (when manual control is enabled)
- Green: On
- Red: Indicates the pump is disabled.

Right-click a component to display pop-up menus.

Schematic

Component	Description
Air Valve	Sets the position of the air valve.
Cell	Controls the movement of the analysis cell. An arrow in the cell symbol indicates the direction of cell movement. **Move Cell Position**. Enter the cell position. **Absolute**. Move the cell position to an absolute (relative to the last beamsplit location) number of steps. For example, an absolute move of 100 steps moves the cell 100 steps above beamsplit. **Relative**. Move the cell position to a relative (relative to current position) number of steps. For example, a relative move of 100 steps moves the cell up 100 steps from its current position. **Cell Position.** Move the cell to the position entered. **Stop Motion.** Stop cell movement. **X-ray intensity Normal / Low**. Select the X-ray intensity setting. **Find Beamsplit.** Zeros the cell position at the proper beamsplit location. **Start**. Progress messages display. **Done**. Close the window.
Cell Pump	**Turn Off / Turn On**. Turns the cell pump off or on. **Flow up / Down in a cell**. Changes flow direction. Arrows in the pump symbol display the current direction. **Increase / Decrease Speed**. Changes the cell pump speed. The speed of the cell pump can be set from 1 to 5, with 1 being the slowest speed.
MasterTech *(if installed)*	**Move Arm Up / Down.** MasterTech arm movement control. **Ultrasonic On / Off**. Turn the ultrasonic probe on or off. **Stirrer On / Off**. Turn the stirrer in the beaker on or off. **Stirrer Speed Fast / Slow.** Stirrer speed control. **Move to beaker.** Move the beaker to the next beaker position.

Schematic (continued)

Component	Description
	Turn On / Off. Turn the MasterTech pump on and off. **Flow Direction Rinse / Load.** Set the flow direction of the MasterTech pump. An arrow in the pump symbol changes to show the current flow direction.
Mix Pump	Turns the mixing pump on or off.
Mixing Chamber	The speed of the mixing chamber magnetic stirrer can be set from 1 to 10, with 1 being the lowest speed. **Set Speed**. Controls the stirrer speed by entering a value from 1 to 10. **Speed**. Displays the Mixing Chamber Speed window. Turns the stirrer on or off.
Rinse Valve	Set the rinse valve position.
Set Temperature	**Set Temperature**. Use to set the target temperature. **Set Point**. Enter a temperature set point. Range 25.0 to 50.0 °C. The set point must be at least 10 °C above ambient temperature for accurate control.
Waste Valve	Set the waste valve position.

For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.

SHOW STATUS

Unit [n] > Show Status

Use to show the current status for each port.

Use this option if:

- There is an automatic operation in progress and a sample file needs to be edited.
- There are two units attached to the computer. Select *Show Status* on each unit menu and have the status for both units displayed simultaneously.
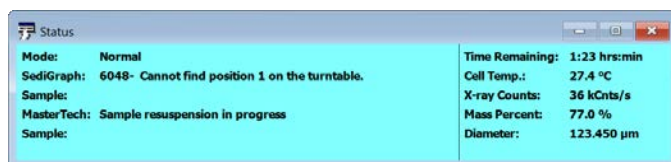
If multiple units are attached to the computer, select *Show Status* on each *Unit [n]* menu. The status for all units displays.

Selections	Description
Cell Temp.	Temperature of the liquid in the analysis cell.
Diameter	Current particle size in the analysis.
Mass Percent	Current mass percent in the analysis.
MasterTech	MasterTech status (if installed).
Mode	Type of operation being performed.
Sample	Sample file involved in the operation.
SediGraph	Analyzer status — such as *Analysis operation in progress*, *Idle*, *Waiting for load*, etc.
Time Remaining	Time remaining on the analysis if an analysis is in progress.
X-ray Counts	Intensity of the X-ray in kilocounts/sec.

EXPORT FILES

File > Export

Provides the option to print the contents of one or more sample or parameter files to either the screen, a printer, or a file. Data can be exported as a .PDF, .TXT, .XML, or .XLS file format. The type of data to include or exclude can be selected during the export process. The data can be imported into other applications that read these file formats when exported to a file.

1. Click **List** and open an .SMP file.
2. Select an experiment and the applicable options.
3. Click **OK**.
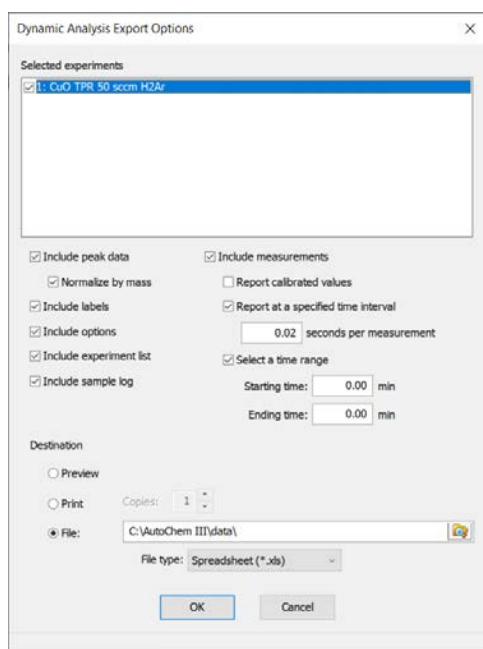
LIST FILES

File > List

Provides the option to create a list of sample file information —such as file name, date, time the file was created or last edited, file identification, and file status.

Select one or more files from the file selector, click **List**, then provide the file destination.

File Listing

No.	File Name	Date	Time	Description	Status
1	13x with CO2 at 0C Port 1B.SMP	8/10/2020	3:53:54 PM	13x with CO2 Port 1	Complete
2	13x with CO2 at 0C Port 2B.SMP	8/10/2020	3:53:54 PM	13x with CO2 Port 2	Complete
3	13x with CO2 at 0C Port 3B.SMP	8/10/2020	3:53:54 PM	13x with CO2 Port 3	Complete
4	13x with N2 and TranSeal Port 2.SMP	8/10/2020	3:53:54 PM	13X Zeol Tube 2 w/ FS @ end of analysis, Port 2	Complete
5	13x with N2 and TranSeal Port 3.SMP	8/10/2020	3:53:54 PM	13X Zeol Tube 1A w/ FS @ end of analysis, Port 3	Complete
6	Activated Carbon with Butane C3 Port 1.SMP	8/10/2020	3:53:55 PM	Activated Carbon Tube C3 Butane Port 1	Complete
7	Activated Carbon with Butane C4 Port 3.SMP	8/10/2020	3:53:55 PM	Activated Carbon Tube C4 Butane Port 3	Complete

Example of File List

SOFTWARE SETUP

If the computer is to be connected to a network, a second Ethernet port on the computer must be used for that purpose.

The *Setup* program is located on the installation media and is used to reinstall the software and make analyzer changes — such as adding, moving, or removing a unit, etc.

If the IP address needs to be changed on the computer connected to the analyzer, refer to the computer's operating system manual or the internet for instructions. The IP address for the computer and the IP address specified in the setup program must match. The IP address must be 192.168.77.100.

SOFTWARE UNINSTALL

The software can be uninstalled in two ways. Either method removes only the files required to run the software, not the analysis files.

■ Click the Windows *Start* icon. Scroll to the Micromeritics entry. Select the *Uninstall [analyzer]* option, then follow the prompts.
■ Locate the *uninstall.exe* file in *C:\Program Files (x86)\Micromeritics\[analyzer name]* (or wherever the application was installed). Double-click the *uninstall.exe* file, then follow the screen prompts.

SOFTWARE UPDATES

A User Account Control in the Windows operating system must be enabled to ensure all components of the Micromeritics application are correctly installed. If UAC is not enabled, right-click the *setup.exe* installer file and select *Run as administrator*.

The most current version of the instrument software can be found on the Micromeritics web page (www.Micromeritics.com).

When performing a software update, existing data files are not overwritten.

Insert the setup media into the media drive. The setup program starts automatically. If the program does not start automatically, navigate to the installation media drive, locate and double-click the *setup.exe* file.

3 SAMPLE FILES

Sample files include the information required by the analyzer to perform analyses and collect data. A sample file identifies the sample, guides the analysis, specifies report options, and may be displayed in *Advanced*, *Basic*, or *Restricted* presentation display mode.

A sample file consists of parameter sets; however, parameter sets can also stand alone. A sample file may be created either before or at the time of analysis.

Parameter files allow for repeated use of parameter sets. For example, if the same analysis conditions exist for multiple analyses, an *Analysis Conditions* file containing the recurring conditions can be created. When the sample file is created, the *Analysis Conditions* file can be selected for the analysis conditions. Once it becomes part of the new sample file, the new file can be edited, as needed, without affecting the original *Analysis Conditions* file.

The analysis application contains a default method. A method is a template for sample files that contains the parameters to be used for an analysis. When a new sample file is created, all the parameters are filled with the values in the default method.

> To change the view for the selected window, use the drop-down list at the bottom of the sample file editor.

CREATE SAMPLE FILES

File > New Sample > [.SMP File]

File > Open > [.SMP File]

Each analysis must be linked with a sample file before the analysis can proceed. A sample file can consist of parameter files; however, parameter files can also stand alone.

Specify or change the option presentation by selecting **Options > Option Presentation** or use the view selector drop-down list at the bottom of the window.

Sample files created in the *Basic* option presentation are selected from parameter files created in the *Advanced* option presentation. The values specified in the parameter portions of the default method are the defaults for new sample files. To navigate from one set of parameters to another, select the parameter tab across the top of the window.

> A bar code reader may be used to enter text into many of the fields on the *Sample Description* window. Use a mouse to click in the field first where information is to be entered then scan the bar code with the bar code reader.

Sample Files

Selections	Description
Add Log Entry [*button***]**	Use to enter information that will display in the sample log report that cannot be recorded automatically through the application. Click the button again to enter multiple log entries.
Bar Code [*text box***] ***	Use to enter additional information about the sample, such as a sample lot number, sample ID, etc.
Comments [*text box***]**	Enter comments to display in the report header about the sample or analysis.
Method [*drop-down box***]**	Select a method from the drop-down list.
Operator [*text box***] ***	Enter operator identification information.
Sample [*text box***] ***	Enter a sample description.
Submitter [*text box***] ***	Enter submitter identification information.

> **For fields and buttons not listed in this table; see** *Common Fields and Buttons on page 2 - 2*.

* This field label may have been renamed or may not display if modified in **Options > Default Methods**.

OPEN A SAMPLE FILE

File > Open > [.SMP File]

> When working with an existing sample file, consider copying the sample file to maintain the original configuration options.

File Status	Displays
No Analysis	Tabbed file editor
Complete Analyzing Entered	MicroActive report window
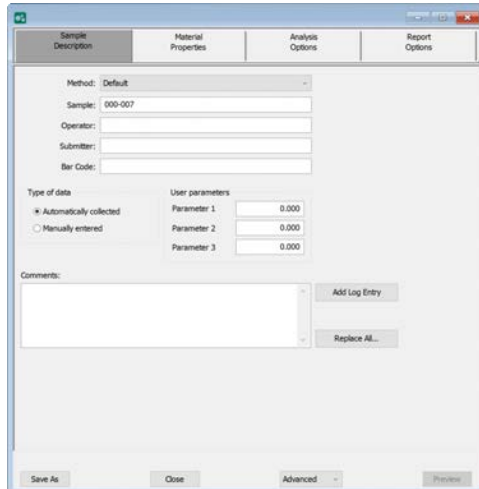
Tabbed file editor in Advanced view
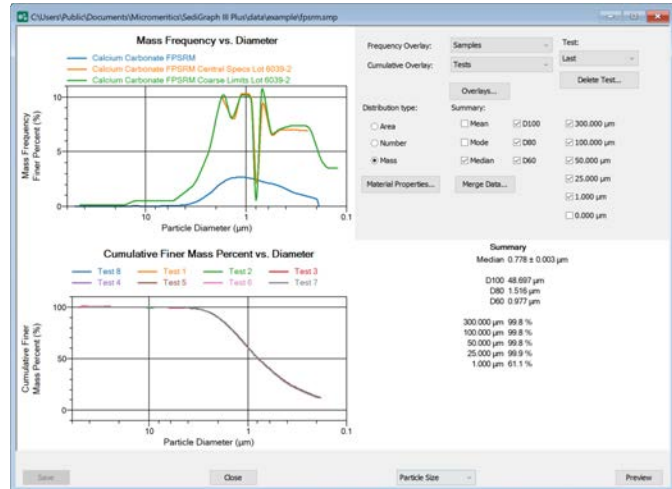
Example of a Report window

To view the tabbed file editor for a sample file with a *Complete* status, select *Advanced* from the view selector drop-down list at the bottom of the window.

MANUALLY ENTER DATA

This process allows the manual entry of data from a sample file with a *Complete* status. There are two methods for manually entering data into a sample file:

- Copy and paste onto the graph area of the interactive window.
- Import data into the interactive window.

COPY AND PASTE MANUALLY ENTERED DATA

> To display the file status in a search window, go to **File > Open**. Right-click the column header then click *More...* Scroll to the *MIC* entries and enable *MIC Status*.This is a snippet

1. Open a sample file with a *Complete* status. The file will open in the interactive reports window.
2. Right-click in the graph area of the interactive reports window, then select *Copy data*.
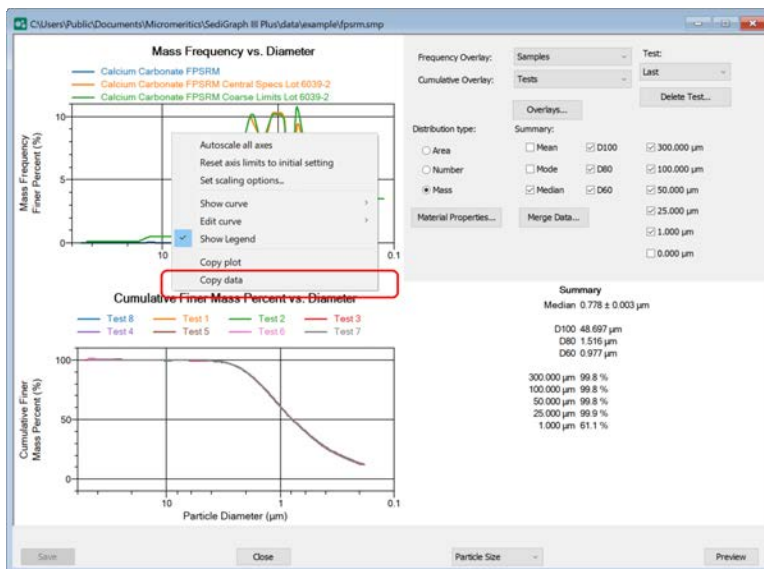
3. Open another sample file using the *Advanced* option presentation.
4. On the *Sample Description* tab, select *Manually entered* in the *Type of Data* group box.
5. In the view selector drop-down list at the bottom of the window, click *Advanced*, then select *Particle Size*.
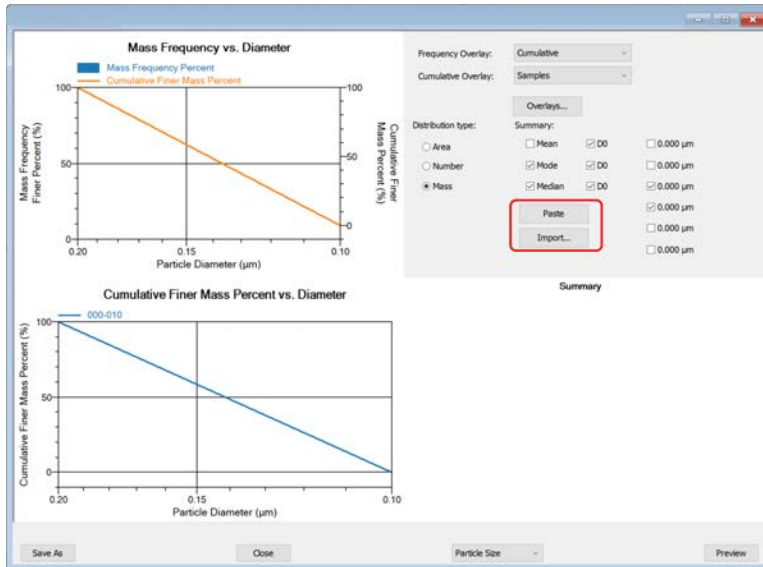
6. Ensure that all parameter fields are set appropriately, then click **Paste**.

IMPORT MANUALLY ENTERED DATA

When importing data from an external ASCII text file using the **Import** button on the interactive window, the ASCII text file must use the following **ASCII text file format** rules:

- Data must be in two columns and separated by a comma or white-space.
- Only cumulative distributions can be imported.
- An acceptable header should be in the format shown below where *Diameter* or *Radius* and *Cumulative Coarser* or *Cumulative Finer* can be used.
- Size units of micrometers are required.
- The distribution can be *Mass*, *Number*, or *Area*.

Example:

> Cumulative Coarser Mass Fraction vs Diameter
> Particle (µm)   Cumulative Coarser Mass Fraction

To import the ASCII text file

1. Open a new sample file in *Advanced* option presentation.
2. On the *Sample Description* tab, select *Manually entered*.
3. In the view selector drop-down list at the bottom of the window, click *Advanced*, then select *Particle Size*.
4. Ensure that all parameter fields are set appropriately, then click **Import**.
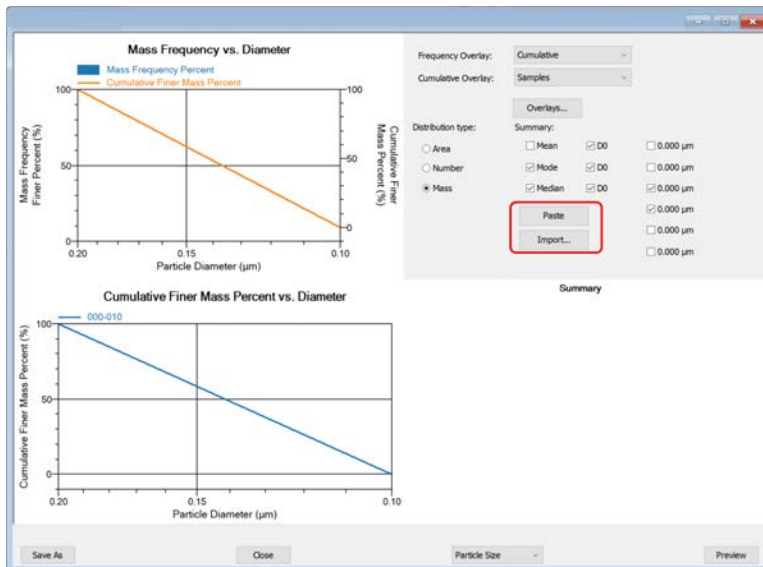
5. Open the .TXT file. The data from the original sample file is imported and displayed. If an error message displays instead, verify that the .TXT file format is correct.

MERGE DATA

Use to merge data collected from an external source.
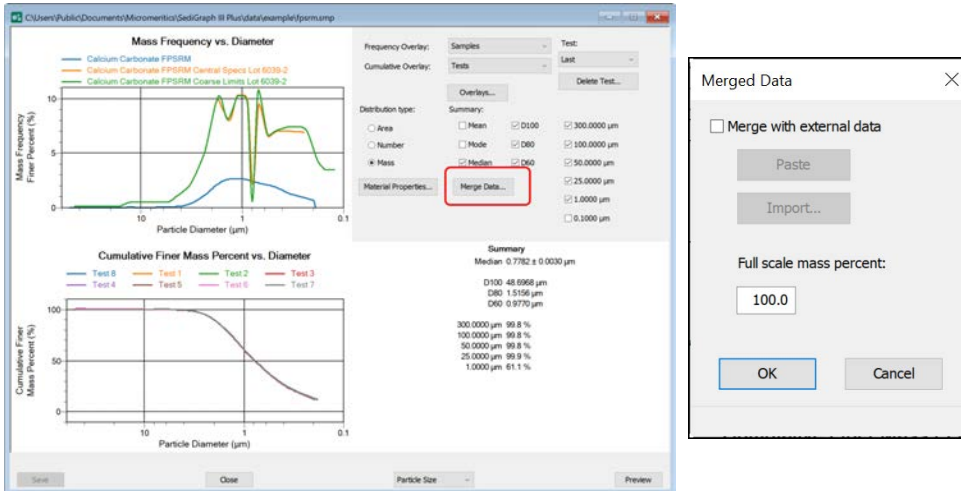
PASTE DATA FROM AN EXTERNAL SOURCE

1. Open the sample file with a *Complete* status.
2. Copy the external source data onto the clipboard.
3. On the Report window, click **Merge Data**, then select *Merge with external data*, then click **Paste**.

IMPORT DATA FROM AN EXTERNAL SOURCE

1. Open the sample file with a *Complete* status.
2. On the Report window, click **Merge Data**, then select *Merge with external data*, then click **Import**
3. Locate the .TXT file to import, then click **Open**.

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4 PARAMETER FILES

Parameter files allow for repeated use of parameter sets. For example, if the same analysis conditions exist for multiple analyses, an *Analysis Conditions* file containing the recurring conditions can be created. When the sample file is created, the *Analysis Conditions* file can be selected for the analysis conditions. Once it becomes part of the new sample file, the new file can be edited, as needed, without affecting the original *Analysis Conditions* file.

Methods include both analysis conditions and report options, offering the most convenient way to repeat most analyses.

Predefined parameter files are included with the program and can be edited as needed, or new parameter files created.

The following file types can exist as part of the sample file as well as individual parameter files.

File Type and File Name Extension

File Type	File Name Extension
Analysis Conditions	.ANC
Liquid Properties	.LIQ
Report Options	.RPO
Sample Information	.SMP
Method	.MTH

MATERIAL PROPERTIES

File > Open > Analysis Conditions

Or, click the *Material Properties* tab when in *Advanced* option presentation.

Material Properties

Selections	Description
Analysis liquid [*group box*]	Displays a list of the *Liquid Properties* files. **Description**. Enter the name of analysis liquids to add to the list. **X-ray Intensity**. Displays the X-ray intensity selected for the analysis liquid. The intensity is selected in *Liquid Properties* window. **Add**. Click to add analysis liquids to the list and change values for an analysis liquid. ▪ **To add analysis liquids**: In the *Description* field, enter the name of the liquid, then click **Add**. ▪ **To change values of an analysis liquid**: Highlight the liquid, then click **Properties**. Enter the new values, then click **OK**. **Add** changes to **Change**; click **Change**. **Delete**. Click to delete the selected liquid from the list. **Properties**. Click to edit the properties of the analysis liquid. See *Liquid Properties on page 4 - 10*.
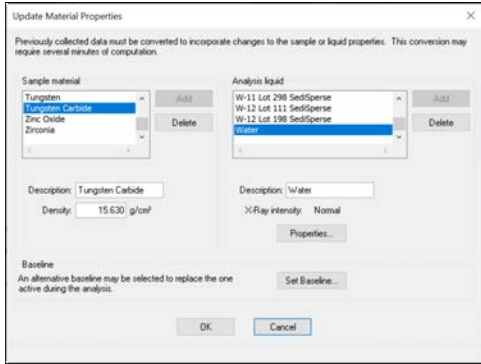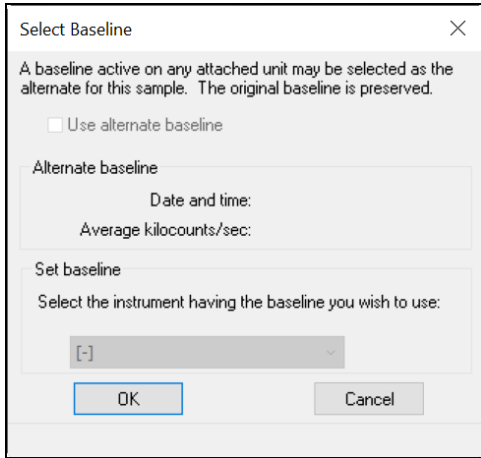
Material Properties (continued)

Selections	Description
Analysis Type [*group box*]	Specifies if the analysis is standard, high speed or high resolution. ■ **Standard**. Provides good resolution and average analysis time. ■ **High speed**. Allows a faster analysis, but a little lower resolution. ■ **High resolution**. Provides high resolution at the smallest diameters, but takes a longer time. **Starting diameter**. Specify the range of sizes to be included in the analysis. The starting diameter generally should be larger than the largest particle expected to be in the sample. **Ending diameter**. The ending diameter must be less than the smallest size particle of interest. Each time the values in these fields are changed, the analysis statistics are updated. A note also is added to the report header indicating changes have been made since the first analysis was performed.
Analysis Unit [*group box*]	Displays a list of the attached units and their temperatures. The displayed temperature is used to compute analysis statistics. ■ **Reynolds number**. Calculated for the starting diameter using the sample's density and the liquid's density and viscosity. If this number is greater than 0.3, large particles falling through the liquid may create turbulence, affecting both their velocity and the velocity of neighboring smaller particles. This results in an incorrect particle size distribution. ■ **Maximum diameter**. Calculated to have a Reynolds number equivalent to the one entered as a default (from the *Options* menu). If the sample has more than a couple percent mass of particles larger than this diameter, the sample should be analyzed in a liquid with a higher viscosity. The Maximum diameter field should be greater than the starting diameter specified in step 8. The Reynolds number should be less than 0.3. ■ **Analysis time.** Calculated based on the sample density, liquid density and viscosity, and ending diameter. The actual analysis time may vary slightly if the analysis compartment temperature is different when the analysis takes place. The *Reynolds number*, *Maximum diameter*, and *Analysis time* fields

Material Properties (continued)

Selections	Description
	display analysis statistics. These values are updated whenever a parameter affecting their computation is changed.

If...	Then...
the maximum diameter and Reynolds number values are not attained	a dispersing liquid with a higher viscosity must be used.
the maximum diameter is much greater than the starting diameter and the Reynolds number is much less than 0.3	a lower viscosity liquid (if available) may be used.

Selections	Description
Description [*text box***]**	Description of the Analysis Conditions file.
Sample Material [*group box***]**	Displays a list of available sample materials. When a sample material is selected, the description and density display. **Description**. Name of sample materials to add to the list. **Density**. Density of the sample material selected from the list. **Add**. Adds sample materials to the list. ■ **To add samples materials**: In the *Description* field, enter the name of the sample material. Click **Add**. ■ **To change values of the sample material density**: Highlight the sample material in the list, then enter the density value in the *Density* field. **Delete**. Deletes sample materials from the list.

Material Properties (continued)

Selections	Description
Update Properties [*button*]	Allows the updating of the material properties of a *completed* analysis. This allows the collected data to be reprocessed based upon the new properties. The material properties for the original analysis remain unchanged. A note is added to the report header describing the change. The contents of the *Sample Material* and *Analysis Liquid* group boxes are described elsewhere in this table. **Set Baseline**. Applies a baseline different than the one active in the original analysis. From the drop-down list, select the instrument containing the baseline to use, then select *Use alternate baseline*. The original baseline is preserved. From the drop-down list, select the instrument containing the baseline to use, then select *Use alternate baseline*. The original baseline is preserved.

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Material Properties (continued)

Selections	Description
	Apply Changes. Select to apply all changes to the material properties. Click **Yes** at the prompt. All test data will be converted to the new data reduction options. *Do you wish to continue*? The data are converted and this prompt displays: *Application of new reduction options [file name] is complete.* Click **OK** to close the message box.

For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.

ANALYSIS OPTIONS

File > Open > Analysis Conditions

Or, click the *Analysis Options* tab when in *Advanced* option presentation.

Provides details for setting up the sample analysis conditions file. Analysis options can be edited as long as the analysis is not in progress and the sample file does not contain manually entered data. Changes made to analysis parameters are noted in the report header upon completion of the analysis.
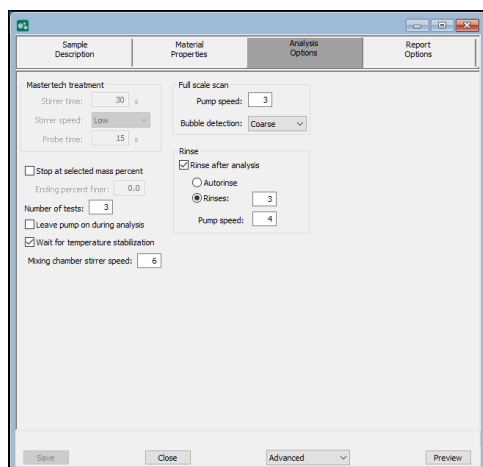
Analysis Options

Selections	Description
Full scale scan [*group box*]	**Pump speed**. The speed at which the cell pump should operate during the full-scale scan. Use a pump speed of 2 or 3 if analyzing fine samples since they pump through the tubing easily. If analyzing coarse particles, especially if dispersed in higher viscosity liquids, a higher pump speed of 4 to 5 should be used. If the analyzer has the smaller 5 mm (3/16 in.) OD tubing, higher speeds may be required for finer particles.
	Bubble detection. Types of bubble detection (*Fine*, *Medium,* or *Coarse*).
	The presence of most bubbles in the cell can be detected during the full-scale scan that takes place at the start of the analysis. Detecting bubbles, however, is somewhat sample-dependent. Samples, which contain very large particles, may appear to have bubbles near the top of the cell, when actually the sudden change in X-ray intensity is due to incomplete filling of the topmost portion of the analysis cell.

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Analysis Options (continued)

Selections	Description
	For samples of this type, select *Coarse* bubble detection.
	If only small particles are present in the sample (less than 1 mm), select *Fine* bubble detection.
	For samples between these two ranges, select *Medium* bubble detection.
Leave pump on during analysis [*check box*]	Coarse materials tend to settle in the tubing during analysis. This option allows the pump to operate during analysis, enabling easier rinsing and resuspension of the sample.
MasterTech treatment [*group box*]	(Applicable only if using a MasterTech.)
	Samples tend to settle in the beakers while waiting for sample analysis, especially if samples are prepared ahead of time, as in most cases when using a MasterTech. Program the MasterTech stirrer and probe to redisperse the sample using options in the group box.
	Stirrer time. The number of seconds to have the stirrer operate during resuspension.
	Stirrer speed. Options include *High* and *Low*. Coarse materials and less-stable dispersions may require more high-speed stirring than finer materials. Range: 1 to 10, with 1 being the slowest
	Probe time. Length of time for the ultrasonic probe to operate during resuspension. Coarse materials and less-stable dispersions may require more high-speed stirring than finer materials.
Mixing chamber stirrer speed [*text box*]	Adjusts the speed of the magnetic stirring bar which stirs the mixture in the mixing chamber. Select a number between 1 and 10. 1 represents the lowest speed and 10 the highest.
Number of tests [*text box*]	The number of analyses to be performed.

Analysis Options (continued)

Selections	Description
Rinse [*group box*]	**Rinse after analysis**. Select if a rinse cycle should be performed after analysis. **Autorinse**. Performs up to 3 cycles of 3 rinses each (a total of 9 rinses) in an attempt to re-establish baseline conditions. If conditions are not re-established after 9 rinses, an error message is displayed. **Rinses**. The number of rinses to be performed. **Pump speed**. The speed for the cell pump to operate during rinsing. The range is 1 to 5, with 1 being the slowest.
Stop at selected mass percent [*check box*]	Stops analysis at a specified mass percent finer. If unsure of the smallest size particle present in the sample, it may be difficult to determine an ending diameter which will include the selected data. With this option, choose to end mass percent at 0%, after having set the ending diameter at a small value of approximately 0.1 μm. Using this method, wait time is lessened at the end of the analysis. **Ending percent finer**. Enabled only if *Stop at selected mass percent* is selected. Enter the point at which the analysis should stop.
Wait for temperature stabilization [*check box*]	Select to have the temperature in the analysis compartment and mixing chamber stabilize to within ± 0.5 °C of the setpoint before the analysis begins.

For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.

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LIQUID PROPERTIES

File > Open > Liquid Properties

Or, click the **Properties** button on the *Materials Property* tab when in *Advanced* option presentation.

Use to edit the properties of an analysis liquid and to specify properties for a new liquid properties file.

The liquid properties are edited by selecting the *Materials Properties* window. Click **Properties** in the *Analysis Liquid* group box.

Liquid Properties

Selections	Description
Current Cell Conditions [*group box*]	Displays the cell conditions of the analysis unit. These conditions are based on the temperature of the cell and are used in computing the analysis statistics displayed on the *Material Properties* window. Select either fixed values or interpolated values based on the cell temperature. **Fixed values**. Enter a value in the *Viscosity* and *Density* fields. These values will be maintained regardless of the cell temperature. **Interpolate using cell temperature**. Enter three sets of values in the *Temp.*, *Density*, and *Viscosity* fields. These values will be used to interpolate the density and viscosity at the current cell temperature. The table requires that the entered values be properly ordered. For example, enter values from left-to-right and from top-to-bottom. Temperature is in ascending order.
Description [*text box*]	If editing an existing file, this field contains the name of the selected file. If defining a new file, enter a name in this field.
X-ray intensity [*selection*]	**Normal**. Optimized for most applications when using high X-ray absorption liquids, such as water. **Low**. Decreases intensity when using low X-ray absorption liquids, such as hydrocarbons.

> **For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.**

REPORT OPTIONS

File > Open > [.RPO File]

Or, click the *Report Options* tab when in *Advanced* option presentation.

About Reports on page 6 - 1

Additional reports are available using the *Reports* menu.

Use to specify report options for data collected from an analysis or manually entered data. *Report Options* files also help in customizing report details such as axis scale, axis range, column headings, and components of thickness curve equations. These files may contain tabular reports, plots, or both, as well as advanced report tables.

Customized report options files can be created then loaded into a sample file, allowing quick generation of reports.

Report Options files may be defined to include overlay options. This system allows the overlay of up to 25 plots of different samples onto a plot of the same type or overlay one plot type onto a different plot type from the same analysis.

Report Options

Selections	Description
Distribution type [*selection*]	Select the type of distribution data to report: Area, Number, or Mass.
Overlays [*button*]	See *Overlay Multiple Sample Files on page 6 - 10*.
Reference [*button*]	Specify a reference sample file to compare analysis results of the current sample.
Report options [*drop-down box*]	Browse for a .RPO file that contains report options parameters to be used in the report.
Selected reports [*group box*]	Select the report names to include in the report.
Specification [*button*]	Select the sample files to be used for the coarse and fine specification boundaries to determine if the results of the current sample are within the specified boundaries.
Test [*drop-down box*]	Select the analysis for the report: First, Last, or Average.

> **For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.**

5 PERFORM AN ANALYSIS

PREPARE FOR ANALYSIS

It is recommended to perform the tasks in the provided order.

CREATE SAMPLE FILES

File > New Sample > [.SMP File]

File > Open > [.SMP File]

Each analysis must be linked with a sample file before the analysis can proceed. A sample file can consist of parameter files; however, parameter files can also stand alone.

Specify or change the option presentation by selecting **Options > Option Presentation** or use the view selector drop-down list at the bottom of the window.

Sample files created in the *Basic* option presentation are selected from parameter files created in the *Advanced* option presentation. The values specified in the parameter portions of the default method are the defaults for new sample files. To navigate from one set of parameters to another, select the parameter tab across the top of the window.

> A bar code reader may be used to enter text into many of the fields on the *Sample Description* window. Use a mouse to click in the field first where information is to be entered then scan the bar code with the bar code reader.

Sample Files

Selections	Description
Add Log Entry [*button***]**	Use to enter information that will display in the sample log report that cannot be recorded automatically through the application. Click the button again to enter multiple log entries.
Bar Code [*text box***] ***	Use to enter additional information about the sample, such as a sample lot number, sample ID, etc.
Comments [*text box***]**	Enter comments to display in the report header about the sample or analysis.
Method [*drop-down box***]**	Select a method from the drop-down list.
Operator [*text box***] ***	Enter operator identification information.
Sample [*text box***] ***	Enter a sample description.
Submitter [*text box***] ***	Enter submitter identification information.

Sample Files (continued)

Selections	Description
	For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.

* This field label may have been renamed or may not display if modified in **Options > Default Methods**.

DRAIN AND LOAD OPERATION

Unit [n] > Drain and Load

Before collecting baseline data or performing an analysis, the cell and mixing chamber must be drained and the sample (or baseline liquid) loaded.

■ Prior to a baseline collection or an analysis, go to **Unit > Drain and Load**.
■ At the beginning of a baseline collection, select the Prepare SediGraph to load baseline liquid check box on the Baseline Measurement window.
■ At the beginning of an analysis, select the Prepare SediGraph to load sample check box on the
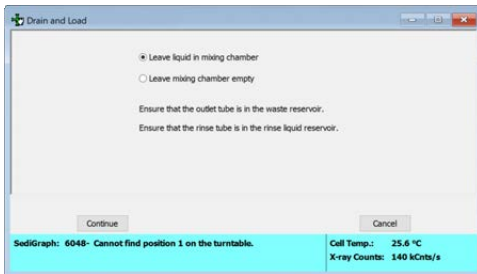
Ensure that the outlet tube is in the waste reservoir and that the rinse tube is in the rinse liquid reservoir.

1. Select to either have the liquid remain in the mixing chamber or leave the mixing chamber empty. Click **Continue**. A progress message appears prior to the following window.
2. Ensure the mixing chamber bezel is inserted in the mixing chamber, then load the sample (or baseline liquid) into the mixing chamber. The mixing speed can be changed using the **Increase** or **Decrease** button. Click **Continue**.

3. Confirm the X-ray intensity reduction over the baseline before it completes:

    ■ **Good**. Indicates reduction is between 30 and 75% meaning that the concentration level is appropriate.
    ■ **Low**. Indicates the reduction is less than 30% meaning that the concentration is too low and sample should be added.
    ■ **High**. Indicates the reduction is more than 75% meaning that the concentration is too high and more dispersant or less sample should be used.

4. When the X-ray reduction level is set, click **Continue** and the cell will move to the normal park position and the load operation will be complete.

BASELINE MEASUREMENT

Unit [n] > Baseline

A baseline measurement is required for data collection. Although it is not necessary to measure a baseline for each analysis, Micromeritics recommends that a baseline measurement be performed once per shift and when changing dispersing agents. Up to seven baselines can be measured; however, only the last one may be saved.

> Ensure that the outlet tube is in the waste container and that no sample is present in the system.
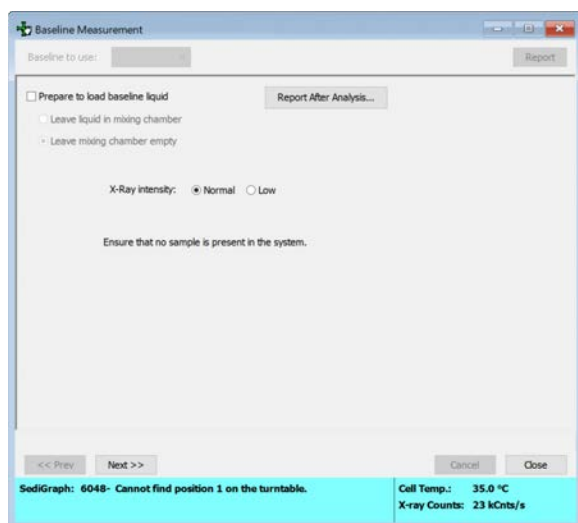
1. If the baseline liquid has not been loaded into the mixing chamber:

   a. Select *Prepare to load baseline liquid*.
   b. Select to have the liquid remain in the mixing chamber or to leave the mixing chamber empty.

> If planning to use a liquid different from the one used for rinsing, select *Leave mixing chamber* empty.

2. To have a baseline report generated, select *Report After Analysis* then select the report destination.
3. Select the *X-ray intensity* setting.

Baseline

Selections	Description
Baseline to use [*drop-down box*]	Select whether to use the latest or the previous baseline **Latest**. Uses the last baseline performed. **Previous**. Uses the baseline which was active before the last series of baselines were performed.
Prepare to load baseline liquid [*check box*]	Select if the baseline liquid is not loaded. Select if the liquid should remain in the mixing chamber or leave the mixing chamber empty. If *Prepare to load background liquid* is selected, a drain and load operation is performed before the baseline measurement begins. Load the baseline liquid when prompted. Click **Next** to begin the baseline measurement. If *Prepare to load baseline liquid* was selected, a drain and load operation is performed first. If this baseline is not satisfactory, click **Next** to perform another baseline. If another baseline is measured, the current one will become inaccessible.
X-ray intensity [*selection*]	**Normal**. Increases intensity when using high X-ray absorption liquids, such as water. **Low**. Decreases intensity when using low X-ray absorption liquids, such as hydrocarbons.

> **For fields and buttons not listed in this table; see _Common Fields and Buttons on page 2 - 2_.**

MASTERTECH AUTOMATIC

Unit[n] > MasterTech Automatic

Option is available only if a MasterTech is connected to the analyzer.

Use to analyze a series of samples of the same type, which contain the same analysis conditions. Sample files are created automatically.
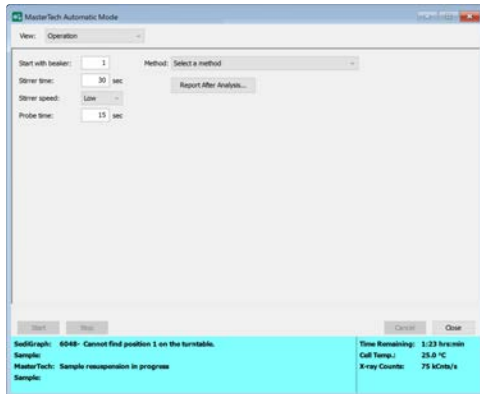
MasterTech Automatic

Selections	Description
Method [*drop-down box***]**	Select the method to be used in the analysis. See ***Methods on page 2 - 10***.
Sample resuspension [*group box***]**	Enter resuspension parameters. All fields in this group box are disabled if an analysis is in progress. Samples tend to settle in the beaker while waiting for analysis, especially if samples are prepared ahead of time, as in most cases when using a MasterTech. Use the options in this group box to program the MasterTech stirrer and probe to re-disperse the sample before analysis. **Stirrer time**. Enter the number of seconds to have the stirrer operate during resuspension. **Stirrer speed**. Select the stirrer speed. Coarse materials and less-stable dispersions may require more high-speed stirring time than finer materials.

MasterTech Automatic (continued)

Selections	Description
	Probe time. Enter how long to have the ultrasonic probe operate during resuspension. Coarse materials and less-stable dispersions may require more probe time than finer materials.
Start with beaker [*text box*]	Enter the position number of the beaker containing the first sample to be analyzed. This field is disabled if an analysis is in progress.

> **For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.**

MASTERTECH SCHEDULE

Unit [n] > MasterTech Schedule
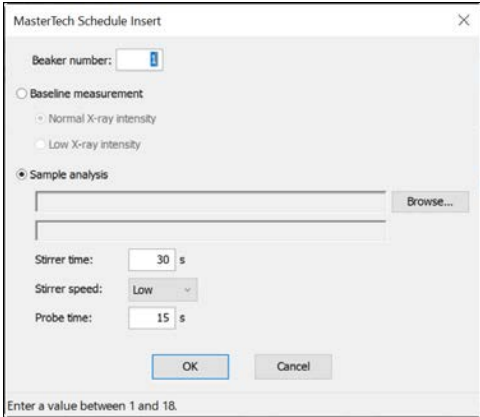
> Option is available only if a MasterTech is connected to the analyzer.

Use to:

- Analyze a series of samples that may be different in size and shape and require different analysis conditions.
- Perform a series of baseline measurements.
- Analyze samples and measure a baseline alternately.
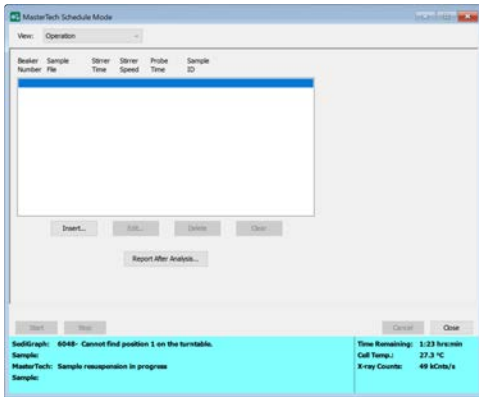
MasterTech Schedule

Selections	Description
Insert [*button***]**	Click to insert sample files to be used for analyses.

MasterTech Schedule (continued)

Selections	Description
	If a sample file is selected, the new file will be inserted before the selected file; otherwise it will be inserted at the end of the list. **Beaker Number**. Enter the beaker number containing the selected sample (or baseline liquid). **Baseline measurement**. Specify either a baseline measurement or sample analysis for the specified beaker. If *Baseline measurement* is selected, select the X-ray intensity. ■ **Normal**. Increases intensity when using high X-ray absorption liquids, such as water. ■ **Low**. Decreases intensity when using low X-ray absorption liquids, such as hydrocarbons. ⚠️ CAUTION — Use this option if planning to change dispersing agents with one of the samples. A baseline measurement can then be scheduled using the beaker preceding the one containing the different dispersant. For example, if planning to change dispersing liquids in beaker position #4, schedule a baseline measurement in beaker position #3. **Sample analysis**. Click **Browse**, then choose the sample file or use with the sample in this beaker position. ■ **Stirrer time**. The number of seconds to have the stirrer operate during resuspension. ■ **Stirrer speed**. Select the stirrer speed. Coarse materials and less-stable dispersions may require more probe time than finer materials. ■ **Probe time**. The length of time to have the ultrasonic probe operate during resuspension. Coarse materials and less-stable dispersions may require more highspeed stirring time than finer materials.

✏️ **For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.**

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1. Enter the position number of the beaker containing the current sample.
2. Select *Baseline measurement* or *Sample analysis*.

   ■ If *Sample analysis* is selected, click **Browse** to select a sample file to use with the sample in this beaker position. The values contained in the fields for *Stirrer time*, *Stirrer speed*, and *Probe time* are copied from the selected sample file.
   ■ If *Baseline measurement* is selected, select the X-ray intensity.

      ○ *Normal* increases intensity when using high X-ray absorption liquids, such as water.
      ○ *Low* decreases intensity when using low X-ray absorption liquids, such as hydro-carbons.

3. Click **OK**. The beaker information displays in the list box.
4. Repeat step 3 and 4 for each beaker containing sample.

   If dispersing liquids will be changed at any time during this series, perform a baseline measurement using the beaker position preceding the one containing the sample with the new liquid. For example, if dispersing liquids are changed with the sample contained in beaker position 4, insert a Baseline measurement for beaker position 3.

5. Click **Report Settings** to generate a report after analysis. Click **OK**.
6. Click **Start** to begin the analysis.

> When the analysis begins, the **Start** button changes to **Stop**. The **Stop** button cancels the remaining analyses. The analysis that is currently in progress will be completed.
>
> To view the analyses in progress, go to *View > Analysis Results*.

QUICK START ANALYSIS

Unit [n] > Quick Start

Use this mode of operation to analyze a series of samples of the same type that contain the same analysis conditions. Sample files are created automatically.
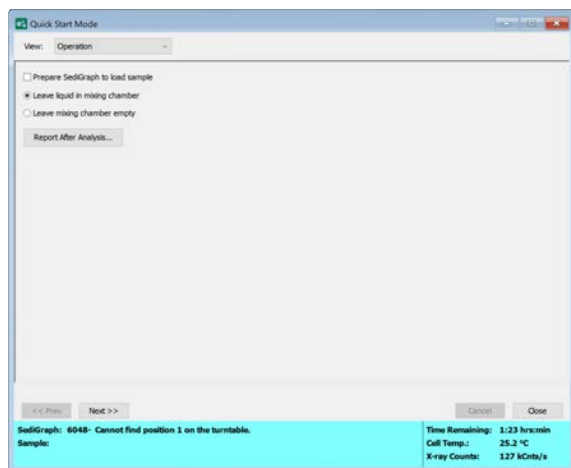
QuickStart Analysis

Selections	Description
Leave liquid in mixing chamber [*button*]	Select to leave liquid in mixing chamber after analysis.
Leave mixing chamber empty [*button*]	Select to leave mixing chamber empty after analysis.
Prepare SediGraph to load sample [*button*]	Select if the sample is not loaded. If selected, an initial drain and load operation is performed.

> **For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.**

1. If the analyzer has not been drained, select *Prepare SediGraph to load sample* to drain the mixing chamber. Then select to have the liquid remain in the mixing chamber after the drain and load operation or to leave the mixing chamber empty.
2. Click **Report After Analysis** to generate a report after analysis is complete.
3. Click **Next**.
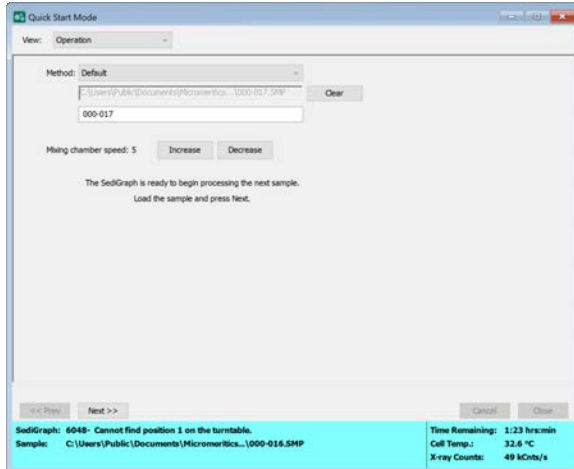
4. Select a *Method* from the drop-down list.
5. To specify a different file name enter the new file name in the text box.
6. Specify a mixing chamber speed using the **Increase** or **Decrease** buttons.
7. Load the sample.
8. Click **Next**. If *Prepare SediGraph to load sample* was selected, a drain is performed before being prompted to load the first sample. Analysis of the first sample begins. The current baseline and data display as they are collected. When analysis is complete, a prompt to load the next sample displays. Repeat steps 7 and 8 until all analyses are complete.
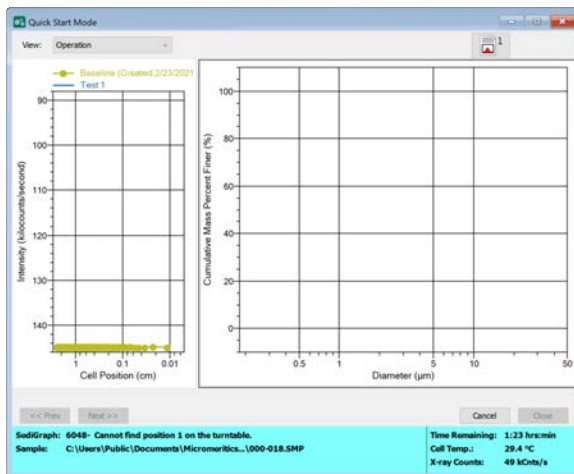
PERFORM A SAMPLE ANALYSIS

Unit [n] > Sample Analysis

1. Click **New** to create a new sample file, or click **Browse** to select an existing sample file.
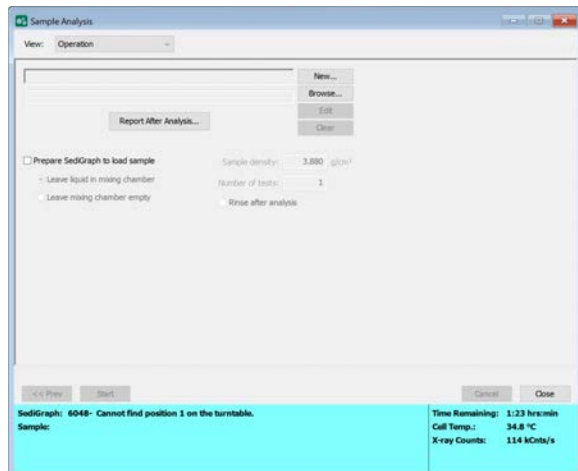
Sample Analysis

Selections	Description
Prepare SediGraph to load sample [_check box_**]**	Select if the sample has not been loaded into the mixing chamber. If selected, a drain and load operation is performed. Select if the liquid should remain in the mixing chamber or leave the mixing chamber empty.
Sample density [_text box_]	Enter the sample density.
Number of tests [_text box_]	Enter the number of tests to be performed.
Rinse after analysis [_check box_]	Select to perform a rinse after analysis.

> 🖉 **For fields and buttons not listed in this table; see** _Common Fields and Buttons on page 2 - 2_.

2. Click **Start**.
3. When the analysis completes, the graph displays.

4. Click the **Report** button to display the report.
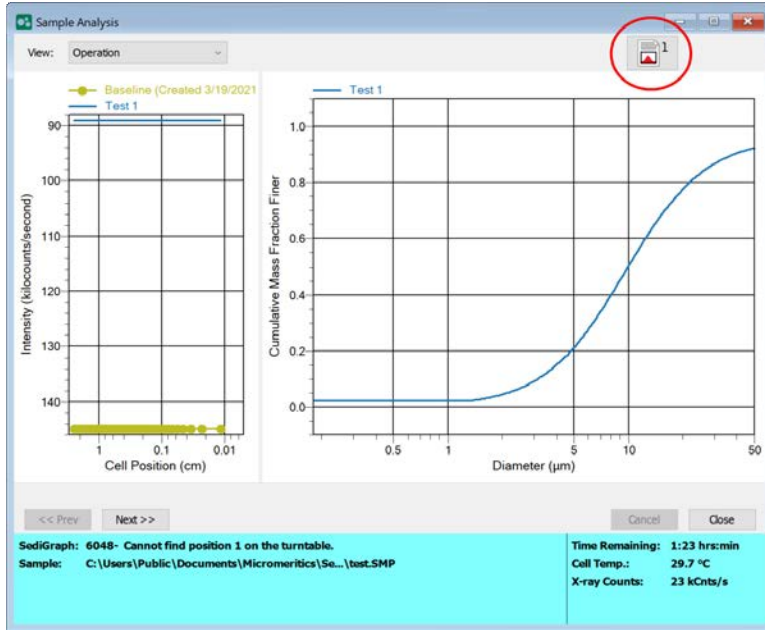
5. Click **Next** to select another sample file for a new analysis.

INITIALIZE MASTERTECH

Unit [n] > Initialize MasterTech
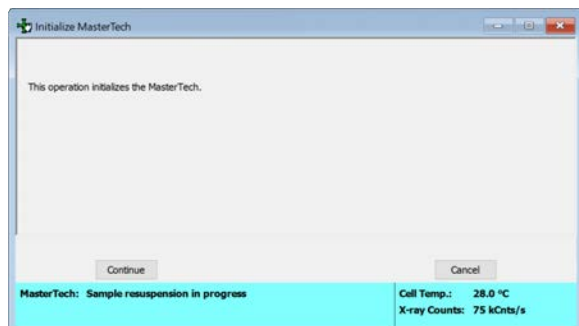
Select this option if:

- Manual operations should be performed with the MasterTech.
- The MasterTech beaker tray has been disturbed.

When the MasterTech is initialized, the tray is aligned so that beaker #1 is in the start position.

PERFORM A RINSE OPERATION

Unit [n] > Rinse > [SediGraph, MasterTech, Both]

> - A rinse operation cannot be performed when an analysis is in progress.
> - The rinse container should be rinsed thoroughly or replaced after each use.

A rinse operation should be performed to rinse the analysis cell, mixing chamber, and tubing of any contaminants or sample materials from the previous analysis. It is best to perform a rinse operation after each analysis. On the *Analysis Options* window, select that a rinse is to be performed after an analysis. See *Analysis Options on page 4 - 7*.

Rinse

Selections	Description
SediGraph	Rinses the analysis cell, mixing chamber, and the analyzer tubing.
MasterTech	Rinses the MasterTech tubing.
Both	Rinses the analysis cell, mixing chamber, the analyzer tubing, and the MasterTech tubing.

> **For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.**

SETUP THE RINSE AND WASTE CONTAINERS

1. Pour approximately 10 liters of water containing a small amount of surfactant into the rinse container. For example, use 0.05% sodium metaphosphate (W/W) in deionized water.
2. Insert the rinse tube into the rinse container.
3. Insert the waste and overflow tubes into the waste container.
4. Turn the caps clockwise to secure.
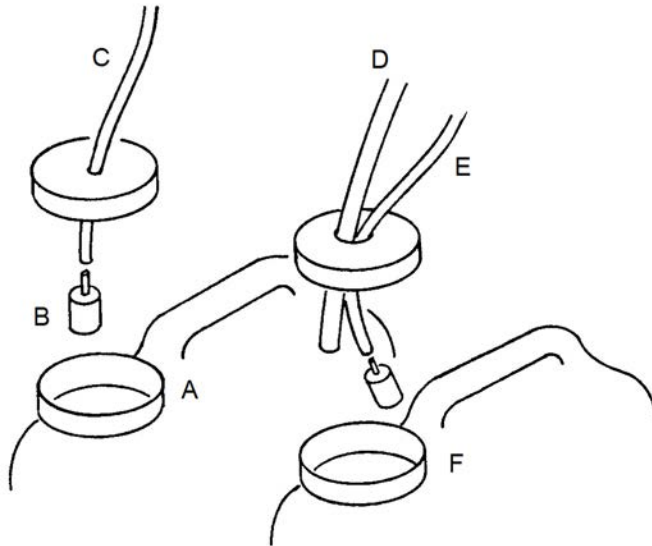
A. Rinse container
B. Tube weight
C. Rinse tube
D. Overflow tube
E. Waste tube
F. Waste container

Ensure that tube weights are attached to the rinse and waste tubes, that the overflow tube and waste tubes are in the waste container, and that the rinse tube is in the rinse liquid container.

RINSE SEDIGRAPH

Unit [n] > Rinse > SediGraph
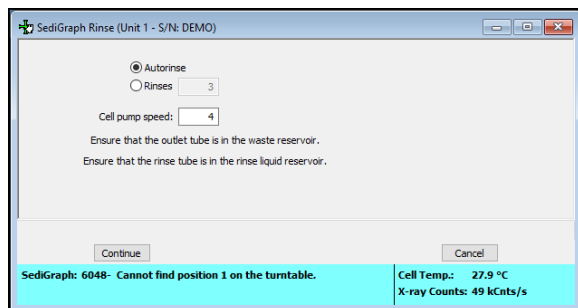
SediGraph Rinse

Selections	Description
Rinse Cycles [*selection*]	**Autorinse**. Performs up to 3 cycles of 3 rinses each (a total of 9 rinses) in an attempt to reestablish baseline conditions. If conditions are not reestablished after nine rinses, an error message is displayed. See ***Autorinse on page 2 - 15***. **Rinses**. Specifies up to five rinses to be performed.
Cell Pump Speed [*text box*]	The speed for the cell pump is to operate during rinsing. The range is 1 to 5, with 1 being the slowest.
Continue [*button*]	Begins the rinse operation. A message displays indicating a rinse operation is in progress. When rinsing is complete, the window closes.

> **For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.**

1. Ensure the rinse and waste containers have been setup. See ***Setup the Rinse and Waste Containers on the previous page***.
2. Select either of the following:

   - **Autorinse**. To have the analyzer automatically determine how many rinse cycles to perform. Autorinse, in an effort to reestablish baseline conditions, performs three cycles of three rinses per cycle (default setting) before displaying an error message that baseline conditions cannot be reestablished.

   - **Rinses**. If Rinses is selected, enter the number of rinse cycles to perform.

3. Enter the operating speed of the cell pump. A speed of 2 usually is sufficient unless the material is difficult to rinse; then it may be necessary to use a higher speed.
4. Click **Continue**. Progress messages display until rinsing is complete.

RINSE MASTERTECH

Unit [n] > Rinse > MasterTech
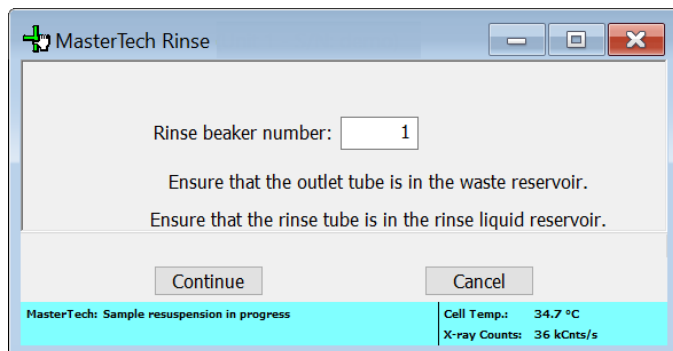
MasterTech Rinse

Selections	Description
Continue [_button_**]**	Begins the rinse operation. A message displays indicating a rinse operation is in progress. When rinsing is complete, the window closes.
Rinse beaker number [_text box_**]**	Enter the position number of the beaker to rinse into. Ensure the beaker is empty.

> **For fields and buttons not listed in this table; see _Common Fields and Buttons on page 2 - 2_.**

1. Ensure the rinse and waste containers have been setup. See _Setup the Rinse and Waste Containers on page 5 - 17_.
2. Enter the position number of the beaker to catch the rinse liquid.
3. Ensure the beaker is empty.
4. Click **Continue**. Progress messages display until rinsing is complete.

RINSE > BOTH

Unit [n] > Rinse > Both
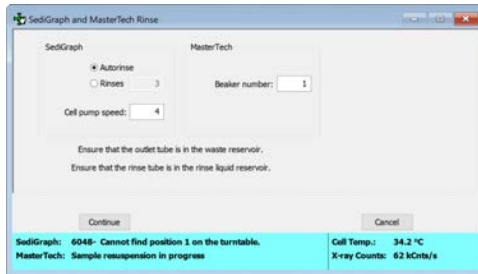
1. Ensure the rinse and waste containers have been setup. See ***Setup the Rinse and Waste Containers on page 5 - 17***.
2. In the SediGraph group box, select:

   ■ **Autorinse**. To have the analyzer automatically determine how many rinse cycles to perform. Autorinse, in an effort to reestablish baseline conditions, performs three cycles of three rinses per cycle (default setting) before displaying an error message that baseline conditions cannot be reestablished.

   ■ **Rinses**. Enter the number of rinse cycles to perform.

3. In the MasterTech group box, enter the position number of the beaker to catch the rinse liquid.
4. Enter a speed in the *Cell pump speed* field.
5. Ensure the beaker is empty.
6. Click **Continue**. Progress messages display until rinsing is complete.

PERFORM A REFERENCE MATERIAL ANALYSIS

A reference material analysis is used to verify the analyzer is operating properly and producing optimum results. These methods provide specifications for critical report quantities and reporting of whether quantities are in or out of specification.

When running a reference material analysis, use the appropriate reference material kit. This kit is available from Micromeritics. The results should match those shown on the label of the reference material bottle, within the tolerance level.

Parts and accessories are located on the Micromeritics web page.

ADVANCED OPTIONS

Options > Advanced Options

> Changing these parameters will affect the performance of the SediGraph III Plus instrument. This program should only be used after consultation with a Micromeritics Service Representative

SediGraph III Advanced Options

Changing these parameters will affect the performance of the SediGraph III Plus instrument. This program should only be used after consultation with a Micromeritics Service Representative.

Baseline/Fullscale

High Speed Analysis

Close

BASELINE/FULLSCALE

SediGraph III Options -- Baseline and Fullscale Treatment

Selection of Baseline and Fullscale treatment

CELL PROFILING is the appropriate choice for particle systems that are readily suspended, such as most pigments and clays. Readily suspended samples would be characterized by particle populations mostly below 50 micrometers and having a moderate density (less than 4 g/cm²)

Cell Profiling uses baseline and full scale readings taken at each cell position to scale mass percent data taken at that position. This prevents cell window defects or contamination from affecting the measured size distribution.

⦿ Cell profiling

BASELINE/FULLSCALE AVERAGING is a choice provided for the analysis of samples having a significant mass percentage of particles showing a very high settling velocity because of some combination of size (50 to 300 micrometers) or density.

Baseline/Fullscale Averaging uses mean baseline and fullscale values to scale mass percent data taken at all cell positions. This procedure largely eliminates the fullscale fluctuations caused by flow variations in the presence of a statistically small number population of the more massive particles. When using this choice, the cell should be checked to verify a flat baseline.

○ Baseline/Fullscale averaging

OK   Cancel

CELL PROFILING

Cell Profiling is the appropriate choice for particle systems that are readily suspended, such as most pigments and clays. Readily suspended samples would be characterized by particle populations mostly below 50 micrometers and having a moderate density less than 4 g/cm^3).

Cell Profiling uses baseline and full scale readings taken at each cell position to scale mass percent data taken at that position. This prevents cell window defects or contamination from affecting the measured size distribution.

BASELINE/FULLSCALE AVERAGING

Baseline/Fullscale Averaging is a choice provided for the analysis of samples having a significant mass percentage of particles showing a very high setting velocity because of some combination of size (50 to 300 micrometers) or density.

Baseline/Fullscale Averaging uses mean baseline and fullscale values to scale mass percent data taken at all cell positions. This procedure largely eliminates the fullscale fluctuations caused by flow variations in the presence of a statistically small number population of the more massive particles. When using this choice, the cell should be checked to verify a flat baseline.

HIGH SPEED ANALYSIS

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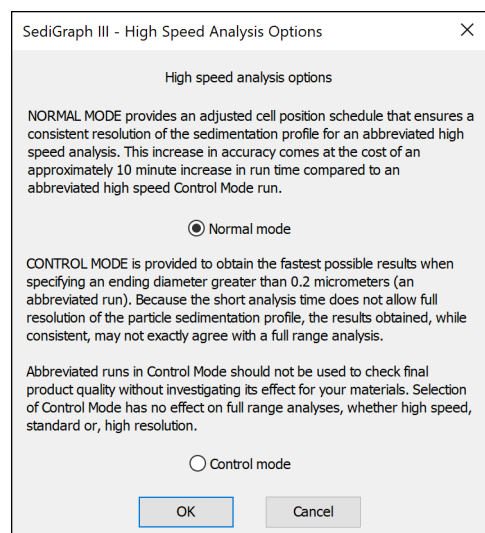
NORMAL MODE

Normal Mode provides an adjusted cell position schedule that ensures a consistent resolution of the sedimentation profile for an abbreviated high speed analysis. This increase in accuracy comes at the cost of an approximately 10 minute increase in runtime compared to an abbreviated high speed Control Mode run.

CONTROL MODE

Control Mode is provided to obtain the fastest possible results when specifying an ending diameter greater than 0.2 micrometers (an abbreviated run). Because the short analysis time does not allow full resolution of the particle sedimentation profile, the results obtained, while consistent, may not exactly agree with a full range analysis.

Abbreviated runs in Control Mode should not be used to check final product quality without investigating its effect for the materials being used. Select of Control Mode has no effect on full range analyses, whether high speed, standard, or high resolution.

6 ABOUT REPORTS

Reports can be generated for data collected on a sample that has completed analysis, collected on a sample currently being analyzed, or manually entered.

Reports > Start Report

Generates a report on a sample analysis.

Reports > Close Reports

Closes all open reports. This option is unavailable if reports are being generated.

Reports > Open SPC Report

Opens the file selector to open or create an SPC report. See *SPC Report on page 6 - 3*.

START REPORTS
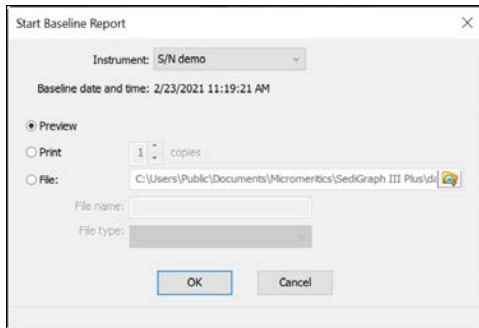
Reports > Start Report

Starts the selected report. Select a file from the *Files* list. Ensure the selected file has a status of either *Complete* or *Analyzing*.

BASELINE REPORT

Reports > Baseline

A graphical report can be generated on an instrument's baseline. This report generates a graph illustrating the X-ray intensity versus the cell height. The report header contains baseline statistics, such as the unit serial number, date the baseline was performed, etc.

Baseline Report

Selections	Description
Baseline Date and Time	Date and time of the last baseline measurement.
Copies [*scroll selection*]	Specifies the number of copies of the report.
Instrument [*drop-down box*]	List of serial numbers of the attached instruments.
File [*text box*]	Specifies the location where the report should be saved.
File name [*text box*]	Specifies the name for the report.
File type [*drop-down box*]	Indicates the report file type: Spreadsheet (.xls), XML (.xml) or Unicode Text (.txt).
Preview [*button*]	Displays a preview of the report.
Print [*button*]	Prints the selected report.

For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.

SPC REPORT

Reports > SPC Report Options

Use to generate reports with various *SPC* (Statistical Process Control) options. All selected variables must be computed for each sample file used in an SPC report; therefore, it is more efficient to select only the necessary variables.
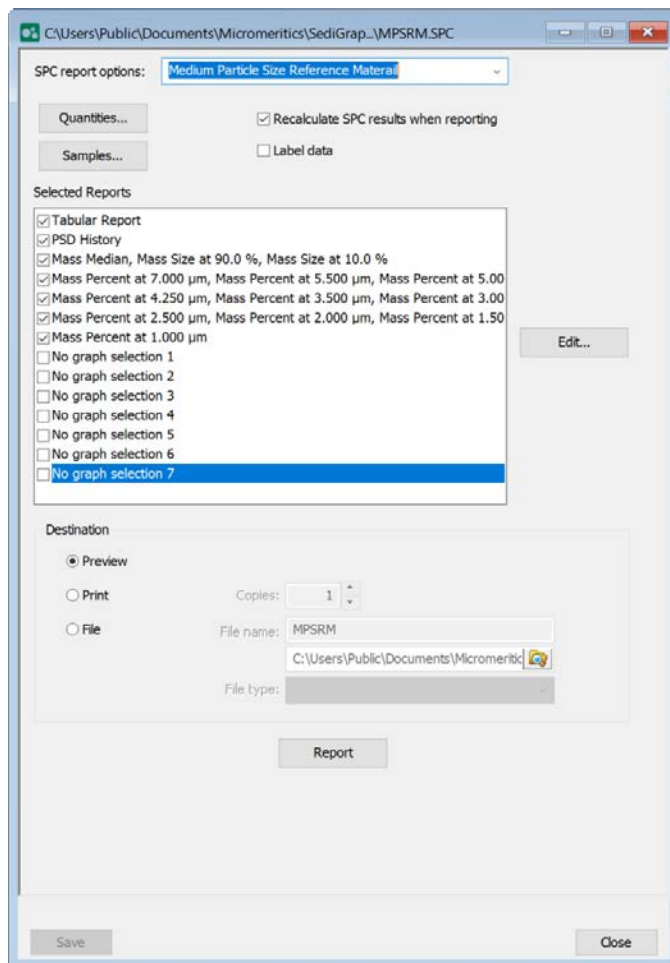
MICROACTIVE REPORTS

MicroActive reports are generated automatically after an analysis is performed. This feature provides a quick and easy way to investigate and manipulate analysis data using a variety of reporting methods.

When a report is opened, plots and summary data are displayed, and in some reports certain parameters are also displayed. Plots may be edited by selecting the data points or data point range to be included in the plots and modifying the parameters. When a report is edited, the results are immediately reflected in the plots and summary data.

INTERACTIVE REPORTS

When opening a sample file that contains data from a complete or in-progress analysis, the interactive reporting feature is enabled.

1. From the view selector drop-down list at the bottom of the window, do either of the following:

   - Change the option presentation of the sample description window to either *Basic* or *Advanced* to modify certain file parameters.
   - Select another plot from the list and edit the data contained in the plot.

2. When ranges are edited, the changes are reflected immediately in the plots and the summary data displayed in the window. Some editing options are:

   - Drag the blue bars to increase or decrease the range of data included in the plot.
   - Right-click to display a popup menu to include reports; enable or select overlays; edit curves, axes, legends, titles; and copy and paste the data in a graph or in tabular format.

3. Click **Save**.

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REPORT FEATURES

Click **Preview** on the MicroActive report window to display additional report information.

- After analysis, reports can be viewed, printed, and/or copied and pasted into other documents.
- The report zoom feature provides the viewing of fine graph details and the ability to shift the axes.
- All reports contain a header displaying file statistics.
- Tabular and graphical reports contain sample and analyzer statistics such as analysis date/-time, analysis conditions, etc.
- The headers contain notes of sample file changes occurring after analysis.
- Summary report headers contain the same information as tabular and graphical reports with the exception of notes.
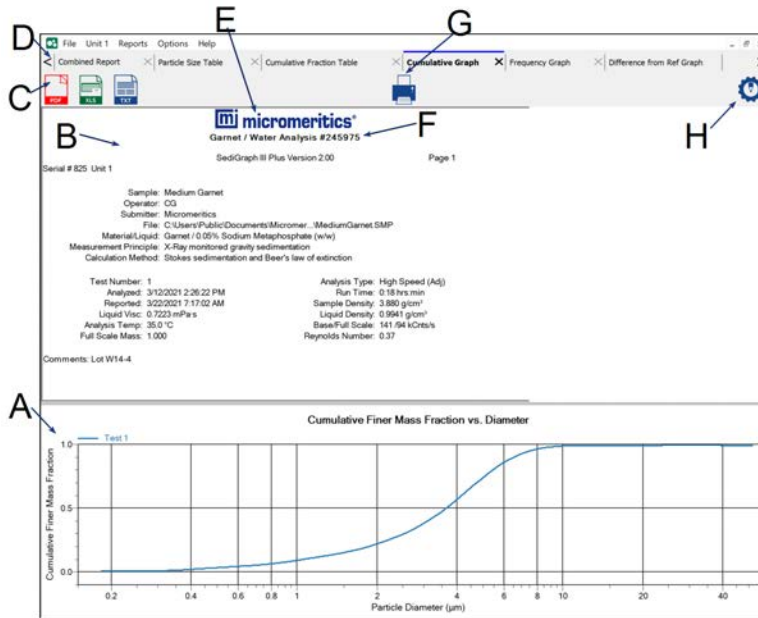
A. Data display (graph or text)
B. Report header area
C. Report export options
D. Generated tabs
E. Report graphic
F. Title
G. Print icon
H. Style icon

Report Features and Shortcuts

Selections	Description
Data Display area	Displays either a graphic or text from the generated report. Click the tabs across the top to display the selected report.
Generated tabs	Tabs represent the reports selected on the *Report Options* window.
Print icon	Click to send the report to a designated printer.
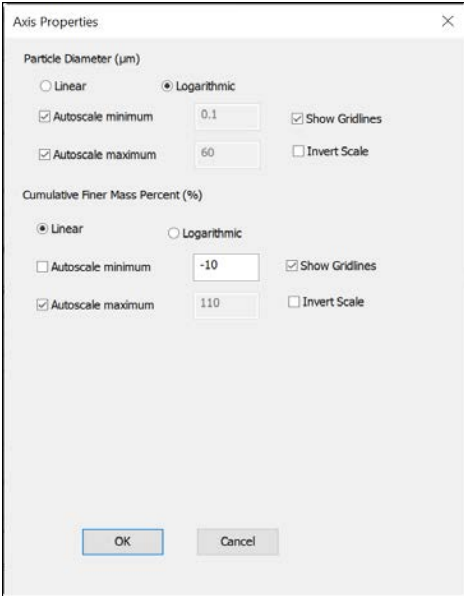
Report Features and Shortcuts (continued)

Selections	Description
Report export options	Select a file format option for the exported report details.
Report graphic	A graphic can be displayed on the report by using the **Style** button.
Report header area	Displays information about the sample, instrument, and software.
Title	A report title can be displayed on the report by using the **Style** button.
Style icon	Click to customize report options, such as font size, graphics, report title, etc.

REPORT SHORTCUTS

Right-click in the graphic or tabular report area to display report shortcuts.

Report Shortcuts

Selections	Description
Autoscale all axes	Returns the report to full view after using the zoom feature.
Copy data	Copies the report data to the clipboard. It can then be pasted into other software programs as tab-delimited columns or copied as an overlay onto another graph.
Copy plot	Copies the graph to the clipboard. It can then be pasted into other software programs.
Copy table	Copies the table to the clipboard.
Edit curve	Edits available curves from the report.
Reset axis limits to initial setting	Removes the cross-hair and returns the graph back to the initial setting.
Set scaling options	Edits the axis properties. **Linear / Logarithmic.** [*button*] Select the option to scale the graph as linear or logarithmic. **Autoscale minimum / maximum.** [*check box*] To manually specify minimum / maximum autoscale, deselect the option and enter the new amount in the text box.

Report Shortcuts (continued)

Selections	Description
	Show Gridlines. [*check box*] Use to enable or disable report gridlines. **Invert scale.** [*check box*] Use to invert the scale.
Show curve	Displays a list of all curves. Select the curve(s) to display.
Show legend	Displays or hides the legend.

AXIS CROSS-HAIR

Left-click on the graph to view the cross-hair coordinates.
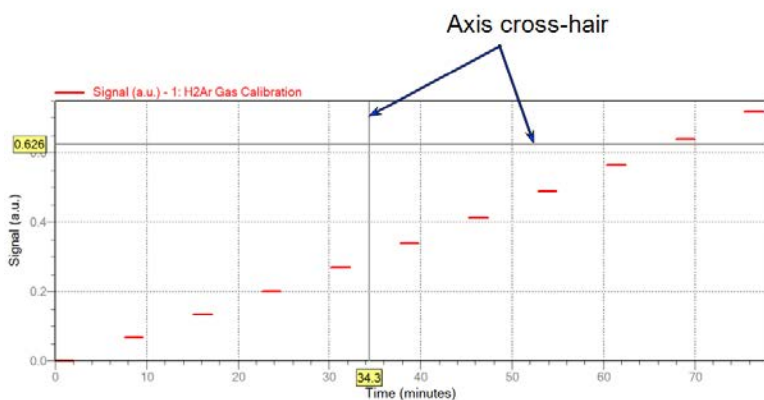
Example of
Axis cross-hair feature

ZOOM FEATURE

Use the zoom feature to examine graph details. Click, hold, and drag the left mouse button on the graphical area to be enlarged. A box will display in the area to be enlarged. To return to normal view, right-click in the graph and select *Autoscale all axes*.

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OVERLAY MULTIPLE SAMPLE FILES

To overlay the same type of graph on multiple samples:

1. Go to **File > Open**.
2. Select a .SMP file, then click **Open**. If the particle size plot displays, select *Advanced* from the view selector drop-down list at the bottom of the window to display the tabbed window view.
3. Click the *Report Options* tab.
4. In the *Selected Reports* list box, highlight a report, then click **Overlays**.
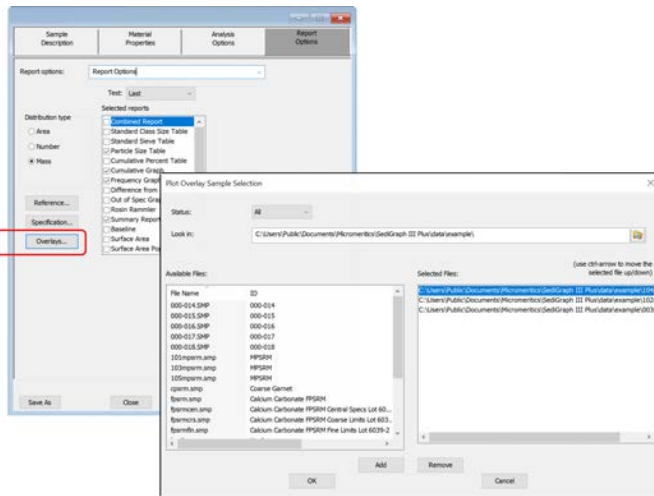
5. In the *Plot Overlay Sample Selection* window, move up to 25 files from the *Available Files* box to the *Selected Files* box.

Overlay Sample Selection

Selections	Description
Available Files [*selection*]	Lists files that meet the selected criteria. Select the files to be combined, then click **Add**. The selected files are moved to the *Selected Files* list box.
Look in [*button*]	Changes the file folder location. Click the **Browse** icon.
Reference [*button*]	Compares analysis results for the current sample to those obtained for a reference sample. Results are shown in the *Difference from Reference Graph* report.
Selected Files [*selection*]	Lists the files selected to be combined. Click **Remove** to move a file back to the *Available Files* list box. Click **OK** to combine the files.

Overlay Sample Selection (continued)

Selections	Description
Specification [*button***]**	Determines if the results for the current sample are within coarse and fine specifications. Results are shown in the *Out of Specification Graph* report.
Status [*drop-down box***]**	Selects the status of files to be combined.

> **For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.**

6. Click **OK**.
7. Click **Preview**.

REPORT EXAMPLES

BASELINE REPORT

COMBINED REPORT

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Serial # 0003 Unit 2

Sample: MPSRM
Operator: AWT
Submitter: Micromeritics
File: C:\Users\Public\Documents\Micromeritic...\003mpsrm.smp
Material/Liquid: Garnet / Water
Measurement Principle: X-Ray monitored gravity sedimentation
Calculation Method: Stokes sedimentation and Beer's law of extinction

Test Number: 8
Analyzed: 9/4/2003 12:11:11 AM
Reported: 2/23/2021 12:49:07 PM
Liquid Visc: 0.7227 mPa·s
Analysis Temp: 35.0 °C
Full Scale Mass: 100.0 %

Analysis Type: High Speed (Adj)
Run Time: 0:19 hrs:min
Sample Density: 3.880 g/cm³
Liquid Density: 0.9941 g/cm³
Base/Full Scale: 135 /84 kCnts/s
Reynolds Number: 0.37

Notes:
o Analysis options changed after first analysis.

Combined Report

Report by Size Table

Low Diameter (µm)	Cumulative Mass Finer (Percent)	Out of Spec (-%<,+%>)	Difference From Reference (% Finer)	Cum. Mass Standard Deviation (8 tests)
7.000	92.2	0.0	0.3	0.3
5.500	79.8	0.0	0.7	0.2
5.000	72.9	0.0	0.9	0.1
4.250	59.8	0.0	0.7	0.1
3.500	44.9	0.0	0.2	0.2
3.000	35.4	0.0	-0.2	0.2
2.500	27.1	0.0	-0.5	0.2
2.000	20.1	0.0	-0.6	0.2
1.500	13.7	0.0	-0.8	0.1
1.000	8.1	0.0	-0.6	0.1

Report by Mass Percent

Low Diameter (µm)	Cumulative Mass Finer (Percent)	Out of Spec (-%<,+%>)	Difference From Reference (% Finer)	Cum. Mass Standard Deviation (8 tests)
6.608	90.0	0.0	0.5	0.0
3.753	50.0	0.0	0.5	0.0
1.176	10.0	0.0	-0.8	0.0

CUMULATIVE FINER MASS PERCENT VS DIAMETER

SediGraph III Plus Operator Manual
512-42835-01 (Rev B) — Sep 2022
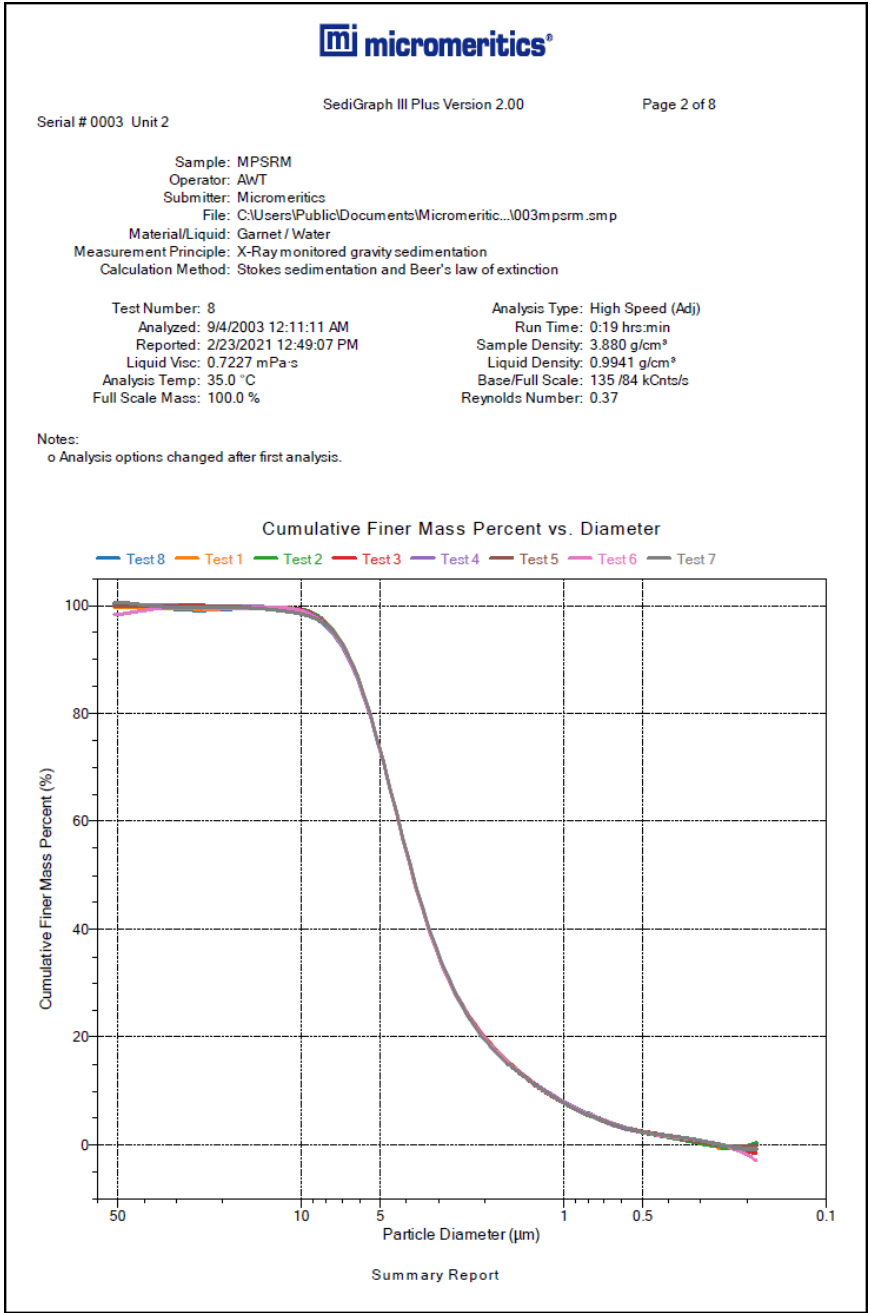
MASS FREQUENCY VS DIAMETER REPORT

![micromeritics]

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Serial # 0003 Unit 2

                Sample: MPSRM
              Operator: AWT
             Submitter: Micromeritics
                  File: C:\Users\Public\Documents\Micromeritic...\003mpsrm.smp
        Material/Liquid: Garnet / Water
  Measurement Principle: X-Ray monitored gravity sedimentation
     Calculation Method: Stokes sedimentation and Beer's law of extinction

       Test Number: 8   Analysis Type: High Speed (Adj)
          Analyzed: 9/4/2003 12:11:11 AM   Run Time: 0:19 hrs:min
          Reported: 2/23/2021 12:49:07 PM   Sample Density: 3.880 g/cm³
        Liquid Visc: 0.7227 mPa·s   Liquid Density: 0.9941 g/cm³
      Analysis Temp: 35.0 °C   Base/Full Scale: 135 /84 kCnts/s
     Full Scale Mass: 100.0 %   Reynolds Number: 0.37

Notes:
  o Analysis options changed after first analysis.

Mass Frequency vs. Diameter

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7 SELECTED REPORT OPTIONS

> To edit reports, open the *Sample* file then select the *Report Options* tab. Highlight the report name in the *Selected Reports* list box and click **Edit**.

ADVANCED REPORTS - PYTHON MODULE

The mic Python module is automatically imported when running a user supplied script. The module provides access to particle size data, and provides support for summary, tabular, and graphical reports.

- **Summary reports.** Consist of summary sections, each containing a two-column table of label and value pairs. Summary reports are created with the *mic.summary* call.
- **Tabular reports.** Consist of one or more tables each containing one or more labeled columns of data. Tabular reports are created with the *mic.table* call.
- **Graphical reports**. Consist of a single graph with one or more curves on one or two y-axes. Graphical reports are created with the *mic.graph* call.

Calls for accessing the sample file data can be found in the *Mic Module Python Calls* section of this appendix. More advanced example python scripts are included in the analyzer software.

Advanced Report Options

Up to five Advanced reports, each with up to 10 summary reports, 10 tabular reports, and 10 graphical reports can be created. To use this feature, a file containing a Python script that imports a "mic" Python module must be created. See *__MicModule Python Calls on page A - 30__* for an example of a Python script and functions for the "mic" Python module.

1. Create the Python script and save it in the *Scripts* directory.
2. Open a sample file with a *Complete* status.
3. Select *Advanced* in the view selector drop-down list at the bottom of the window to return to the tabbed view.
4. On the *Report Options* tab, select *Advanced* in the *Selected Reports* list box, then click **Edit**.
5. On the *Advanced Report Options* window, click **Add** in the *Available Scripts* group box to locate and select the Python script. Repeat for each script to be added.

6. In the *Selected Reports* group box, click the drop-down arrows to select up to five Python scripts previously added in the *Available Scripts* box.
7. On the *Report Options* tab, click **Preview**. The Python Reports will be included on the tabs across the top portion of the *Reports* window.

Advanced Reports

Selections	Description
Advanced Report 1 through 5 [*drop-down box*]	Use the drop-down lists to select currently-defined functions used to define the report calculations and output.
Available Scripts [*group box*]	Lists the available reports and provides the option to add, replace, edit, or remove reports.

For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.

BASELINE OPTIONS REPORT

The *Baseline* report shows a baseline measurement of the x-ray intensity as a function of cell elevator position.
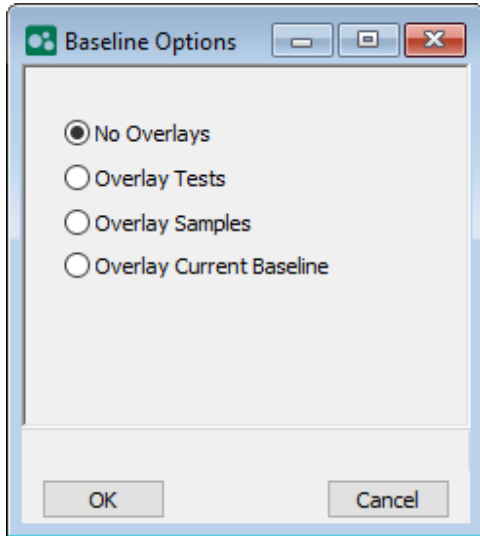
Select the options to include in the Baseline report.

COMBINED REPORT

The *Combined* report combines a selection of any SediGraph report onto a single page.
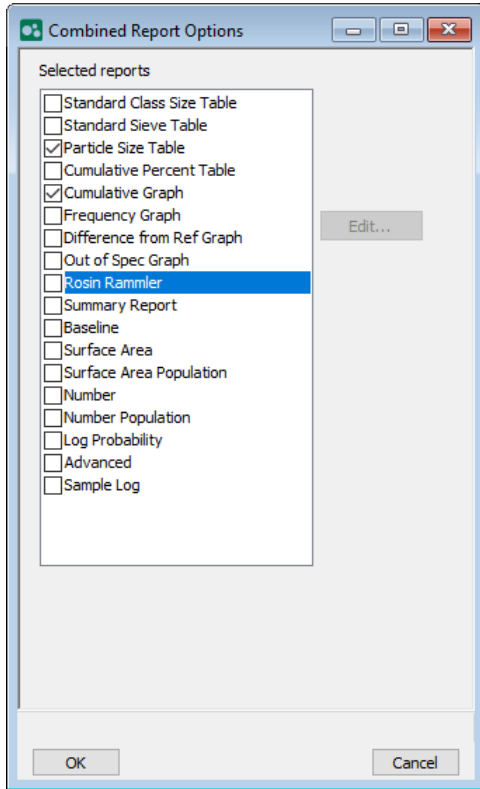
CUMULATIVE TABLE

This tabular report shows the SediGraph's collected data interpolated to a user specified set of cumulative values rather than being reported at the instrument defined standard particle sizes. Select which quantities to show in each column of the table.

Cumulative Percent Table

If Percent is selected in **Options > Units**, then the *Cumulative Percent Table* is available.
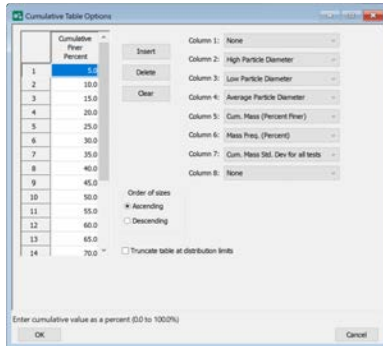
Cumulative Fraction Table

If Percent is selected in **Options > Units**, then the *Cumulative Fraction Table* is available.
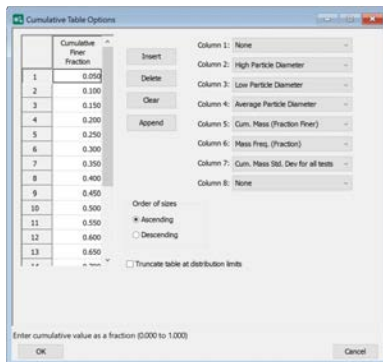
GRAPH OPTIONS

- Cumulative Graph Options
- Frequency Graph
- Difference from Ref Graph
- Out of Spec
- Surface Area
- Surface Area Population Options
- Number
- Number Population
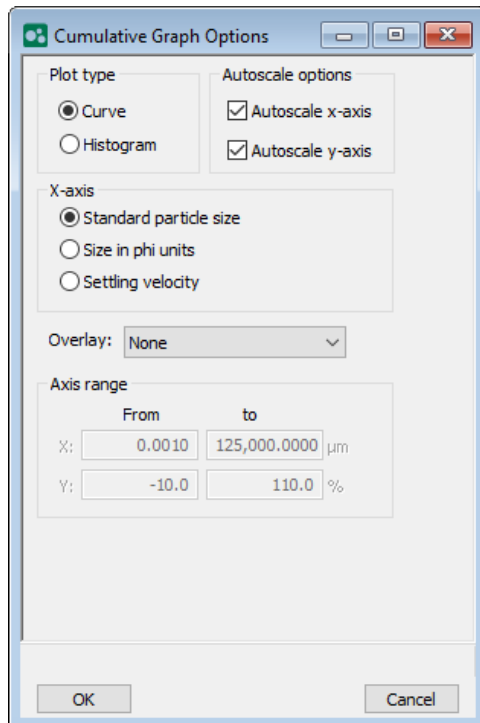
LOG PROBABILITY REPORT

The *Log Probability* report plots the particle size distribution with particle size on the x-axis and the logarithm of the probability on the y-axis

PARTICLE SIZE TABLE

This tabular report shows the SediGraph's collected data interpolated to a user specified set of particle sizes rather than being reported at the instrument defined standard particle sizes. Select which quantities to show in each column of the table.

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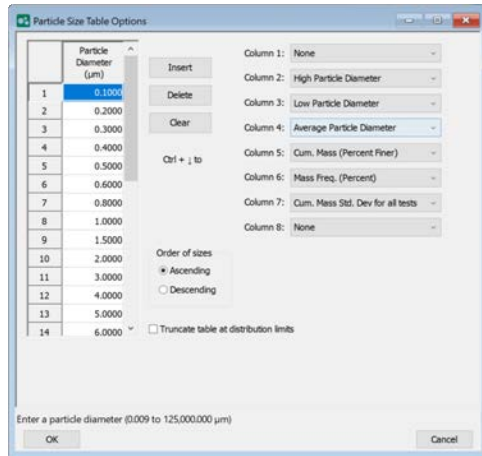
ROSIN RAMMLER

> The Rosin Rammler report cannot be edited.

This report shows the sample's particle distribution using a graph of the Rosin Rammler parameter as a function of the particle diameter.

SAMPLE LOG REPORT

> Sample Log reports cannot be edited.

Inserts a log of sample operations in the reports.

This report provides information on:

- Manual control operations performed during analysis.
- Information entered using *Add Log Entry* on the sample file editor.
- Warnings and/or errors which occurred during analysis.

STANDARD CLASS SIZE TABLE REPORT

This tabular report shows the SediGraph's collected data measured at the instrument defined standard set of particle sizes. Select which quantities to show in each column of the table.
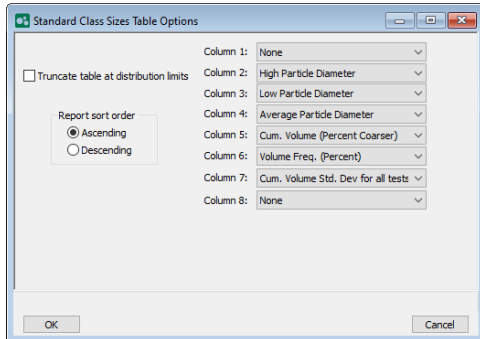
STANDARD SIEVE TABLE

This tabular report shows the SediGraph's collected data interpolated to a set of standard sieves rather than reported at the instrument defined standard particle sizes. Select which quantities to show in each column of the table.
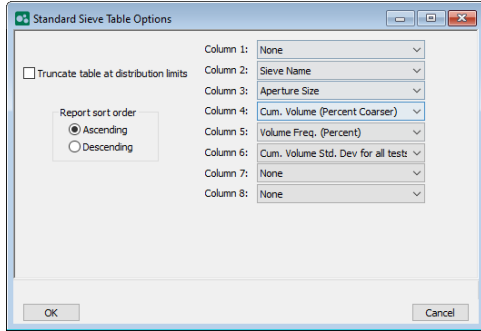
SUMMARY REPORT OPTIONS

The *Summary* report allows the user to select relevant statistical measures to characterize the sample and show these results on a single report page.
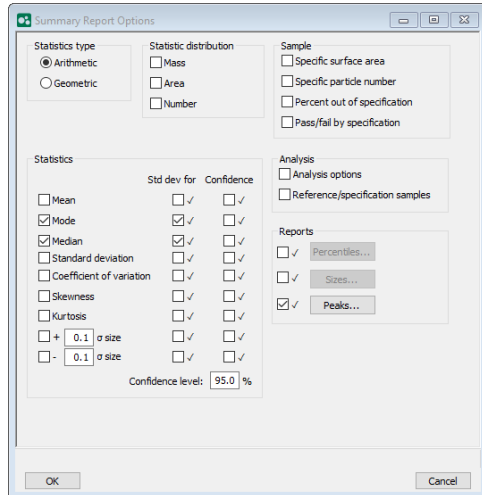
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8 DIAGNOSTICS
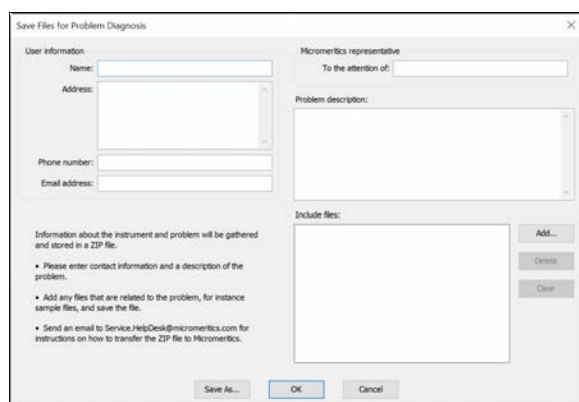
Unit [n] > Diagnostics

Use to display diagnostic readings, start diagnostic tests, and open saved diagnostic reports. Each test generates a file to the default directory name and path of *...\...\Service\userdiag* unless another directory name was specified. These reports can be sent to a Micromeritics Service Representative for examination.

SAVE FILES FOR PROBLEM DIAGNOSIS

Unit [n] > Diagnostics > Save Files for Problem Diagnosis

Use to compress pertinent diagnostic information into a single zip file. This file can be sent to a Micromeritics Service Representative for problem resolution.

1. Complete the form. A default file named *Diagnostics-[date].zip* is created unless another file name is specified.
2. Add any files that are related to the problem — such as sample files — and save the file.
3. Send an email to Service.Helpdesk@Micromeritics.com for instructions on how to transfer the .ZIP files to Micromeritics.

Save Files for Problem Diagnostics

Selections	Description
Problem description [*text box*]	Enter information that would be helpful to the Micromeritics rep-resentative.
Include Files	**Add.** Click to select additional files to send with this problem diagnosis. **Delete.** Select the file in the *Include Files* box, then click **Delete** to remove the file from the list. **Clear.** Click to clear all files from the *Include Files* box.

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Save Files for Problem Diagnostics (continued)

Selections	Description
Save As [*button***]**	Click to specify the name and location of the compressed file. Make a note of the file name and location. This file will need to be sent to your Micromeritics representative for problem resolution.
Micromeritics representative [*text box***]**	Enter the name of your Micromeritics representative. This inform-ation will remain on the window each time files for problem diagnosis need to be submitted (can be modified as necessary).
User Information [*text box***]**	Enter information for the person to be contacted by a Micromeritics representative. This information will remain on the window each time files for problem diagnosis need to be submitted (can be modified as necessary).

For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.

9 MAINTENANCE AND TROUBLESHOOTING

⚠ Do not modify this instrument without the authorization of Micromeritics Service Personnel.

⚠ Improper handling, disposing of, or transporting potentially hazardous materials can cause serious bodily harm or damage to the instrument. Always refer to the MSDS when handling hazardous materials. Safe operation and handling of the instrument, supplies, and accessories is the responsibility of the operator.

⚠ When lifting or relocating the instrument, use proper lifting and transporting devices for heavy instruments. Ensure that sufficient personnel are available to assist in moving the instrument. The 5125 SediGraph II Plus weighs approximately 43 kg (95 lb). The MasterTech weighs approximately 18 kg (40 lb).

⚠ Use of a power cord or power supply not provided with the instrument could cause personal injury or damage to the equipment. If a replacement is needed, contact your Micromeritics Service Representative. Detachable power supply cords with an inadequate rating could cause significant instrument damage or physical harm.

Do not add anything between the power cord and the power source that would compromise the earth ground.

Do not remove or disable the grounding prong on the instrument power cord.

If the equipment needs to be relocated, check with your Micromeritics service representative. The equipment must be positioned such that the mains supply is not obstructed and is easily accessible to disconnect the equipment from the AC main power supply.

The analyzer has been designed to provide efficient and continuous service; however, certain maintenance procedures should be followed to obtain the best results over the longest period of time. When unexpected results occur, some common operational problems not indicated on the window and their respective causes and solutions are provided.

The following can be found on the Micromeritics web page (www.Micromeritics.com).

- Error Messages document (PDF)
- Parts and Accessories

Most operational problems are caused by:

- Deteriorated or blocked tubing
- Air leaks
- An unlevel analyzer

When unexpected analysis results occur, check the above first. Some common operational problems not indicated on the window and their respective causes and solutions are provided below:

Cell cannot be filled or drained.

Cause A: Blocked or damaged tubing.

Action A: Locate and replace blocked or damaged tubing. See *Replace the Flexible Tubing on page 9 - 18*.

Cause B: Blocked cell input or output port.

Action B: Clean analysis cell. See *Replace the Analysis Cell Assembly on page 9 - 9*.

Cause C: Valve or pump not working properly.

Action C: From *Manual Control* window, check pump and valve operation. If either is not working properly, contact authorized service personnel.

Cause D: Tubing improperly installed.

Action D: Install the tubing. See *Replace the Flexible Tubing on page 9 - 18*.

Cell cannot be raised or lowered

Cause: Elevator which moves cell is stuck.

Action: Check flexible tubing for possible obstruction to elevator movement. If necessary, reposition tubing. Also check for any other obstruction to elevator movement.

Mixing chamber cannot be filled or drained.

Cause A: Blocked or damaged tubing.

Action A: Locate and replace blocked or damaged tubing. See *Replace the Flexible Tubing on page 9 - 18*.

Cause B: Blocked mixing chamber input or output port.

Action B: Clean mixing chamber. See *Clean the Mixing Chamber and Bezel on page 9 - 17*.

Cause C: Valve or pump not working properly.

Action C: From Manual Control window, check pump and valve operation. If either is not working properly, contact authorized service personnel.

Cause D: Tubing improperly installed.

Action D: Install the tubing. See ***Replace the Flexible Tubing on page 9 - 18***.

Mixing chamber suspension is turning brown

Cause: Teflon coating on stirring bar is worn.

Action: Replace stirring bar.

X-RAY ON indicator is turned on, but the computer display shows 0 kilocounts.

Cause A: Analysis compartment door not completely closed.

Action A: Close analysis compartment door.

Cause B: Cell is in a position which blocks beam.

Action B: Move cell to proper operating position. Enable Manual Control, access the pop-up menu on the cell, and select Move Cell Position.

Cause C: Cell is clogged.

Action C: Remove and clean cell. See ***Clean the Analysis Cell Assembly on page 9 - 11***.

Cause D: Slits in collimator blocked.

Action D: Clean the collimator. See ***Clean the Collimator Slits on page 9 - 14***.

Cause E: X-ray source or detector has failed.

Action E: Contact authorized service personnel.

X-RAY STANDBY indicator was turned on, but when keyswitch is placed in X-RAY ON position, XRAY ON indicator does not turn on.

Cause A: Keyswitch is between positions.

Action A: Move keyswitch to X-RAY STANDBY position and then back to X-RAY ON position while observing indicator.

Cause B: X-RAY ON indicator lamp is burned out.

Action B: Replace lamp. See ***Replace the X-ray Indicator Lamps on page 9 - 23***.

Cause C: X-ray filament supply not available or X-ray unit damaged.

Action C: Contact authorized service personnel in accordance with service contract.

Cause D: Rear panel is off, the top cover is off, or the fluid module is not fully installed.

Action D: Replace all panels.

*See **Cause of Bubbles on page 9 - 27** first to determine the cause of the bubbles. Perform the*

outlined procedure then return to this table for corrective action.

Bubble elimination problem.

Cause A: Windows are dirty or misaligned.

Action A: Clean or replace the windows.See ***Clean the Analysis Cell Assembly on page 9 - 11***.

Cause B: Inlet port on the cell assembly is loose.

Action B: Replace the cell assembly. See ***Replace the Analysis Cell Assembly on page 9 - 9***.

Cause C: A valve has failed.

Action C: Contact authorized service personnel.

SAFE SERVICING

> ⚠️ Do not modify this instrument without the authorization of Micromeritics Service Personnel.

To ensure safe servicing and continued safety of the instrument after servicing, service personnel should be aware of the following risks:

Product specific risks that may affect service personnel:

- **Electrical**. Servicing or repair could require opening the outer panels and exposing energized electrical components.
- **MasterTech Fuses**. Only use fuses rated as:

Power Source	Required Fuses
100-120VAC	Single fuse, 3AG (Slo-Blo) 250V, 2.0AL, 6.35 mm x 31.7 5 mm. Single pole input.
220-240VAC	Double fuse, Time-lag (Slo-Blo), 250V, 1.25AL, 5 mm x 20 mm. Double pole input.

Protective measures for these risks:

- **Electrical**. The electrical components operate at low voltage (24V or less) and pose low risk when energized. Maintenance, troubleshooting, and repairs should be performed with the instrument de-energized whenever possible, in accordance with standard electrical safety guidelines.
- **MasterTech Fuses**. Use of improperly rated fuses could cause damage to the equipment.
- Power off and unplug the analyzer from the power outlet prior to servicing.

Verification of the safe state of the instrument after repair:

- All instrument panels and covers installed.

PARTS AND ACCESSORIES

Parts and accessories are located on the Micromeritics web page.

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POWER

The SediGraph is designed to operate with universal input power supply (100/120/220/240 VAC, 47/63 Hz, 450 VA). The power outlet should be able to supply 15 amps@ 100 or 115 VAC ±10% or 7.5 amps @ 240 VAC ±10%. These requirements can be checked by using a circuit analyzer (available at most hardware or electronic supply houses) or a multimeter. There should also be sufficient outlets for the computer, monitor, printer, and any other peripheral devices. The power cord, IEC, 300V, 10A (available in the accessories kit) should be connected to noise-free power of the correct voltage and frequency, with a safety earth ground, through a standard wall receptacle.

The MasterTech 052 leaves the factory set for 120 VAC and with the line fuse removed. The correct setting of the universal power entrance must be checked, and the appropriate fuse installed before the MasterTech can be operated. The MasterTech is designed to operate with either 100/120/220/240 VAC at 50/ 60 Hz. Voltage selection and fusing are made at the power connector which is located on the rear panel of the unit.

The instrument should be connected to a switch which meets relevant requirements of IEC 60947-3 or a circuit breaker which meets the relevant requirements of IEC 60947-2.

Noise-free power of the correct voltage and frequency, with a safety earth ground, should be available through a standard wall receptacle. There should be a minimum 15A rated breaker @ 100/120 VAC and a minimum 7.5A @ 240 VAC.

CAUTION	The analyzer and peripheral devices **must** be installed on their own dedicated power line. Other devices — such as motors, generators, or ovens — **should not** be placed on the same power line.

	Replacement power supply cords must be rated for the specifications stated above.

ENABLE MANUAL CONTROL

Unit [n] > Enable Manual Control

Show Instrument Schematic on page 2 - 20

Use to enable the manual control of certain system valves and pump components on the analyzer schematic. When this option is enabled, a checkmark appears to the left of ***Unit [n] > Enable Manual Control***. If the analyzer schematic is not immediately visible, go to ***Unit [n] > Show Instrument Schematic***.

PREVENTIVE MAINTENANCE

Perform the following preventive maintenance procedures to keep the analyzer operating at peak performance. Micromeritics also recommends that preventive maintenance procedures and calibration be performed by a Micromeritics Service Representative every 12 months.

A Micromeritics service technician should perform the following procedures every 12 months. Do not attempt to perform these procedures yourself.

- Clean the high voltage area
- Calibrate the X-ray control system
- Calibrate the fluid control system
- Calibrate the temperature control system

Maintenance Required	Frequency
Perform a reference material run	Every week
Clean the analyzer	Every 30 days*
Clean the mixing chamber and bezel	As needed
Clean the analysis cell	Every 30 days*
Replace the mixing pump and cell pump tubing	Every 30 days*
Replace the analysis cell tubing	As needed
Clean the air filter	Every 30 days*
Check the operation of the mixing pump	Every 30 days*
Check the operation of the cell pump	Every 30 days*
Check the level of the analyzer	Every 30 days*
Clean the collimating slits	As needed

* Or every 160 analyses, which ever comes first

ANALYSIS CELL ASSEMBLY

Replace the Analysis Cell Assembly

If the analysis cell assembly becomes damaged, it may be necessary to replace it.

1. Go to **Unit [n] > Drain and Load**.
2. Select *Leave mixing chamber empty*.
3. Click **Continue**.
4. When prompted to load the sample, click **Cancel**.
5. Power OFF the Pump Control.
6. Open the transparent sliding door to the analysis compartment.
7. Loosen the cell mounting screw and remove the cell from the retaining bracket.
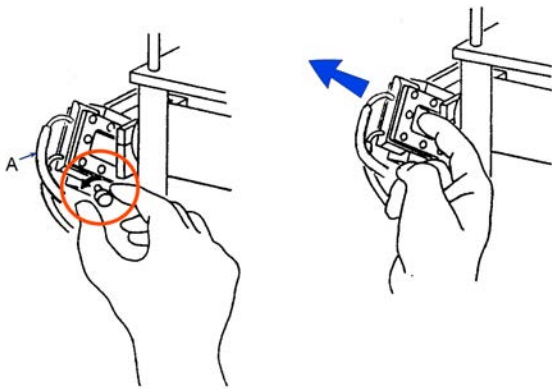
A. Flexible analysis cell tubing

8. Carefully remove the flexible tubing from the two ports on the cell.
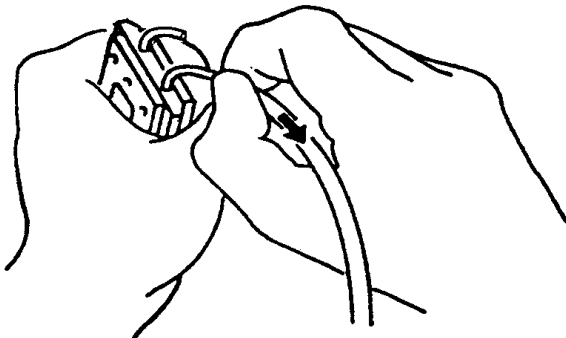
9. Connect the flexible tubing to the ports on the new analysis cell
10. Insert the cell in the retaining bracket and tighten the cell mounting screw.
11. Power ON the Pump Control.

Replace the Analysis Cell Tubing

1. Drain the system. See *Drain the System on page 9 - 22*.
2. Place the Pump Control switch on the analyzer front panel in the OFF position
3. Open the transparent sliding door to the analysis compartment.
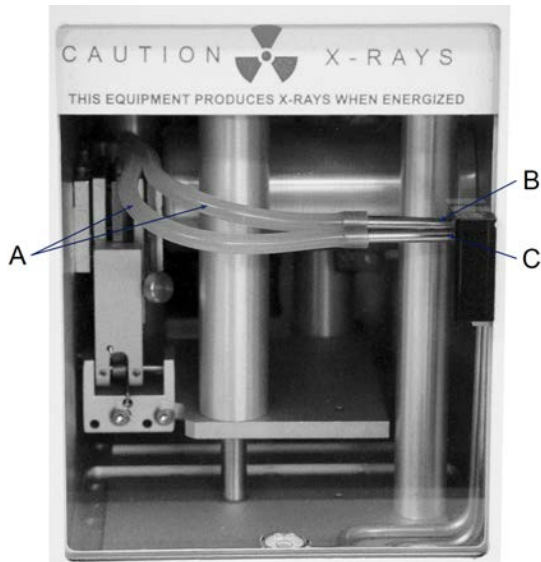
A. Flexible analysis cell tubing
B. Back connector (for back cell port tubing)
C. Front connector (for front cell port tubing)

4. Remove the flexible analysis cell tubing from the rigid tubing connector in the analysis compartment.
5. Loosen the cell mounting screw and remove the cell from the retaining bracket as shown below.
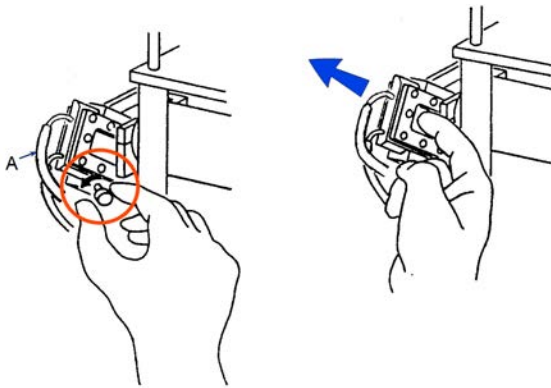
A. Flexible analysis cell tubing

6. Remove the flexible analysis cell tubing from the two ports on the cell.
7. Connect the new flexible analysis cell tubing to the ports on the new analysis cell and to the rigid tubing connector. The tubing for the front port of the cell connects to the front rigid tubing connector and the tubing for back port of the cell connects to the back rigid tubing connector.

8. Insert the cell in the retaining bracket and tighten the cell mounting screw.
9. Close the analysis compartment door.
10. Power ON the Pump Control.

Clean the Analysis Cell Assembly

The analysis cell should be removed periodically and cleaned to remove any residue.

1. Go to **Unit [n] > Drain and Load**.
2. Select *Leave mixing chamber empty*.
3. Click **Continue**.
4. When prompted to load the sample, click **Cancel**.
5. Place the *Pump Control* switch on the analyzer front panel in the OFF position.
6. Open the transparent sliding door to the analysis compartment. Loosen the cell mounting screw and remove the cell from the retaining bracket.
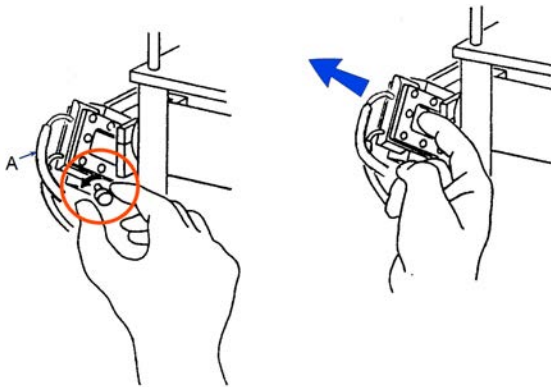
A. Flexible analysis cell tubing

7. Carefully remove the flexible tubing from the rigid tubing connector which is mounted along the right side of the analysis compartment.
8. Carefully remove the flexible tubing from the two ports on the cell.
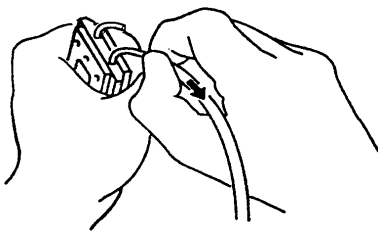
9. Disassemble the cell by removing the ten screws in the cell window retaining plates.

![micromeritics® logo]
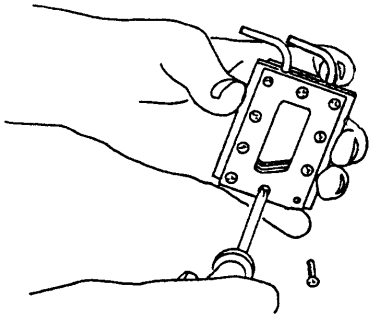
> **CAUTION** Do not use cloth made of a coarse material or abrasive cleansers when cleaning the cell windows. Particles may lodge in scratches, which could alter X-ray pulse rates and cause invalid analysis results.

10. Use either IPA or a mild detergent to clean the cell windows. Use an air blower to remove any debris from the cell body, window retaining plates, and ports.

11. Assemble the cell by placing a cell window and a cell window retaining plate on each side of the cell body. The cell window retaining plate must be positioned so that the sloped part matches that of the cell body and other plate.
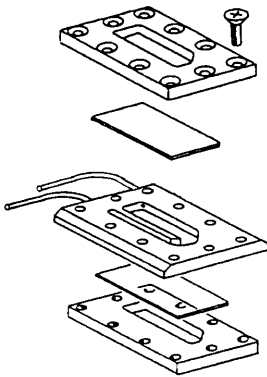
Ensure the sloped portions of the cell body and retaining plates are aligned.

12. Insert the ten screws removed in step 8 into the window retaining plates, but do not tighten.

> **CAUTION** When assembling the cell, alternate the tightening of screws. Failure to do so could result in air entering the cell, causing bubble elimination problems.

13. Using a screwdriver, tighten the screws around the cell by tightening one screw and then tightening the screw diagonally opposite that screw. See the following illustration for the tightening sequence. This sequence helps to ensure uniform closure around the cell.
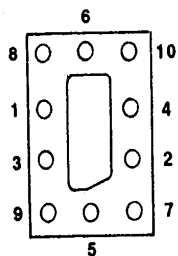
14. Connect the flexible tubing to the ports on the analysis cell and to the rigid tubing connector. The tubing for the front port of the cell connects to the front rigid tubing connector. The tubing for the back port of the cell connects to the back rigid tubing connector.
15. Insert the cell in the retaining bracket and tighten the cell mounting screw.
16. Place the Pump Control switch in the ON position.
17. Go to **Unit [n] > Rinse > SediGraph**.
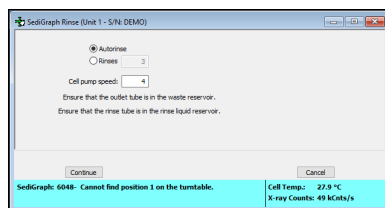
18. Select *Autorinse* then click **Continue** to rinse the analysis cell.

CLEAN THE COLLIMATOR SLITS

Replace the Analysis Cell Assembly on page 9 - 9

The collimator slits may become blocked by dust or debris which accumulates in the analysis compartment over a period of time, causing inaccurate results.

1. Power OFF the analyzer.
2. Remove the retaining screws from the top of the analyzer; then remove the top panel.
3. Remove the analysis cell. See *Replace the Analysis Cell Assembly on page 9 - 9* for removal instructions.
4. Remove the two foam plugs in the top of the analysis module.
5. Use a hex driver with an extension to remove the collimator retaining screws.
6. Reach through the door of the analysis compartment to lift the top collimator out of the analysis module.
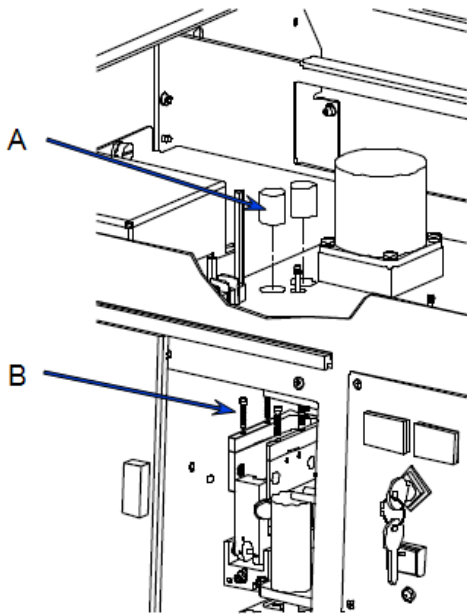
A. Foam plugs
B. Collimator retaining screws

7. Use a lint-free cloth to clean the shiny area near the center of the collimator removed and the corresponding area of the collimator remaining in the analysis module.

> **CAUTION** Do not use cloth made of a coarse material or abrasive cleansers when cleaning the collimating slits.

8. Replace the top collimator and the retaining screws.

> **CAUTION** Tighten the collimator retaining screws only enough to securely hold the collimator in place. Over-tightening the screws can close the collimating slits, reducing the intensity of (or completely blocking) the X-rays.

9. Tighten the retaining screws for the top collimator.
10. Replace the two foam plugs in the top of the analysis module.
11. Replace the analysis cell and the top panel.
12. Power ON the analyzer.

CLEAN THE AIR FILTER

The air filter on the analyzer should be cleaned every 30 days (more often in environments with increased levels of dust) and replaced once a year.

1. Slide out the drip tray on the front of the analyzer.

A. Air filter
B. Drip tray
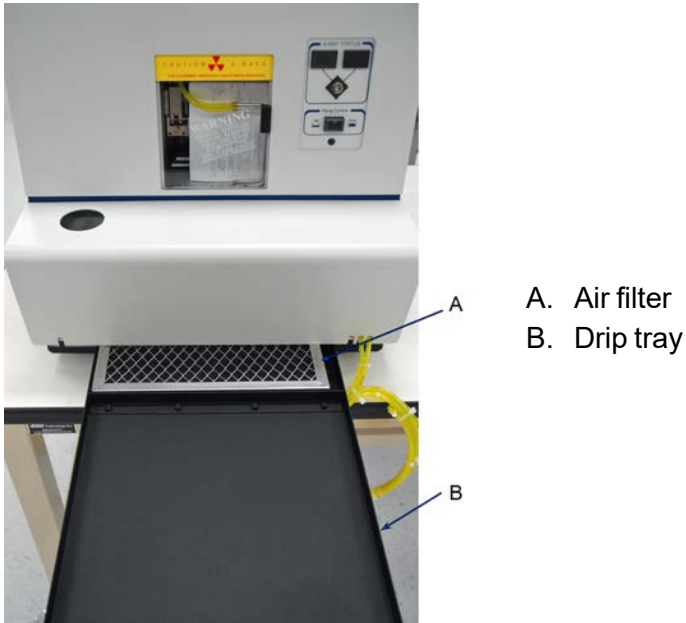
2. Remove the air filter from drip tray by squeezing the filter while pulling it away from the drip tray.
3. Rinse the filter thoroughly and shake out the excess water. Place it aside and allow it to dry.
4. Install a new filter or after the filter has dried, replace it.
5. Check to see that the analyzer is level.

CLEAN THE INSTRUMENT

The exterior casing of the instrument may be cleaned using a clean, lint-free cloth dampened with isopropyl alcohol (IPA), a mild detergent, or a 3% hydrogen peroxide solution. Do not use any type of abrasive cleaner. It is not necessary to remove knobs, screws, etc. while cleaning. If a MasterTech is installed, clean it in the same manner.

> **CAUTION**
> - Do not allow liquid to penetrate the casing of the analyzer. Doing so could result in damage to the unit.
> - Use only a mild detergent in water to clean safety shields. The use of isopropyl alcohol can damage the shield surface.

CLEAN THE MIXING CHAMBER AND BEZEL

The mixing chamber bezel should be cleaned periodically to prevent contaminants from entering the mixing chamber. To clean the bezel:

- Remove the bezel and clean using a mild detergent. Rinse, then dry thoroughly before replacing it on the mixing chamber.

The mixing chamber should be removed and cleaned periodically to remove any residue.

> **CAUTION**
> When cleaning the mixing chamber, avoid getting the electrical connections wet. Do not immerse the chamber in liquid. Doing so could damage the system.

1. Drain the mixing chamber.

    a. Go to **Unit [n] > Drain and Load**.
    b. Select *Leave mixing chamber empty*.
    c. Click **Continue**.
    d. When prompted to load the sample, click **Cancel**.

2. Disconnect the flexible tubing from the mixing chamber, exercising caution to prevent damage to the tubing.
3. Disconnect the electrical cable.

A. Flexible tubing
B. Flexible tubing
C. Flexible tubing
D. Flexible tubing
E. Flexible tubing
F. Electrical cable
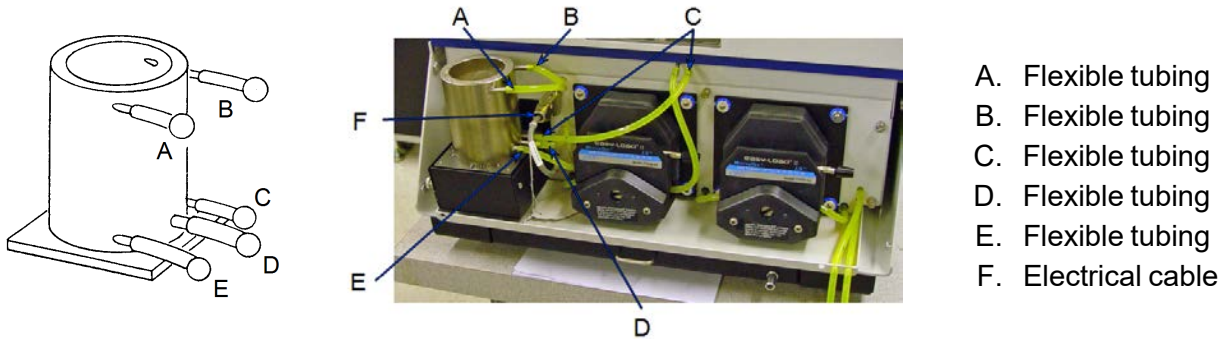
4. Clean the chamber using IPA or a mild detergent. Rinse thoroughly. All ports should be cleaned using an air blower.
5. Reconnect the tubing to the mixing chamber.
6. To reconnect the mixing chamber, ensure the tubing is securely fastened at each port.
7. Reconnect the electrical cable.

REPLACE THE FLEXIBLE TUBING

Drain and Load Operation on page 5 - 2

The analyzer includes a complete plumbing system for circulation of sedimentation liquid and particle suspension between the cell, the mixing chamber, an external rinse container, and an external waste container. In order for the system to operate properly, damaged or deteriorated tubing must be replaced. Tubing from the mixing pump, the cell pump, and the analysis cell can be replaced independently.

> Use the tube installation tool to help install the tubing. It is included in the tool accessories kit.

When replacing tubing, always drain the system first.

CHECK THE MIXING PUMP OPERATION

The mixing pump should be checked every 30 days (or every 160 runs, whichever comes first) to see if it is operating correctly.

1. Go to **Unit [n] > Enable Manual Control** to display the instrument schematic.
2. Right-click the *Mixing Pump* icon, then select *Turn on* from the pop-up menu.
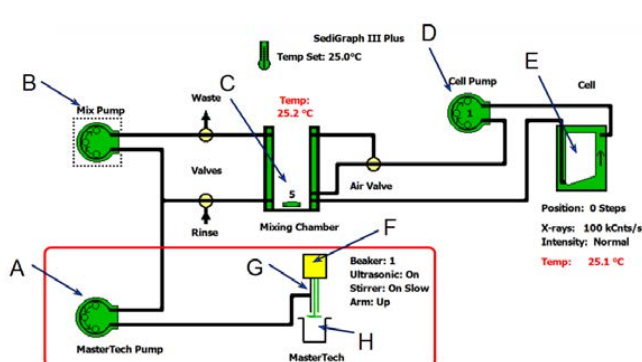
A. MasterTech pump
B. Mixing pump
C. Mixing chamber
D. Cell pump
E. Analysis cell
F. MasterTech arm
G. MasterTech stirrer
H. MasterTech Beaker

Items in the red box show only if MasterTech is installed

3. If the pump fails to start, refer to the ***Reset the Mixing Pump and Cell Pump on page 9 - 21***.
4. Right-click on the *Mixing Pump* icon.
5. Select *Turn off* from the pop-up. If the pump fails to stop, the fluid control board may need replacing. Contact your service representative.

CHECK THE CELL PUMP OPERATION

Reset the Mixing Pump and Cell Pump on the facing page

The cell pump should be checked every 30 days (or every 160 runs, whichever comes first) to see if it is operating correctly.

1. Go to **Unit [n] > Enable Manual Control** to display the instrument schematic.
2. Right-click the *Cell Pump* icon, then select *Turn on* from the pop-up.
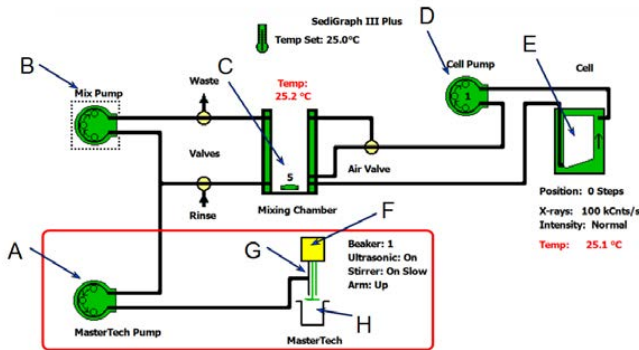
A. MasterTech pump
B. Mixing pump
C. Mixing chamber
D. Cell pump
E. Analysis cell
F. MasterTech arm
G. MasterTech stirrer
H. MasterTech Beaker

Items in the red box show only if MasterTech is installed

3. Perform the following steps. If any of these steps fail, see*Reset the Mixing Pump and Cell Pump on the facing page* .

    For each of the following steps, right-click the *Cell Pump* icon, then select the item listed:

    - Increase speed
    - Decrease speed
    - Flow up in cell
    - Flow down in cell
    - Increase speed
    - Decrease speed

4. Right-click the *Cell Pump* icon, then select **Turn off**. If the pump fails to stop, the fluid control board may need replacing. Contact a service representative.

RESET THE MIXING PUMP AND CELL PUMP

If an electrical overload occurs with the mixing pump or the cell pump, the pumps should be rest.

1. Power OFF the Pump Control.
2. Allow the internal varistor to cool down (approximately two to three minutes).
3. Check the tubing to verify that it is routed properly.
4. Place the Pump Control switch in the AUTO position.
5. Check the pump operation.

Contact your Micromeritics service representative if the problem continues.

REPLACE THE CELL WINDOWS

Clean the Analysis Cell Assembly on page 9 - 11

X-ray photons from the X-ray source pass through the cell windows to the X-ray detector on the other side of the cell. If cell windows become scratched or damaged, settling particles may become entrapped. This could alter X-ray pulses, resulting in invalid analyses. The analysis cell windows should be replaced when necessary.

DRAIN THE SYSTEM

Unit [n] > Drain and Load

Ensure that the outlet tube is in the waste reservoir and the rinse tube is in the rinse liquid reservoir.
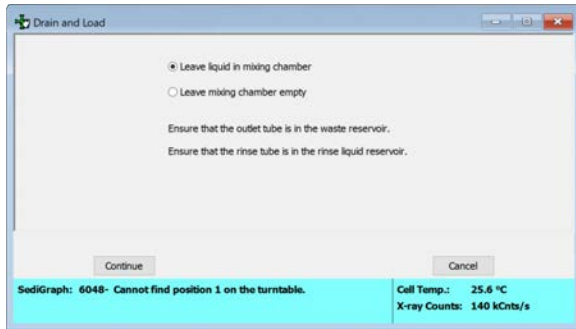
1. Select *Leave mixing chamber empty*.
2. Click **Continue**. A progress message displays.
3. Click **Cancel**.

CHECK THE LEVEL OF THE ANALYZER

An unlevel analyzer may cause inaccurate analyses. Check every 30 days to see if the analyzer is level.

1. Open the analysis compartment door and locate the level indicator.
2. Look straight down at the indicator. The analyzer is level when the bubble is centered inside the black circle on the level indicator.

Level indicator

3. If the analyzer is not level, lift the corner of the analyzer then turn the appropriate foot counterclockwise to raise the unit or clockwise to lower the unit.

4. Set the analyzer down and observe the indicator. The bubble should be centered inside the black circle on the level indicator.

REPLACE THE X-RAY INDICATOR LAMPS

The X-RAY STANDBY indicator and the X-RAY ON indicator on the front panel of the analyzer contain an internal lamp.

> **CAUTION**   If the X-RAY ON indicator lamp is burned out or installed incorrectly, the instrument will be inoperative.

> **CAUTION**   Disconnect the analyzer power cord from the AC power source before attempting to replace the lamp. Failure to do so could result in electrical shock or damage to the instrument.

1. Remove the cover lens from the analyzer by prying with a flat object.
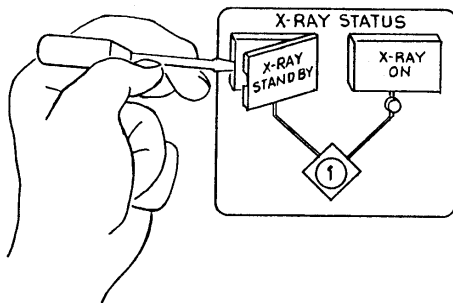
2. Using a flat object, pull the lever which raises the lamp socket out of the lamp compartment.
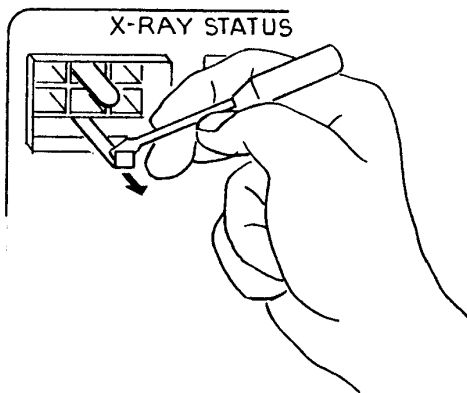
3. Remove the lamp by pulling it away from the socket.

![X-RAY STATUS illustration showing a hand adjusting the lamp socket]
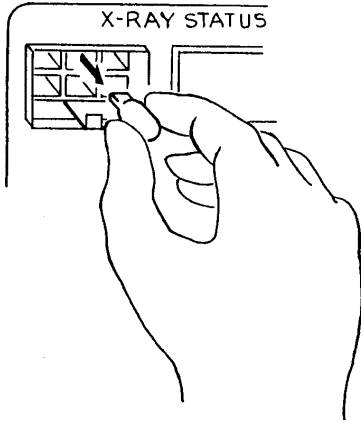
4. Push lamp socket lever toward the analyzer and insert replacement lamp into socket.

![X-RAY STATUS illustration showing a hand inserting the replacement lamp]
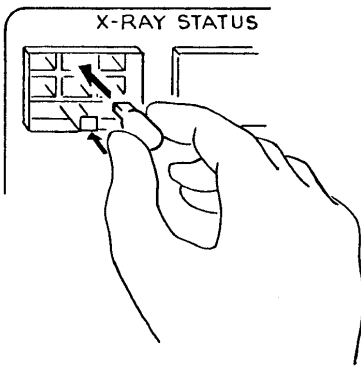
5. Replace the indicator cover lens.
6. Connect the analyzer power cord to an AC power source.
7. Power ON the analyzer.
8. Place the keyswitch in the appropriate position.
9. Verify that the lamp is working.

REPLACE THE MIXING PUMP TUBING

1. Place the analyzer on the edge of a table or flat surface.
2. Remove the pump chassis cover.
3. Drain the system. See *Drain the System on page 9 - 22*.
4. Power OFF the Pump Control.
5. Rotate the mixing pump lever to the left (the mixing pump is the pump on the right) to place the mixing pump housing in the open position.

    A. Mixing pump lever (open position)
    B. Mixing pump tubing

6. Remove the mixing pump flexible tubing from the rigid tubing connectors on both sides of the pump. Discard the used tubing.
7. Using the tube installation tool supplied in the accessories kit, attach one end of the new flexible mixing pump tubing to the rigid tubing connector on the right.
8. Thread the tubing through the pump as shown below.

9. Attach the other end of the tubing to the rigid connector on the left.
10. Rotate the mixing pump lever to the right to place the mixing pump housing in the closed position.
11. Replace the pump chassis cover.
12. Power ON the Pump Control.

![micromeritics® logo]

PERFORM A REFERENCE MATERIAL ANALYSIS

It is a good practice to perform a reference material analysis every week to ensure that the analyzer is operating within specifications. Reference material kits, including instructions for performing the reference material analysis, are available from Micromeritics.

CAUSE OF BUBBLES

If bubble problems continue to exist, perform the following steps to determine their source.

1. Install a clean, cell assembly in the cell holder and ensure it is free of bubbles.
2. Go to *Unit [n] > Baseline* and perform the steps for collecting baseline data.

   If the analyzer is successful in obtaining a baseline, the cell proceeds to a parked position, indicating that bubbles are caused by:

   - improper tubing routing,
   - a failed valve,
   - window misalignment, or
   - a loose inlet / outlet port on the cell assembly.

   If the analyzer is unable to obtain a baseline, an error message appears in the lower status window. This indicates X-ray detection and / or generation problems may be present. Contact your Micromeritics service representative for corrective action.

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POWER INSTRUMENT ON AND OFF

> **CAUTION** DO NOT connect or disconnect cables when the instrument is powered ON.

Power ON the equipment in the following order:

1. Computer, monitor, and printer.
2. Place the Pump Control switch (located on the front panel) in the AUTO position.
3. Analyzer.
4. Insert the X-ray key into the X-ray keyswitch then turn the switch to the X-RAY ON position.
5. Wait 30 minutes for the analyzer to warm up before performing an analysis.

> **CAUTION** It is recommended that the analyzer remain on unless it is going to be idle for a period of more than 24 hours. Leaving the analyzer on helps prolong the life of its major components.

Power OFF the equipment in the following order:

> **CAUTION** Always exit the analysis program before turning off the computer. Failure to do so could result in loss of data.

1. Exit the analysis program. If an analysis is in progress when closing the application, the following message is displayed:

   Instrument is busy. Continue program exit?

   Select Yes and the analysis program closes. The analysis continues and data continue to be collected. Queued reports under the printer will print. If a power failure occurs and an uninterruptible power supply (UPS) is not attached to the analyzer, the data collected after exiting the analysis program are lost.

   Select **No** to continue the analysis. Select **Yes** to close the application.

2. Computer, monitor, printer.
3. Analyzer.

RECOVER FROM A POWER FAILURE

The analyzer saves entered and collected data in case of power failure. File parameters and any other data entered will still be present when power is restored. If an analysis was in progress when the power failure occurred, it will be canceled when the analyzer restarts. Any data collected during the analysis will still be present, but the analysis should be restarted in order to produce complete results.

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MASTERTECH TROUBLESHOOTING AND MAINTENANCE

Power failure

Cause A: Power cable not connected or switch not in ON position.

Action A: Make sure power cable is plugged into the power source and the power ON/OFF switch is in the ON position.

Cause B: Input power fuse blown.

Action B: Replace the fuse. See ***Replace the Input Power Fuse on the facing page***.

Stirrer will not work.

Cause: Stirrer is improperly connected.

Action: Check the stirrer's electrical connection.

Turntable will not move.

Cause: Arm is in the LOAD position.

Action: Press the AUTO/LOAD switch on the front panel to lower the arm.

MasterTech pump will not run.

Cause: Pump switch on the front panel may be in the OFF position.

Action: Press the pump AUTO/ OFF switch on the front panel.

Ultrasonic probe will not work.

Cause: Probe improperly connected to the MasterTech.

Action: Check the MasterTech connector cable.

Ultrasonic agitation diminished.

Cause: The ultrasonic probe tip may need replacing.

Action: See ***Replace the MasterTech Ultrasonic Probe Tip on the facing page***.

MasterTech will not initiate commands from the computer.

Cause: The cable may be connected improperly from the MasterTech to the computer.

Action: Check the cable connections.

Pump leaks or is not operating efficiently.

Cause: Tubing is leaking or clogged.

Action: See *Replace the Flexible Tubing on page 9 - 18*.

REPLACE THE MASTERTECH ULTRASONIC PROBE TIP

Parts and accessories are located on the Micromeritics web page.

After extended periods of use, the tip of the ultrasonic probe on the MasterTech may become pitted, causing diminished agitation.

1. Remove the damaged tip from the probe using the wrenches provided.
2. Attach the new probe tip to the probe body. Use the wrenches to tighten securely.

⚠ CAUTION	Never hold the probe by the tip. Doing so may cause damage to the probe.

REPLACE THE INPUT POWER FUSE
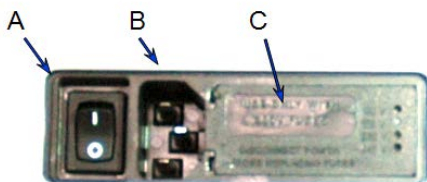
A. Power switch
B. Power connector
C. Fuse cover

⚠	■ The power cord should be disconnected from the instrument before removing the cover from the input power connector. Failure to disconnect the power cord could result in electrical shock.
	■ The input power connector can be used with either a single-fuse arrangement or a double-fuse arrangement. Use the appropriate fuse(s) for the input power source. The fuses must be identical in type and rating to that specified. Use of other fuses could result in electrical shock and/or damage to the instrument. Fuse requirements are listed in the following table.

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Fuses may be obtained from Micromeritics or a vendor of your choice as long as they meet the requirements specified in this section.

Power Source	Required Fuses
100-120VAC	Single fuse, 3AG (Slo-Blo) 250V, 2.0AL, 6.35 mm x 31.7 5 mm. Single pole input.
220-240VAC	Double fuse, Time-lag (Slo-Blo), 250V, 1.25AL, 5 mm x 20 mm. Double pole input.

1. Ensure the instrument is powered OFF and the power cord is disconnected.
2. Open the cover to the right of the power entrance and remove the fuse block by inserting the tip of a small pocket screwdriver (or pointed object) in the left side of the power module then gently prying the cover open.

CAUTION   Do not to pry in the middle of the cover near the hinges. Doing so may break the hinge.
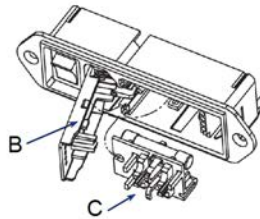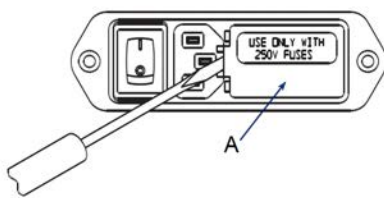
A. Fuse cover closed
B. Fuse cover opened (swing to the left)
C. Fuse block removed

3. Gently lift until the cover opens approximately 1/4 inch, then swing the hinged cover to the left.
4. Remove the fuse block. If necessary, use needle-nose pliers to grasp the block.
5. Insert the appropriate fuse(s) for the input power source.
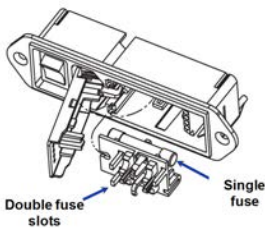
6. Position the fuse block so that the side containing the fuse(s) is facing the power module and insert it into the connector. Do not close the cover.
7. Fuse the power line according to local safety practices.
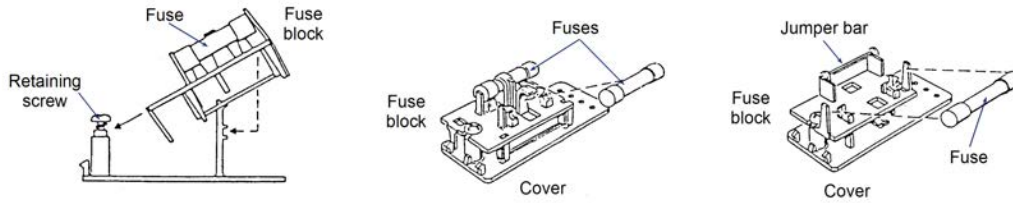
- If the *single*-fuse arrangement is used, the fuse block is positioned so that the side with the single-fuse slot and the jumper bar is away from the cover.
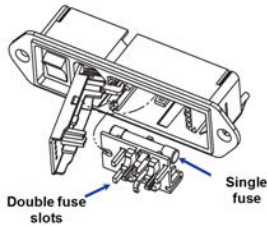
- If the *double*-fuse arrangement is used, the fuse block is positioned so that the side with the double-fuse slots is away from the cover (insert just opposite of single-fuse arrangement).

8. Snap the fuse block and cover assembly back into the input power connector. If the fuse block does not seat properly:

   a. Remove the fuse block retaining screw.
   b. Lift the fuse block from the cover.
   c. Rotate the fuse block.
   d. Mount the fuse block to the cover.
   e. Replace the retaining screw.

Once the fuse block and cover assembly are in place, the position of the indicator pin shows the input power selected.
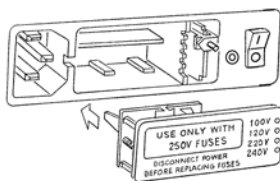
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A ADVANCED REPORTS - PYTHON MODULE

The mic Python module is automatically imported when running a user supplied script. The module provides access to particle size data, and provides support for summary, tabular, and graphical reports.

- **Summary reports.** Consist of summary sections, each containing a two-column table of label and value pairs. Summary reports are created with the *mic.summary* call.
- **Tabular reports.** Consist of one or more tables each containing one or more labeled columns of data. Tabular reports are created with the *mic.table* call.
- **Graphical reports**. Consist of a single graph with one or more curves on one or two y-axes. Graphical reports are created with the *mic.graph* call.

Calls for accessing the sample file data can be found in the *Mic Module Python Calls* section of this appendix. More advanced example python scripts are included in the analyzer software.

ADVANCED REPORT OPTIONS

Up to five Advanced reports, each with up to 10 summary reports, 10 tabular reports, and 10 graphical reports can be created. To use this feature, a file containing a Python script that imports a "mic" Python module must be created. See ***MicModule Python Calls on page A - 30*** for an example of a Python script and functions for the "mic" Python module.

1. Create the Python script and save it in the *Scripts* directory.
2. Open a sample file with a *Complete* status.
3. Select *Advanced* in the view selector drop-down list at the bottom of the window to return to the tabbed view.
4. On the *Report Options* tab, select *Advanced* in the *Selected Reports* list box, then click **Edit**.
5. On the *Advanced Report Options* window, click **Add** in the *Available Scripts* group box to locate and select the Python script. Repeat for each script to be added.

6. In the *Selected Reports* group box, click the drop-down arrows to select up to five Python scripts previously added in the *Available Scripts* box.
7. On the *Report Options* tab, click **Preview**. The Python Reports will be included on the tabs across the top portion of the *Reports* window.

Advanced Reports

Selections	Description
Advanced Report 1 through 5 [*drop-down box*]	Use the drop-down lists to select currently-defined functions used to define the report calculations and output.
Available Scripts [*group box*]	Lists the available reports and provides the option to add, replace, edit, or remove reports.

> **For fields and buttons not listed in this table; see *Common Fields and Buttons on page 2 - 2*.**

SCRIPTS

Run a Script

1. Open a sample file with a *Complete* file status.
2. Select *Advanced* in the view selector drop-down list at the bottom of the window.
3. Select the *Report Options* tab.
4. Highlight *Advanced* in the *Selected Reports* list box, then click **Edit**.
5. On the *Advanced Report Options* window, click **Add**.
6. Locate and select one or more python scripts then click **Select**. The selected scripts become a part of the drop-down list in the *Available Scripts* section of the *Advanced Report Options* window.
7. In the *Select Reports* section, select up to five *Advanced* reports in the drop-down lists.
8. Click **OK**.
9. Click **Preview** on the *Report Options* tab to view all reports selected in the previous window.

Remove a Script

Select the script in the *Available Scripts* box then click **Remove**. The script is removed from the application however, the original .py text file is not affected.

Edit a Script

Selections	Description
Add [*button***]**	Adds one or more scripts to the *Available Scripts* box. The added scripts then become available as options in the *Selected Reports* section.
Edit [*button***]**	Edits the script stored within the application but does not affect the original .py text file.
Remove [*button***]**	Removes the script from the *Available Scripts* box but does not affect original .py text file.
Replace [*button***]**	Replaces the contents of the selected script however, the script name remains the same.

PYTHON REPORTS

Graphic Report

This script is an example of the mic module producing a graph with two curves:

```python
1   import mic
2   import numpy as np
3
4   mic.graph( 'My Graph', 'X', 'F(X)' )
5   myx = np.array( [0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0 ] )
6   mic.graph.add( 'X2', myx, myx*myx, marker='o' )
7   mic.graph.add( 'sin(X)', myx, np.sin(myx), marker='^' )
```

The results are:

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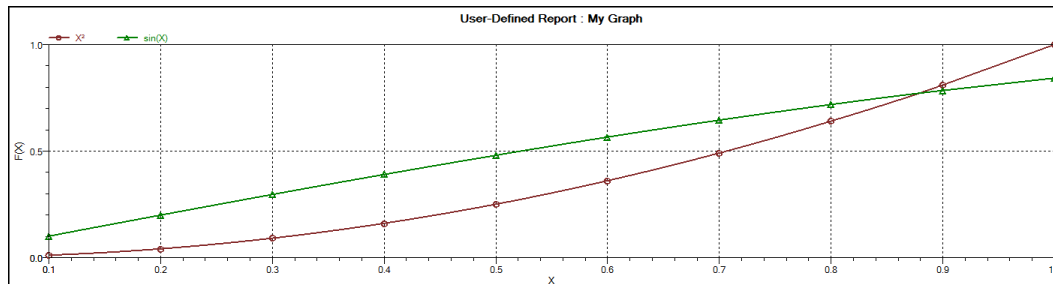
Summary Report

This script produces a summary report with two summaries:

```
1   import mic
2   import numpy as np
3
4   mic.summary( "My Summaries" )
5   mic.summary.add( "Summary A",
6                    ["Label 1:", "Label 2:", "Label 3:"],
7                    ["val1", "val2", "val3"] )
8   mic.summary.add( "Summary B",
9                    ["Label 4:", "Label 5:", "Label 6:"],
10                   ["val4", "val5", "val6"] )
```

The result is:

Summary A
Label 1: val1
Label 2: val2
Label 3: val3

Summary B
Label 4: val4
Label 5: val5
Label 6: val6

Tabular Report

If more than one column is required, the call *mic.table* is employed. This script produces a tabular report consisting of two tables.

This script uses the Python package *numpy* and *c*-style formatting of the numerical values.

```python
11   import mic
12   import numpy as np
13
14   mic.table( "My Tables" )
15   mic.table.addtable( "My Set A" )
16   mic.table.addcolumn( "X", ["1.0", "2.0", "3.0"] )
17   mic.table.addcolumn( "Y", ["0.5", "1.0", "1.5"] )
18   x1 = 0.2
19   x2 = 0.5
20   x3 = 3.14159/2
21   mic.table.addtable( "My Set B" )
22   mic.table.addcolumn( "X", ['{:8.3f}'.format(x1),
23                              '{:8.3f}'.format(x2),
24                              '{:8.3f}'.format(x3)] )
25   mic.table.addcolumn( "sin(X)", ['{:8.3f}'.format(np.sin(x1)),
26                                   '{:8.3f}'.format(np.sin(x2)),
27                                   '{:8.3f}'.format(np.sin(x3))] )
28   mic.table.addcolumn( "cos(X)", ['{:8.3f}'.format(np.cos(x1)),
29                                   '{:8.3f}'.format(np.cos(x2)),
30                                   '{:8.3f}'.format(np.cos(x3))] )
```

The result is:

My Set A

X	Y
1.0	0.5
2.0	1.0
3.0	1.5

My Set B

X	sin(X)	cos(X)
0.200	0.199	0.980
0.500	0.479	0.878
1.571	1.000	0.000

ACQUIRE BASIC INFORMATION

The following script generates a report that lists sample information, material properties, analysis options, and collected sedimentation data. See *Get Particle Sizing Sample on page A - 18* for API information.

```python
1   from math import log
2   import numpy as np
3   import mic
4
5   sample_data = mic.particle_sizing_sample()
6   coarser_data = mic.particle_sizing_coarser()
7   finer_data = mic.particle_sizing_finer()
8   reference_data = mic.particle_sizing_reference()
9   overlays_data = mic.particle_sizing_overlay(0)
10
11  sample_information = sample_data["SampleInfo"]
12  mat_props = sample_data["MaterialProperties"]
13  anl_opts = sample_data["AnalysisOptions"]
14  collected_data = sample_data["CollectedData"]
15
16  # Sample information
17  mic.summary(title="Summary Report")
18  params = sample_information["params"]
19  params_summary = []
20  sampleinfo_summary = [
21      ['Description:', sample_information["sample description"]],
22      ] + [["Parameter {} - {}:".format(i + 1, params[i]['name']),
23          "{}".format(params[i]['value'])]
24          for i in range(len(sample_information["params"]))]
25  mic.summary.add('Sample Information',
26              [desc for desc, value in sampleinfo_summary],
27              [value for desc, value in sampleinfo_summary])
```

```python
28
29    # Material properties
30    interp_tbl = mat_props["interpolation table"]
31    matprops_summary = [
32        ['Analysis type:',          mat_props["analysis type"]],
33        ['Starting size:',          "{} µm diameter".format(mat_props["starting
      size"])],
34        ['Ending size:',            "{} µm diameter".format(mat_props["ending
      size"])],
35        ['Sample ID:',              mat_props["sample ID"]],
36        ['Sample density:',         "{} g/cm³".format(mat_props["sample
      density"])],
37        ['Liquid ID:',              mat_props["liquid ID"]],
38        ['Liquid fixed density:',   "{} g/cm³".format(mat_props["liquid fixed
      density"])],
39        ['Liquid fixed viscosity:', "{} mPa*s".format(mat_props["liquid fixed
      viscosity"])],
40        ['X-ray intensity:',        mat_props["xray intensity"]],
41        ] + [["Interpolation table row {}:".format(i + 1),
42              "Cell temperature: {} °C, Density: {} g/cm³, Viscosity: {} mPa*s"
43              .format(interp_tbl[i]["cell temperature"],
44                      interp_tbl[i]["density"],
45                      interp_tbl[i]["viscosity"])]
46         for i in range(len(interp_tbl))]
47    mic.summary.add('Material Properties',
48                    [desc for desc, value in matprops_summary],
49                    [value for desc, value in matprops_summary])
50
51    # Analysis options
52    anlopts_summary = [
53        ['MasterTech stir time:',   "{} sec".format(anl_opts['mt stir time'])],
54        ['MasterTech stir speed:',  anl_opts['mt stir speed']],
55        ['MasterTech probe time:',  "{} sec".format(anl_opts['mt probe time'])],
56        ['Stop at mass percent:',   anl_opts['stop at mass percent']],
```

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```python
57        ['Ending percent:',            "{}%".format(anl_opts['ending percent'])],
58        ['Number of tests:',          anl_opts['number of tests']],
59        ['Leave pump on:', 'yes' if anl_opts['leave pump on'] else 'no'],
60        ['Wait for temperature stabilization:',
61         'yes' if anl_opts['wait for temp stabilization'] else 'no'],
62        ['Mixing stir speed:',        anl_opts['mix stir speed']],
63        ['Full scale pump speed:',   anl_opts['full scale pump speed']],
64        ['Bubble detection:',         anl_opts['bubble detection']],
65        ['Rinse after analysis:',    anl_opts['rinse after analysis']],
66        ['Auto rinse:',               anl_opts['is auto rinse']],
67        ['Rinse cycles:',             anl_opts['rinse cycles']],
68        ['Rinse pump speed:',         anl_opts['rinse pump speed']],
69    ]
70    mic.summary.add('Analysis Options',
71                    [desc for desc, value in anlopts_summary],
72                    [value for desc, value in anlopts_summary])
73
74    # Collected data
75    colldata_summary = [
76        ["Mean base/Full:", '{:.4f} kCnts/s'.format(collected_data["mean base/-
    full"])],
77        ["Base/Full scale:", '{:.4f} kCnts/s'.format(collected_data["base/full
    scale"])],
78    ]
79    mic.summary.add('Collected Data',
80                    [desc for desc, value in colldata_summary],
81                    [value for desc, value in colldata_summary])
82
83    # Cumulative mass graph
84    test = 'avg'
85    dist = 'mass'
86    mic.graph(title='Cumulative Mass Test Average',
87              xlabel='Particle size (µm diameter)', ylabel='Cumulative')
```

```python
88   xs = collected_data['low diameter'][test][dist]
89   ys = collected_data['cumulative'][test][dist]
90   mic.graph.add("Cumulative", xs, ys)
91
92   # Sedimentation data table
93   test = '1' # First test
94   sedtimes = collected_data['unsmoothed']['sedimentation times'][test]
95   sedheights = collected_data['unsmoothed']['sedimentation heights'][test]
96   sedperiods = collected_data['unsmoothed']['sedimentation periods'][test]
97   mic.table(title="Sedimentation Data for Test {}".format(test))
98   mic.table.addtable('Sedimentation Data')
99   mic.table.addcolumn('Sedimentation time (sec)', [sedtime/100.0 for sedtime
     in sedtimes])
100  mic.table.addcolumn('Sedimentation height (cm)', ['{:.4f}'.format(height)
     for height in sedheights])
101  mic.table.addcolumn('Sedimentation period (µs)', ['{:.4f}'.format(period)
     for period in sedperiods])
```

ACQUIRE REPORT RESULTS

The Advanced Reports provide a way to access Log Probability, Rosin Rammler, Baseline, and Fullscale data.

```python
1   import mic
2   import numpy as np
3
4   # Returns slope, intercept, r² information.
5   def get_linear_fit(xs, ys):
6       slope, intercept = np.polyfit(xs, ys, 1)
7       correlation_matrix = np.corrcoef(xs, ys)
8       correlation_xy = correlation_matrix[0,1]
9       r_squared = correlation_xy ** 2
10      return slope, intercept, r_squared
11
12  sample_data = mic.particle_sizing_sample()
13  collected_data = sample_data["CollectedData"]
14
15  # Log probability graph
16  test = 'avg'
17  dist = 'mass'
18  mic.graph(title='Log Probability for {} using {} Distribution'.format(test,
            dist),
19          xlabel='Particle size (µm)', ylabel='Logprob')
20  logprob = collected_data['logprob'][test][dist]
21  slope, intercept, r_squared = get_linear_fit(logprob['X'], logprob['Y'])
22  mic.graph.add("Logprob: slope={:.4f}, intercept={:.4f}, r²={:.4f}"
23              .format(slope, intercept, r_squared),
24              logprob['X'], logprob['Y'])
25
26  # Rosin Rammler graph
27  test = '1' # First test
28  dist = 'mass'
```

```
29  mic.graph(title='Rosin Rammler for Test {} using {} Distribution'.format
    (test, dist),
30          xlabel='Particle size (µm)', ylabel='RR')
31  rosinrammler = collected_data['rosinrammler'][test][dist]
32  slope, intercept, r_squared = get_linear_fit(rosinrammler['X'], rosinrammler
    ['Y'])
33  mic.graph.add("RR: slope={:.4f}, intercept={:.4f}, r²={:.4f}"
34              .format(slope, intercept, r_squared),
35              rosinrammler['X'], rosinrammler['Y'])
36
37  # Baseline graphs
38  mic.graph(title='Raw Baseline', xlabel='Cell position (cm)', ylabel='Intens-
    ity (µs)')
39  xs = collected_data['baseline']['heights']
40  ys = collected_data['baseline']['periods']
41  mic.graph.add("Baseline", xs, ys)
42  mic.graph(title='Reported Baseline', xlabel='Cell position (cm)',
    ylabel='Intensity (1000/µs)')
43  reported_xs = [0.01 if x < 1.0e-6 else x for x in xs]
44  reported_ys = [1.0e3 / y if y > 1.0e-6 else 0.0 for y in ys]
45  mic.graph.add("Baseline", reported_xs, reported_ys)
46
47  # Fullscale graphs
48  mic.graph(title="Raw Fullscale for Test {}".format(test),
49          xlabel='Cell position (cm)', ylabel='Intensity (µs)')
50  xs = collected_data['fullscale'][test]['heights']
51  ys = collected_data['fullscale'][test]['periods']
52  mic.graph.add('Fullscale raw', xs, ys)
53  mic.graph(title="Reported Fullscale for Test {}".format(test),
54          xlabel='Cell position (cm)', ylabel='Intensity (1000/µs)')
55  reported_xs = [0.01 if x < 1.0e-6 else x for x in xs]
56  reported_ys = [1.0e3 / y if y > 1.0e-6 else 0.0 for y in ys]
57  mic.graph.add("Fullscale", reported_xs, reported_ys)
58
```

ACQUIRE OVERLAY SAMPLE DATA

There are four functions that can be used to get overlay information. The *Report Options* must have:

- Reference (corresponds to particle_sizing_reference),
- Specification (corresponds to def particle_sizing_coarser() and def particle_sizing_finer()),
- Overlays (corresponds to def particle_sizing_overlays(number)) selection

```
1    Acquire Overlay Sample Data
2    def particle_sizing_coarser():
3        '''Get particle_sizing sample information, material properties, analysis
         options,
4            and collected data of the coarser reference file.
5
6        Usage:
7
8           coarser = particle_sizing_coarser()
9
10       The returned dict has the same layout as the structure returned by
11       particle_sizing_sample()
12       '''
13
14   def particle_sizing_finer():
15       '''Get particle_sizing sample information, material properties, analysis
         options,
16           and collected data of the finer reference file.
17
18       Usage:
19
20          finer = particle_sizing_finer()
21
22       The returned dict has the same layout as the structure returned by
23       particle_sizing_sample()
```

```
24      '''
25
26  def particle_sizing_reference():
27      '''Get particle_sizing sample information, material properties, analysis
    options,
28          and collected data of the reference reference file.
29
30      Usage:
31
32          reference = particle_sizing_reference()
33
34      The returned dict has the same layout as the structure returned by
35      particle_sizing_sample()
36      '''
37
38  def particle_sizing_overlay(sample_number):
39      '''Get particle sizing sample information, material properties, analysis
    options,
40          and collected data of the sample_number overlay reference files.
41
42      Usage:
43
44          first_overlay = particle_sizing_overlay(0)
45
46      The returned dict has the same layout as the structure returned by
47      particle_sizing_sample()
48      '''
49
50  This is an example code block that makes use of it:
51  import mic
52
53  sample_data = mic.particle_sizing_sample()
54  collected_data = sample_data["CollectedData"]
```

```
55   finer_data = mic.particle_sizing_finer()
56   reference_data = mic.particle_sizing_reference()
57   coarser_data = mic.particle_sizing_coarser()
58   first_overlay = mic.particle_sizing_overlay(0)
59
60
61   # Cumulative mass graph
62   test = 'avg'
63   dist = 'mass'
64   mic.graph(title='Cumulative Mass Test Average',
65            xlabel='Particle size (µm diameter)', ylabel='Cumulative')
66   xs = sample_data['CollectedData']['low diameter'][test][dist]
67   ys = sample_data['CollectedData']['cumulative'][test][dist]
68   mic.graph.add("Sample", xs, ys)
69   xs = finer_data['CollectedData']['low diameter'][test][dist]
70   ys = finer_data['CollectedData']['cumulative'][test][dist]
71   mic.graph.add("finer", xs, ys)
72   xs = coarser_data['CollectedData']['low diameter'][test][dist]
73   ys = coarser_data['CollectedData']['cumulative'][test][dist]
74   mic.graph.add("finer", xs, ys)
75   xs = reference_data['CollectedData']['low diameter'][test][dist]
76   ys = reference_data['CollectedData']['cumulative'][test][dist]
77   mic.graph.add("finer", xs, ys)
78
79
80
```

GET PARTICLE SIZING SAMPLE

```python
def particle_sizing_sample():
    '''Get particle_sizing sample information, material properties, analysis options,
        and collected data.

    Usage:

       sample = particle_sizing_sample()

    The returned dict has the following layout.

    sample = {
            'SampleInfo' : {
                    'sample description': str,
                    'params' :  list( {'name': str, 'value': float } )
                    },
            'MaterialProperties' : {
                    'analysis type': str,
                    'starting size': float,
                    'ending size': float,
                    'sample ID': str,
                    'sample density': float,
                    'liquid ID': str,
                    'liquid fixed density': float,
                    'liquid fixed viscosity': float,
                    'xray intensity': str,
                    'interpolation table': {
                            'cell temperature': double,
                            'density': double,
                            'viscosity': double,
```

```
30                         },
31                     },
32             'AnalysisOptions' : {
33                 'mt stir time': float,
34                 'mt stir speed': float,
35                 'mt probe time': double,
36                 'stop at mass percent': bool,
37                 'ending percent': double,
38                 'number of tests': int,
39                 'leave pump on': bool,
40                 'wait for temp stabilization': bool,
41                 'mix stir speed': double,
42                 'full scale pump speed': double,
43                 'bubble detection': str,
44                 'rinse after analysis': bool,
45                 'is auto rinse': bool,
46                 'rinse cycles': double,
47                 'rinse pump speed': double,
48             },
49             'CollectedData': {
50                 'analysis times': dict( {'0': str,
51                                          '2': str,
52                                          ...,
53                                          '7': str } ),
54                 'unsmoothed': dict( { 'sedimentation heights': dict( { '0':
    list(float),
55                                                                       '1':
    list(float),
56                                                                       ...
57                                                                       '7':
    list(float) } ),
58                                       'sedimentation times' : dict( { '0':
    list(float),
59                                                                       '1':
```

```
      list(float),
60                                                  ...
61                                                 '7':
      list(float) } ),
62                      'sedimentation periods' : dict( { '0':
      list(float),
63                                                 '1':
      list(float),
64                                                  ...
65                                                 '7':
      list(float) } ),
66                      'masses' : dict( { '0': list(float),
67                                     '1': list(float),
68                                          ...
69                                     '7': list(float) } ),
70                      'sizes' : dict( { '0': list(float),
71                                     '1': list(float),
72                                          ...
73                                     '7': list(float) } ),
74                          } )
75           'smoothed': dict( { 'masses' : dict( { '0': list(float),
76                                          '1': list(float),
77                                               ...
78                                          '7': list(float) } ),
79                          'sizes' : dict( { '0': list(float),
80                                          '1': list(float),
81                                               ...
82                                          '7': list(float) } ) }
      ),
83           'mean base/full' : float,
84           'base/full scale' : float,
85           'low diameter' : dict( { '0' : dict( {
86                                          'mass': list(float)
87                                          'area': list(float)
```

```
 88                                              'volume': list(float)
 89                                              'number': list(float)
 90                                        } ),
 91                            '1' : dict( { ... } ),
 92                            ...
 93                            '7' : dict( {... } ),
 94                            'avg' : dict( {... } ) } )
 95            'high diameter': dict( { '0' : dict( {
 96                                                'mass': list(float)
 97                                                'area': list(float)
 98                                                'volume': list(float)
 99                                                'number': list(float)
100                                        } ),
101                            '1' : dict( { ... } ),
102                            ...
103                            '7' : dict( {... } ),
104                            'avg' : dict( {... } ) } ),
105            'average diameter': dict( { '0' : dict( {
106                                                'mass': list(float)
107                                                'area': list(float)
108                                                'volume': list
(float)
109                                                'number': list
(float)
110                                        } ),
111                            '1' : dict( { ... } ),
112                            ...
113                            '7' : dict( {... } ),
114                            'avg' : dict( {... } ) } ),
115            'cumulative': dict( { '0' : dict( {
116                                            'mass': list(float)
117                                            'area': list(float)
118                                            'volume': list(float)
```

```
119                                          'number': list(float)
120                                    } ),
121                        '1' : dict( { ... } ),
122                        ...
123                        '7' : dict( {... } ),
124                        'avg' : dict( {... } ) } ),
125        'frequency': dict( { '0' : dict( {
126                                    'mass': list(float)
127                                    'area': list(float)
128                                    'volume': list(float)
129                                    'number': list(float)
130                              } ),
131                        '1' : dict( { ... } ),
132                        ...
133                        '7' : dict( {... } ),
134                        'avg' : dict( {... } ) } ),
135        'rosin rammler': dict( { '0' : dict( {
136                                        'mass': list(float)
137                                        'area': list(float)
138                                        'volume': list(float)
139                                        'number': list(float)
140                                  } ),
141                          '1' : dict( { ... } ),
142                          ...
143                          '7' : dict( {... } ) } ),
144        'specific area': dict( { '0' : dict( {
145                                        'mass': list(float)
146                                        'area': list(float)
147                                        'volume': list(float)
148                                        'number': list(float)
149                                  } ),
150                          '1' : dict( { ... } ),
```

```
151                                              ...
152                                     '7' : dict( {... } ),
153                                     'avg' : dict( {... } ) } ),
154              'area in interval': dict( { '0' : dict( {
155                                                  'mass': list(float)
156                                                  'area': list(float)
157                                                  'volume': list
      (float)
158                                                  'number': list
      (float)
159                                                    } ),
160                                     '1' : dict( { ... } ),
161                                              ...
162                                     '7' : dict( {... } ),
163                                     'avg' : dict( {... } ) } ),
164              'specific number': dict( { '0' : dict( {
165                                                  'mass': list(float)
166                                                  'area': list(float)
167                                                  'volume': list
      (float)
168                                                  'number': list
      (float)
169                                                    } ),
170                                     '1' : dict( { ... } ),
171                                              ...
172                                     '7' : dict( {... } ),
173                                     'avg' : dict( {... } ) } ),
174              'number in interval': dict( { '0' : dict( {
175                                                  'mass': list
      (float)
176                                                  'area': list
      (float)
177                                                  'volume': list
      (float)
178                                                  'number': list
```

```
                    (float)
179                                                          } ),
180                                        '1' : dict( { ... } ),
181                                        ...
182                                        '7' : dict( {... } ),
183                                        'avg' : dict( {... } ) } ),
184          'log probability': dict( { '0' : dict( {
185                                            'mass': list(float)
186                                            'area': list(float)
187                                            'volume': list
          (float)
188                                            'number': list
          (float)
189                                              } ),
190                                    '1' : dict( { ... } ),
191                                    ...
192                                    '7' : dict( {... } ),
193                                    'avg' : dict( {... } ) } ),
194          'phi size': dict( { '0' : dict( {
195                                        'mass': list(float)
196                                        'area': list(float)
197                                        'volume': list(float)
198                                        'number': list(float)
199                                          } ),
200                              '1' : dict( { ... } ),
201                              ...
202                              '7' : dict( {... } ),
203                              'avg' : dict( {... } ) } ),
204          'settling velocity': dict( { '0' : dict( {
205                                            'mass': list
          (float)
206                                            'area': list
          (float)
207                                            'volume': list
```

```
         (float)
208                                              'number': list
         (float)
209                                          } ),
210                                    '1' : dict( { ... } ),
211                                    ...
212                                    '7' : dict( {... } ),
213                                    'avg' : dict( {... } ) } ),
214              'phi size low': dict( { '0' : dict( {
215                                            'mass': list(float)
216                                            'area': list(float)
217                                            'volume': list(float)
218                                            'number': list(float)
219                                        } ),
220                                '1' : dict( { ... } ),
221                                ...
222                                '7' : dict( {... } ),
223                                'avg' : dict( {... } ) } ),
224              'settling velocity low': dict( { '0' : dict( {
225                                                   'mass': list
         (float)
226                                                   'area': list
         (float)
227                                                   'volume': list
         (float)
228                                                   'number': list
         (float)
229                                              } ),
230                                        '1' : dict( { ... } ),
231                                        ...
232                                        '7' : dict( {... } ),
233                                        'avg' : dict( {... } ) } ),
234
235              'baseline' : dict( { 'heights' : list(float), 'periods' : list
```

```
        (float) } ),
236              'fullscale' : dict( { '0' : dict( { 'heights' : list(float),
        'periods' : list(float) } ),
237                                      '1' : dict( { ... } ),
238                                      ...
239                                      '7' : dict( { ... } ),
240                                      'avg' : dict( {... } ) } ),
241          'logprob'    : dict( {'0': {'mass': { 'X' : list(float),
242                                            'Y' : list(float) }
243                                    'area': { ... },
244                                    'number': { ... },
245                                    'volume': { ... },
246                                    },
247                              '1': {...},
248                              ...
249                              '7': {...},
250                              'avg': {...},
251                              } )
252          'rosinrammler': dict( {'0': {'mass': { 'X' : list(float),
253                                            'Y' : list(float), }
254                                    'area': { ... },
255                                    'number': { ... },
256                                    'volume': { ... },
257                                    },
258                              '1': {...},
259                              ...
260                              '7': {...},
261                              'avg': {...},
262                              } )
263          }
264      }
265      '''
266
```

```
267   def particle_sizing_coarser():
268       '''Get particle_sizing sample information, material properties, analysis
      options,
269           and collected data of the coarser reference file.
270
271       Usage:
272
273         coarser = particle_sizing_coarser()
274
275       The returned dict has the same layout as the structure returned by
276       particle_sizing_sample()
277       '''
278
279   def particle_sizing_finer():
280       '''Get particle_sizing sample information, material properties, analysis
      options,
281           and collected data of the finer reference file.
282
283       Usage:
284
285         finer = particle_sizing_finer()
286
287       The returned dict has the same layout as the structure returned by
288       particle_sizing_sample()
289       '''
290
291   def particle_sizing_reference():
292       '''Get particle_sizing sample information, material properties, analysis
      options,
293           and collected data of the reference reference file.
294
295       Usage:
296
```

```
297         reference = particle_sizing_reference()

298

299     The returned dict has the same layout as the structure returned by

300     particle_sizing_sample()

301     '''

302

303 def particle_sizing_overlay(sample_number):

304     '''Get particle sizing sample information, material properties, analysis
    options,

305         and collected data of the sample_number overlay reference files.

306

307     Usage:

308

309       first_overlay = particle_sizing_overlay(0)

310

311     The returned dict has the same layout as the structure returned by

312     particle_sizing_sample()

313     '''

314
```

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ENABLE THE USE OF OVERLAY DATA

1. On the *Report Options* tab, click **Overlays**.
2. On the *Plot Overlay Sample Selection* window, to move a file from the *Available Files* list box to the *Selected Files* list box, either double-click a file name in the *Available Files* list box or click one or more files in the *Available Files* list box then click **Add**.
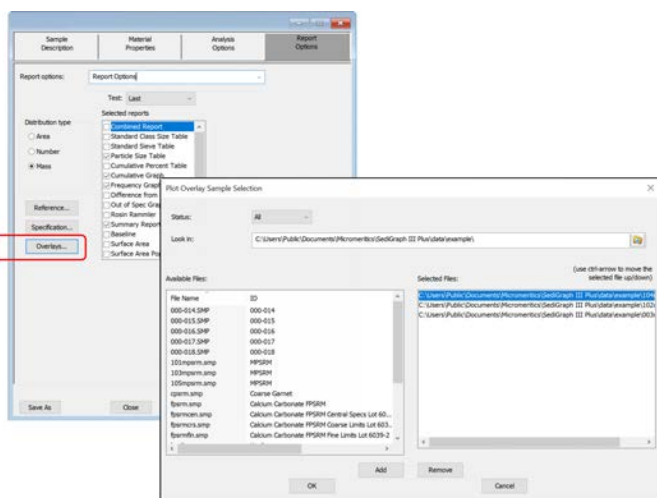
3. Click **OK**.
4. On the *Report Options* tab, highlight *Advanced* in the *Selected Reports* list box.
5. On the *Advanced Report Options* window, click **Add** in the *Available Scripts* group box and select a Python script.
6. In the *Select Reports* group box, select the drop-down arrow to select a report to be used in the overlay.
7. Click **OK**.
8. Run the script using the instructions found in ***Scripts on page A - 4***.

MICMODULE PYTHON CALLS

Tables

Available Mic Python calls for tables:

- Create a new tabular report
- Add a column
- Add a table

Add a Table

This script adds a table to the last created tabular report:

```
1   mic.table.addtable( name )
2
3   Keyword arguments:
4
5     name --- the table name
```

Add a Column

This script adds a column to the last created table:

```
1   mic.table.addcolumn(header, values, align='r'):
2
3   Keyword arguments:
4
5     header --- column header; must be a string (or convertible)
6     values --- column values; must be a list of strings (or convertible)
7     align  --- column alignment; 'r', 'l', 'c' for right, left, and center jus-
    tified
```

Create a New Tabular Report

```
1   mic.table( title='User Table' )
2
3   Keyword arguments:
4
5     title --- the tabular report title (default = 'User Table')
```

Summary Reports

Add a Summary Section

This script adds a summary section to the last created summary report:

```
1   mic.summary.add(name, labels, values):
2
3   Keyword arguments:
4
5     name    --- summary section name
6     labels --- column of labels; must be a list of strings
7              (or convertible) and the same length as values
8     values --- column of values; must be a list of strings
9              (or convertible) and the same length as labels
```

Create a New Summary Report

```
1   mic.summary( title='User Summary' )
2
3   Keyword arguments:
4
5     title --- the summary title
```

Graphic Reports

Add a Curve

This script adds a curve to the last created graphical report:

```
1   mic.graph.add(name, x, y, yyaxis=False, color=None, linestyle='-',
2                 marker='a', graphtype='both', interpolation='akima'):
3
4   Keyword arguments:
5
6     name       --- the curve name
7     x          --- list of x values; must be a list of floats
8                    (or convertible) and the same length as y
9     y          --- list of y values; must be a list of floats
10                   (or convertible) and the same length as x
11    yyaxis     --- place this curve on the yy-axis if True
12                   otherwise place on the y-axis (default = False)
13    color      --- RGB color as an HTML hex string (e.g., '#4169e1')
14                   or a three-element list or tuple (e.g., [65,105,225]);
15                   if None, color is automatically selected (default = None)
16    linestyle --- line style; (default = '-')
17                     '-'       : solid
18                     '--'      : dash
19                     '.'       : dot
20                     '-.'      : dash dot
21                     '-..'     : dash dot dot
22    marker     --- marker shape; (default = 'a')
23                     '+'       : plus
24                     'o' or '0' : circle
25                     'x'       : cross
26                     '^'       : up triangle
27                     'v'       : down triangle
28                     's'       : square
```

```
29                          'd'        : diamond
30                          '8'        : hourglass
31                          '~'        : horizontal hourglass
32                          '' or None : no marker
33                          'a'        : automatically selected
34    graphtype --- graph type; (default = 'both')
35                          'curve'  or 'c' : curve
36                          'points' or 'p' : points
37                          'both'   or 'b' : curve-and-points
38                          'hist'   or 'h' : histogram
39    interpolation -- linear or akima spline interpolation (default='akima')
40                          'akima' use akima spline
41                          'linear' use linear interpolation
```

Add a Curve Using the Second Y-Axis

This script adds a curve to the last created graphical report using the second y-axis:

```
1    mic.graph.addyy(name, xx, yy):
2
3    Add a curve to the last created graphical report using the second
4    y-axis. The arguments to this call are the same as to mic.graph.add.
```

Create a New Graphical Report

```
1  mic.graph(title='User Graph', xlabel='X axis', ylabel='Y axis',
2            yylabel='YY axis',
3            xlinear=True, ylinear=True, yylinear=True,
4            xinvert=False, yinvert=False, yyinvert=False,
5            xrange=None, yrange=None, yyrange=None, xbars_id=''):
6
7  Keyword arguments:
8
9    title    --- the graphical report title (default = 'User Graph')
10   xlabel   --- x-axis label (default = 'X axis')
11   ylabel   --- y-axis label (default = 'Y axis')
12   yylabel  --- yy-axis label (default = 'YY axis')
13   xlinear  --- x-axis linear scale; if false, use log scale
14              (default = True)
15   ylinear  --- y-axis linear scale; if false, use log scale
16              (default = True)
17   yylinear --- yy-axis linear scale; if false, use log scale
18              (default = True)
19   xinvert  --- Invert x-axis if true (default = False)
20   yinvert  --- Invert y-axis if true (default = False)
21   yyinvert --- Invert yy-axis if true (default = False)
22   xrange   --- None, or two values giving the min and max
23              range of the axis.
24   yrange   --- None, or two values giving the min and max
25              range of the axis.
26   yyrange  --- None, or two values giving the min and max
27              range of the axis.
28   xbars_id --- None, or the id of an xbar control created
29              via the mic.control() object
```

Get Sample Information Item

```
1   mic.sample_information( item, sample_number = 0 ):
2
3   Keyword arguments:
4
5     item          --- string identifying the item to be returned.
6                        For example; 'sample mass', or 'sample description'
7                        The default is an empty string for which the return
8                        value is a list of all available keywords
9
10    sample_number --- Sample to retrieve
11                        0              : current sample file (default)
12                        1 through 8 : corresponding overlay sample file
13
14  Usage:
15
16    all_keywords = sample_information()
17    mass         = sample_information('sample mass')
18    mass         = sample_information('sample mass',0)
```

B CHEMICAL AIDS FOR PARTICLE DISPERSION

Name	Type	Active Ingredient
Aerosol 22	Anionic	Tetrasodium N-(1,2-dicarboxyet hyl)-Noct-adecysulfosuccinanate, 35%
Aerosol OT	Anionic	Dioctyl ester of sodium sulfosuccinic acid, 70%
Atlas G-3300	Anionic	Amine salt of alkylaryl sulfonate
Calcium Chloride	Cationic	$CaCl_2$
Calgon	Anionic	Sodium hexametaphosphate, unadjusted
Calgon T	Anionic	Part of sodium replaced by other cations, predominantly zinc
Cobaltous Chloride	Cationic	$CoCl_2$
Cobalt Citrate	Anionic	$Co_3(C_6H_5O7)_2$
Daxad 23	Anionic	Sodium salt of polymerized carboxylic acid, 25%
Daxad 30	Anionic	Sodium salt of polymerized carboxylic acid, 25%
FC-134	Cationic	Fluorochemical surfactant
FC-161	Anionic	Fluorochemical surfactant
FC-170	Nonionic	Fluorochemical surfactant
Igepal CO-530	Nonionic	Nonylphenoxypoly (ethyleneoxy) ethanol, 100%
Oleic Acid	Anionic	$CH_3(CH_2)_7CH=CH(CH_2)_7COOH$
Renex 648	Nonionic	Ethoxylated nonylphenol, 100%
Sodium Silicate	Anionic	Na_2SiO_3
Triton X-100	Nonionic	Octyl phenoxy polyethoxy ethanol, 100%
Tamol SN	Anionic	Sodium salt of condensed naphthalene sulfonic acid, 100%
TSPOP	Anionic	Tetrasodiumpyrophosphate, $Na_4P_2O_7$
Twitchell Base 8240	Anionic	Sodium salt of low molecular weight, sulfonated oil, parafin oil, water, and diethylene glycol
Tween 20	Nonionic	Polyoxyethylene Sorbitan monolaureate (polysorbate 20), 100%
Zonyl S-13	Anionic	Fluoroalkyl phosphate
Zonyl A	Nonionic	Ethylene oxide-ester condensate

Data extracted from McCutcheon's Detergents and Emulsifiers, McCutcheon Division, MC Publishing Co., Glen Rock, NJ, 1980.

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C DATA REDUCTION

DATA ACQUISITION

The basic data acquired are in the form of cumulative mass percent finer vs. diameter. An explanation of the method for acquiring the data are provided below.

DIAMETER

Diameter for a given set of sedimentation conditions is given by Stokes equation as follows:

$$D\left[\frac{18\eta}{(\rho-\rho o)g}\right]^{1/2} \times \left[\frac{h}{t}\right]^{1/2}$$

where

D	=	diameter (cm, multiply by 10000 for micrometers)
η	=	liquid viscosity (poise, multiply by 0.01 for cp)
h	=	sedimentation height (cm)
ρ	=	sample density (g/cm^3)
ρo	=	liquid density (g/cm^3)
g	=	acceleration due to gravity (981 cm/s/s)
t	=	sedimentation time (sec)

All data are acquired at one of 220 predetermined sedimentation heights, ranging from 2.54 cm to 0.0079375 cm.

Sample density is user-entered. Liquid viscosity and density are user-entered, or they are calculated using the sedimentation cell temperature and interpolating from the user-selected Liquid Properties Set (see Liquid Properties Interpolation).

Target diameters for data collection are determined as follows:

Up to 250 target diameters are selected, evenly spaced on a log diameter basis, between the user selected starting diameter and ending diameter. Note that this gives the operator some choice in the resolution of the data relative to the log diameter axis: selecting a narrower range of analysis provides more data points in a given range of diameters. Maximum resolution is obtained by selecting starting and ending diameters spanning only one decade (factor of 10), providing 250 data points per decade resolution.

Target sedimentation heights and times are selected based on run type (high speed, standard, or high resolution) and Stokes' equation.

During analysis, mass % data will be taken at these target heights, and as close to these target times as possible, allowing for cell movement, data acquisition delay time, and sequential collection of data points. The actual time of data collection will be recorded for each point, so that actual diameter may be calculated later.

Height, time, density, and viscosity data are stored separately, so that corrections to density and viscosity can be made after the analysis and diameters are recalculated.

LIQUID PROPERTIES INTERPOLATION

The density and viscosity of the sedimentation liquid at the time of analysis are interpolated as follows, using a liquid properties table of three points of density and viscosity versus temperature, and the cell temperature reading at the start of analysis.

DENSITY

$$\beta = \frac{((d2-d1)-(d3-d1)\times((t2-t1)/(t3-t1)))}{(d1\times(2-t3))}$$

$$A = (1 - (d2/d1) + \beta \times (t2 - t1)^2)/(t2 - t1)$$

$$\rho o = d1(1 - A(tc - t1) + \beta(tc - t1)^2)$$

t1, t2, t3	=	temperatures from liquid properties table (degrees C)
d1, d2, d3	=	densities at t1, t2, t3 respectively (g/cm^3)
A	=	first order coefficient
β	=	second order coefficient
tc	=	cell temperature reading at start of analysis (degrees C)
ρo	=	liquid density at analysis temperature (g/cc)

VISCOSITY

$$C = (\nu1(1 - (t1 - t2)/(t1 - t3)) - \nu2 + \nu3(t1 - t2)/(t1 - t3))/((t1 - t2)(t2 - t3))$$

$$\beta = (\nu1 - \nu2 - (C \times (t1^2 - t2^2)))/(t1 - t2)$$

$$A + \beta/tk + C/tk^2$$

$$\eta = e^{A+\beta/tk+C/tk^2}$$

t1, t2, t3	=	1/(t + 273.15) for t = each of the 3 temperatures in the liquid properties table (t in degrees C)
υ1, υ2, υ3	=	ln(υ) for υ = each of the 3 viscosities (cp)
A, B, C	=	0th, 1st, and 2nd order coefficients, respectively
tk	=	cell temperature at start of analysis (K, i.e., 273.15 + degrees C)
η	=	viscosity at analysis temperature (cp)

MASS PERCENT

The mass percent of sample present at a given sedimentation height after a given time is determined by relating the x-ray transmission intensity at that point to the intensity with no sample present (baseline), and the intensity with all of the sample present (full scale):

$$mass\% = (log(Im) - log(Ib))/(log(If) - log(Ib)) \times 100$$

Im	=	intensity at data point (mass % being determined)
Ib	=	intensity at baseline (mass % = 0)
If	=	intensity at full scale (mass % = 100)

The Ib and If values are average values to minimize random variations in the X-ray intensity. The average of these values is used to compute the mass percent.

One set of baseline data may be used for scaling multiple analyses until another set of baseline data are collected.

After the sample is loaded while the cell pump is still on and the sample fully suspended and evenly distributed throughout the cell, bubble elimination data are collected at between 110 and 220 predetermined analysis heights, based on the type of bubble elimination selected. In addition, a single average full-scale value is computed at the starting analysis height.

Mass percent data appearing on the 'Analysis Results' screen has been smoothed with an 11-point evenly weighted running average.

When data are saved permanently after all analyses on a sample are completed, the mass percent values are smoothed before storage in the sample file as follows:

The mass percent values are smoothed with an 11-point running average, just as for the 'Analysis Results' screen. From these data, a set of mass percent values are interpolated at 250 evenly spaced intervals on a log diameter basis, using linear interpolation between the two adjacent collected points to get each evenly spaced point. This is done because the next smoothing step requires evenly spaced data points, and the collected data can vary from even log diameter spacing due to limitations on time of collection, as noted above.

The evenly spaced mass percent values are smoothed using a digital filter which removes high-frequency variations from the data. The final, stored mass percent values are obtained by interpolating to a standard size table with 40 logarithmicly, evenly-spaced sizes per decade.

REDUCTION OF COLLECTED DATA

MASS DATA

In order to obtain cumulative mass percent data, the smoothed mass percent data scaled to the specified full scale value:

For each of the total number of points collected:

$$\mathbf{CumMassFiner}\ (\%) = MassFiner \times \frac{FullScale}{100.0}$$

Cumulative mass percent coarser data are simply the difference of scaled mass percent finer data from 100:

For each of the total number of points collected:

$$\mathbf{CumMassCoarser}\ (\%) = 100.0\ (\%) - \mathbf{CumMassFiner}\ (\%)$$

These cumulative mass data (finer and coarser) are represented directly in tabular form and as y-axis data in the CUMULATIVE MASS FINER VS. DIAMETER and CUMULATIVE MASS COARSER VS. DIAMETER plots (cumulative mass distribution curve). Also, cumulative mass data are used to derive mass frequency and log probability data.

MASS FREQUENCY DATA

The mass frequency of a particle size interval is the difference between the cumulative mass percent interpolated at the end points of the interval. The interpolation is performed using a spline fit to the cumulative mass data.

CUMULATIVE DATA

Any cumulative quantity can be expressed as Coarser or Finer (Retained or Passed on the Tabular Report by Sieve Size).

For data defined by the standard class sizes (Summary, Tabular Defined by Size Class, and Graphs):

CumFracCoarser$_i$ = $\sum$FreqFrac$_k$ for all classes k such that AvgDiam$_k$ > AvgDiam$_i$

CumFracFiner$_i$ = $\sum$FreqFrac$_k$ for all classes k such that AvgDiam$_k$ > AvgDiam$_i$

CumFracRetain$_i$ = $\sum$FreqFrac$_k$ for all classes k such that AvgDiam$_k$ > AvgDiam$_i$

CumFracPass$_i$ = $\sum$FreqFrac$_k$ for all classes k such that AvgDiam$_k$ < AveDiam$_i$

or equivalently,

CumFracFiner$_i$ = 1.0 - CumFracCoarser$_{i-1}$

CumFracRetain$_i$ = CumFracCoarser$_{i-1}$

CumFracPass$_i$ = 1.0 - CumFracCoarser$_{i-1}$

For Tabular Defined by SizeTable or by Sieve Sizes:

CumFrac (Coarser or Finer, Retained or Passed) is calculated for the standard size classes as defined above. CumFrac is then interpolated from CumFrac vs. Particle Size at each particle size in the Size table or aperture size in the Sieve table.

PEAK REPORT DATA

Peak report data are calculated as:

$$\mathbf{DiffFreqFrac_i} = \frac{FreqFrac_i}{log\left(\frac{HighDiam_i}{LowDiam_i}\right)}$$

Starting at the small particle size end of the frequency distribution:

1. Scan DiffFreqFrac$_i$ for a local maximum, i.e.,

    DiffFreqFrac$_k$ > DiffFreqFrac$_{k+1}$, and

    DiffFreqFrac$_k$ > DiffFreqFrac$_{k-1}$

    AvgDiam$_k$ is the mode of the candidate peak.

2. Scan DiffFreqFrac$_i$ from class k toward smaller particle sizes to find a local minimum, i.e.,

    DiffFreqFrac$_m$ = 0, or

    DiffFreqFrac$_m$ < DiffFreqFrac$_m$+1 and DiffFreqFrac$_m$ < DiffFreqFrac$_{m-1}$

    LowDiam$_m$ is the low diameter of the candidate peak.

3. Scan DiffFreqFrac$_i$ from class k toward larger particle sizes to find a local minimum, i.e.,

    DiffFreqFrac$_n$ = 0, or

    DiffFreqFrac$_n$ < DiffFreqFrac$_{n+1}$ and DiffFreqFrac$_n$ < DiffFreqFrac$_{n-1}$

    HighDiam$_n$ is the high diameter of the candidate peak.

4. Sum values of FreqFrac$_i$ from i=m to i=n.

    If the sum is greater than or equal to the Minimum Fraction to Report, the candidate peak is qualified and the sum is the Fraction of Distribution. Other peak quantities are calculated using the same formulas as for the entire distribution, except the only range from class m to class n is used.

    Otherwise, the candidate peak is disqualified.

In either case, peak identification repeats from step 1, starting with class n. When the end of the distribution is reached by scanning in either step 1 or step 3, peak identification is complete.

In step 1 if the end of the distribution is reached on an increasing frequency slope, i.e., DiffFreqFrac$_k$ > DiffFreqFrac$_{k-1}$, then class k is treated as the mode of a candidate peak and as the high size end of the candidate peak.

If the beginning or end of the distribution is reached while scanning for a local minimum in step 2 or 3, the beginning or ending class is treated as the local minimum.

For calculating Standard Deviation for N tests, peaks from the various tests are simply matched by their order, i.e., peak 1 from test 1 is matched with peak 1 from test 2, etc. If all tests do not have the same number of peaks, Standard Deviation for N tests is reported as N/A (not available). If the peak numbers are not the same and the user chose average of n tests, a single row is filled in with all N/A (including the peak number).

NUMBER FREQUENCY DATA

The number frequency is computed from the mass frequency distribution as defined by the standard size classes.

For each class:

$$\mathbf{NumFreq_i} = \frac{MassFreq_i/\text{AvgDiam}_i{}^3}{\sum\limits_{k}\text{MassFreq}/AvgDiam_k{}^3}$$

where

NumFreq$_N$	=	NumberfFrequency for class N
MassFreq$_N$	=	Mass frequency for class N
AvgDiam	=	Average diameter for class N

The cumulative number percent for a class is computed as the summation of the non-negative frequencies for all smaller classes.

SURFACE AREA FREQUENCY DATA

The surface area frequency is computed from the mass frequency distribution as defined by the standard size classes.

$$Area\mathbf{Freq_i} = \frac{MassFreq_i/\text{AvgDiam}_i}{\sum\limits_{k}\text{MassFreq}/AvgDiam_k}$$

For each class:

where

AreaFreq$_N$	=	NumberfFrequency for class N
MassFreq$_N$	=	Mass frequency for class N
AvgDiam	=	Average diameter for class N

The cumulative number percent for a class is computed as the summation of the non-negative frequencies for all smaller classes.

SIZE STATISTICS

STANDARD DEVIATION OF QUANTITY FOR N TESTS

For quantity, substitute the variable name for which the standard deviation is being determined. The subscript k refers to the test number.

If NumTests < = 1, StdDevTestQuantity = 0.

Otherwise,

$$MeanTestQuantity = \frac{\Sigma Quantity_k}{NumTests}$$

$$StdDevTestQuantity = \sqrt{\frac{\Sigma(Quantity_k - MeanTestQuantity)^2}{NumTests - 1}}$$

MODE

In order to do a mode calculation, the definition of the standard classes is extended over the range of input for all the data; frequencies are calculated for these classes. It is this frequency data that is used in determining the peak quantities so that all the classes are of the same width.

ModeDiam = AvgDiam$_i$ such that DiffFreqFrac$_i$ is the maximum DiffFreqFrac

MEDIAN

MedianDiam = Diameter interpolated from HighDiam vs. CumFracCoarser at CumFracCoarser = 0.5.

If the calculation is being performed on a peak, the interpolation point is at CumFracCoarser = (Cum-FracCoarser$_m$ + CumFracCoarser$_n$)/2.

ARITHMETIC CALCULATIONS

MEAN

$$\mathrm{MeanDiam} = \frac{\Sigma FreqFrac \cdot AvgDiam_i}{\Sigma FreqFrac_i}$$

STANDARD DEVIATION (OF THE DISTRIBUTION)

$$\mathrm{StdDevDiam} = \sqrt{\frac{\Sigma FreqFrac_i (\mathrm{AvgDiam} - \mathrm{MeanDiam})^2}{\Sigma \mathrm{FreqFrac}_i}}$$

COEFFICIENT OF VARIATION

$$\mathrm{CoefVar} = \frac{StdDevDiam}{\mathrm{MeanDiam}}$$

SKEWNESS

$$Skew = \frac{\Sigma FreqFrac_i (\mathrm{AvgDiam}_i - MeanDiam)^3 / \Sigma FreqFrac_i}{(\Sigma FreqFrac_i (\mathrm{AvgDiam}_i - MeanDiam^2)/\Sigma \mathrm{FreqFrac}_i)^{3/2}}$$

KURTOSIS

$$Kurt = \frac{\Sigma FreqFrac_i (\mathrm{AvgDiam}_i - MeanDiam)^4 / \Sigma FreqFrac_i}{(\Sigma FreqFrac_i (\mathrm{AvgDiam}_i - MeanDiam^2)/\Sigma \mathrm{FreqFrac}_i)^2} - 3$$

+Xδ

$$PlusNSig = MeanDiam + \times \cdot StdDevDiam$$

where x is a user-selected number.

-Xδ

$$MinusNSig = MeanDiam - \times \cdot STdDevDiam$$

where x is a user-selected number.

GEOMETRIC CALCULATIONS

MEAN

$$\frac{\Sigma(FreqFrac_i log(AvgDiam_i))}{\Sigma FreqFrac_i}$$

GeoMeanDiam = 10

STANDARD DEVIATION (OF THE DISTRIBUTION)

$$10^{StdDevLogDiam}$$

STANDARD DEVIATION OF LOG

$$StdDevLogDiam = \sqrt{\frac{\Sigma FreqFrac_i(log(AvgDiam)-log(GeoMeanDiam))2}{\Sigma FreqFrac_i}}$$

SKEWNESS OF LOG

$$SkewLog = \frac{\Sigma FreqFrac_i(log(AvgDiam_i)-log(GeoMeanDiam))^3/\Sigma FreqFrac_i}{\Sigma FreqFrac_i(log(AvgDiam_i)-log(GeoMeanDiam))^2/\Sigma FreqFrac_i^{3/2}}$$

KURTOSIS OF LOG

$$KurtLog = \frac{\Sigma FreqFrac_i(log(AvgDiam_i)-log(GeoMeanDiam))^4/\Sigma FreqFrac_i}{\Sigma FreqFrac_i(log(AvgDiam_i)-log(GeoMeanDiam))^2/\Sigma FreqFrac_i^2} - 3$$

+Xδ

$$PlusNSigLog = 10^{log(GeoMeanDiam)+\times log \ (GeoStdDevDiam)}$$

-Xδ

$$MinusNSigLog = 10^{log(GeoMeanDiam)-\times log \ (GeoStdDevDiam)}$$

SPECIFICATION / REFERENCE QUANTITIES

OUT OF SPEC

$SampCumFrac_i$ = cumulative fraction coarser/finer/passed/retained for class i from sample distribution.

$CoarseSpecCumFrac_i$ = cumulative fraction coarser/finer/passed/retained for class i from Coarse Specification distribution interpolated if the bins are of different size. This is always the average of all tests in the named sample file.

$FineSpecCumFrac_i$ = cumulative fraction coarser/finer/passed/retained for class i from FineSpecification distribution interpolated if the bins are of different size. This is always the average of all the tests in the named sample file.

If $\{SampCumFracCoarser_{i-1} > CoarseSpecCumFracCoarser_{i-1}\}$

$OutSpecFracCoarser_i = SampCumFracCoarser_{i-1} - CoarseSpecCumFrac$
$Coarser_{i-1}$

If $\{SampCumFracCoarser_{i-1} < FineSpecCumFracCoarser_{i-1}\}$

$OutspecFracCoarser_i = SampCumFracCoarser - FineSpecCumFrac$

$Coarser_{i-1}$

or,

$OutSpecFracFiner_i = -OutSpecFracCoarser_{i-1}$

$OutSpecFracRetain_i = OutSpecFracCoarser_{i-1}$

$OutSpecFracPass_i = OutSpecFracCoarser_{i-1}$

DIFFERENCE FROM REFERENCE

$SampCumFrac_i$ = cumulative fraction coarser/finer/passed/retained for class i from sample distribution.

$RefSpecCumFrac_i$ = cumulative fraction coarser/finer/passed/retained for class i from Reference Specification distribution interpolated if the bins are of different size. This is always the average of all the tests in the named sample file.

$DiffRefCoarser_i = SampCumFrac_i - RefCumFrac_i$

or,

$DiffRefFiner_i = DiffRefCoarser_{i-1}$

$DiffRefRetain_i = DiffRefCoarser_{i-1}$

$DiffRefPass_i = DiffRefCoarser_{i-1}$

MAXIMUM OUT OF SPEC

$MaxOutSpecFrac = maximum (abs value (OutSpecFrac_i))$

PASS / FAIL BY SPECIFICATION

If MaxOutSpecFrac = 0, PassFail = Passed by Specification

Otherwise, PassFail = FAILED by Specification

SPC REPORT VARIABLES

REGRESSION CHART VARIABLES

The line of best fit for the Regression Chart is calculated by the usual least squares method. [1] If there is only a single point or all *N* points have the same x-value, there can be no line of best fit in the standard form.

$$\bar{x} = \frac{\sum x_i}{N}$$

$$\bar{y} = \frac{\sum y_i}{N}$$

$$\text{Slope} = \frac{\sum (x_i - \bar{x})(y_i - \bar{y})}{\sum (x_i - \bar{x})^2}$$

$$\text{Intercept} = \bar{y} - \text{Slope} \cdot \bar{x}$$

The coefficient of correlation for this line is also calculated in the usual way. [2]

$$\sigma_x = \sqrt{\frac{\sum (x_i - \bar{x})^2}{N}}$$

$$\sigma_y = \sqrt{\frac{\sum (y_i - \bar{y})^2}{N}}$$

$$\text{Cov}(x, y) = \frac{\sum (x_i - \bar{x})(y_i - \bar{y})}{N}$$

$$\text{CorrelationCoeff} = \frac{\text{Cov}(x,y)}{\sigma_x \sigma_y}$$

CONTROL CHART VARIABLES

$$\text{Mean} = \frac{\sum y_i}{N}$$

---

[1] *BASIC Scientific Subroutines Vol II*, by F.R. Ruckdeschel, Copyright 1981 BYTE Publications/McGraw Hill, p. 16.
[2] *Mathematical Handbook for Scientists and Engineers*, G.A. Korn and T.M. Korn, McGraw Hill, Sec. 18.4. (1968)

$$StandardDeviation = \sqrt{\frac{\sum(y_i - Mean)^2}{N-1}}$$

$$C.V. = \frac{StdDev}{Mean}$$

$$+n\sigma = Mean + n \cdot StandardDeviation$$

$$-n\sigma = Mean - n \cdot StandardDeviation$$

REYNOLDS NUMBER

The Reynolds Number is calculated as follows:

$$\text{Reynolds Number} = \left[\frac{D(\mu m)}{10000(\mu m/cn)}\right]^3 \times \left[\frac{\rho o(\text{g/cc}) \times (\rho - \rho o)(\text{g/cc}) \times g(cm/s/s)}{K \times (\eta(cp) \times 0.01 \ (\text{poise/centipoise})) \times 2^2}\right]$$

where

D	=	specified starting diameter
ρ_o	=	liquid density
ρ	=	sample density
η	=	liquid viscosity
g	=	acceleration due to gravity
K	=	Stokes' constant = 18

The Reynolds Number is displayed on the tabular report.

LOG PROBABILITY

Log probability data are a transformation of cumulative mass finer data as a means of determining how well cumulative and differential mass data represent statistical normal distributions. Since cumulative mass finer data are essentially data indicating the probabilities of finding particles of mass finer at given diameters, log normal probability data are a fit of the cumulative mass data to the defined, symmetrical probabilities tabulated for a normal distribution.

The log probability table used is a subset of 99 points, ranging from (-2.88, 0.2%) to (0.0, 50.0%) to (+2.88, 99.8%), from a standard normal distribution table (see log probability interpolation table). The x-axis and y-axis data which are plotted on a log probability graph are calculated as follows:

1. X-axis boundaries are determined by the spline interpolation at 0.2% and 99.8% from cumulative mass finer vs. log diameter. This gives Xprob_beg and Xprob_end, respectively.

2. For each of the number of points collected,

    If Diameter value is between Xprob_beg and Xprob_end and

    if CumMassFiner value is between 0.2% and 99.8%, then

    Xprob value = Diameter value

    Yprob value = Spline interpolation at CumMassFiner values of the x vs. y log probability table values

Log Probability Interpolation Table

X(%)	Y	X(%)	Y	X(%)	Y
0.20	-2.88	33.00	-0.44	68.08	0.47
0.99	-2.33	34.83	-0.39	69.15	0.50
2.02	-2.05	35.94	-0.36	69.85	0.52
3.01	-1.88	37.07	-0.33	70.88	0.55
4.01	-1.75	37.83	-0.31	71.90	0.58
4.95	-1.65	38.97	-0.28	72.91	0.61
5.94	-1.56	40.13	-0.25	73.89	0.64
6.94	-1.48	40.90	-0.23	74.86	0.67
7.93	-1.41	42.07	-0.20	76.11	0.71
9.01	-1.34	42.86	-0.18	77.04	0.74
10.03	-1.28	44.04	-0.15	77.94	0.77

Log Probability Interpolation Table (continued)

X(%)	Y	X(%)	Y	X(%)	Y
10.93	-1.23	44.83	-0.13	79.10	0.81
11.90	-1.18	46.02	-0.10	79.95	0.84
12.92	-1.13	46.81	-0.08	81.06	0.88
14.01	-1.08	48.01	-0.05	82.12	0.92
14.92	-1.04	48.80	-0.03	82.89	0.95
16.11	-.099	50.00	0.00	83.89	0.99
17.11	-0.95	51.20	0.03	85.08	1.04
17.88	-0.92	51.99	0.05	85.99	1.08
18.94	-0.88	53.19	0.08	87.08	1.13
20.05	-0.84	53.98	0.10	88.10	1.18
20.90	-0.81	55.17	0.13	89.07	1.23
22.06	-0.77	35.96	0.15	89.97	1.28
22.96	-0.74	57.14	0.18	90.99	1.34
23.89	-0.71	57.93	0.20	92.07	1.41
25.14	-0.67	59.10	0.23	93.06	1.48
26.11	-0.64	59.87	0.25	94.06	1.56
27.09	-0.61	61.03	0.28	95.05	1.65
28.10	-0.58	62.17	0.31	95.99	1.75
29.12	-0.55	62.93	0.33	96.99	1.88
30.15	-0.52	64.06	0.36	97.98	2.05
30.85	-0.50	65.17	0.39	99.01	2.33
31.92	-0.47	67.00	0.44	99.80	2.88

Standard Report Tables

Standard Diameter	Standard Mass %
300	95
250	90
200	85
150	80
100	75
80	70
60	65
50	60
40	55
30	50
25	45
20	40
15	35
10	30
8	25
6	20
5	15
4	10
3	5
1.5	
1	
0.8	
0.6	
0.5	
0.4	
0.3	
0.2	
0.1	

D EXPORTED DATA EXAMPLE

This exported data has been truncated for this manual.

```
Sample Information File



            Sample Information


      Sample:    MPSRM
    Operator:    AWT
   Submitter:    Micromeritics
  Parameter 1    0.000
  Parameter 2    0.000
  Parameter 3    0.000
Type of data:    Automatically collected


                  Analysis Conditions


  Parameter set name:    Garnet Medium Particle Size Reference


Sample Properties






  Particle description:    Garnet
            Density:    3.880 g/cm³


        Liquid Properties


  Parameter set name:    Water
    Classification:    Interpolated
```

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```
Table of User Entered Densities and Viscosities


  Temperature     Viscosity      Density
    (°C)           (mPa·s)       (g/cm³)
---
  26.0            0.8737        0.9968
  32.0            0.7679        0.9951
  38.0            0.6814        0.9930


   Analysis Control Parameters


 Starting diameter:    50.00 µm
   Ending diameter:    0.18 µm
     Analysis type:    High Speed


                 Analysis Options


            MasterTech stir time:    30 s
         MasterTech stirrer speed:    Low
           MasterTech probe time:    15 s
      Stop at selected mass percent:    No
            Ending percent finer:    0.0
                Number of tests:    1
       Leave pump on during analysis:    No
 Wait for temperature stabilization:    Yes
       Mixing chamber stirrer speed:    6
            Full scale pump speed:    3
           Bubble detection method:    Medium
             Rinse after analysis:    Yes
                  Rinse method:    Fixed Cycles
                  Rinse cycles:    3
```

```
                   Rinse pump speed:    4


                   Report Options


 Report ID:    Garnet Medium Particle Size Reference




 Distribution Type:    Mass

    Selected Test:    Last


                           Reference Sample:


  1)    C:\Users\Public\Documents\Micromeritics\SediGraph III
Plus\data\example\MPSRMCEN.SMP


                         Specification Samples:


  1)    C:\Users\Public\Documents\Micromeritics\SediGraph III
Plus\data\example\MPSRMCRS.SMP

  2)    C:\Users\Public\Documents\Micromeritics\SediGraph III
Plus\data\example\MPSRMFIN.SMP


                            Overlay Samples:


  1)    C:\Users\Public\Documents\Micromeritics\SediGraph III
Plus\data\example\MPSRMCEN.SMP

  2)    C:\Users\Public\Documents\Micromeritics\SediGraph III
Plus\data\example\MPSRMCRS.SMP

  3)    C:\Users\Public\Documents\Micromeritics\SediGraph III
Plus\data\example\MPSRMFIN.SMP
```

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Peak selection type:	Automatic
Minimum percent of dist. to report:	5.0 %
Minimum valley depth to separate peaks:	0.00

Reports

Combined Report	Yes
Standard Class Size Table	No
Standard Sieve Table	No
Particle Size Table	No
Cumulative Fraction Table	No
Cumulative Graph	Yes
Frequency Graph	Yes
Difference from Ref Graph	Yes
Out of Spec Graph	Yes
Rosin Rammler	No
Summary Report	No
Baseline	Yes
Surface Area	No
Surface Area Population	No
Number	No
Number Population	No
Log Probability	No
Advanced Reports	No
Sample Log	No

Combined Report

Standard Class Size Table	No
Standard Sieve Table	No
Particle Size Table	Yes
Cumulative Fraction Table	Yes

Cumulative Graph	Yes
Frequency Graph	No
Difference from Ref Graph	No
Out of Spec Graph	No
Rosin Rammler	No
Summary Report	Yes
Baseline	No
Surface Area	No
Surface Area Population	No
Number	No
Number Population	No
Log Probability	No
Advanced Reports	No
Sample Log	No

Cumulative Finer Mass Fraction vs. Diameter

Plot Type:	Curve
Overlay:	Samples
Autoscale x-axis:	Yes
Autoscale y-axis:	Yes
X axis range:	0.0090 to 125,000.0000 µm
Y axis range:	-0.100 to 1.100

Mass Frequency vs. Diameter

Plot Type:	Curve
Overlay:	Tests
Autoscale x-axis:	Yes
Autoscale y-axis:	Yes
X axis range:	0.0090 to 125,000.0000 µm
Y axis range:	-0.100 to 1.100

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Cumulative Finer Mass Fraction Difference From Reference Graph

Plot Type:	Curve
Overlay:	Tests
Autoscale x-axis:	No
Autoscale y-axis:	Yes
X axis range:	1.0000 to 7.0000 µm
Y axis range:	-1.0000 to 1.1000

Cumulative Finer Mass Fraction Out of Specification Graph

Plot Type:	Curve
Overlay:	Tests
Autoscale x-axis:	Yes
Autoscale y-axis:	Yes
X axis range:	0.0090 to 125,000.0000 µm
Y axis range:	-1.0000 to 1.1000

Collected Data

Sample recorded at first analysis:	Garnet
Liquid recorded at first analysis:	Water
Use auxiliary baseline:	No
Mean baseline value:	135 kCnts/s

Test Summary:

Test Number	Cell Temperature (°C)	Liquid Density (g/cm³)	Viscosity (mPa·s)	Mean Full Scale (kCnts)

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```
-----
    1           35.0        0.9941       0.7226         84
    2           35.0        0.9941       0.7227         84
    3           35.0        0.9941       0.7227         84
    4           35.0        0.9941       0.7227         84
    5           35.0        0.9941       0.7227         84
    6           35.0        0.9941       0.7227         84
    7           35.0        0.9941       0.7227         84
    8           35.0        0.9941       0.7227         84
```

```
  Instrument name:    0003
    Serial number:    0003
```

Test 1

	Cumulative		Cumulative		Cumulative
Particle	Mass	Particle	Mass	Particle	Mass
Diameter	Finer	Diameter	Finer	Diameter	Finer
(μm)	(Fraction)	(μm)	(Fraction)	(μm)	(Fraction)

51.5822	0.997	7.7179	0.958	1.1548	0.099
48.6968	0.997	7.2862	0.943	1.0902	0.091
45.9727	0.997	6.8786	0.924	1.0292	0.084
43.4010	0.996	6.4938	0.900	0.9716	0.077
40.9732	0.996	6.1306	0.871	0.9173	0.0-

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70						
64	38.6812	0.995	5.7876	0.837	0.8660	0.0-
58	36.5174	0.995	5.4639	0.799	0.8175	0.0-
52	34.4747	0.995	5.1582	0.756	0.7718	0.0-
46	32.5462	0.995	4.8697	0.711	0.7286	0.0-
41	30.7256	0.995	4.5973	0.663	0.6879	0.0-
37	29.0068	0.995	4.3401	0.615	0.6494	0.0-
33	27.3842	0.994	4.0973	0.568	0.6131	0.0-
30	25.8523	0.994	3.8681	0.522	0.5788	0.0-
27	24.4062	0.993	3.6517	0.478	0.5464	0.0-
24	23.0409	0.993	3.4475	0.437	0.5158	0.0-
22	21.7520	0.993	3.2546	0.400	0.4870	0.0-
20	20.5353	0.994	3.0726	0.366	0.4597	0.0-
18	19.3865	0.994	2.9007	0.335	0.4340	0.0-
15	18.3021	0.996	2.7384	0.307	0.4097	0.0-
13	17.2783	0.997	2.5852	0.283	0.3868	0.0-
11	16.3117	0.998	2.4406	0.261	0.3652	0.0-
08	15.3993	0.998	2.3041	0.242	0.3447	0.0-
06	14.5378	0.998	2.1752	0.224	0.3255	0.0-
	13.7246	0.998	2.0535	0.209	0.3073	0.0-

03					
12.9569	0.997	1.9387	0.194	0.2901	0.0-
01					
12.2321	0.996	1.8302	0.181	0.2738	-
0.002					
11.5478	0.994	1.7278	0.168	0.2585	-
0.004					
10.9018	0.992	1.6312	0.156	0.2441	-
0.005					
10.2920	0.990	1.5399	0.145	0.2304	-
0.006					
9.7163	0.987	1.4538	0.135	0.2175	-
0.006					
9.1728	0.983	1.3725	0.125	0.2054	-
0.005					
8.6596	0.977	1.2957	0.116	0.1939	-
0.003					
8.1752	0.969	1.2232	0.107	0.1830	-
0.001					

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E Sample Dispersion

Use of the SediGraph requires that each powder be well dispersed in a liquid of known density and viscosity and that the difference between the powder and liquid densities be accurately known. Viscosity and density data for some common liquids are given in *Sources of Dispersing Aids on page I - 1*. Handbook values for other liquids are usually sufficiently accurate, so the latter requirement means that only the powder density must be determined if it is unknown and if composition information does not permit calculation from handbook values. For this, one of Micromeritics' pycnometers is recommended. For materials likely to have dead-end pores into which liquid may not completely penetrate, the effective density[1] may need to be determined using the sedimentation liquid to be employed and a gas pycnometer.

The liquid should be one in which the powder can be completely dispersed (separated into unattached particles) for accurate size results to be obtained. Obviously, the liquid should be nontoxic, readily available, and one in which the sample is insoluble. Complete insolubility may be difficult to achieve in some instances. Solubility problems may be minimized by allowing the liquid to stand in contact with the particle material prior to using the liquid for the test sample. This cannot completely eliminate problems, however, because particle solubility is a function of particle size. Small particles are more soluble than large ones. In a dispersion of different sizes, the smallest particles tend to go into solution while precipitation occurs on the larger particles. In making a particle size distribution analysis, particle solubility is indicated if the recorded distribution consistently fails to attain zero percent even long after the analysis is complete.

There are no established rules or laws by which complete particle dispersion can be assured. Only guidelines can be offered. Some powders disperse easily in any of several liquids and remain so while others require careful attention to conditions in order to achieve dispersion and are prone to reagglomerate if conditions shift a small amount. A few can be dispersed only after extended treatments.

Agitation, resulting in the application of strong shear forces, aids dispersion. The more violent the agitation — perhaps carried out in a high-speed blender, homogenizer, or an ultrasonic device — the better generally is the dispersion. Stirring a suspension while subjecting it to ultrasonic dispersion generally achieves the best dispersion because this ensures that all portions of the mix are brought into the zones of greatest energy.

For a few friable materials such agitation can result in comminution of the particles for which measurements are preferred. This is not likely to be the case with solid particles, particularly when the particles are under 50 to 100 µm in diameter.

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[1] The procedure for determining the effective density is discussed in Application Note #94. Contact your local sales representative or the Micromeritics sales office to request a copy.

Air bubbles cause misleading results if trapped in the liquid during agitation. Care should be taken to avoid bubble entrapment, especially when the liquid is highly viscous. The SediGraph performs bubble elimination routines and checks to verify their effectiveness, but the best agitation procedure is one that does not introduce them in the first place. The magnetic stirrer built into the instrument is a convenient means for maintaining a homogeneous particle dispersion but will cause flocculation in certain magnetically susceptible materials. With such particles, stirring can be accomplished by using the ultrasonic dispersion accessory or the MasterTech.

Chemical wetting or dispersing agents also generally aid dispersion. A great variety of such products are marketed. *Chemical Aids for Particle Dispersion on page B - 1* and *Sources of Dispersing Aids on page I - 1* list some of the more useful dispersing aids, as well as sources for some of these materials. These agents have been found useful for particle dispersion in Micromeritics' Materials Analysis Laboratory but are not the only agents available. It is to be noted that liquid density and viscosity values may need slight adjustment if more than about 0.1% by weight (based on the dry weight of the sample) of dispersing agent is added and precise measurements are needed.

Some commercial surfactants are intended for use in specific pH ranges and in particular nonaqueous solutions. Slight solution composition differences may alter the effectiveness of any agent. The chemical supplier should be contacted about this type of problem. Sometimes merely shifting the pH of an aqueous dispersion will yield great improvements in the degree of dispersion. Metal oxides and metals that are likely to have oxide layers on their surface ordinarily are most easily dispersed in mildly alkaline media. Metal powders with any likelihood of grease on them should always be degreased prior to a dispersion attempt. Noble metal powders usually need a wetting agent for good dispersion. Dispersions involving hydrocarbon liquids that are immiscible with water are often difficult to make unless the powder is quite dry. Sometimes moisture picked up from the air is more than enough to cause difficulties.

Micromeritics offers Sedisperse liquids in three series for dispersing particles at low solids concentrations. A- and P-series are stable, balanced formulations containing highly purified, saturated aliphatic hydrocarbons and added surfactants. A-series Sedisperse liquids are colorless while the P-series are pale yellow. These liquids produce nearly universal dispersion of powder-liquid systems with solids concentrations below three weight percent generally, and as much as five weight percent in some cases. Sedisperse liquids solubilize adsorbed moisture.

W-series Sedisperse liquids are slightly anionic, non-foaming, aqueous formulations. They also produce nearly universal dispersion of systems with concentrations generally below three weight percent. Sedisperse liquids contain built-in surfactants and dispersants so that nothing else needs to be added for the dispersion of particles except mechanical and / or ultrasonic energy. These liquids are available over a range of densities and viscosities, thus making them applicable to particles of widely varying properties. Sedisperse liquids are designed to be used without dilution or the addition of surfactants, and exhibit good shelf life and stability. A data sheet is supplied with each liquid giving handling details, density, and viscosity data over a temperature range of 24 to 45 °C.

The A-series Sedisperse liquids are the most widely useful and will disperse most powders, including metals, oxides, silicates, pigments, Portland cements, propellants, and many other powders. Those few materials not dispersing well in the A-series liquids can usually be dispersed in the P-series Sedisperse liquids. These are special formulations, slightly cationic, developed to disperse difficult metal and pigmented resin powders. The W-series Sedisperse liquids should be used to disperse those materials which are soluble in the organic Sedisperse liquids. See *Sedisperse Particle Dispersion Liquids on page H - 1*.

Some powders flocculate upon standing a few moments after having been dispersed. Such flocculation is quite readily detected with the SediGraph. The indicated size distribution as plotted by the instrument during a test will proceed normally until flocculation starts. The first evidence of flocculation will likely be an increase in the indicated particle concentration and this will then be followed by a precipitous drop in the plotted percentage. Flocculation, of course, prevents accurate particle size analysis, and better dispersion and stabilization techniques must be sought.

As a general guide, the best dispersing technique (includes agent and procedure) is the one producing consistently the finest distribution of sizes by SediGraph analysis. We make this assertion because of the high reproducibility of the SediGraph when presented identical samples. If the sample preparation technique is deficient in freeing particles one from another or if, though unlikely, is producing particle fracture, this will be evidenced by an inconsistency of results.

The rheological behavior of high concentrations of fine powder in a liquid gives a good preliminary indication of the suitability of both the liquid medium and the dispersing agent. Some powders containing as much as 50 percent liquid act as if they were almost a solid mass, but a few tenths of a percent of wetting agent can cause the mass to take on the consistency of soup. This reaction is indicative of a very good agent. The effect will not often be so dramatic, but working the mass with a spatula will give a good indication of the efficacy of an agent.

A test for the optimum quantity of a dispersing agent is conducted by measuring the sediment volume from a slurry of about 5 weight percent concentration. The slurry and agent must be mixed and allowed to stand in a sedimentation tube undisturbed by either mechanical vibrations or thermal currents. The minimum sediment volume indicates the best agent concentration level. If several dispersing agents are compared at the same time, the minimum sediment volume is also a measure of the best dispersing agent.

No particular sample concentration is required in using the SediGraph as long as the dispersed sample reduces the radiation beam intensity by 13 to 70 percent. The recommended procedure for initial testing is to prepare a dispersion of approximately 5 volume percent concentration. Portions of this preparation are added to pure suspending liquid until an adequate concentration for analysis is achieved. The advantage of this procedure is that less concentrated dispersions can generally be produced without fear of flocculation once the initial preparation is made.

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F SEDIGRAPH RESULTS RELATIVE TO OTHER METHODS

The SediGraph 5100 Analyzer, sieve analysis, and hydrometer measurements yield particle size distributions on a mass (weight) basis. Microscopic measurements result in size data as a function of the number of particles. Measurements that involve light scattering, transmission, or diffraction relate size most appropriately to particle cross sectional area. Particle counting systems, electric zone sensing, gives size in terms of particle volume.

Mass-based measurements can be expected to be in agreement with respect to their reliability and the applicability to the size range involved, provided the particles are spherical and solid. When the particles are irregular, close agreement should not necessarily be anticipated. Sieve analysis, for example, must be very carefully performed with fine particles to ensure complete separation according to size without damaging the sieves. Even so, the size determined is not necessarily the same as that measured by the SediGraph. The SediGraph determines the size of all particles in terms of the E.S.D. (equivalent spherical diameter). Since sieve openings are usually square, elongated particles sometimes pass a given sieve in one orientation and at other times are retained. These differences obviously lead to differences in results.

Light-based instruments incorporate various means for tuning, calibrating, and data reduction, which can make them agree satisfactorily for some materials with most any one of the other techniques. Any setting is dependent to a degree on the refractive index of the measured particles; however, so agreement cannot be general or over all particle size ranges. The shape of the particles also influences all results.

Mass and volume measurements are equivalent numerically. Therefore, analyses with the SediGraph and the electric sensing zone can be expected to agree if the particles are spherical, solid, and if their size range is sufficiently narrow for all of them to be accurately detected by the electric sensing zone.

Again, precise agreement is not to be expected with irregular particles, for the electric sensing zone measures something closely akin to the diameter an irregular particle would assume were it melted into a sphere. This is not necessarily the equivalent spherical diameter.

Microscopic measurements yield particle diameters that, for spheres, are essentially E.S.D. As before, measured sizes will deviate from E.S.D. when the particles are irregular— the greater the irregularity, the greater the deviation. The numbers will not correspond even approximately because, as noted above, the measurements are on a different basis. However, number-based measurements are readily converted into mass-based (or volume-based) results by applying the relationship to incremental sizes.

$$Y = \frac{nD^3}{\sum(nD^3)}$$

where Y is the mass percent of particles having the diameter D and n the number of particles of that diameter. The denominator, therefore, represents the entire spectrum of sizes. The following tabulation presents number-based data and calculations leading to the number-based and mass-based diameter distributions.

Particle Diameter Range (μm)	D Largest Diameter Within Range (μm)	n Number of Particles Within Range	Percent by Number Less than Diameter	nD^3	$\dfrac{nD^3}{\sum(nD^3)}$	Percent by Mass Less Than Diameter
5.4 - 5.0	5.4	10	100.0	1575	0.0481	0.0481 100.0
4.9 - 4.5	4.9	51	99.2	6000	0.1833	95.2
4.4 - 4.0	4.4	65	95.3	5537	0.1692	76.9
3.9 - 3.5	3.9	70	90.3	4152	0.1269	59.9
3.4 - 3.0	3.4	133	84.9	5227	0.1597	47.3
2.9 - 2.5	2.9	160	74.6	3902	0.1192	31.3
2.4 - 2.0	2.4	288	62.3	3981	0.1216	19.4
1.9 - 1.5	1.0	271	40.1	1859	0.0568	7.2
1.4 - 1.0	1.4	162	19.2	445	0.0136	1.5
0.9 - 0.5	0.9	72	6.7	52	0.0016	0.2
0.4 - 0	0.4	14	1.1	1	0.0000	0.0
		$1296 = \sum n$		$32731 = \sum nD^3$		

G SEDIMENTATION THEORY

CALCULATIONS

Sedimentation size analysis is based upon the fact that the measured equilibrium velocity of a particle through a viscous medium, resulting from the action of the gravitational force, can be related to the size of the particle by Stokes' law. For spherical particles, Stokes' law is expressed by:

$$D = KV^{1/2} \tag{1}$$

where

$$K = [18\frac{\eta}{(\rho-\rho o)g}]^{1/2} \tag{2}$$

and D is the diameter of the spherical particle, v its equilibrium sedimentation velocity, and ρ its density. The fluid medium is characterized by viscosity η and density ρo ; g is the acceleration of gravity. These equations apply rigorously as long as the particle Reynolds number, Dvρo/η, is less than 0.3 and they apply up to a Reynolds number of 0.5, with about 3% error.[1]

In practice, truly spherical particles are seldom encountered, and Stokes' law is not exact for any other shape. Since irregular shapes cannot in any case be described by a single linear dimension, it is accepted practice to specify the size of non-spherical particles in terms of the diameter of a sphere of the same material that would have the same sedimentation velocity. Thus, for non-spherical particles, the terms "Stokes' diameter" or "equivalent spherical diameter" are universally understood. The term "equivalent spherical diameter" (E.S.D.) is sometimes used in a different context to mean the diameter of a sphere of the same material that would have the same mass as the particle in question; that is, the results of measurements of particle dimensions from electron micrographs are frequently reduced to size distribution curves in terms of mass E.S.D. In general, the relationship between these two measures of size is given by the inequality.

$$\frac{\text{Sedimentation E.S.D.}}{\text{Mass E.S.D.}} \leq 1 \tag{3}$$

The ratio expressed in equation (3) is usually close to unity.

Data on the sedimentation velocity of suspended particles may be obtained in two ways: (a) by measuring the concentration of particles remaining in suspension as a function of time, or (b) by measuring the quantity of sediment produced as a function of time. The latter approach is less desirable mathematically because of the graphical differentiation required to reduce the data to a size distribution curve.

---

[1] Lapple, C.E., et al, *Fluid and Particle Mechanics*, University of Delaware, Newark, 1956.

Tests based on the first approach are traditionally performed in the following way. A dilute, dispersion of the fine particle material is stirred to render it homogeneous and then allowed to stand undisturbed while undergoing sedimentation. Time is measured from the beginning of the settling period. By Stokes' law, a particle of diameter D will settle a distance h in time t according to the expression:

$$D = K\left(\frac{h}{t}\right)^{1/2} \tag{4}$$

where K is given by equation (2). Consequently, after a given time t_i all particles larger than the corresponding diameter D_i will have fallen below a given distance h from the surface of the suspension. If the initial (uniform) concentration of material is C_o g/cm^3 and the concentration after time t_i at distance h is C_i g/cm^3, then P_i, the weight percent of material finer than D_i, is given by:

$$P_i = 100\left(\frac{C_i}{C_o}\right) \tag{5}$$

By obtaining values of C_i after various times, the corresponding values of P_i and D_i may be calculated, which when plotted yield an integral, or cumulative distribution of particle size in terms of Stokes' E.S.D.

The SediGraph uses a finely collimated X-ray beam to measure particle concentration in terms of the transmitted intensity of the X-ray beam through the suspension relative to the clear or particle-free suspending fluid. This transmittance is a function of the weight concentration of the suspended solid at the depth of measurement. Since the X-ray beam can be made extremely small and because it does not disturb the suspension, it constitutes an ideal measuring technique.

If a sample container or cell of rectangular cross section is irradiated from a direction perpendicular to one of its sides by a collimated X-ray beam, the fraction of the incident radiation transmitted by the cell when filled with the suspension under study is given by:

$$\frac{I}{I_o} = e^{-(a_1\phi_1 + a_s\phi_s)L_1 - a_cL_2} \tag{6}$$

where I and Io are the transmitted and incident intensities; a_1, a_s, and a_c the X-ray absorption coefficients of the liquid, the particulate solids, and the cell walls, respectively; ϕ_1 and ϕ_s the weight fractions of liquid and solid present in the suspension; L_1 the internal cell thickness in the direction of irradiation; L_2 the total thickness of the cell walls. By using the relation $\phi_1 = 1 - \phi_s$ and by defining a transmittance T as the ratio of the transmission of the cell when filled with a sample dispersion to its transmission when filled with pure suspending liquid, there is obtained:

$$T = e^{-\phi_s(a_s - a_i)L_i} \tag{7}$$

or

$$InT = -A\phi_s \tag{8}$$

where A is a constant for the particular apparatus and suspension components.

By collimating the X-ray beam through horizontal slits with a vertical dimension small compared to the sedimentation depth, h, the measured values of T can be used in calculating the particle size distribution; that is:

$$P = 100\left(\frac{InT_i}{InT_o}\right) \tag{9}$$

where T_o refers to the transmittance of the initial suspension.

METHOD OF ANALYSIS

Generally, the sedimentation method derives its results from the rates that different size particles fall in a liquid due to the force of gravity. Rate, as used here, is the distance that a particle falls in a certain period of time. The scientific law which describes the rate that particles fall in a liquid is called Stokes' Law. Large particles fall at a faster rate than smaller particles, as shown in the following illustration.

A. Lowest Falling Rate
B. Highest Falling Rate
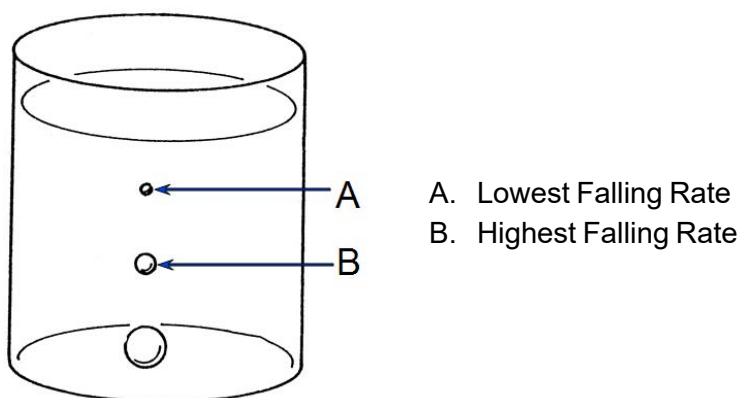
In order to determine particle diameters accurately using the falling rates of particles, the density and viscosity of the liquid used must be known as well as the density of the particles. Density is the mass of a material that it takes to fill a unit of space. Viscosity may be thought of as the resistance of the liquid applied to falling particles. For example, a particle falls much slower in syrup than in water because syrup has a higher viscosity. It should also be noted that temperature affects both the density and viscosity of liquids; therefore, the temperature of the liquid must be known for particle size determinations to be accurate.

The falling rates for various particle sizes are computed before analysis using Stokes' Law. A vertical distance and an elapsed time are selected for each falling rate such that a particle falling at a certain rate will fall a certain distance in a selected time. Relative particle concentration is then measured at the selected distance and time.

Initially, a completely mixed (homogeneous) suspension of particles is established in a container by rapidly circulating the mixture. The circulation is stopped, and the relative concentrations of particles are measured at the selected vertical distances from the top of the container and at the selected elapsed times after circulation is stopped.

The particle size associated with each concentration measurement is the size of the largest particle present at the height and time of the measurement. All particles larger than that size have higher falling rates, and have fallen to a lower point in the container. Smaller particles are still present at equal concentrations just above and below the specified point. Thus, the concentration measured at the specified point is the concentration of particles smaller than or equal to that size.

This series of relative concentrations of particles smaller than various sizes is the particle size distribution.
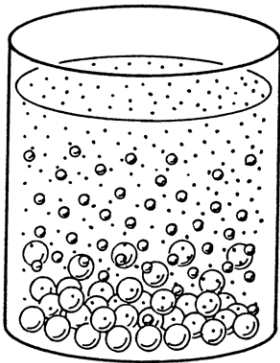
% Maximum Concentration at Typical Specified Points

Since different particles usually have different shapes, the standard measure used to report particle size is Equivalent Spherical Diameter. This is the diameter of a sphere (or perfectly rounded mass) of the same material with the same falling rate.

SYSTEM OPERATION

The sedimentation method is used for particle size analysis in the SediGraph. The rates of particle fall due to gravity are calculated and X-ray absorption (concentration) of particles at different heights and points in time are determined, and the results of those determinations are provided as graphs and tabular reports. Sedimentation analysis takes place in the analyzer. Data are sent to the computer which provides the graphs and tabular reports.

The material to be analyzed is dispersed in a liquid, according to the type of analysis to be performed. (For more information concerning the relationship of dispersion to the type of analysis, see appendices B and C.) At the appropriate time, the dispersed mixture is poured into the mixing chamber on the front of the analyzer.

A magnetic stirrer located under the mixing chamber keeps the particles suspended (that is, keeps the particles from sedimenting) until it is time for the analysis. The stirring speed can be adjusted as required to properly suspend the particles. If the particles to be analyzed are attracted to the magnetic stirrer, the magnetic stirrer can be replaced with a mechanical stirrer. If the dispersion energy required to keep the particles in a dispersed state in the mixing chamber is more than can be provided by the stirrer used, an ultrasonic probe can be inserted into the mixing chamber.

Sedimentation takes place inside an analysis cell as shown in the following illustration. At the appropriate time, the particle mixture is transferred by the analyzer from the mixing chamber to the analysis cell. Particle circulation is stopped, and the particles are allowed to sediment (or fall) inside the analysis cell under the influence of gravity. The SediGraph then determines the particle size distribution.
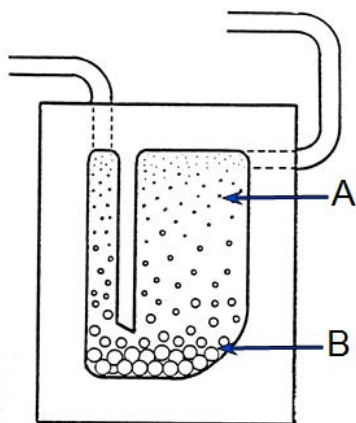
A. Lowest Falling Rate
B. Highest Falling Rate

An X-ray beam (made up of a number of fine parallel rays) is provided from a source inside the analyzer. A unit which detects X-rays is placed directly across from the X-ray source. The analysis cell is placed in the path of the X-ray beam, between the X-ray source and the detector. The cell contains a window on each side so that the X-rays can pass through the cell to the detector. Sedimenting particles (particles falling under the influence of gravity) inside the cell cross the path of the X-ray beam. The particles in the path of the beam absorb X-rays (that is, the particles keep some X-rays from reaching the detector). The amount of X-ray absorption at the point in the cell where the beam is located is determined as a percentage of the X-ray absorption with the highest particle concentration for that sample. Based upon particle falling rates, this percentage is related to the maximum particle size above that point in the cell.

![micromeritics®]
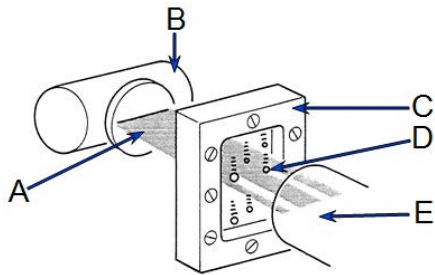
A. X-Rays
B. X-Ray Source
C. Sample Cell
D. Particle
E. X-Ray Detector

The SediGraph system uses both particle falling rates and the amount of X-ray absorption for particle size analysis. Particle falling rates (according to Stokes' Law) are used to determine the points in the cell beyond which certain size particles have fallen. X-ray absorption is used to determine the percentage of total particle mass at different points in the cell. The resulting particle size distribution data are processed by the system computer and used to provide graphs and tabular reports which provide details of the analysis.

PARTICLE FALLING RATES

Particle falling rates are very significant in the determination of particle size distribution. However, there are several important considerations in the accurate determination of particle falling rates. There must be a reference point for measuring particle falling distances. The SediGraph uses an automatic beam-split feature for establishing a reference point. Small particles have a low falling rate, which could require considerable amounts of time for analysis. The SediGraph uses cell movement during analysis to shorten analysis times by measuring small particle concentration at very short sedimentation distances. Cell movement does not affect particle falling rates within the cell. Particle dispersion also affects falling rates; therefore, proper particle dispersion is required when using the SediGraph.

Beam-Split
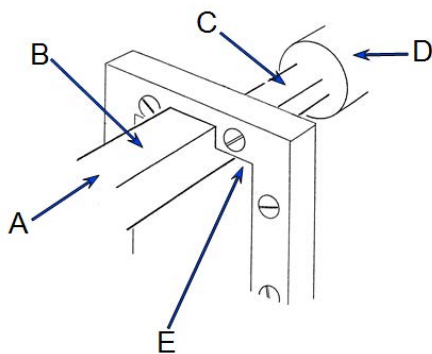
A. X-Ray Source
B. 100% Beam
C. 50% Beam
D. Detector
E. Inside Top of Cell

Since the top of the cell is used as the reference point for measuring particle falling rates, the exact position of the cell (relative to the X-ray beam) must be known in order for particle falling rates to be correct. The SediGraph determines the position of the cell by moving the cell to the point where the top edge of the cell splits the X-ray beam (exactly in half), and by storing this beam-split data in the system computer so that this position can be located for the next analysis. Beam-split is done automatically by the system at the start of any automatic scanning operation; no message is displayed on the monitor unless beam-split cannot be performed for some reason.

Cell Movement
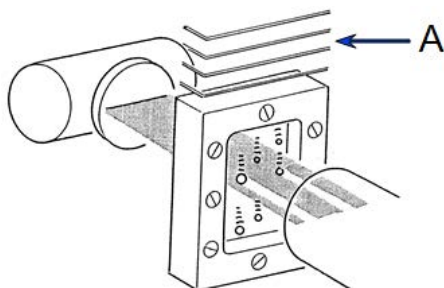
A. Cell is Moved Down

The cell is attached to an elevator assembly which moves the cell down during analysis to speed the data collection process. The system computer performs the calculations associated with particle falling rates as the distances and times are changed according to the movement of the cell. For example, as shown in the cell movement illustration, it might take 30 minutes for the particle shown to fall the distance from the top of the cell to the X-ray beam; however, by moving the cell down, the particle reaches the beam in, perhaps, three minutes. The system computer uses this time and distance in determining the particle falling rate.

Particle Dispersion

The particle falling rates also depend upon how well the particles in the cell are dispersed (or separated). Joined particles behave as a single particle with a greater falling rate than if the joined particles were separate (as shown in the following illustration).
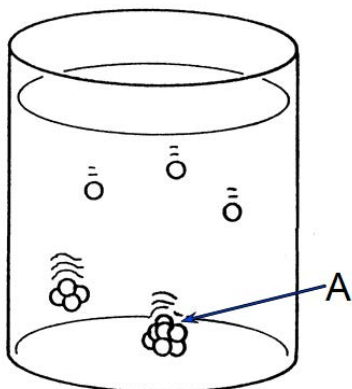
A. Joined Particles Have Higher Falling Rate

X-RAY ABSORPTION

In addition to particle falling rates, the SediGraph uses the relative amount of X-ray absorption as part of the analysis process. As falling particles in the cell cross the path of the X-ray beam, they absorb X-rays. In order for X-ray absorption to be used for measuring the distribution of particle masses in the cell: (1) the minimum and maximum X-ray absorption must be determined for each X-ray absorption measurement point in the cell; (2) any bubbles in the cell must be detected and eliminated; and (3) the particles must be properly dispersed, as explained in Appendices B and C.

Baseline (Minimum) Absorption

In order for the X-Ray absorption values to be accurate, a reference (or baseline) must be used with each value. This baseline is the amount of X-ray absorption with no particle mass present. However, since the sedimentation liquid also absorbs X-rays, the amount of X-ray absorption for the liquid must be included in the baseline. The shape of the cell, or cell profile, affects the accuracy of baseline X-ray absorption values. The SediGraph automatically determines the baseline and makes baseline corrections for any changes in the shape of the cell. This feature is called baseline correction. Let's look at how it works.

When instructed, the SediGraph performs an X-ray scan of the cell filled only with the selected sedimentation liquid. The reason for this scan is to determine the amount of X-ray absorption of the cell and liquid alone before any particles are introduced. The scan progresses from the bottom of the cell toward the top in exactly the same manner as will be done when sample particles are present.

As the cell is scanned, X-ray absorption reference values (referred to as baseline values) are determined at many points along the cell. The baseline value is the amount of X-ray absorption at that point in the cell. The baseline value is for 0% concentration since the cell contains only the sedimentation liquid and no particles.
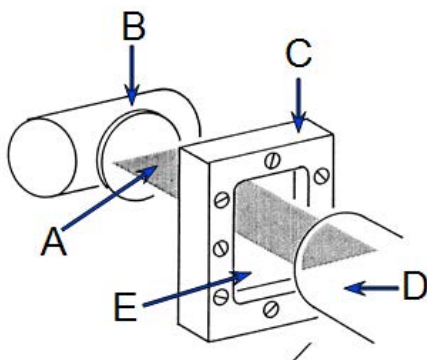
A. X-Rays
B. X-Ray Source
C. Sample Cell
D. X-Ray Detector
E. Clear Liquid in Cell

Slight differences in the cell thickness at the measurement points (up to 250) along the cell change the amount of X-ray absorption for those points. The amount of X-ray absorption at each point is stored in the system computer and recalled during the analysis to adjust the baseline at those same points in the cell.

The baseline values do not change unless the sedimentation liquid changes, the shape of the cell changes, or the X-ray intensity changes. It is, however, recommended that you obtain a baseline measurement at the beginning of each shift or whenever a different dispersant (or a new batch) is to be used. This assures accurate analysis results. The baseline operation is selected from the Unit [n] menu.

Full-Scale (Maximum) Absorption

Before each analysis, the SediGraph examines the cell filled with particles suspended in liquid (particles not allowed to sediment). As the cell is being examined, a full-scale X-ray absorption value (or maximum absorption) is determined for each point along the cell as shown in the following illustration. This full-scale absorption value is for 100% concentration, since the cell contains suspended particles, which represents the highest particle concentration for that analysis. The full-scale absorption values change with each analysis since a different number and composition of particles is used.

A. X-Rays
B. X-Ray Source
C. Sample Cell
D. Particle
E. X-Ray Detector
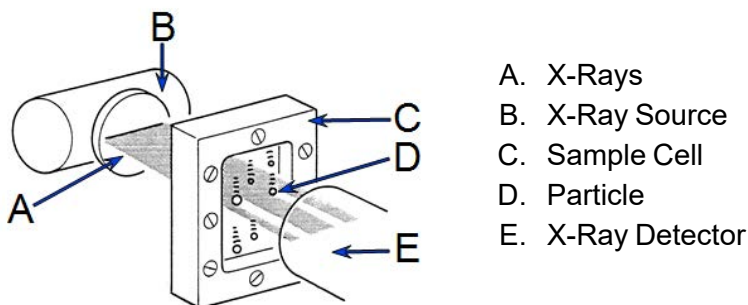
The X-ray absorption is measured at up to 250 positions in the cell. This may be reported on the Baseline / Full scale report. The full scale scan used in the analysis is computed as the average of 10 readings measured at a fixed position.

The full-scale absorption profile operation is performed automatically by the system. Since baseline absorption and full-scale absorption are known for each analysis point in the cell before the analysis, the absorption during the analysis is a percentage somewhere between baseline and full-scale. Using particle falling rate determinations, the system determines the size of the particles which have fallen beyond the specific analysis point in the cell. Therefore, the absorption percentage at each specific analysis point in the cell indicates the percentage of particles that are below a certain particle size. When this is done for a number of points in the cell, the particle size distribution can be determined.

Bubble Detection / Elimination

If air bubbles are formed in the cell during analysis, the amount of X-ray absorption at those points will be detected as a sharp, discrete change. This would make the analysis results invalid. In order to prevent this, the SediGraph has a built-in bubble detection and elimination feature. This feature automatically detects and removes bubbles from the cell. A message is displayed on the screen indicating this operation is in process.
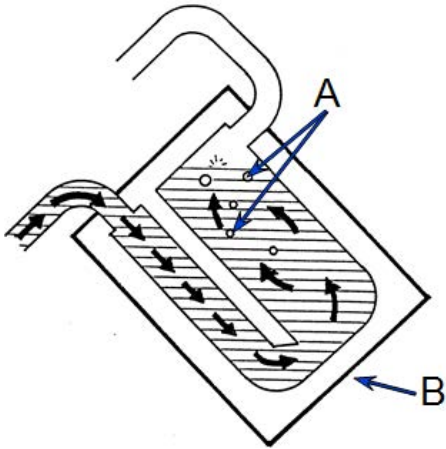
A. Bubbles
B. Cell Tilted for Bubble Discharge

SediGraph III Plus Operator Manual
512-42835-01 (Rev B) — Sep 2022

H SEDISPERSE PARTICLE DISPERSION LIQUIDS

Sedisperse A-series and P-series liquids are stable, balanced formulations for dispersing insoluble particles. These liquids are primarily saturated aliphatic hydrocarbons. Sedisperse A-series liquids are colorless while P-series liquids are pale yellow. These liquids produce nearly universal dispersions of powder-liquid systems with solids concentrations below three weight percent and to as much as five weight percent in some cases. Sedisperse liquids solubilize adsorbed moisture.

Sedisperse W-series liquids are slightly anionic, non-foaming, aqueous formulations for dispersing insoluble particles. They also produce nearly universal dispersions of systems with solids concentrations generally below three weight percent.

Sedisperse liquids are non-irritating, non-toxic, non-carcinogenic, and non-explosive. The organic Sedisperse liquids will burn, but will not support combustion at room temperature.

STORAGE REQUIREMENTS

Keep containers closed. Keep containers from freezing. If a container develops a leak during storage, transfer it to another clean container. Spillage may be cleaned using detergent and water. Sometimes particles may crystallize and settle out of Sedisperse liquids during storage. This is usually a result of exposure to cold temperatures. It is corrected by warming the Sedisperse to 40-50 °C and then vigorously shaking the liquid in a closed container to re-dissolve the particulates. Micro-organisms may also begin to grow in Sedisperse W-series liquids. These can usually be removed by filtering and the liquid is again usable for particle dispersion.

TECHNICAL DATA

Recommended techniques for using these liquids:

1. Disperse particles using energy from an ultrasonic bath or probe accompanied by continuous, moderate mechanical agitation to force particles through the nodes of the standing ultrasound waves.

2. For sedimentation particle size analysis, first disperse the powder in Sedisperse and estimate the size of the largest particles using a microscope. Next, calculate the liquid viscosity needed by using the relationship.

$$\eta = 0.0023 D_{max} \sqrt{D_{max}(\rho - 1)}$$

where

η = minimum viscosity permitted in mPa•s (or cp)

D_{max} = equivalent spherical diameter of the largest particles in µm

ρ = density of the particles in g/cm^3

MATERIAL PROPERTIES

A Material Safety Data Sheet (MSDS) is supplied with each purchase. It should be consulted for the following information:

- Oral toxicity
- Local effect on eyes
- Local effect on skin
- Shock sensitivity
- Decomposition characteristics
- Heat generation characteristics
- Recommended extinguishing agents
- Hazard by inhalation

FIRST AID TREATMENT

The Material Safety Data Sheet (MSDS) supplied with each liquid should be consulted for the following first aid information:

- Skin contact
- Eye contact
- Inhalation
- Antidote in case of swallowing

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I SOURCES OF DISPERSING AIDS

Dispersant	Source
Aerosol OT Aerosol 22	American Cyanamid Company, Process Chemicals Department, One-T Cyanamid Plaza, Wayne, NJ 07470
Calcium Chloride	Can be purchased at most laboratory supply houses.
Calgon Calgon T	Calgon Corporation, Water Management Division, Calgon Center, P. O. Box 1346, Pittsburgh, PA 15230
Cobalt Citrate	Shepherd Chemical Company, Cincinnati, OH 45212
Cobaltous Chloride	Can be purchased at most laboratory supply houses.
Daxad 23, 30	Hampshire Chemical Corporation, 55 Hayden Avenue, Lexington, MA 02173
Dispex 40	Allied Colloids, 2301 Wilroy Road, Suffolk, VA 23434
FC-134, -161 and -170	3M Company, Chemical Division, St. Paul, MN 55141
Igepal CO-530	GAF Corporation, 1361-T Alps Road, Wayne, NJ 07470
Lomar D	Henkel, 300 Brookside Avenue, Ambler, PA 19002
Oleic Acid	Can be purchased at most laboratory supply houses.
Renex 648 Tween 20 Atlas G-3300	ICI Americas, Inc., Chemical Division, New Concordville Pike, Wilmington, DE 19897
Triton X-100 Tamol SN	Rohm and Haas Company, Independence Mall West, Philadelphia, PA 19105
Sodium Silicate *N* Brand	Philadelphia Quartz Company, 1301-T E. Fort Avenue, Baltimore, MD 21230
Pyrophosphate (TSPP)	Can be purchased at most laboratory supply houses.
Zonyl A, S-13	E. I. DuPont de Nemours and Company, Dyes and Chemical Division, 1000-T Market Street, Wilmington, DE 19898

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J STOKES' LAW

A particle falling due to gravity in a viscous liquid is acted upon by three forces: a gravitational force acting downward, a buoyant force acting upward, and a drag force acting upward. The descriptive equation of this motion is

$$mg - m_0 g - F_D = m_o \frac{dv}{dt} \tag{1}$$

where m is the mass of the particle, mo the mass of a volume of liquid equal to the volume of the particle, g the acceleration of gravity, F_D the drag force, v the particle velocity, and t the time.

Small particles reach a stable, or terminal, velocity very rapidly; hence, dv/dt quickly becomes zero. The equation of motion for a sphere of diameter D and density ρ falling in a liquid of density ρo then becomes

$$F_D = \frac{\pi}{6}(\rho - \rho o)gD^3 \tag{2}$$

Dimensional analysis reveals that stable particle motion through a liquid is governed by two dimensionless groups: the particle Reynolds number Re

$$Re = Dv\frac{\rho o}{\eta} \tag{3}$$

where η is the liquid viscosity, and a drag coefficient C_D expressed by

$$C_D = \frac{(\text{drag force})}{(cross-\text{sectional area of particle})(\text{dynamic pressure on particle})} = \frac{F_D}{\frac{\pi D^2}{4} \times \frac{\rho_o v^2}{2}} \ast \tag{4}$$

The relationship between Re and C_D for laminar (not turbulent) flow conditions is well established experimentally for low values of the Reynolds number to be

$$C_D = \frac{24}{Re} \tag{5}$$

Combining equations (2) through (5) yields

$$D^2 = \frac{18v\eta}{(\rho - \rho o)g} \updownarrow$$

which has come to be identified as the Stokes law equation[1] .

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[1] Stokes, G.G., Mathematical and Physical Paper III, Cambridge University Press, 1891.

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mi micromeritics®

EU DECLARATION OF CONFORMITY

This declaration of conformity is issued under the sole responsibility of the manufacturer:

Micromeritics Instrument Corporation
4356 Communications Drive
Norcross, GA 30093, USA

Hereby declares that the product:

Sedigraph™ III Plus 5125 Particle Size Analysis System

is in conformity with the following **EU harmonization legislation**:

2014/35/EU - LVD Directive
2014/30/EU - EMC Directive
2011/65/EU - RoHS Directive

and that the equipment is in conformity with the following harmonized and other appropriate standards;

2014/35/EU (LVD)
EN 61010-1:2010/A1:2019 - *Safety requirements for electrical equipment for measurement, control, and laboratory use — Part 1: General requirements.*
EN 61010-2-081:2020 - *Particular requirements for automatic and semi-automatic laboratory equipment for analysis and other purposes*

2014/30/EU (EMC)
EN 61326-1:2020 - *Electrical equipment for measurement, control and laboratory use — EMC requirements — Part 1: General requirements*

EN 61000-3-2:2018 - *Part 3-2: Limits — Limits for harmonic current emissions (equipment input current ≤ 16 A per phase)*
EN 61000-3-3:2013;+A1:2017 - *Part 3-3: Limits — Limitation of voltage changes, voltage fluctuations and flicker in public low-voltage supply systems, for equipment with rated current <= 16 A per phase and not subject to conditional connection*

2011/65/EU (RoHS)
EN 63000:2018 - *Technical documentation for the assessment of electrical and electronic products with respect to the restriction of hazardous substances*

Name: <u>John McCaffrey, Ph.D.</u>

Signature: _____

Location: <u>Norcross, GA USA</u>

Title: <u>Vice President, R & D</u>

Date of issue: <u>08/19/2021</u>

mi micromeritics®

EU DECLARATION OF CONFORMITY

This declaration of conformity is issued under the sole responsibility of the manufacturer:

Micromeritics Instrument Corporation
4356 Communications Drive
Norcross, GA 30093, USA

Hereby declares that the product:

MasterTech 052 Automatic Sample Feeder

is in conformity with the following **EU harmonization legislation**:

2014/35/EU - LVD Directive
2014/30/EU - EMC Directive
2011/65/EU - RoHS Directive

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Date of issue: <u>08/18/2022</u>