



Operating Manual

# HAPSITE<sup>®</sup> ER



INFICON

Two Technology Place

East Syracuse, NY 13057-9714

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# 1 Declaration of Conformity



This declaration is issued under the sole responsibility of the manufacturer INFICON. The object of the declaration is to certify that this equipment, designed and manufactured by:

**INFICON Inc.**  
**Two Technology Place**  
**East Syracuse, NY 13057**  
**USA**

is in conformity with the relevant Community harmonization legislation. It has been constructed in accordance with good engineering practice in safety matters in force in the Community and does not endanger the safety of persons, domestic animals or property when properly installed and maintained and used in applications for which it was made.

**Equipment Description:** HAPSITE ER, HAPSITE Smart Plus Portable GC/MS with wireless communications, including the HAPSITE Service Module, Headspace Accessory, Situ-Probe Accessory, SPME and Thermal Desorber Accessory.

**Applicable Directives:** 2014/35/EU (LVD)  
 1999/5/EC (R&TTE / EMC)  
 (The required compliance statement concerning this directive can be found in Chapter 4 of this manual.)  
 2014/30/EU (General EMC)  
 2011/65/EU (RoHS)

**Applicable Standards:**

Safety:	EN 61010-1:2010 3.0 Edition
Emissions:	ETSI EN 300 328 v1.8.1 (2.4 Ghz) (ERM for equipment operating in the 2.4 GHz ISM band) ETSI EN 301 893 v1.7.1 (5 Ghz) EN 61326-1: 2013 (Radiated & Conducted Emissions) (EMC – Measurement, Control & Laboratory Equipment) CISPR 11/EN 55011 Edition 2009-12 Emission standard for industrial, Scientific and medical (ISM) radio RF equipment FCC Title 47 Part 18 Class A emission requirements (USA)

Immunity: EN 61326:2013 (Industrial EMC Environments)  
 (EMC – Measurement, Control & Laboratory Equipment)  
 Immunity per Table 2

ETSI EN 301 489-17 V2.2.1: 2012 (General EMI)  
 (ERM - EMC - Specific conditions for 2.4 GHz)

Wireless Restrictions:

Countries	Restrictions
France	Outdoor use limited to 10mW e.i.r.p. within the band 2454 to 2483.5 MHz.
Italy	If used outside of own premises, general authorization is required.
Luxembourg	General authorization is required for public service.
Romania	On a secondary basis. Individual license required.
Austria, Denmark, Finland, Germany, Greece, Iceland, Ireland, Liechtenstein, Luxembourg, The Netherlands, Norway, Portugal, Spain, Sweden, Switzerland, The United Kingdom	None

Authorized Representative:

Lukas Winker  
 President, ISS

ANY QUESTIONS RELATIVE TO THIS DECLARATION OR TO THE SAFETY OF INFICON'S PRODUCTS SHOULD BE DIRECTED, IN WRITING, TO THE AUTHORIZED REPRESENTATIVE AT THE ABOVE ADDRESS

## 2 Two Year Warranty

WARRANTY AND LIABILITY - LIMITATION: Seller warrants the products manufactured by it, or by an affiliated company and sold by it, and described on the reverse hereof, to be, for the period of warranty coverage specified below, free from defects of materials or workmanship under normal proper use and service. The period of warranty coverage is specified for the respective products in the respective Seller instruction manuals for those products but shall not be less than two (2) years from the date of shipment thereof by Seller. Seller's liability under this warranty is limited to such of the above products or parts thereof as are returned, transportation prepaid, to Seller's plant, not later than thirty (30) days after the expiration of the period of warranty coverage in respect thereof and are found by Seller's examination to have failed to function properly because of defective workmanship or materials and not because of improper installation or misuse and is limited to, at Seller's election, either (a) repairing and returning the product or part thereof, or (b) furnishing a replacement product or part thereof, transportation prepaid by Seller in either case. In the event Buyer discovers or learns that a product does not conform to warranty, Buyer shall immediately notify Seller in writing of such non-conformity, specifying in reasonable detail the nature of such non-conformity. If Seller is not provided with such written notification, Seller shall not be liable for any further damages which could have been avoided if Seller had been provided with immediate written notification.

THIS WARRANTY IS MADE AND ACCEPTED IN LIEU OF ALL OTHER WARRANTIES, EXPRESS OR IMPLIED, WHETHER OF MERCHANTABILITY OR OF FITNESS FOR A PARTICULAR PURPOSE OR OTHERWISE, AS BUYER'S EXCLUSIVE REMEDY FOR ANY DEFECTS IN THE PRODUCTS TO BE SOLD HEREUNDER. All other obligations and liabilities of Seller, whether in contract or tort (including negligence) or otherwise, are expressly EXCLUDED. In no event shall Seller be liable for any costs, expenses or damages, whether direct or indirect, special, incidental, consequential, or other, on any claim of any defective product, in excess of the price paid by Buyer for the product plus return transportation charges prepaid.

No warranty is made by Seller of any Seller product which has been installed, used or operated contrary to the Seller's written instruction manual or which has been subjected to misuse, negligence or accident or has been repaired or altered by anyone other than the Seller or which has been used in a manner or for a purpose for which the Seller product was not designed nor against any defects due to plans or instructions supplied to the Seller by or for Buyer.

This manual is intended for private use by INFICON Inc. and its customers. Contact INFICON before reproducing its contents.



**These instructions do not provide for every contingency that may arise in connection with the installation, operation or maintenance of this equipment. Should you require further assistance, please contact INFICON.**

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## 3 Disclaimer and Copyright

### **Disclaimer**

The information contained in this manual is believed to be accurate and reliable. However, INFICON assumes no responsibility for its use and shall not be liable for any special, incidental, or consequential damages related to the use of this product.

Due to our continuing program of product improvements, specifications are subject to change without notice.

### **Copyright**

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## 4 Definition of Note, Hint, Danger, Warning and Caution Paragraphs



Notes provide additional information about the current topic.



### CAUTION

Failure to heed these messages could result in instrument damage or the loss of data.



### DANGER

Immediate danger

Death or very serious injuries can occur.



### WARNING

Failure to heed these messages could result in personal injury.



### WARNING

Dangerous voltages are present, which could result in personal injury.



### WARNING

High temperatures are present, which could result in personal injury.

## 5 Operating Manual Style Conventions

The following information describes the conventions used throughout this manual.

When holding down a key and then pressing another key, this is expressed as (for example) “Press Ctrl+C.”

It is assumed that the CD drive used is drive **d**. If using another drive, substitute the drive letter being used for

“d:”.

It is assumed that the hard drive used is drive **c**. If using another drive, substitute the hard drive letter being used for

“c:”.

Left-click means to press and release the left mouse button (LMB) and right-click means to press and release the right mouse button (RMB).

The HAPSITE software operates in the Windows environment using the Windows® Graphical User Interface (GUI). Actions in the HAPSITE software GUI that are common to the Windows GUI are not explained in detail in this manual. Refer to the Windows documentation supplied by Microsoft®.

## 6 Customer Support

### 6.1 How to Contact Customer Support

Please read the HAPSITE ER Operating Manual before contacting Customer Support. To contact support, please request:

- Technical Support - for information and questions regarding general operation of software assistance for the HAPSITE ER
- Applications Support - for information and questions regarding the ability of the HAPSITE ER to detect various compounds and for assistance creating calibration libraries
- Sales - for pricing requests and purchasing
- Service and Repair - for troubleshooting advice and for information on repairing HAPSITE ER

If experiencing a problem with your instrument, please have the following information readily available:

- The serial number for your instrument, located on the white sticker labeled HAPSITE ER inside the front panel door



- A description of your problem
- A summary of any corrective action that has been attempted
- The exact wording of any error messages

For current customer support phone numbers, please refer to Service at [www.inficon.com](http://www.inficon.com).

### 6.2 Returning Your Instrument to INFICON

Do not return any component of the instrument to INFICON without first speaking with a Service Engineer.

Prior to returning the instrument, a Declaration of Contamination (DOC) online form will need to be completed. The online DOC form can be accessed at [www.inficon.com/service](http://www.inficon.com/service). All chemicals that have been analyzed by the HAPSITE ER should be reported on the DOC form in order for INFICON's service personnel to take the proper safety precautions when performing the repair.

Once the DOC has been received, the Customer Support Coordinator will provide shipping instructions and a Return Materials Authorization (RMA) Number, which signifies that INFICON has authorized the return.

If a laptop is purchased through INFICON, the laptop warranty is the responsibility of the customer and is not supported by INFICON.



Failure to follow these procedures will delay the repair of the instrument.

---

## 7 Introduction

### 7.1 System Description

HAPSITE ER Chemical Identification System is designed to identify and quantify volatile organic compounds from the parts-per-million (PPM) to the parts-per-trillion (PPT) level. HAPSITE ER is a portable unit that collects and analyzes samples in the field using self-contained gas canisters and a chemically maintained vacuum source, while operating on battery power. The HAPSITE ER system can be operated with the front panel touchscreen or with a laptop computer. Near real-time data will be displayed on the front panel touchscreen for immediate review.

### 7.2 Instrument and Accessories

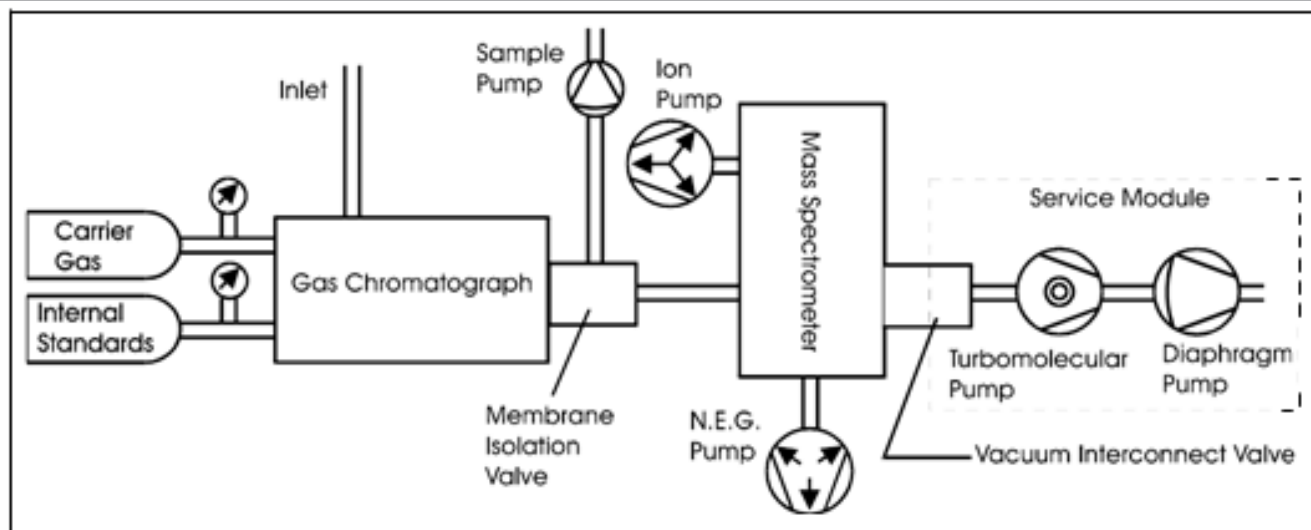
HAPSITE ER	Also known as the Analytical Module (AM). HAPSITE ER contains the Gas Chromatograph and Mass Spectrometer, a vacuum chemical pump for portable operation, control electronics, battery, gases, keypad, display, and a battery charger.
Air sampling probe	Consists of a hand-held sampling device, a heated inlet line, small display and buttons. The inlet line connects to HAPSITE ER and provides a flexible heated sample flow path.
Service module	Also known as the SM, consists of a turbo-molecular high-vacuum pump, roughing pump, battery-charger and power supply.
Headspace sampling system	Also known as the HSS, an accessory for the HAPSITE ER, used for testing volatile compounds in liquids and solids in vials.
SituProbe purge and trap system	SituProbe is a water sampling device that provides portable field testing of water samples without the need for vials.
Thermal desorber sampling system	Also known as the TDSS, an accessory for the HAPSITE ER, used for testing VOCs in air.
SPME sampling system	Solid phase microextraction (SPME) sampling system is a high sensitivity device used for in-situ testing of VOCs and SVOCs for quick, qualitative analysis with HAPSITE ER.

## 7.3 Specifications

Operating temperature range	5°C to 45°C (41°F to 113°F)
Dimensions (LxWxH)	46 cm x 43 cm x 18 cm (18 in. x 17 in. x 7 in.)
Weight	19 kg (42 lb) with battery
Battery life	Approximately 2 to 3 hours (using the Air Probe)
Power requirement	24 V(dc), 30 watts at normal operating conditions
Hard drive	16 GB internal storage
Flash drive	USB
Display	6.5 in. VGA color display with touch
Mass range	41-300 amu (1-300 using SIM)
Scan rate	up to 1000 amu/sec at 10 points per amu
Ionization mode	70 eV electron impact
Carrier gas	nitrogen
Column temperature range	45°C to 200°C (113°F to 392°F)
Maximum sample moisture content	90% Non-condensing
pH range of sample	2 to 11
Boiling point of sample (approx)	<270°C (<518°F)
Vapor pressure of sample (approx)	0.01-250 mmHg
GC column	5% diphenyl/95% dimethyl polysiloxane
SIM channels	up to 20 mass fragments
External communications	802.11G wireless or direct Ethernet

## 7.4 Instrument Overview

A diagram of the major HAPSITE ER components is shown below, including the pumps used to provide flow and vacuum. Service Module components are also identified. Service and HAPSITE ER Modules contain a Vacuum Interconnect Valve and electrical connectors through which vacuum systems join.



## 7.5 Description of Subsystems

HAPSITE ER combines two analytical techniques, gas chromatography and mass spectrometry, to separate and identify the organic components in a gas phase sample. The HAPSITE ER software also allows for the quantification of analytes.

HAPSITE ER is comprised of the following subsystems:

- Gas Chromatograph, see Gas Chromatograph [▶ 23]
- Mass Spectrometer, see Mass Spectrometer [▶ 24]
- Vacuum System, see Vacuum System [▶ 26]
- Electronic Systems, see Electronic Systems [▶ 27]
- Software systems, see Software Systems [▶ 27]

## 7.6 Gas Chromatograph

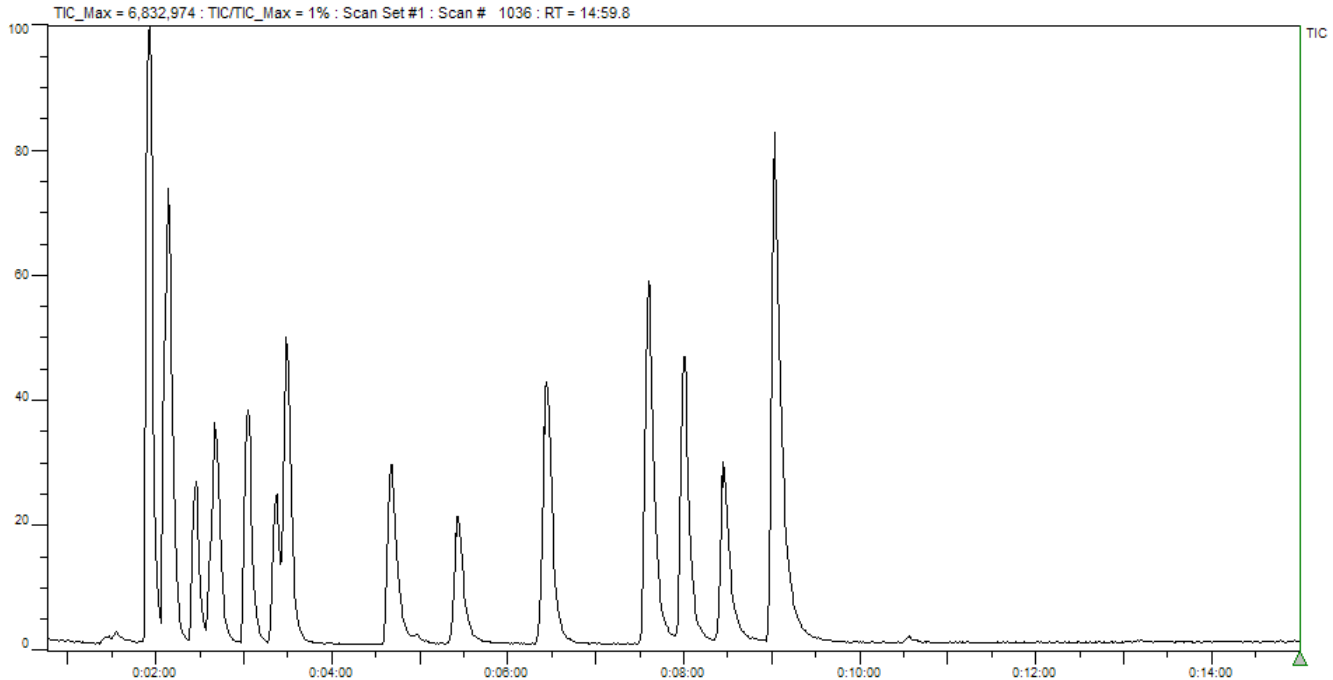
Gas Chromatograph (GC) performs a time separation of the sample compounds. The separation order is primarily based on the volatility of the sample components.

HAPSITE ER GC system utilizes nitrogen as the carrier gas to transport analytes through a column, of which the standard column is a narrow-bore fused silica tube 15 meters in length. The carrier gas is referred to as mobile phase. The inside of the column is coated with a thin layer of a material known as stationary phase.

The time needed by an individual compound to travel through the GC column to the detector is referred to as retention time (RT). If the GC conditions remain constant, the compound will elute from the column at the same retention time on every analysis.

HAPSITE ER uses internal standards to verify the performance of the Gas Chromatograph and Mass Spectrometer. The internal standard is composed of two volatile organic gases which are injected into the sample inlet flow. The internal standards' retention times and responses are used to ensure proper instrument performance.

A graph of eluting gases from the Gas Chromatograph is shown below. This graph is called a Total Ion Chromatogram (TIC) and is plotted as a function of time (x-axis) versus response (y-axis).



### 7.6.1 Membrane Isolation Valve

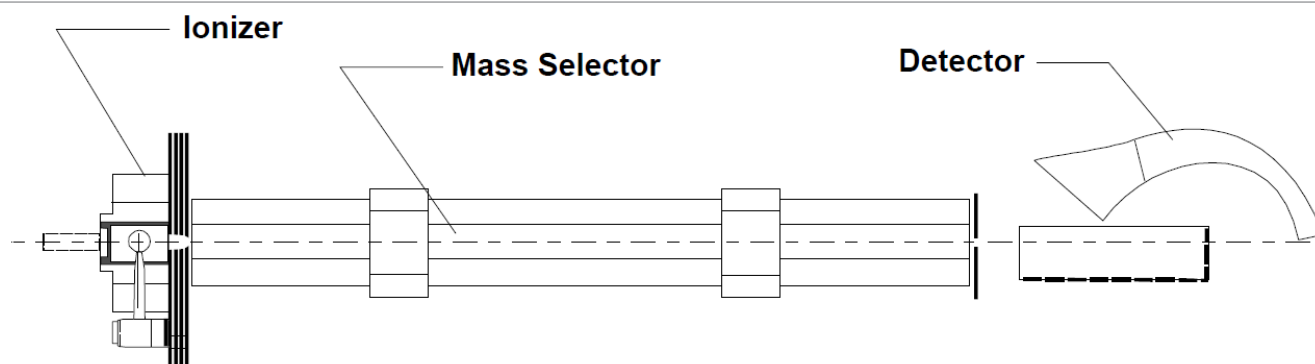
Gas eluting from the GC column passes through the membrane isolation valve. When the membrane isolation valve is opened, organic compounds are permitted to enter the Mass Spectrometer.

In the Survey mode of operation, in which air samples bypass the GC directly to the Mass Spectrometer, the sample pump draws the air sample directly across the membrane with the isolation valve in the open position.

## 7.7 Mass Spectrometer

The mass spectrometer is comprised of three basic physical systems: ionizer, mass selector, and ion detector. These are mounted together in a vacuum manifold which also includes: an inlet, two vacuum pumps, and a portion of the vacuum interconnect valve, as shown in the figure in Instrument Overview [▶ 22]. The figure below is a representation of the three sub-systems of the mass spectrometer.





The inlet flow from the membrane isolation valve is brought directly to the ionizer. Within the ionizer, the compound introduced from the inlet flow is subjected to a bombardment of electrons which are boiled off the hot filament. Collisions with the energetic electrons remove one electron from some of the gas molecules, leaving them with a net positive charge. This process is termed ionization. Other gas molecules are fractured into smaller molecules, some of which are also ionized. The remaining stream of gas is pumped away by the vacuum pump system.

The ionized molecules, or ions, are driven from the ionizer toward the mass selector by the different voltages on the ion volume and focusing plates. As the ions move through the orifices in these plates, the ions are formed into a nearly parallel beam of mixed ions of nearly the same energy.

The mass selector (or mass filter) is a quadrupole analyzer. The quadrupole analyzer is comprised of four parallel rods, mounted with precise alignment and spacing. Opposing rods are electrically connected together. The two pairs of rods are connected to a radio frequency (RF) voltage 180° out of phase with each other. In addition, the two pairs of rods have a direct current (DC) voltage applied to them; positive on one pair, negative on the other.

The ion beam is directed down the center of the array of rods. At any specific combination of RF and DC fields, some ions are light enough to oscillate harmonically with the RF field. This oscillation causes them to increase in energy and in speed until the ions impact one of the rods and are neutralized. The DC field acts upon the heavier ions resulting in their movement from the center towards the rods. Once on the rod, the heavier ion is neutralized. At a specific combination of RF and DC fields, ions of a specific mass will be able to transit the rod structure and emerge at the exit where detection occurs.

When the ions emerge from the mass selector, the ions are directed to the detector. The active element of the detector is an electron multiplier. The electron multiplier responds to the arrival of each individual ion with a cascade of electrons, each of which generates more electrons. The result is a small burst of electrical current in response to each ion emerging from the mass selector. The signal from the electron multiplier is connected to the electronic amplifier and data-handling system outside the vacuum.

In order to determine the constituents of the gas mixture, the ratio of RF to DC field strengths is varied (swept) to permit progressively heavier ions to transit the mass selector. The sweep, or scan, over the full range of masses (from 1 to 300 amu) only takes about 100 milliseconds; the scan is usually repeated multiple times to statistically improve the quality of the data. This scanning produces the mass spectrum, a plot of the partial pressure or intensity of each mass.

The mass spectrum of the unknown compound is compared to a library of mass spectra. The HAPSITE ER identifies the unknown compound based upon this comparison.

## 7.8 Vacuum System

The mass spectrometer is operated in a vacuum for several reasons.

- The ions must travel 0.3048 m (12 in.) from the ionizer through the quadrupole to the electron multiplier without colliding with another molecule (A collision would modify their trajectory and possibly their charge.)
- The sample gas must be free from interference from other unknown gases.
- The hot filament, which generates the electrons, would be destroyed if operated at atmospheric pressure in the presence of oxygen.

The vacuum is initially created by the turbo-molecular and diaphragm pumps in the Service Module. When a good vacuum is achieved, the pumps in HAPSITE ER are turned on and the vacuum interconnect valve is closed. At this point, the Service Module can be disconnected.

The two vacuum pumps of HAPSITE ER continue to provide the pumping necessary for operation. These two pumps are the non-evaporable getter (NEG) pump and the smaller sputter-ion pump. The NEG pump incorporates a special zirconium alloy, arranged in sintered disks, which aggressively adsorbs gas molecules when heated.

Over time, the sintered disks gradually become saturated with gas molecules, which causes the adsorption ability to drop. The instrument detects the resulting rise in operating pressure (loss of vacuum) and the software signals that the pump must be replaced.

The NEG pump can effectively remove active gases, but not noble gases. An ion pump is necessary to pump out noble gases, which would accumulate in the mass spectrometer. The accumulation would raise the mass spectrometer pressure and interfere with operation.

The turbomolecular pump in the Service Module is actually a compound pump, incorporating turbo molecular stages for high pumping speeds at low pressure, and molecular drag stages to provide good compression of the gas at higher pressures. However, even with drag stages, the turbo molecular pump is unable to exhaust gas into atmospheric pressure. An additional diaphragm roughing pump is provided for this purpose.

The diaphragm pump consists of four stages. The diaphragm pump draws the gas from the exhaust of the compound pump and sufficiently compresses exhaust gas in order to discharge the exhaust into the atmosphere.

## 7.9 Electronic Systems

The electronic systems in HAPSITE ER are considered in four groups:

<b>Mass Spectrometer Control</b>	The mass spectrometer control electronics include the programmable DC and RF power supplies for the mass selector, DC power supplies for the filament, electron multiplier, ion pump, and A/D converter for the signal from the electron multiplier.
<b>Gas Chromatograph Control</b>	The Gas Chromatograph (GC) control circuitry includes the power supplies for the solenoid valves, ovens and heated inlet line. It also controls the logic for all the valves and heaters of the GC system.
<b>Main Processor</b>	The main processor is supported by solid state memory and is located in the central electronics assembly. The main processor controls all the other electronic sub-assemblies for routine operation.
<b>Interfaces</b>	There are several input/output devices within HAPSITE ER. These include the front panel touchscreen, keypad and display, USB drive, crossover cable connection, wireless connection, probe, power and logic connections to the Service Module, HSS, SituProbe, TDSS, and SPME accessory.

## 7.10 Software Systems

HAPSITE ER operates with two software systems.

- Control software accepts inputs from the touchscreen, keypad and other interfaces. It commands the operation and sequencing of all systems and subsystems. The control software allows a method to be started from the front panel. Design or modifications of a method require the use of ER IQ™ software on an external laptop.
- Analysis software analyzes the data from the mass spectrometer, accesses the libraries as required, and displays the results of the analyses on the front panel.

Additionally, HAPSITE ER application software, ER IQ, is a Windows XP, Windows 2000, Windows 7, and Windows 10 based system for laptop use. ER IQ is used to design and modify methods, view data, analyze results, and generate reports. The laptop is linked to HAPSITE ER via a specific crossover cable or wireless connection. This linkage permits data and methods to be uploaded from HAPSITE ER. It also allows for new or modified methods to be downloaded to HAPSITE ER.



The specific Windows version supported is based on the specific HAPSITE ER hardware version and date of manufacture.

## 8 HAPSITE Components and Assemblies

### 8.1 Ship Kit Packing Lists

#### 8.1.1 930-850-G5, G6, G7, G8 Ship Kit Contents

The following items are provided in a typical 930-850-G5, G6, G7, G8 HAPSITE ER Ship Kit.

036-0015	Shoulder strap
074-290	Instruction sheet (shoulder strap)
059-0329	Quick disconnect stem
070-0972	Plunger contact (bag of 4)
074-490-P1	Quick use guide
074-5009-G1	Manual CD
074-5012-P2	Basic front panel training CD
600-1319-P2	Ethernet cable
930-021-G1	Gasket kit
930-022-G1	Tool kit
930-0221-G1	Concentrator nut and ferrule
930-0231-G1	Probe nut and ferrule
930-2020-G2	Decontamination cap plug kit
930-4652-P1	Permanent marker
930-612-P1	USB flash drive
930-251-G1	Tenax Concentrator Kit
930-705-G1	Sample Loop Kit

Ship Kit	Location	Cord
930-850-G5	USA	N/A
930-850-G6	Europe	068-0151
930-850-G7	UK	068-0388
930-850-G8	Australia	068-0393

Extra Cords for SM and Battery Charger (Qty. 2)



930-470-G1 battery charger

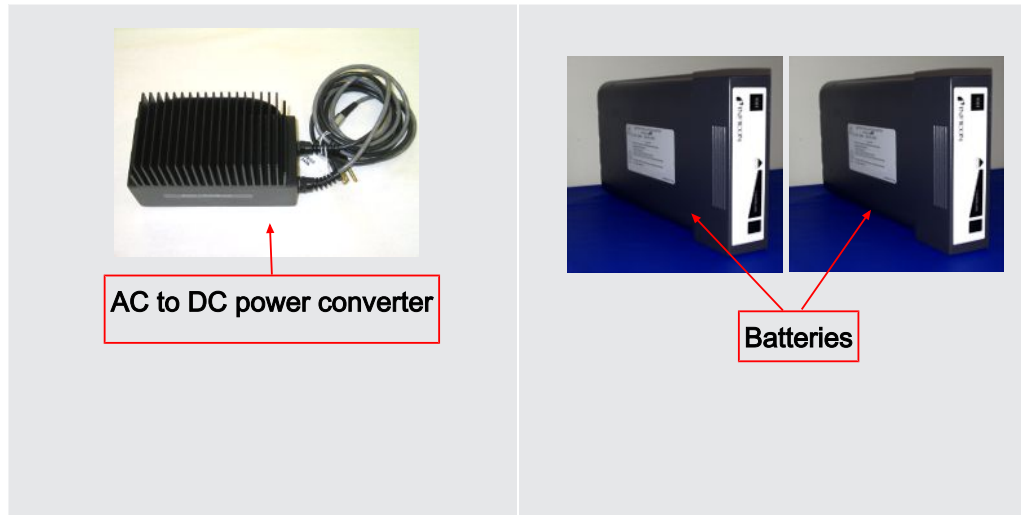


24 V power supply (see table below)

Power Supply	Ship Kit	Usage
930-469-P1	930-850-G5	110 V USA
930-469-P2	930-850-G6	230 V European
930-469-G3	930-850-G7	230 V UK
930-469-G4	930-850-G8	230 V Australia



In two separate boxes, HAPSITE battery (930-4062-G1)



A laptop computer and its accessories will be shipped. The ship kits for the laptops will vary; the items in the laptop ship kit are based upon the type of laptop ordered. The laptop kits will include the ER IQ Software CD and NIST Library Install CD.

## 8.2 Basic Assembly



### ⚠ CAUTION

**HAPSITE ER must be operated a minimum of every 3 weeks.  
Recommended storage is in Extended Standby.**



### 8.2.1 Attaching the Probe

The probe attaches on the top of HAPSITE ER. The probe has two connections: a LEMO® communication line and a Valco connector.

- 1 Remove the silver LEMO port cap from the HAPSITE ER by pulling it outwards. Store the port cap for future use.



- 2 Unscrew the Valco connector port cap. Store the port cap for future use.



- 3 Align the red dots on the LEMO communication line with the red dots on the port. Insert the line into the port.



- 4 Insert the Valco connector into the top of the HAPSITE ER. Screw the Valco connector into place.



**Save all of the port caps for further use. These caps are necessary when decontaminating HAPSITE ER. Spare caps are provided in the Ship Kit.**

## Installing the Gas Canisters



## 8.2.2

**⚠ CAUTION**

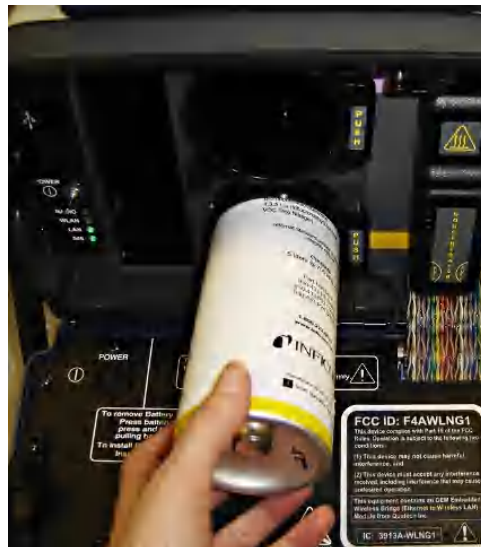
Do not open the front panel in a contaminated area.

The carrier and internal standard gas canisters must be installed inside HAPSITE ER prior to sampling. Follow the instructions below to install the gas canisters into the spring-loaded slots inside the unit.

- 1 Open the panel by placing thumbs on the top of panel and pulling downwards. This technique avoids damaging the sealing gasket with fingernails.



- 2 Insert a yellow banded internal standard canister into the bottom round opening. This opening is marked with a yellow stripe.



- 3 Press the PUSH lever while inserting the standard canister.



- 4 Once inserted, press in the canister and PUSH lever together, then release the PUSH lever.



- 5 Gently pull on the internal standard canister outwards. It should remain fastened inside the HAPSITE ER.



**⚠ CAUTION**

Closing the front panel when the canisters are not properly installed may damage the HAPSITE ER and/or canisters.

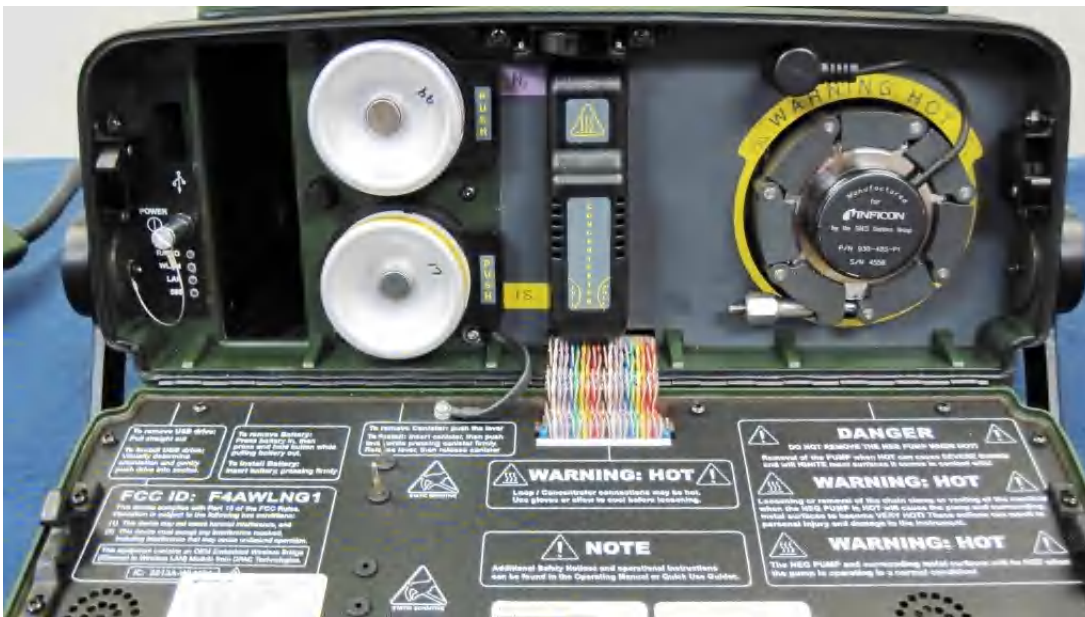
- 6 Insert a purple banded carrier gas canister into the bottom round opening. This opening is marked with a purple stripe.



- 7 Press the PUSH lever while inserting the carrier gas canister.



8 Once inserted, release the PUSH lever.



9 Gently pull the carrier gas canister outwards. It should remain fastened inside HAPSITE ER.

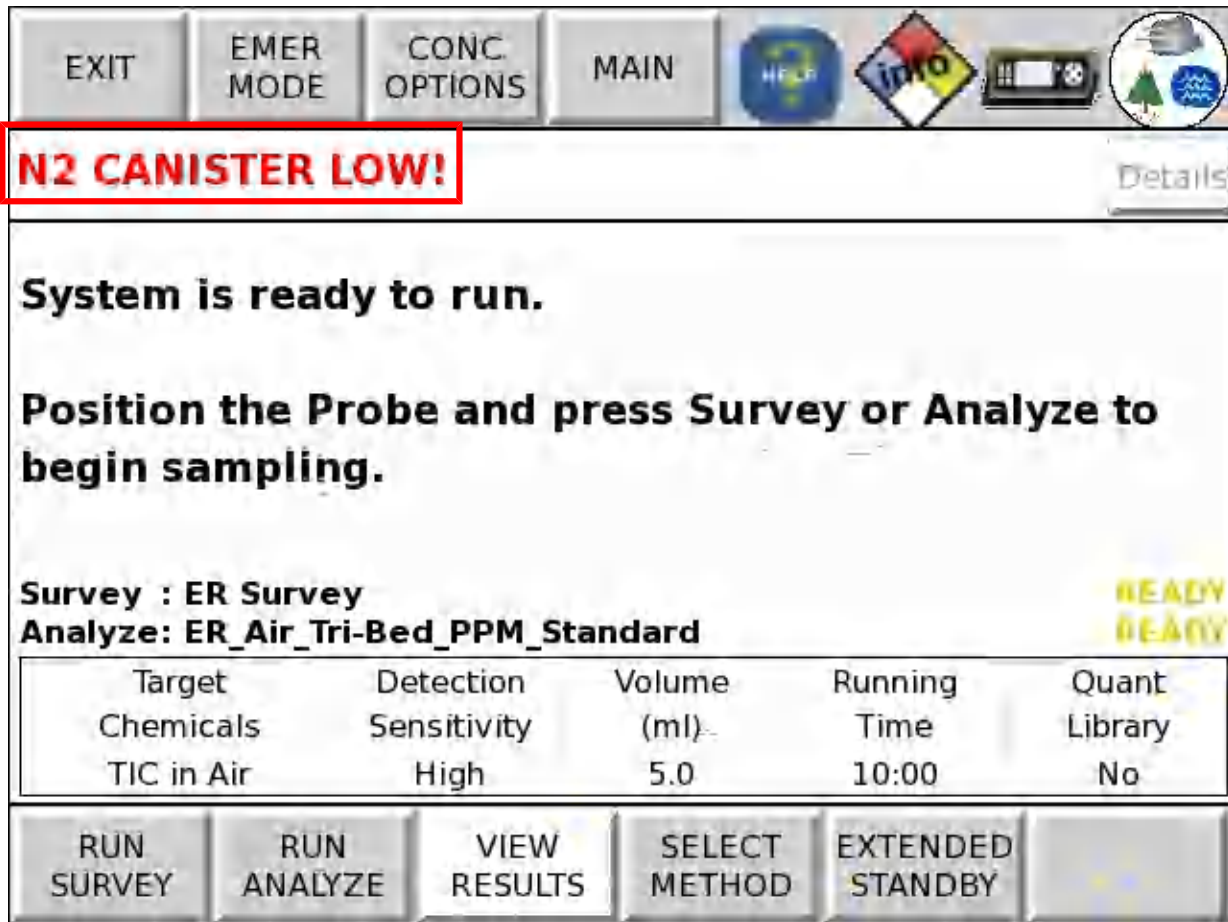


The position of the gas canisters should not be interchanged. To prevent improper placement, the internal standard canister has a Teflon® ring which surrounds the inner stem on the top of the can. Do not force the canisters into the wrong location as this will contaminate and/or damage HAPSITE ER.



### 8.2.3 How to Remove a Gas Canister

Removing the gas canisters is advised when HAPSITE ER has been placed into Extended Standby. Also, the gas canister will need to be replaced when the canister is low. A low canister warning will be displayed on the front panel when the canister needs replacement. Follow the instructions below to remove a gas canister.



- ▶ Press the PUSH lever located to the right of the canister.



- ⇒ The canister will release.



► Remove the canister.



The carrier gas canister will need to be replaced after approximately 12 hours of use. The internal standard canister will need to be replaced after 3 days of continuous use. These numbers are guidelines and will vary.



**⚠ WARNING**

**Do not refill canisters.**

Bodily injury may result. Canisters are designed to be disposable and may fail if filling is attempted.

A slight twist on the canister may be required.



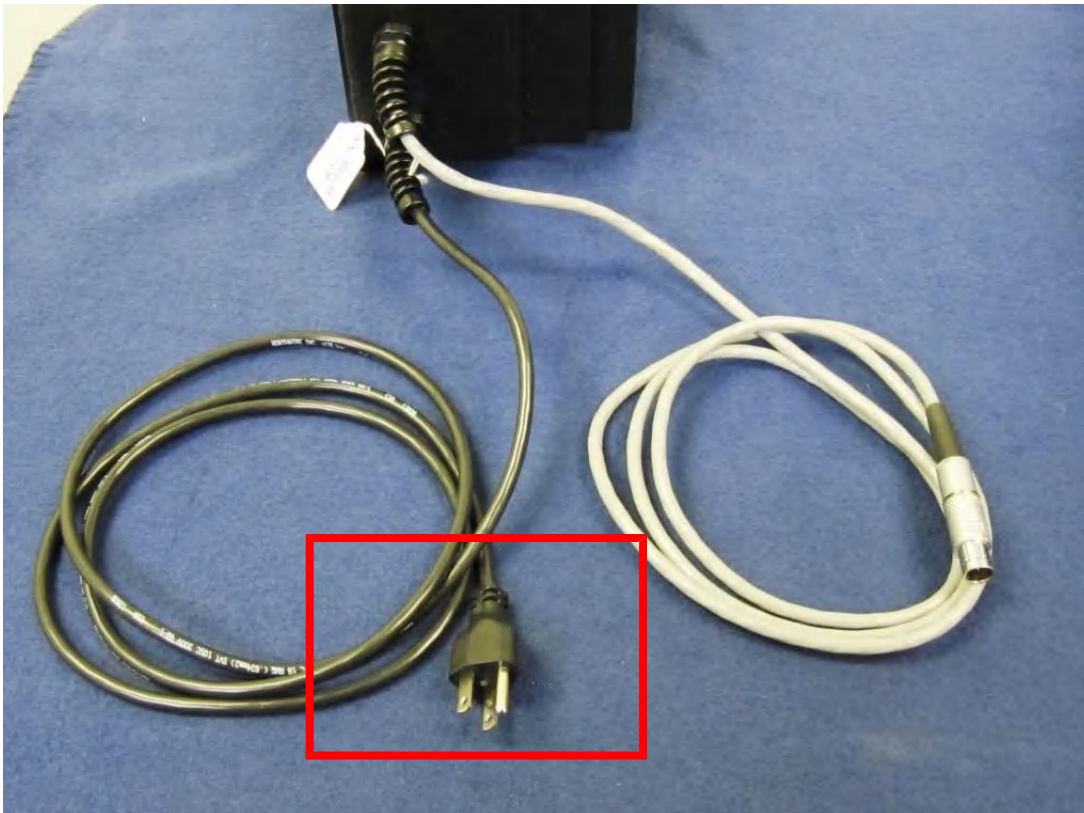
### CAUTION

Closing the front panel when the canisters are not properly installed may damage HAPSITE ER and/or canisters.

## 8.2.4 Connect the Power Supply

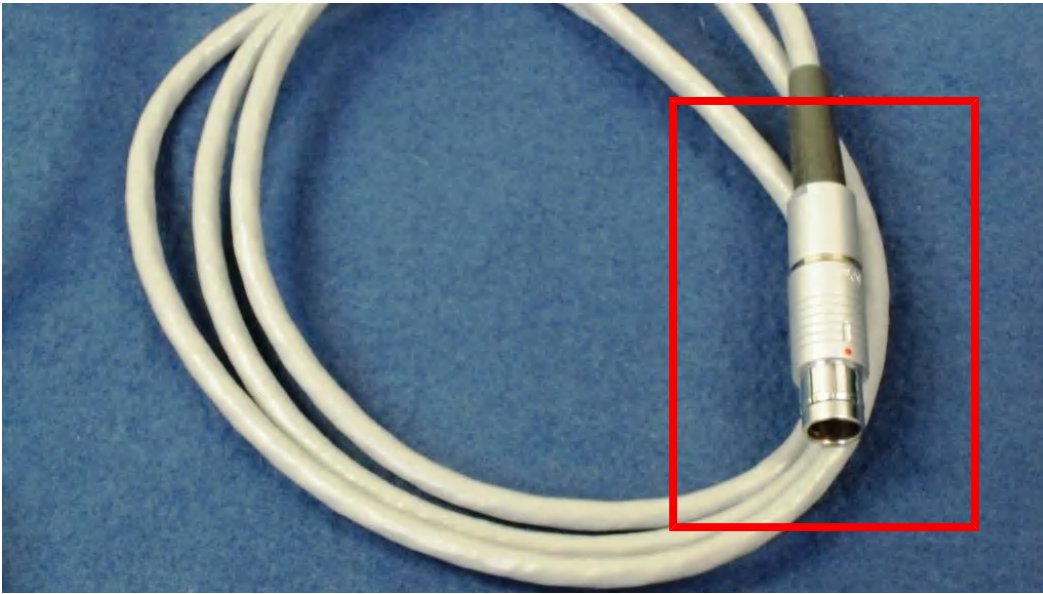
HAPSITE ER uses an AC to DC power converter power supply. This power supply connects to HAPSITE ER and a power outlet.

- 1 The connection with the black cord if fitted with a standard power plug. Plug this cord into a power outlet.

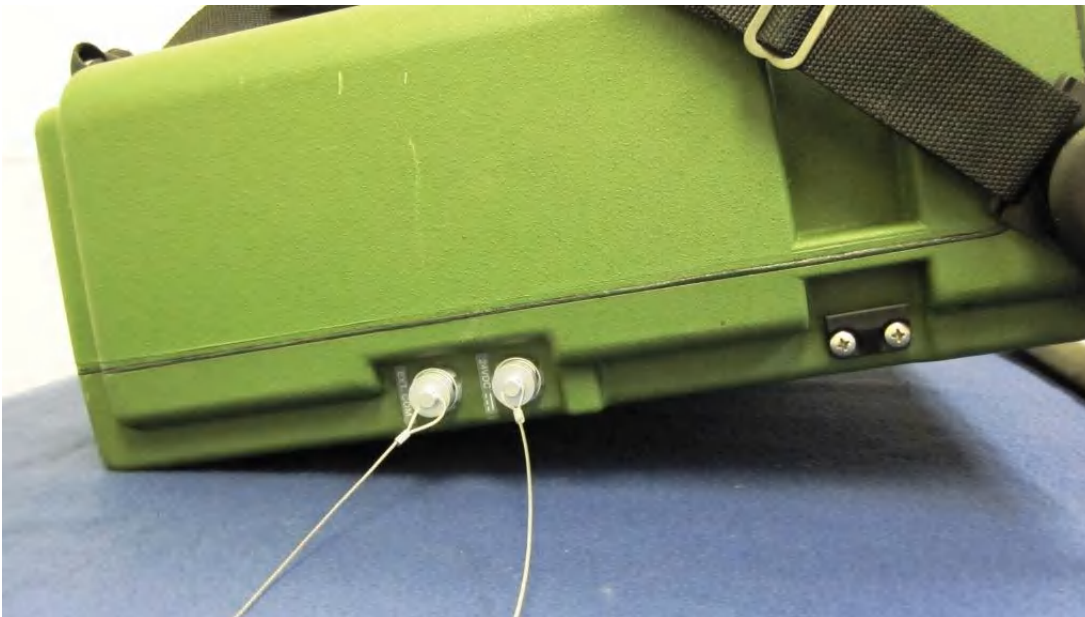


- 2 The connection with the gray cord is fitted with a LEMO connection. When facing the front panel, this cord will plug into the left side of HAPSITE ER.





- 3 Remove the silver plugs from HAPSITE ER . Store the plugs for future use. These plugs will be necessary when decontaminating the unit.



- 4 Align the red dots on the LEMO connection with the red dots on HAPSITE ER. Insert the connection into the power port.



## 8.2.5 Connecting the Laptop

has two possible configurations for connecting a laptop computer:

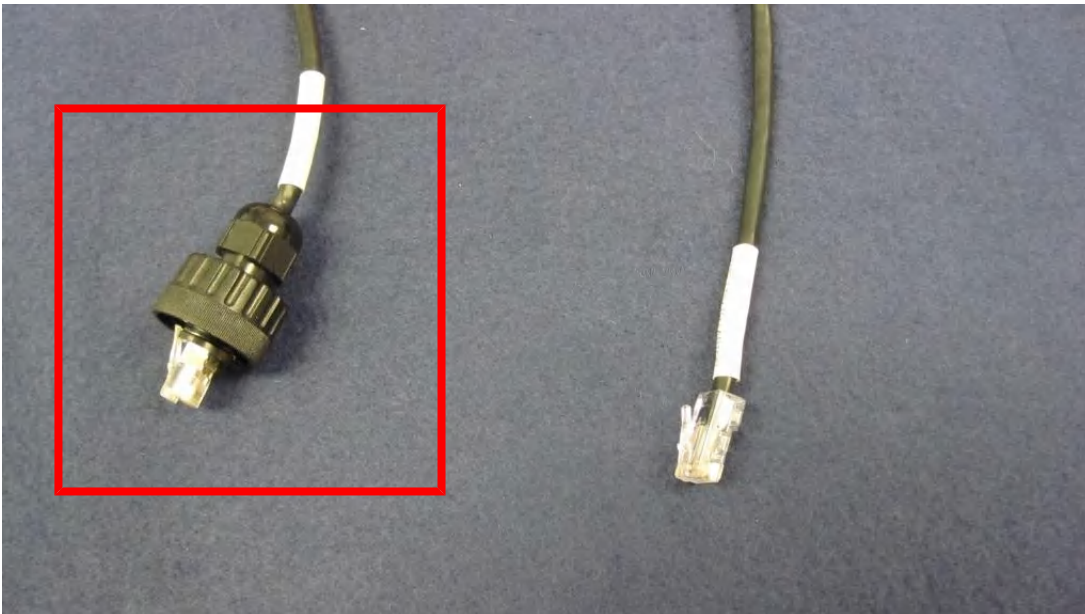
- via the black crossover cable
- via the wireless connection

### 8.2.5.1 Connect the Laptop with the Black Crossover Cable

- 1** Unscrew the cap on the port which is located on the top, left side of HAPSITE ER.



- 2 The crossover cable has two ends. One end has a screw top on the modular connector. This end connects to HAPSITE ER.



- 3 Plug the modular connector with the screw top into the HAPSITE ER port. Screw the plug into place.



4 Plug the opposite end into the laptop.



⇒ Once connected, the crossover cable communication between HAPSITE ER and laptop computer is enabled.

### 8.2.5.2 Connect Laptop with Wireless Connection

Refer to Communications and Touch Screen Options [▶ 110] for information on enabling the wireless connection.

To troubleshoot or set up communications for a new laptop, see Connecting the Laptop [▶ 42].

## 8.3 Battery

The battery provides power to HAPSITE ER when portability is desired. Under optimum conditions, the battery has a two hour life. The battery can be charged using the battery charger. Alternately, it can be charged in the HAPSITE ER when it is connected to external power. However, the battery will charge more slowly when charging inside HAPSITE ER.

### 8.3.1 Battery Charger

The auxiliary battery charger (part number 930-470-G1) uses AC power to charge up to three HAPSITE ER batteries in 15 hours or less.



#### **⚠ CAUTION**

**The battery charger is not sealed against moisture, debris, or contamination.**

The battery charger operates from a range of normal AC voltages from 100 to 230 V(ac). It will continue to operate without internal damage at a voltage as low as 90 V(ac) and as high as 253 V(ac). The frequency can be from 50 to 60 Hz. The battery charger draws 120 W when fully loaded.

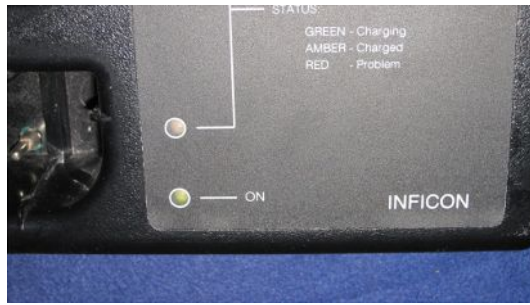
The battery charger is designed for indoor use at ambient temperatures from 5°C to 35°C (41°F to 95°F). The battery charger is not designed for exposure to contaminants, as it cannot be decontaminated.

### 8.3.2 Battery Charger Connections and Startup

- 1 Plug the power cord into the connector at the right rear of the battery charger.



- 2 Plug the battery charger into a grounded outlet.
  - ⇒ The **ON** indicator on the battery charger illuminates. The battery charger does not have a power switch.



- ⇒ As the battery charger performs a self-test, all the indicators turn amber.
- ⇒ The indicators for the empty receptacles then turn green. If a receptacle contains a battery, its indicator turns red.
- ⇒ All lights except for the **ON** indicator will extinguish. No further warm-up is required, it is ready to charge batteries.

### 8.3.3 Loading the Battery Charger

The battery charger receptacles are identical and batteries in any state of charge can be loaded.

- ▶ Place the discharged battery into one of the charging receptacles.



- ⇒ The respective indicator will turn green and charging will commence immediately.



#### **⚠ CAUTION**

**Do not use excessive force when placing battery in the battery charger.**



**⚠ CAUTION**

**Do not charge batteries in a moving vehicle.**

### 8.3.4 Understanding the Battery Charger Indicators

Each battery receptacle is associated with an indicator light which can be illuminated in the colors listed below.

Green	The battery is being charged. If a battery with a severely depleted charge is inserted, the green light will flash. If it flashes for more than 10 minutes, the battery will not accept a charge and should be replaced. The actual state of the battery charge can be assessed by using the <b>TEST</b> button on the battery. A fully discharged battery will charge in approximately 15-20 hours.
Amber	The battery is fully charged. The rate of charge has been reduced to a maintenance level. Remove the battery when fully charged.
Red	The receptacle and/or the battery, if one is installed, is experiencing a problem. A flashing red light indicates that the charger cannot communicate with the battery.
Off	The receptacle is ready to charge a battery. If the indicator remains extinguished when a battery is inserted, the battery is severely depleted. In this case, leave the battery in the receptacle and unplug the power cord. Reconnect the power cord and the battery will start to charge.

After achieving a full charge, the battery should be removed from the charger and stored until needed.

#### 8.3.4.1 Testing Battery

- ▶ To test a battery, press the **TEST** button on the end of the battery.



- ⇒ In the elongated triangle, green lighted numbers will be displayed. The highest illuminated number indicates the remaining percentage of battery charge, which is reported in 20% increments.



**If OVER is illuminated, the battery is fully charged.**

### 8.3.5 Installing the Battery

- 1 Insert a fully charged battery by sliding it into the rectangular opening to the left of the gas canisters. The battery should be inserted with the release arrow pointing towards the release button.



- 2 Push firmly and listen for the battery to click into place.



- 3 Once in place, gently pull the battery outwards to ensure that the battery is securely fastened.

### 8.3.6 Removing the Battery

- 1 Firmly push in the battery until a faint click is heard.



- 2 Push in the **Release** button, the black round button to the right of the battery.





- 3 Pull the battery out of its compartment while pressing the release button.



### CAUTION

Do not expose the battery compartments to rain or other foreign material. Ensure that the area is dry and contaminant-free before opening the front panel.

## 8.4 Helpful Guidelines

DON'T...	DO...
<ul style="list-style-type: none"> <li>• Don't leave batteries installed on battery charger for more than 24 hours.</li> <li>• Ship with a battery installed.</li> <li>• Draw liquid into the instrument.</li> <li>• Go into a potentially explosive environment without an LEL meter and safety checks. HAPSITE ER is not intrinsically safe.</li> <li>• Pressure wash HAPSITE ER or immerse in water.</li> <li>• Sample strong acids (below pH 2) or strong bases (above pH 11).</li> <li>• Use force when assembling any HAPSITE ER system components.</li> <li>• Modify default methods without changing their name.</li> <li>• Sample for Sulfur Mustard (HD) with the VX conversion tube installed.</li> <li>• Abort and Analyze (GC/MS) method during a sample run.</li> <li>• Over-tighten the concentrator nuts.</li> <li>• Block the exhaust vent on HAPSITE ER.</li> <li>• Use the NEG pump and Service Module pumps together.</li> <li>• Use expired internal standard gas.</li> <li>• Attach a bag sample without first checking the ferrules in the probe nut.</li> </ul>	<ul style="list-style-type: none"> <li>• Run a background blank once per week or more.</li> <li>• Use Extended Standby instead of powering off HAPSITE ER.</li> <li>• Place appropriate caps over openings before decontaminating.</li> <li>• Use 5% to 10% bleach solution or local SOP to decontaminate HAPSITE ER.</li> <li>• Only use thumbs to open the front panel.</li> <li>• Attempt to reboot as a first step to troubleshooting operational problems.</li> <li>• Screen samples with the Survey method to reduce the risk of saturation.</li> <li>• Use the VX conversion tube for identification (and quantification) of VX and R-33.</li> <li>• Take a training course.</li> <li>• Contact INFICON at reachus@inficon.com, +1.315.434.1100 for help.</li> </ul>

## 9 Operate the Instrument in Portable Mode

### 9.1 Start HAPSITE ER in Portable Mode

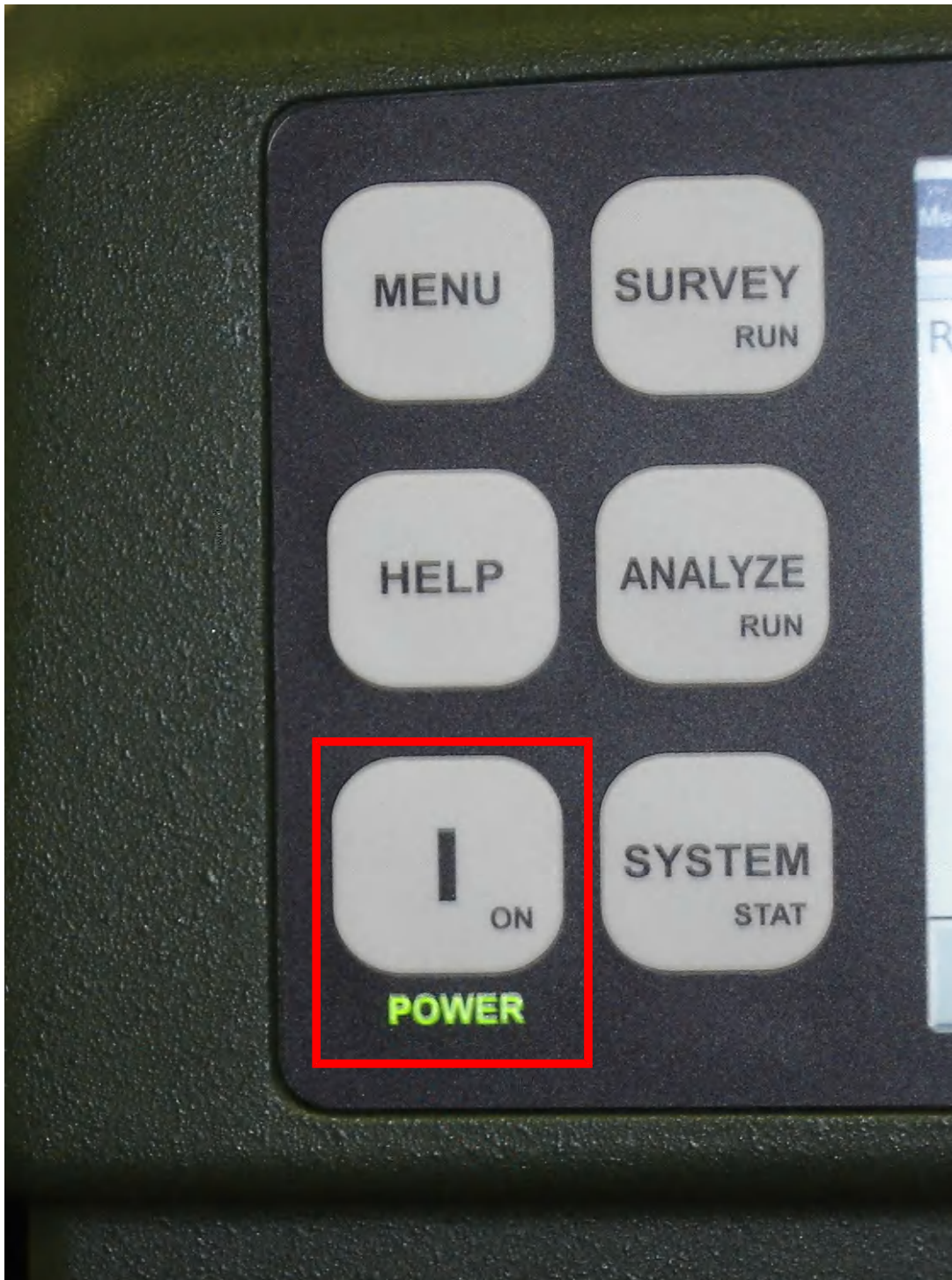
Portable mode refers to using HAPSITE ER without the laptop computer.

**Required Materials:**

- HAPSITE ER (analytical module)
- internal standard gas canister
- carrier gas canister
- charged battery
- AC to DC power converter power supply
- probe

**Procedure:**

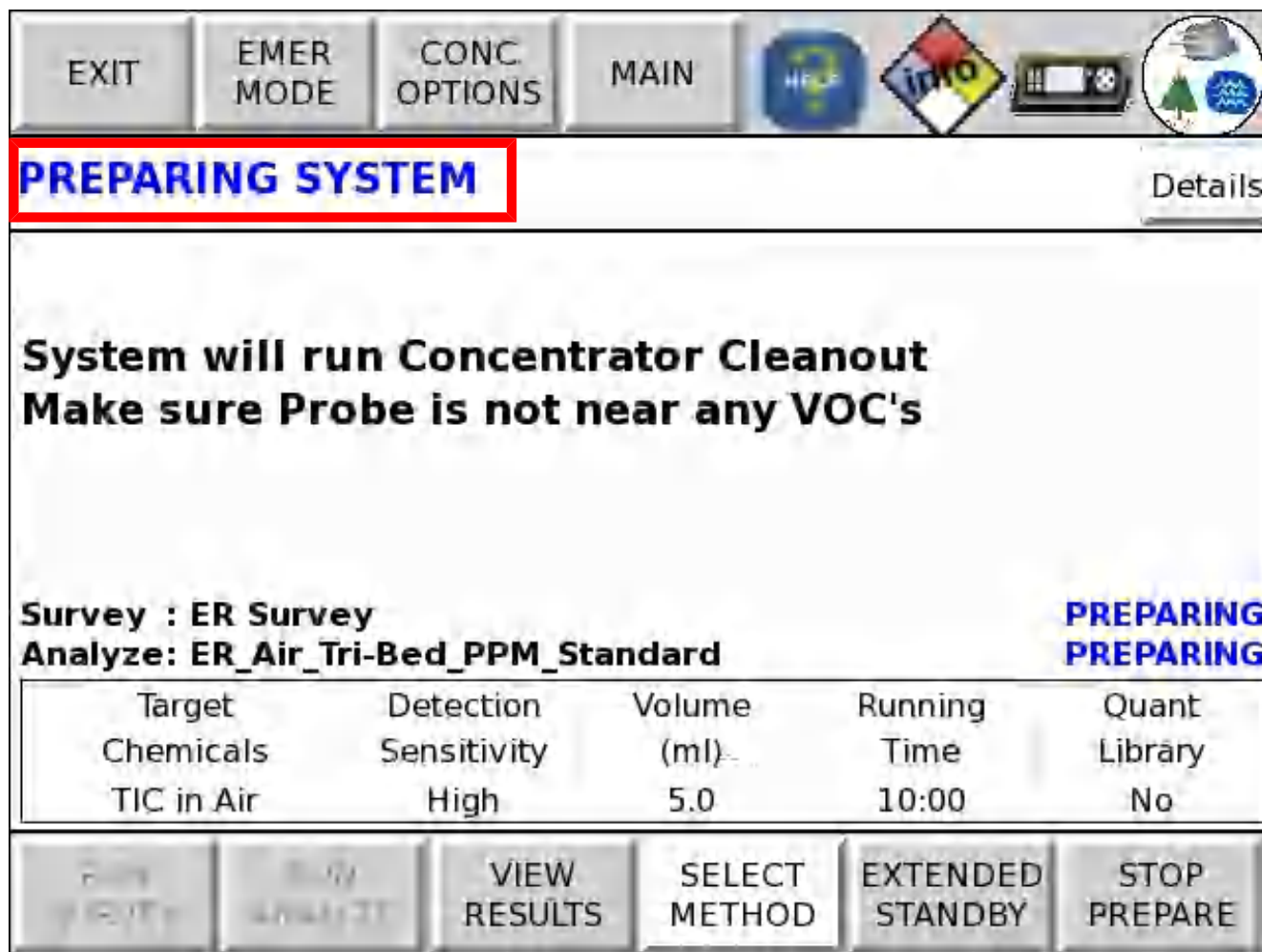
- 1 Assemble HAPSITE ER as shown in Basic Assembly [▶ 30].
- 2 Press the **POWER** button on the front panel. The word **POWER** illuminates. Powering on HAPSITE ER takes one to two minutes.



**Power on HAPSITE ER while connected to AC power. Using battery power to turn on and heat HAPSITE ER will consume over 40% of the battery's charge.**

- 3 HAPSITE ER boots in approximately one minute and senses which sample configuration (for example, concentrator) has been installed. It begins to prepare the default method for this sample configuration.

- 4 HAPSITE ER begins to prepare various components. These components include heating the HAPSITE ER and accessory heaters, running AutoTune, powering the NEG, and if necessary, running a concentrator cleanout.
- 5 During the preparation period, the front panel displays the **PREPARING SYSTEM** message. Depending upon the chosen default method, this screen may show **PREPARING ANALYZE** or **PREPARING SURVEY**. This message occurs when the methods have different temperature setpoints.



- 6 To view the preparation details' progress, touch the **Details** button.

**PREPARING SYSTEM** Details

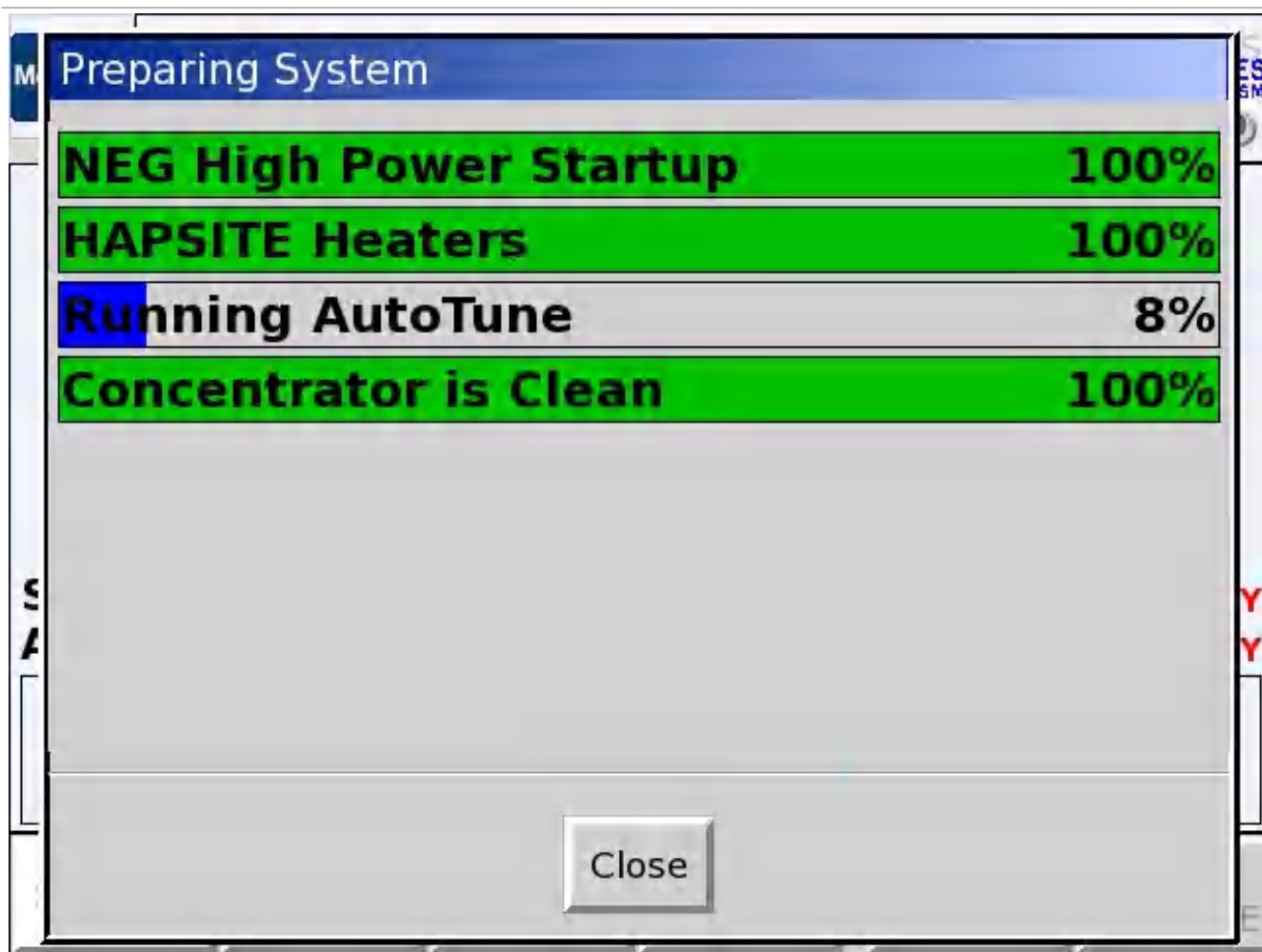
**System will run Concentrator Cleanout  
Make sure Probe is not near any VOC's**

**Survey : ER Survey** **PREPARING**  
**Analyze: ER\_Air\_Tri-Bed\_PPM\_Standard** **PREPARING**

Target	Detection	Volume	Running	Quant
Chemicals	Sensitivity	(ml)	Time	Library
TIC in Air	High	5.0	10:00	No

VIEW RESULTS    SELECT METHOD    EXTENDED STANDBY    STOP PREPARE

- The progress of the preparation is shown by a bar graph. If a component is in the process of being prepared, it is shown in blue. When a component is ready, it is shown in green. If a component is going to be prepared, but the preparation process has not started, it is shown in yellow. If the system is not ready, the items that need to be prepared is shown in red.







- 8 When the heating sequence is completed, the software checks the mass spectrometer tune and automatically makes any necessary adjustments. The automatic tune adjustment is called AutoTune. If AutoTune fails, see Performing Manual Tune [▶ 283].
- 9 As part of the preparation, a concentrator cleanout occurs when the concentrator is installed. This cleanout heats the concentrator to 180°C to remove residue. The cleanout occurs when the unit has been turned on, taken out of **Extended Standby**, the concentrator has been changed, or the concentrator has been saturated.



**A concentrator cleanout can also be skipped, although skipping the concentrator cleanout is not recommended and may lead to poor results.**

- 10 Hold the probe in a clean environment for the duration of the cleanout. If the concentrator cleanout is not successful, see Concentrator Cleanout Failure [▶ 69].
- 11 When HAPSITE ER is ready to run samples, a green **SYSTEM READY**, **SURVEY READY**, or **ANALYZE READY** message displays.

EXIT   EMER MODE   CONC OPTIONS   MAIN      

**ANALYZE READY** Details

**Analyze is ready to run.**

**Position the Probe and press Survey or Analyze to begin sampling.**

**Survey : ER Survey01** **NOT READY**  
**Analyze: ER\_Air\_Tri-Bed\_PPM\_Standard** **READY**

Target	Detection	Volume	Running	Quant
Chemicals	Sensitivity	(ml)	Time	Library
TIC in Air	High	5.0	10:00	No

PREPARE SURVEY   RUN ANALYZE   VIEW RESULTS   SELECT METHOD   EXTENDED STANDBY



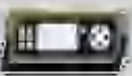



EXIT

EMER  
MODE

CONC  
OPTIONS

MAIN

SYSTEM READY

Details

**System is ready to run.**

**Position the Probe and press Survey or Analyze to begin sampling.**

**Survey : ER Survey**

**Analyze: ER\_Air\_Tri-Bed\_PPB\_Standard**

READY

READY

Target	Detection	Volume	Running	Quant
Chemicals	Sensitivity	(ml)	Time	Library
TIC in Air	High	100.0	10:00	No

RUN  
SURVEY

RUN  
ANALYZE

VIEW  
RESULTS

SELECT  
METHOD

EXTENDED  
STANDBY



If the methods have different temperature setpoints, the method that has been prepared to run will have a green READY message next to the method name.

12 If SURVEY READY is displayed, touch RUN SURVEY or push SURVEY RUN.

The screenshot shows the instrument's main menu. At the top, there are several buttons: EXIT, EMER MODE, CONC OPTIONS, MAIN, a blue globe icon, a yellow diamond icon with 'info', a cassette tape icon, and a circular icon with a tree and water. Below these buttons, the text 'SURVEY READY' is displayed in green. To the right of this text is a 'Details' button. The main display area contains the following text:

**Survey is ready to run.**

**Position the Probe and press Survey or Analyze to begin sampling.**

Survey : ER Survey01 READY  
 Analyze: ER\_Air\_Tri-Bed\_PPM\_Standard NOT READY

Target	Detection	Volume	Running	Quant
Chemicals	Sensitivity	(ml)	Time	Library
TIC in Air	High	5.0	10:00	No

At the bottom of the screen, there are several buttons: RUN SURVEY (highlighted with a red box), PREPARE ANALYZE, VIEW RESULTS, SELECT METHOD, EXTENDED STANDBY, and a blank button.

- 13 If ANALYZE READY is displayed, touch RUN ANALYZE or push ANALYZE RUN.

The screenshot shows the instrument's main menu. At the top, there are buttons for 'EXIT', 'EMER MODE', 'CONC OPTIONS', and 'MAIN'. To the right are icons for a globe, 'info', a cassette tape, and a circular environmental icon. Below this is a green banner that says 'ANALYZE READY' with a 'Details' button on the right. The main display area contains the text: 'Analyze is ready to run. Position the Probe and press Survey or Analyze to begin sampling.' Below this, it shows 'Survey : ER Survey01' and 'Analyze: ER\_Air\_Tri-Bed\_PPM\_Standard'. To the right of this text, 'NOT READY' is written in red and 'READY' is written in green. A table below shows parameters: Target Chemicals (TIC in Air), Detection Sensitivity (High), Volume (ml) (5.0), Running Time (10:00), and Quant Library (No). At the bottom, there are buttons for 'PREPARE SURVEY', 'RUN ANALYZE' (highlighted with a red box), 'VIEW RESULTS', 'SELECT METHOD', and 'EXTENDED STANDBY'.



If the system is preparing a SURVEY run and an ANALYZE method is desired, touch the PREPARE ANALYZE button. Likewise, if an ANALYZE method is being prepared and a SURVEY is desired, touch the PREPARE SURVEY button.

### 9.1.1 Emergency Mode (EMER MODE)

In an emergency, the concentrator cleanout can be bypassed to allow for faster startup. This is not recommended for everyday use. While Emergency Mode is active, the concentrator cleanout will continue to be skipped until Emergency Mode is exited. To place the system into Emergency Mode:

- 1 Touch **EMER MODE** while the **PREPARING SYSTEM** message is displayed.

**EXIT** **EMER MODE** **CONC OPTIONS** **MAIN**

**PREPARING SYSTEM** Details

**System will run Concentrator Cleanout  
Make sure Probe is not near any VOC's**

**Survey : ER Survey** **PREPARING**  
**Analyze: ER\_Air\_Tri-Bed\_PPM\_Standard** **PREPARING**

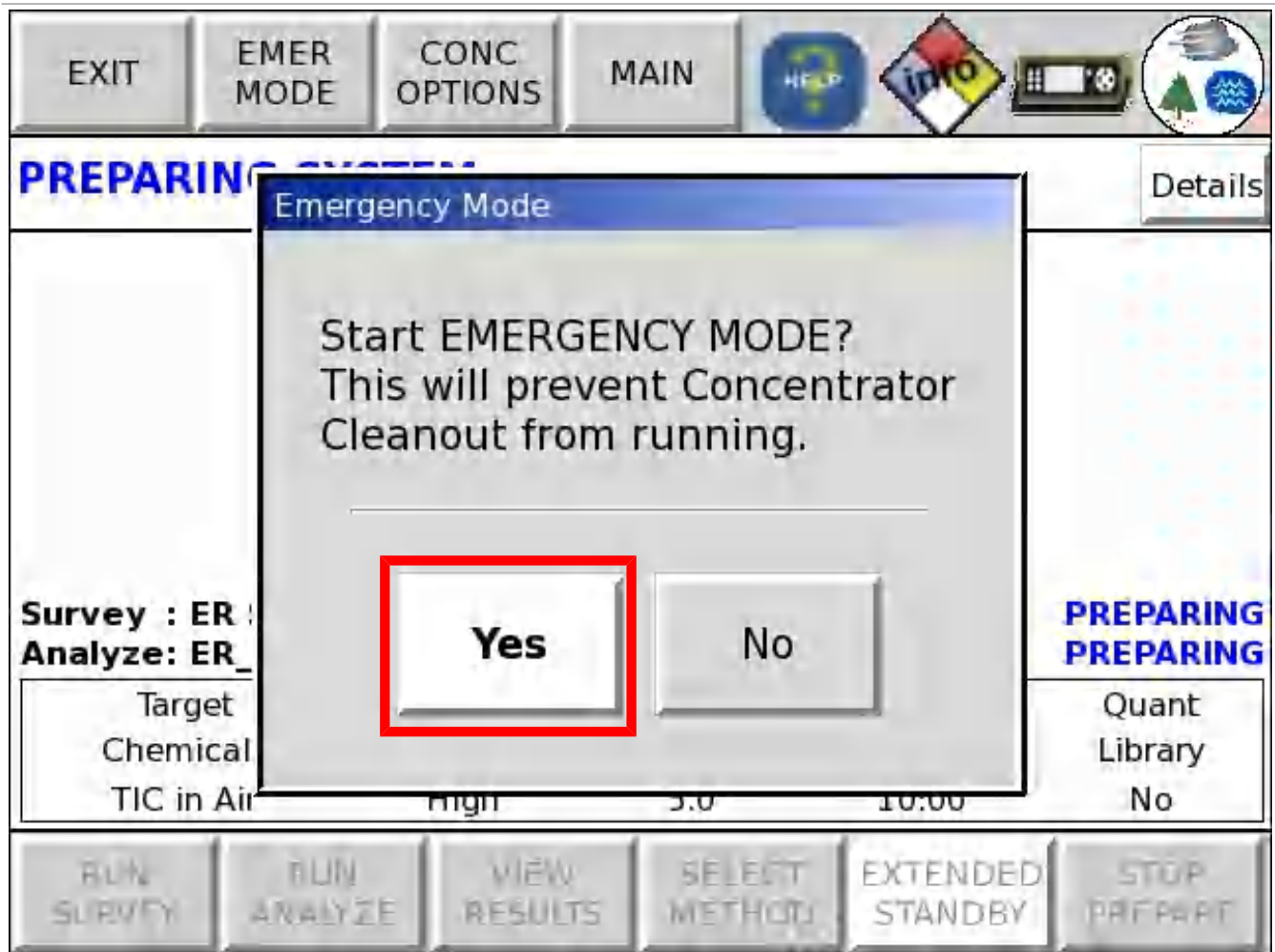
Target Chemicals	Detection Sensitivity	Volume (ml)	Running Time	Quant Library
TIC in Air	High	5.0	10:00	No

**VIEW RESULTS** **SELECT METHOD** **EXTENDED STANDBY** **STOP PREPARE**

- Alternately, use the arrow keys to highlight the **EMER MODE** button and push **OK SEL**.



- A confirmation message will be displayed. Touch **Yes** or push **OK SEL** to continue.



4 The **EMER MODE** button will turn red when Emergency Mode is activated.

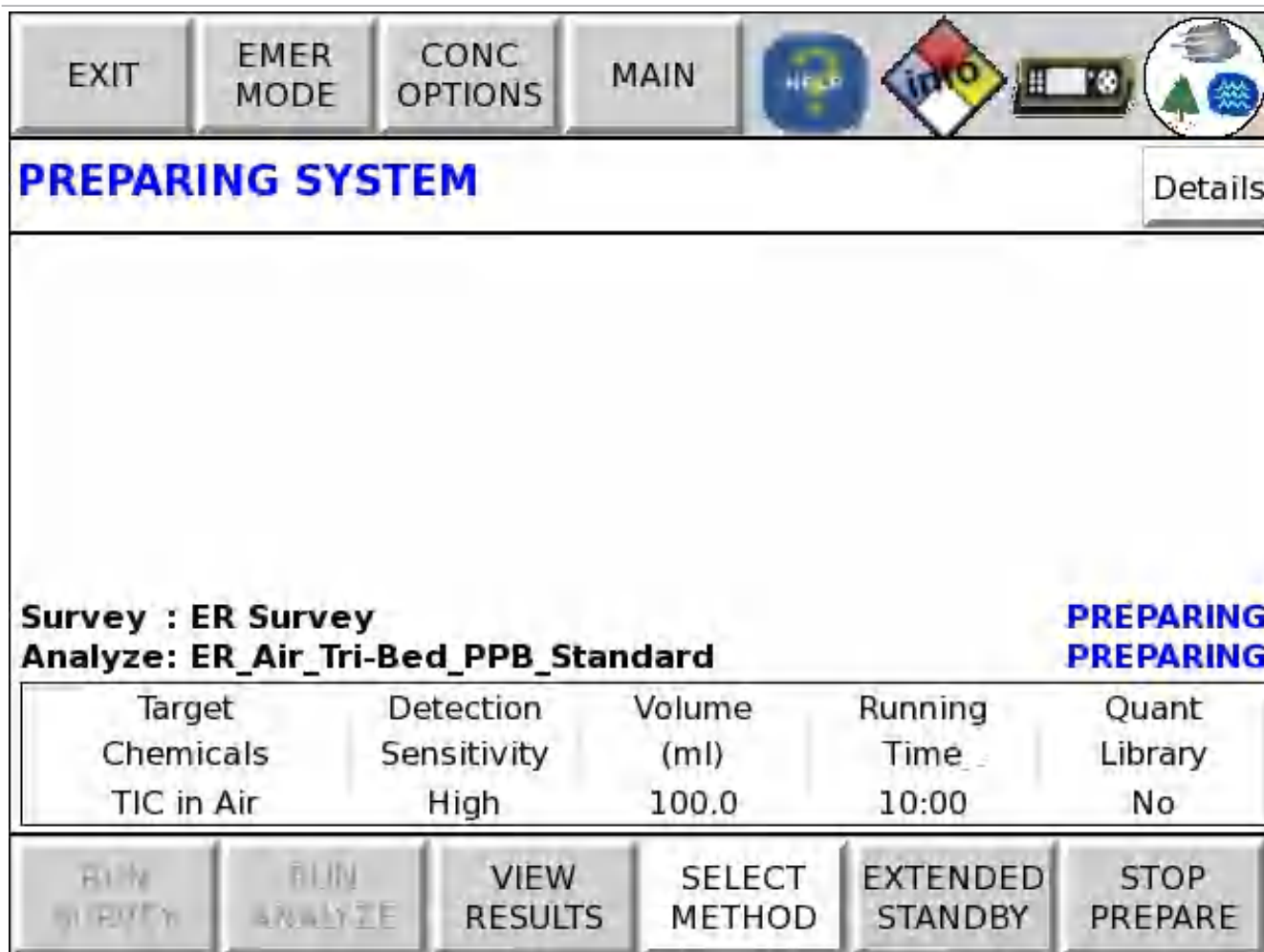
**PREPARING SYSTEM** Details

**Survey : ER Survey** **PREPARING**  
**Analyze: ER\_Air\_Tri-Bed\_PPM\_Standard** **PREPARING**

Target	Detection	Volume	Running	Quant
Chemicals	Sensitivity	(ml)	Time	Library
TIC in Air	High	5.0	10:00	No

RUN SURVEY RUN ANALYZE VIEW RESULTS SELECT METHOD EXTENDED STANDBY STOP PREPARE

- 5 To exit Emergency Mode, touch the **EMER MODE** button. Alternately, use the arrow keys to highlight the **EMER MODE** button and push **OK SEL**. The **EMER MODE** button will turn gray.



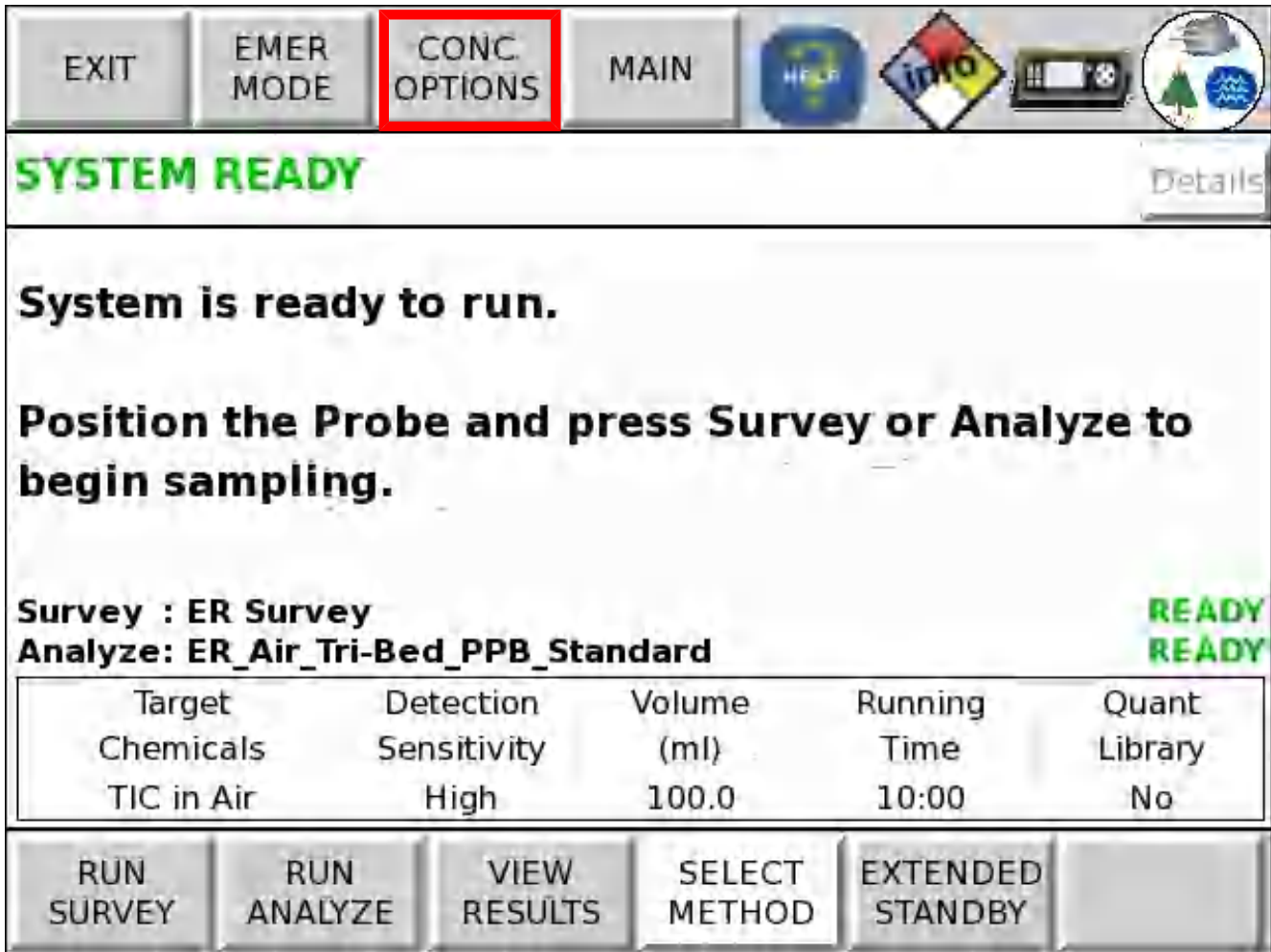
- 6 The HAPSITE ER will run a concentrator cleanout and prepare for general (non-emergency) use. See Start HAPSITE ER in Portable Mode [ 51].

### 9.1.2 Concentrator Options (CONC OPTIONS)

The **CONC OPTIONS** button has two selections: **Concentrator Cleanout** and **Skip Conc Cleanout**. When **Concentrator Cleanout** is selected, the HAPSITE ER will run a manual cleanout. When **Skip Conc Cleanout** is selected, HAPSITE ER will bypass the concentrator cleanout once while the HAPSITE ER is preparing.

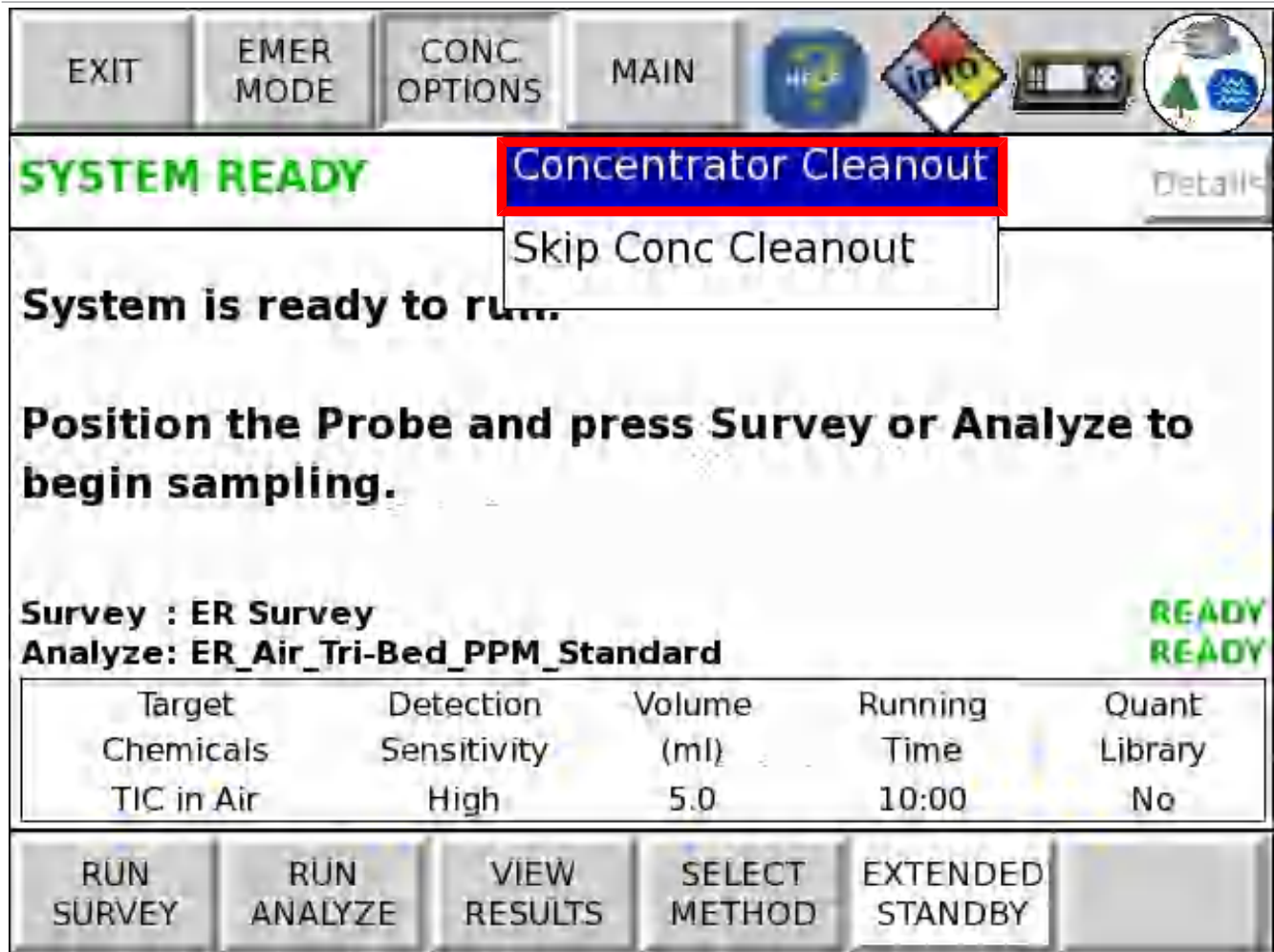
#### 9.1.2.1 Concentrator Cleanout

- 1 Touch **CONC OPTIONS** or use the arrow keys to highlight the **CONC OPTIONS** button and push **OK SEL**.

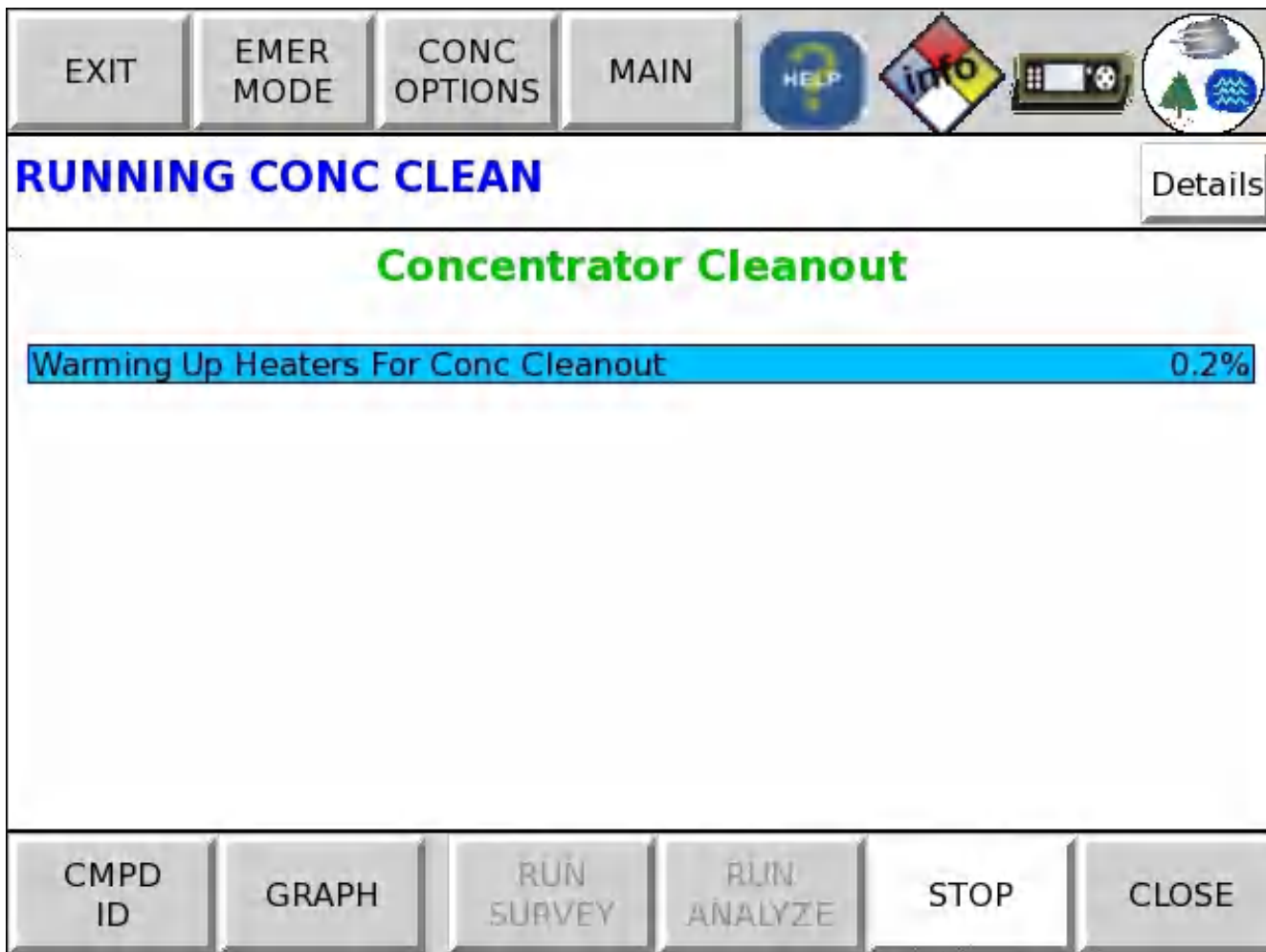


- 2 Touch **Concentrator Cleanout** or highlight **Concentrator Cleanout** using the arrow keys. Push **OK SEL**.

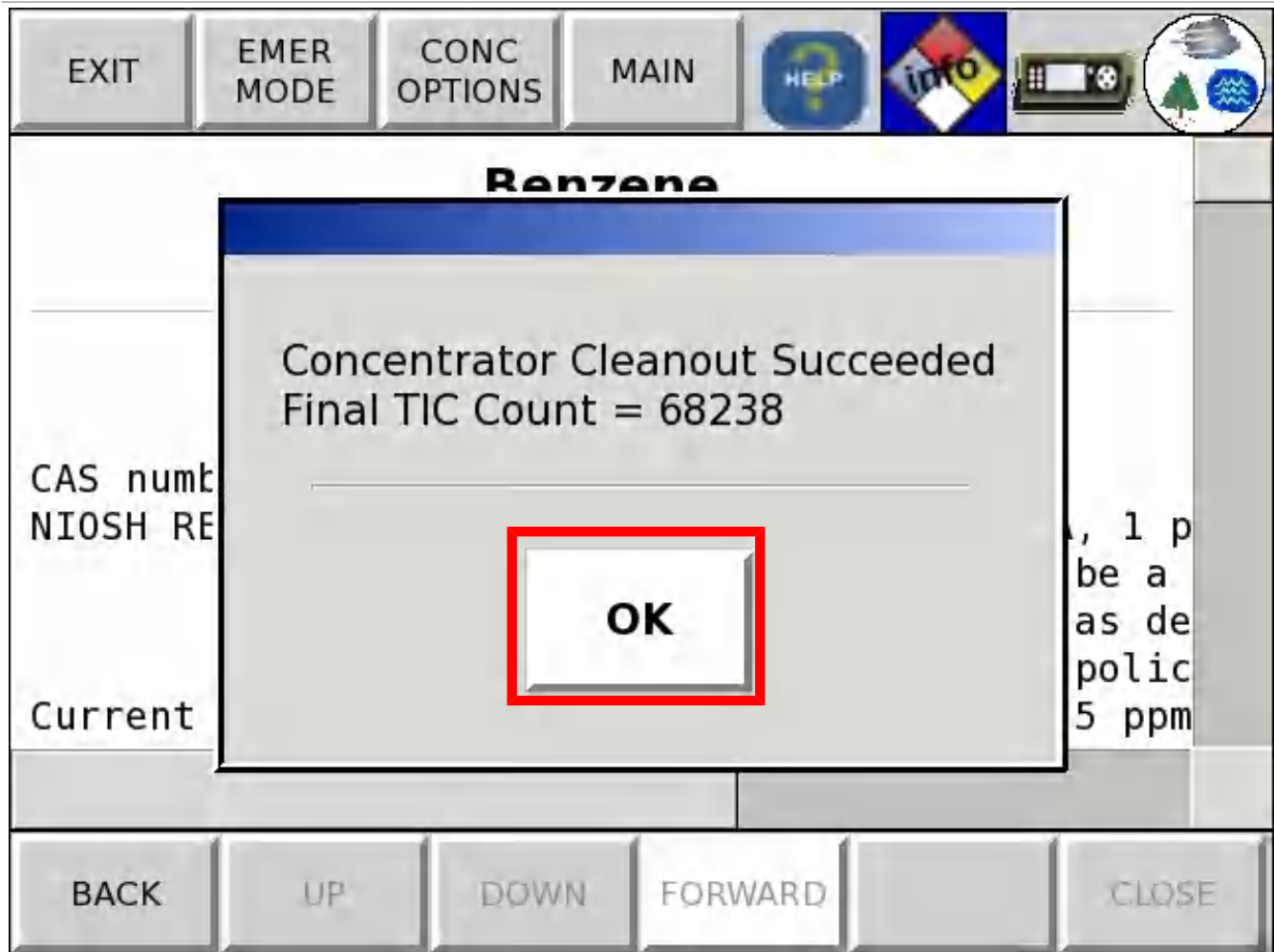




⇒ The HAPSITE ER will run a concentrator cleanout.



- 3 When the cleanout is successful, the **Concentrator Cleanout Succeeded** message will be displayed along with the final TIC. Push **OK** to exit the screen.



### 9.1.2.2 Skip Cleanout

- 1 Touch **CONC OPTIONS** or use the arrow keys to highlight the **CONC OPTIONS** button and push **OK SEL**.

**PREPARING SYSTEM** Details

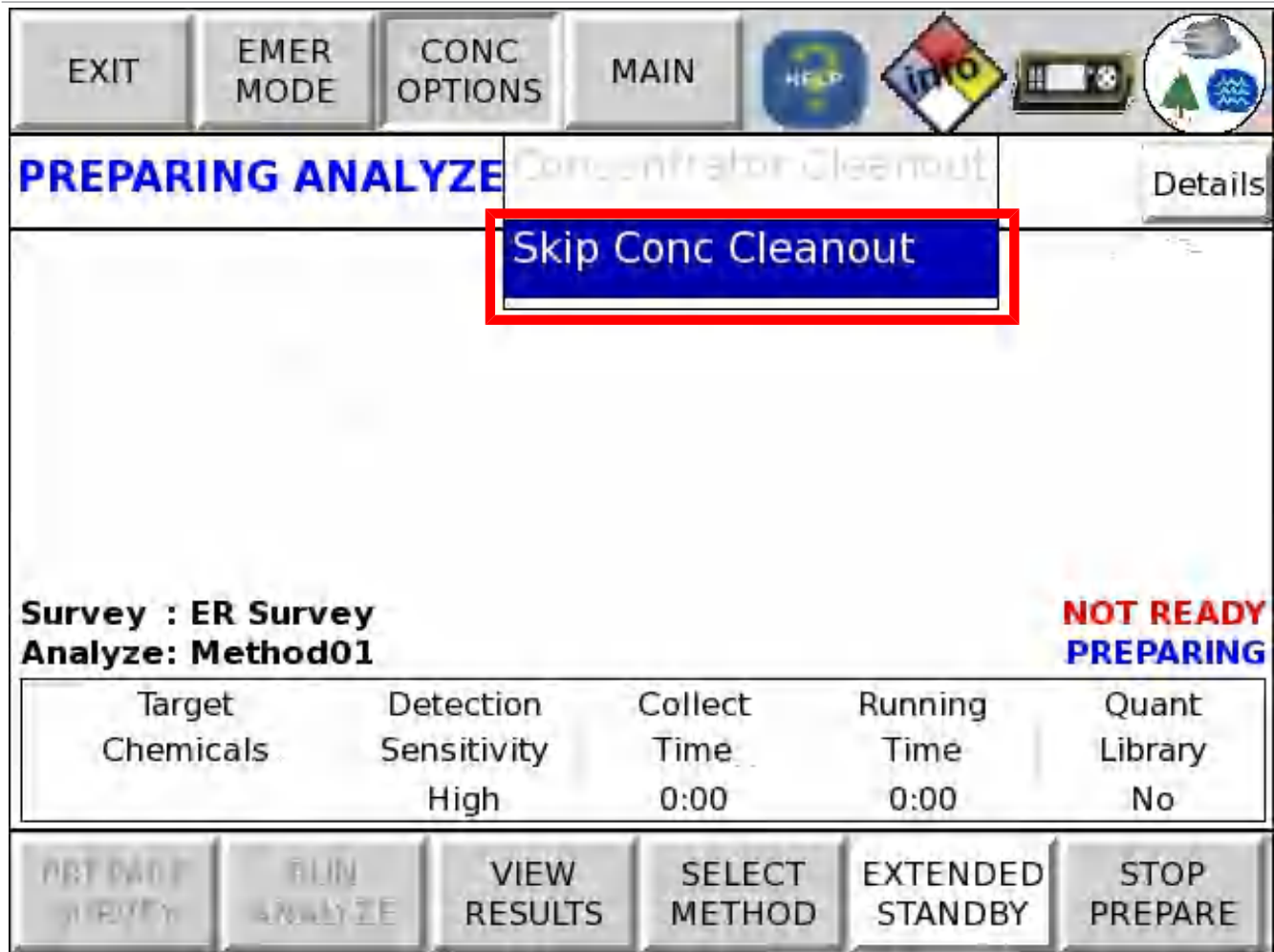
**System will run Concentrator Cleanout  
Make sure Probe is not near any VOC's**

**Survey : ER Survey** **PREPARING**  
**Analyze: ER\_Air\_Tri-Bed\_PPM\_Standard** **PREPARING**

Target	Detection	Volume	Running	Quant
Chemicals	Sensitivity	(ml)	Time	Library
TIC in Air	High	5.0	10:00	No

SKIP CLEANOUT VIEW RESULTS SELECT METHOD EXTENDED STANDBY STOP PREPARE

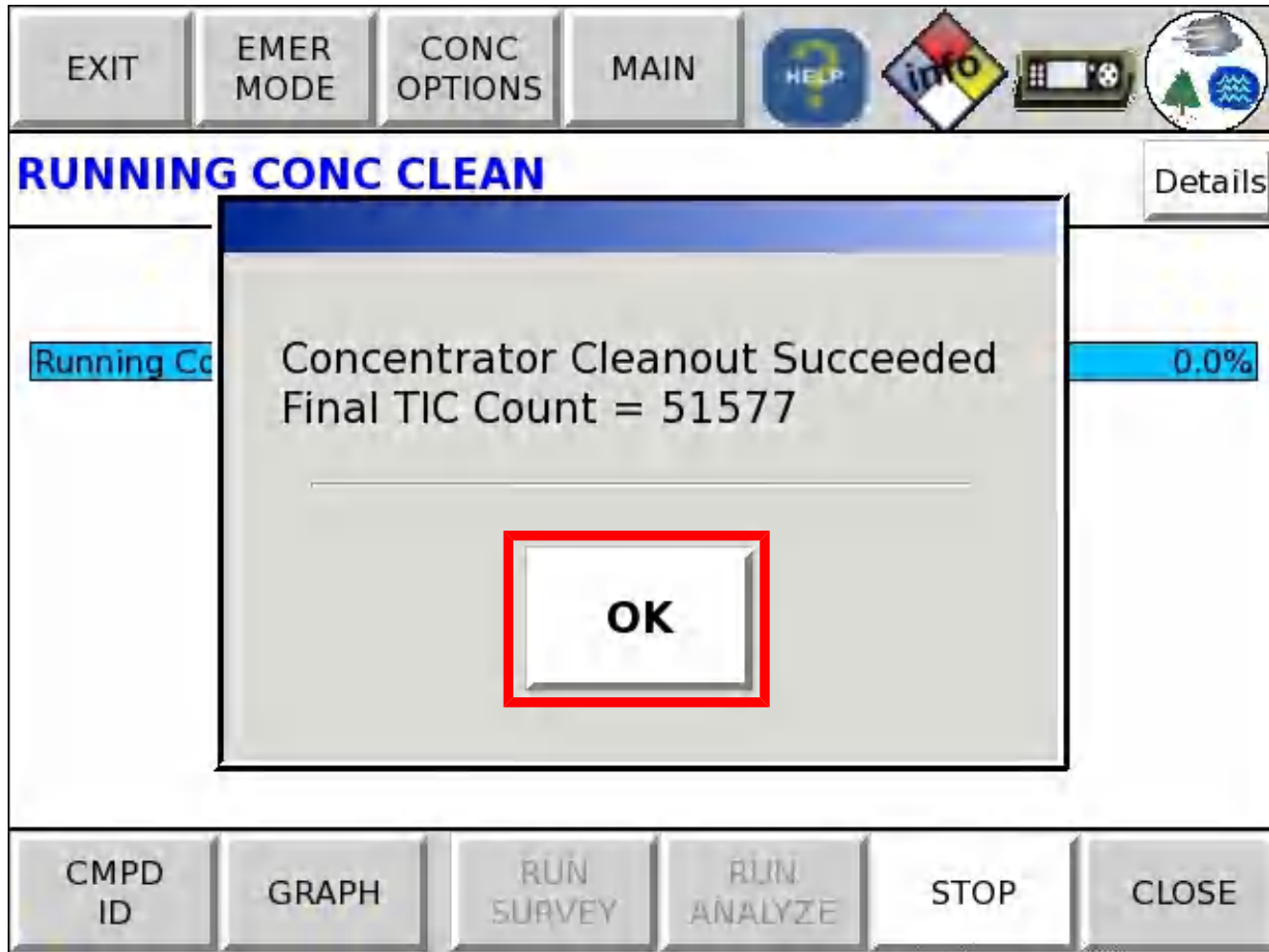
- 2 Touch **Skip Cleanout** or highlight **Skip Cleanout** using the arrow keys. Push **OK SEL.**



⇒ The system will not run a cleanout as part of its preparation.

### 9.1.3 Concentrator Cleanout Failure

If the concentrator cleanout is successful, the screen will display the final TIC.



If the concentrator cleanout is unsuccessful, the screen will display a concentrator cleanout failed message. See the instruction below for cleanout options.

- 1 Touch **Retry** to start another concentrator cleanout sequence.
- 2 Touch **Skip** to start running a concentrator Analyze method.
- 3 Touch **Abort** to return to the Main Screen.



If **Abort** is touched, HAPSITE ER will show that the **SYSTEM IS NOT READY**.

- 4 HAPSITE ER will re-run the cleanout as part of its preparation.
- 5 If the failure box appears again, check the concentrator to verify that it is not cracked or chipped. Also, try re-installing the concentrator to ensure that it is not properly seated.

## 9.1.4 Quick Reference SOP- Heat-up and Tune

### CAUTION

Do not open the front panel in a wet or contaminated area.

- 1 Insert the internal standard and carrier gas canisters.
- 2 Insert a charged battery.
- 3 Connect the AC to DC power converter power supply.
- 4 Verify that the appropriate sample configuration (i.e., concentrator) is installed.
- 5 Press the **POWER** button on the front panel.
- 6 HAPSITE ER will heat the necessary components and perform AutoTune. A prompt to run **SURVEY** or **ANALYZE** will appear when HAPSITE ER is ready to run a sample.
- 7 If the default method is not the desired method, touch **STOP PREPARE**.
- 8 Touch **SELECT METHOD**. Highlight the desired method. Touch **SELECT**.



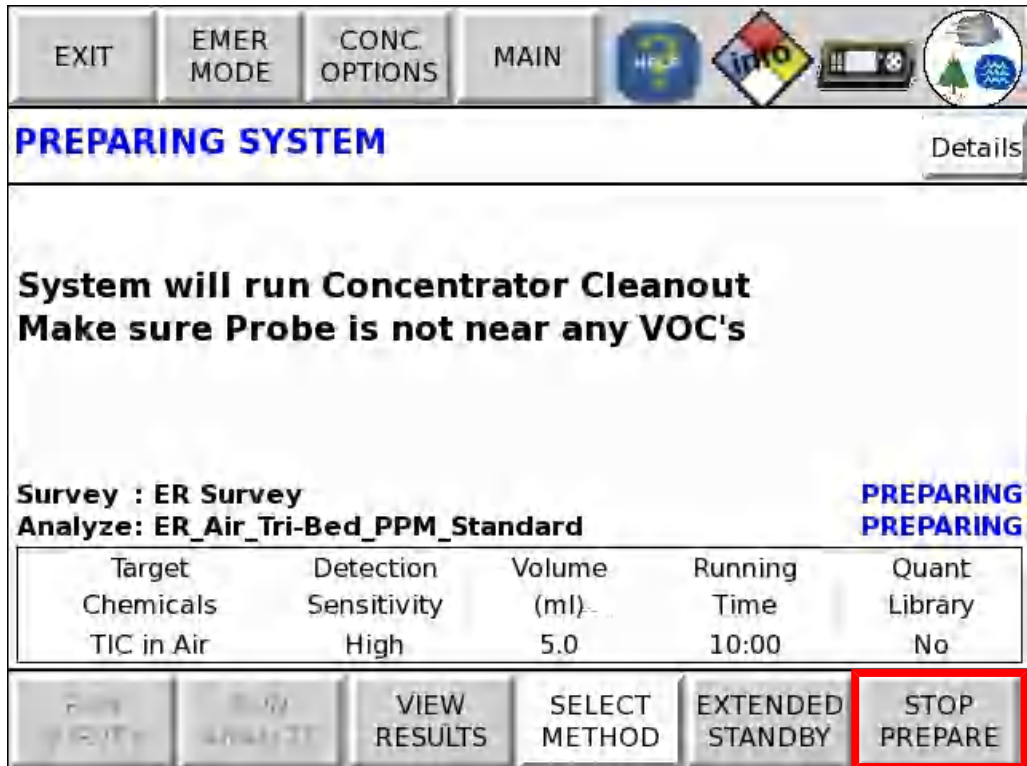
When the **SYSTEM READY** message is displayed, touch either **RUN SURVEY** or **RUN ANALYZE**. If using the push buttons, push **SURVEY RUN** or **ANALYZE RUN**.

If connecting wirelessly to the laptop, see Communications and Touch Screen Options [▶ 110].

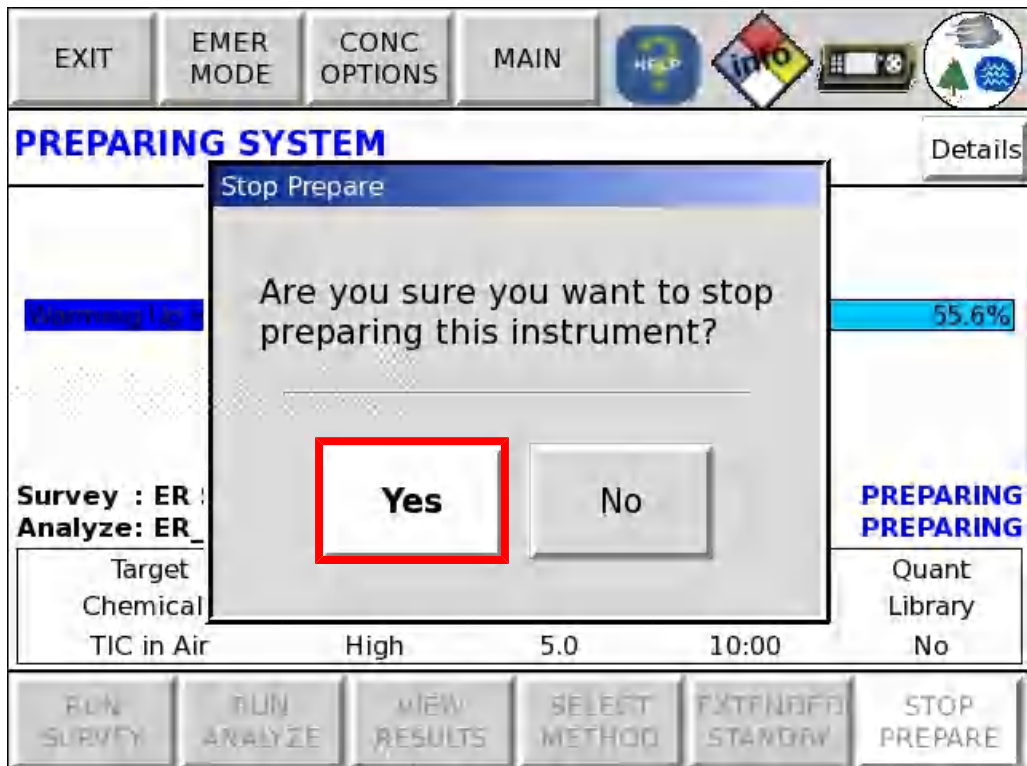
## 9.2 Select a Different Method Using the SELECT METHOD Icon

If the default method is not the desired method, the method can be changed. Changing the method can occur when the system is preparing or when another method has finished preparing.

- 1 When the **PREPARING SYSTEM** screen is displayed, touch **STOP PREPARE**. Alternately, use the arrow keys to highlight **STOP PREPARE** and push **OK SEL**.

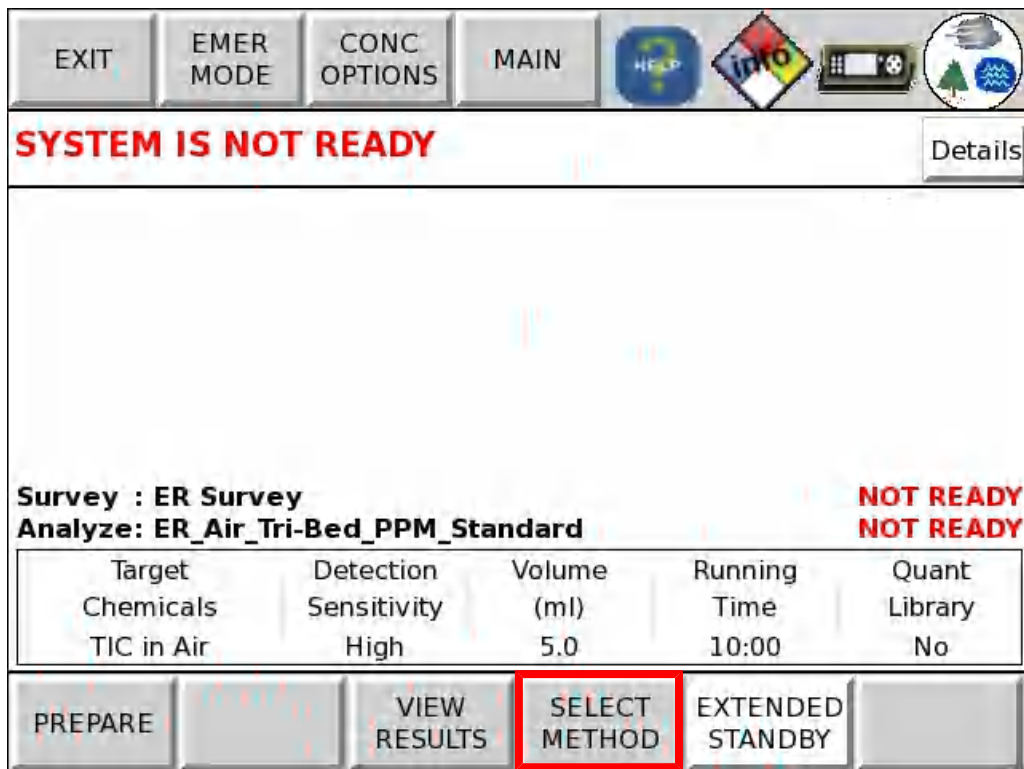


- The screen prompts, **Are you sure you want to stop preparing this instrument?** Touch **Yes** or using the arrow keys, highlight **Yes** and push **OK SEL**.

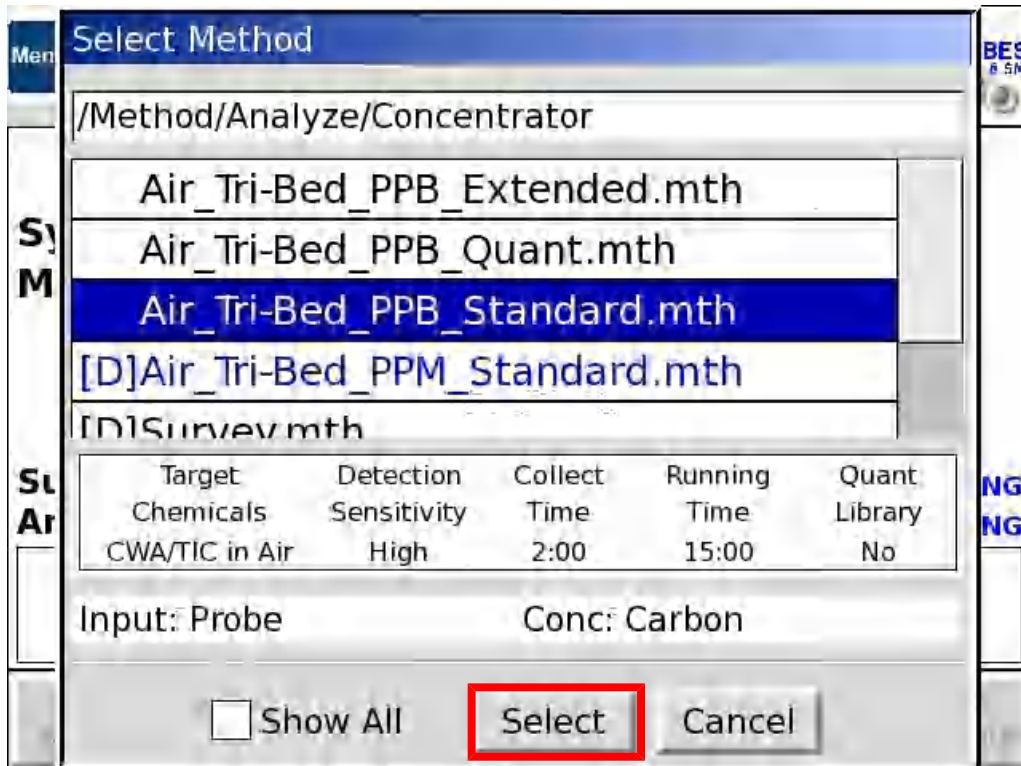




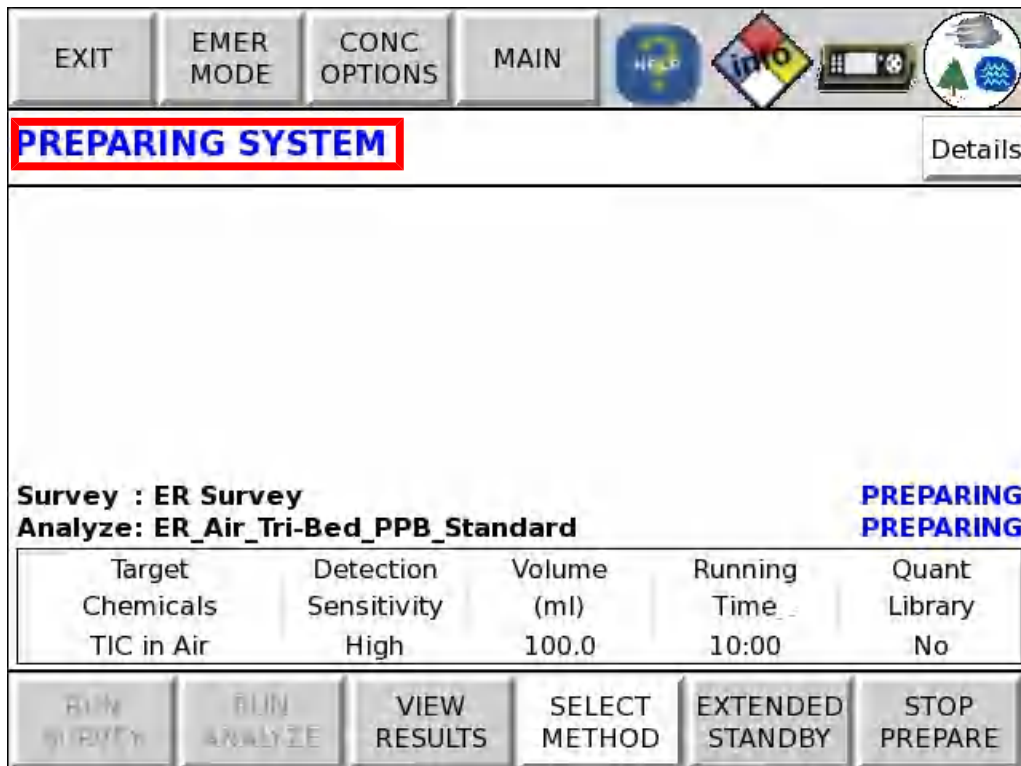
- Repeat steps 1 and 2 for both the **ANALYZE** method and the **SURVEY** method. The **SYSTEM IS NOT READY** screen appears. To select a new method, touch **SELECT METHOD** or using the arrow keys, highlight **SELECT METHOD** and push **OK SEL**.



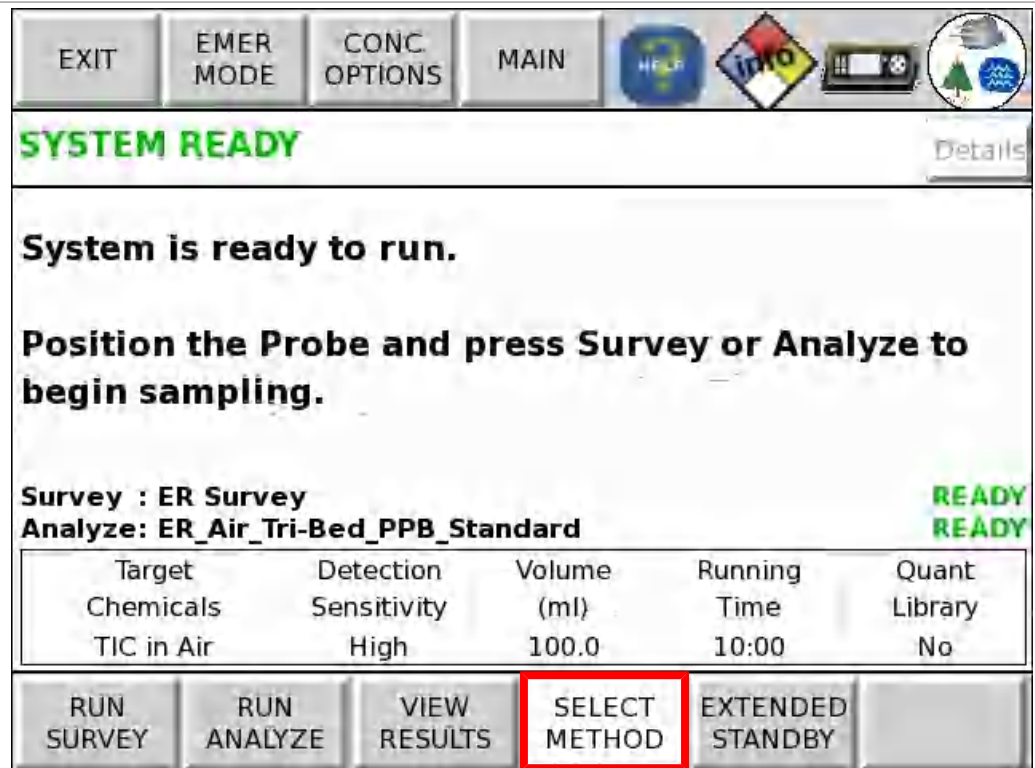
- Scroll up or down using the scroll bar and touch the desired method to highlight it. When the desired method is highlighted, touch **Select**. Alternately, scroll up or down using the arrow keys. When the desired method is highlighted, push **OK SEL**.



- 5 The **PREPARING** message is displayed. Refer to steps 4–9 of section Select a Different Method Using the SELECT METHOD Icon [▶ 71] for further instructions on system preparation.



- 6 If the **SYSTEM READY, ANALYZE READY** or **SURVEY READY** message is already displayed and the prepared method is not the desired one, touch **SELECT METHOD**.



- 7 Scroll up and down with the scroll bar or use the arrow keys to highlight the desired method, as shown in Step 4 of Select a Different Method Using the SELECT METHOD Icon [▶ 71]. Touch **Select** or highlight **Select** using the arrow keys and push **OK SEL**.
- 8 HAPSITE ER begins preparing the new method.

## 9.2.1 Change the Default Method

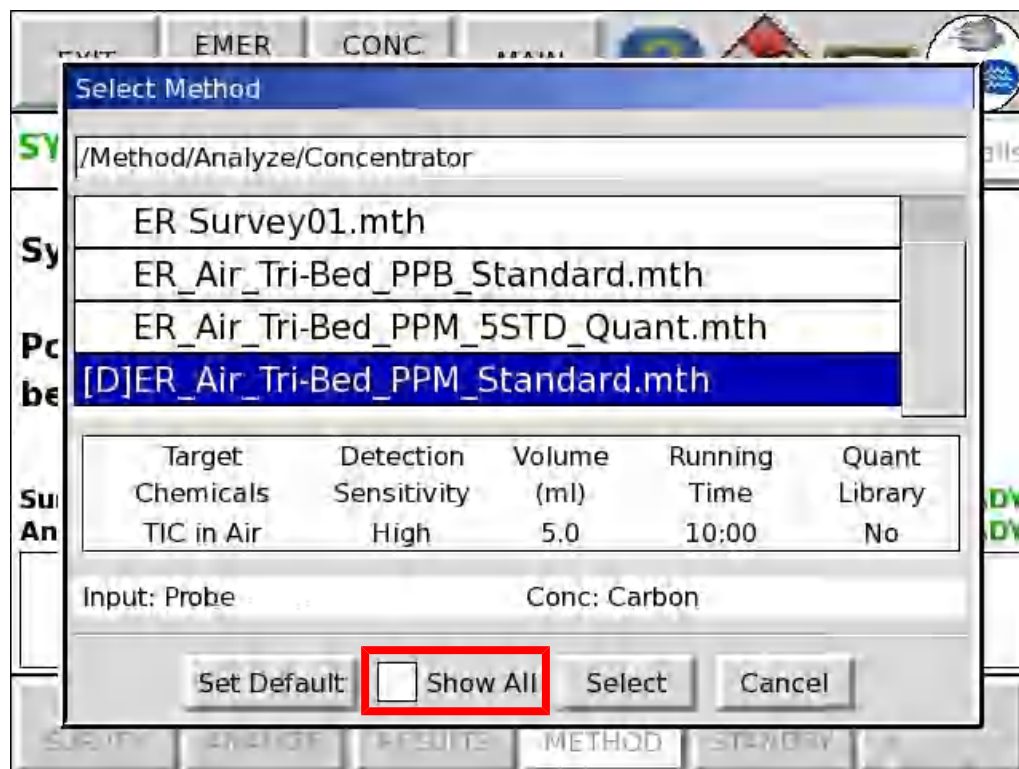
The default method for HAPSITE ER can be changed. By changing the default method, HAPSITE ER will prepare the newly selected method upon startup.

- 1 Touch **SELECT METHOD**.



## 9.2.2 Show All

HAPSITE ER will only show methods that are compatible with the current sample and/or accessory configuration. By checking the **Show All** box, all loaded HAPSITE ER methods will appear in the text box, regardless of configuration. Non-compatible methods will be shown in a lighter gray. The non-compatible methods are for reference only and cannot be selected to run.



## 9.3 Survey Mode

The **Survey Mode** is used for quick analysis and tentative results. When sampling unknown compounds, it is recommended that a **Survey** run be completed before running **Analyze**.

### Overview

- Using the probe, sample the air away from the area of concern for one minute. This establishes the background of VOCs currently present in the area.



### ⚠ CAUTION

**Do not touch the sample with the probe. Do not allow liquids to enter the probe.**

- When a background has been established, sample directly over the point of concern. Once the TIC begins to increase, slowly move the probe away from the sample. If a compound has been identified, it is displayed on the screen.

## Procedure

- 1 If an **Analyze** method is going to be run after **Survey**, verify that the appropriate sample configuration (concentrator) is installed.
- 2 When powered on or taken out of **Extended Standby**, HAPSITE ER automatically starts preparing an **ER Survey** and **Analyze** method if the probe is attached. Refer to Operate the Instrument in Portable Mode [p 51].
- 3 Verify that the desired **Analyze** method is listed under the **Survey** method. In the figure below, the **Analyze** method is **ER\_Air\_Tri-Bed\_PPB\_Standard**.

**SYSTEM READY** Details

**System is ready to run.**

**Position the Probe and press Survey or Analyze to begin sampling.**

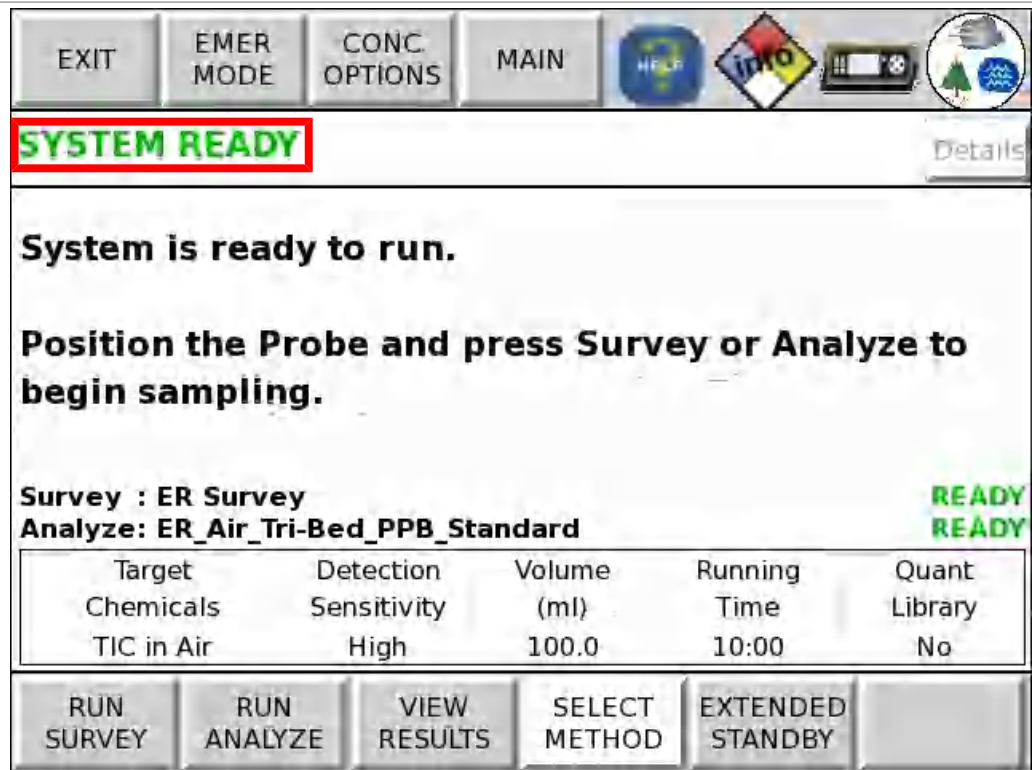
Survey : ER Survey READY

**Analyze: ER\_Air\_Tri-Bed\_PPB\_Standard** READY

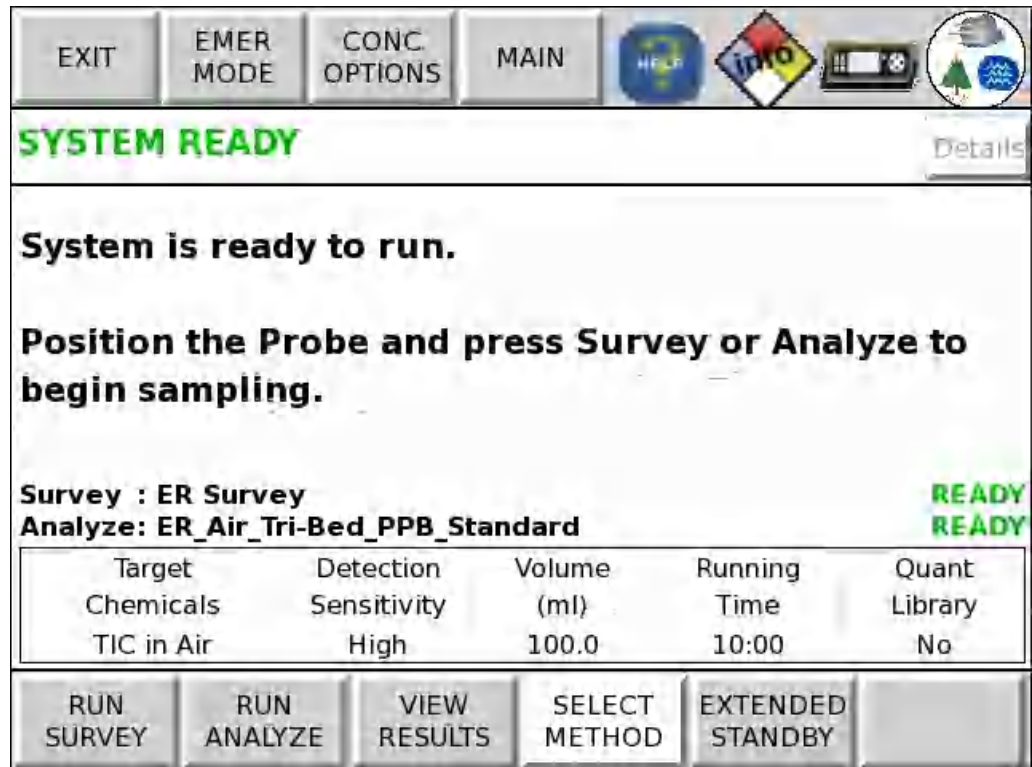
Target Chemicals	Detection Sensitivity	Volume (ml)	Running Time	Quant Library
TIC in Air	High	100.0	10:00	No

RUN SURVEY    RUN ANALYZE    VIEW RESULTS    SELECT METHOD    EXTENDED STANDBY

- 4 A **SYSTEM READY** message is displayed with a prompt to press **Survey** or **Analyze** when HAPSITE ER is ready to sample.



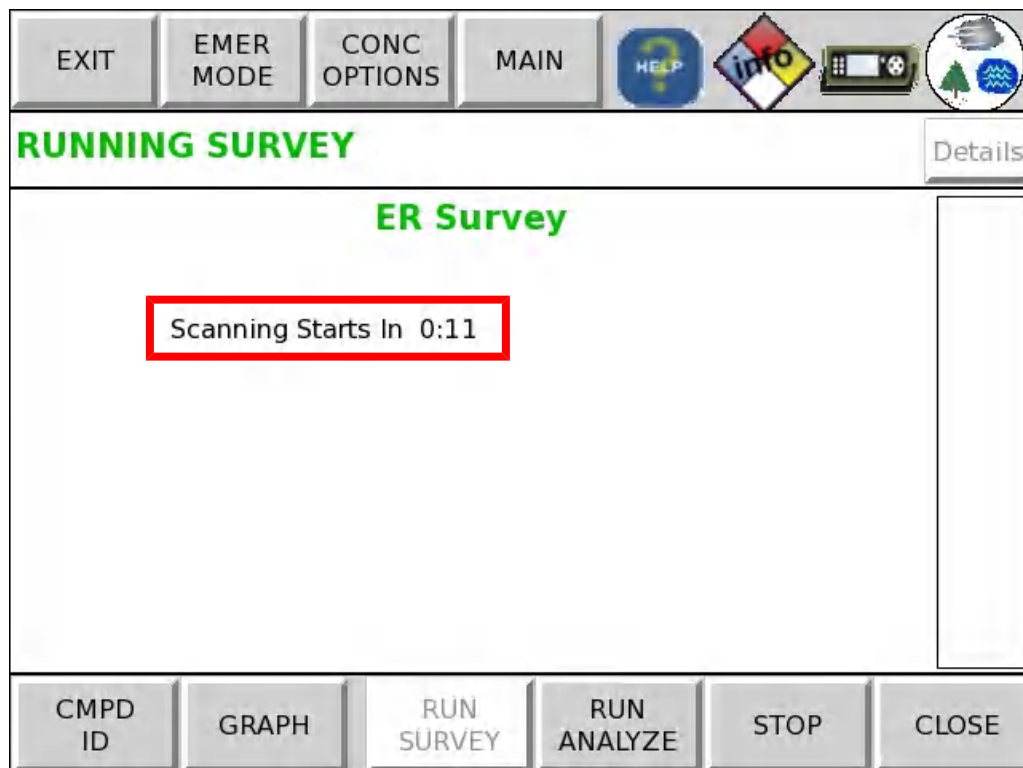
5 Using the touch screen, touch **RUN SURVEY**.



6 Alternately, push **SURVEY RUN** using the push buttons.

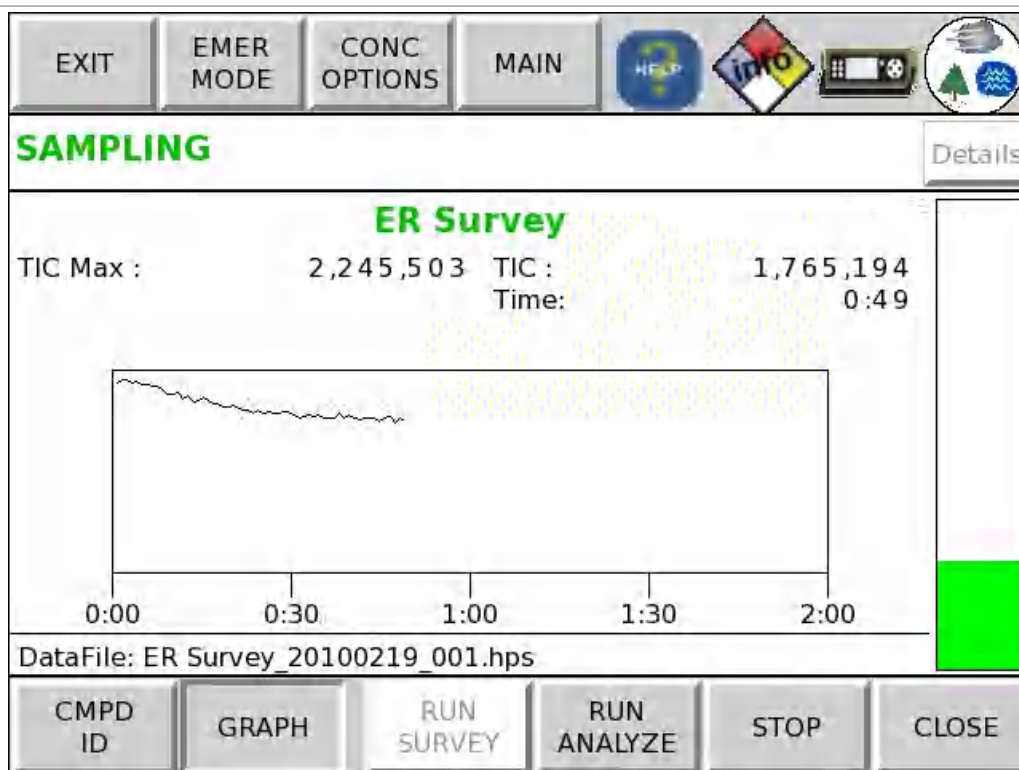


- 7 The front panel momentarily displays a **Scanning Starts In** message before the **Survey** run starts.

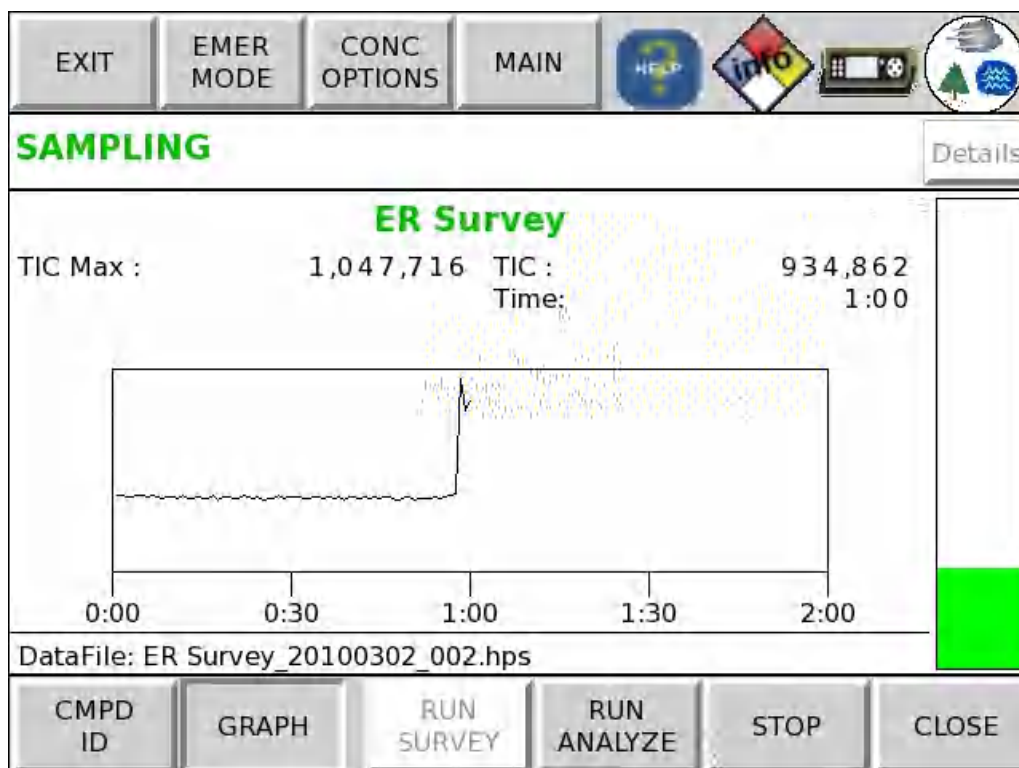


- 8 Sample air away from the point of the concern for one minute. Remember to note the background TIC.





- 9 Hold the probe over the sample of interest for up to one minute. A peak may appear if the compound present is greater than 1 ppm. A compound identification may also be present on the HAPSITE ER screen.





### ⚠ CAUTION

**Do not touch the sample with the probe.**

**Do not allow liquids to enter the probe.**

- 10** By touching **CMPD ID**, a list of identified compounds appears. The CAS number, the **Fit**, and the retention time for each compound is also displayed. this screen states the TIC (total ion count, a measure of response) maximum, the current TIC, and the elapsed time of the method.

EXIT	EMER MODE	CONC. OPTIONS	MAIN					
<b>SAMPLING</b>							Details	
<b>ER Survey</b>								
TIC Max :	5,474,273		TIC :	583,647				
			Time:	1:26				
<b>1: sec-Butylamine</b>			ET: 1:16					
CAS#:	13952-84-6		FIT:	72.0%				
1: 2-Butanamine, (S)-			ET: 1:16					
CAS#:	513-49-5		FIT:	72.0%				
<b>2: 2-Propanamine</b>			ET: 1:24					
CAS#:	75-31-0		FIT:	74.0%				
2: sec-Butylamine			ET: 1:24					
CAS#:	13952-84-6		FIT:	70.0%				
DataFile: ER Survey_20100302_003.hps								
CMPD ID	GRAPH		RUN ANALYZE	STOP	CLOSE			



Touching a compound on the list will display Synonym and Exposure Limit information.

- 11** The **CMPD ID** screen can also be accessed by using the arrow keys to highlight **CMPD ID** and pushing **OK SEL**.
- 12** To view the chromatogram while the method is running, touch **GRAPH**. Alternately, use the arrow keys to highlight **GRAPH** and push **OK SEL**.

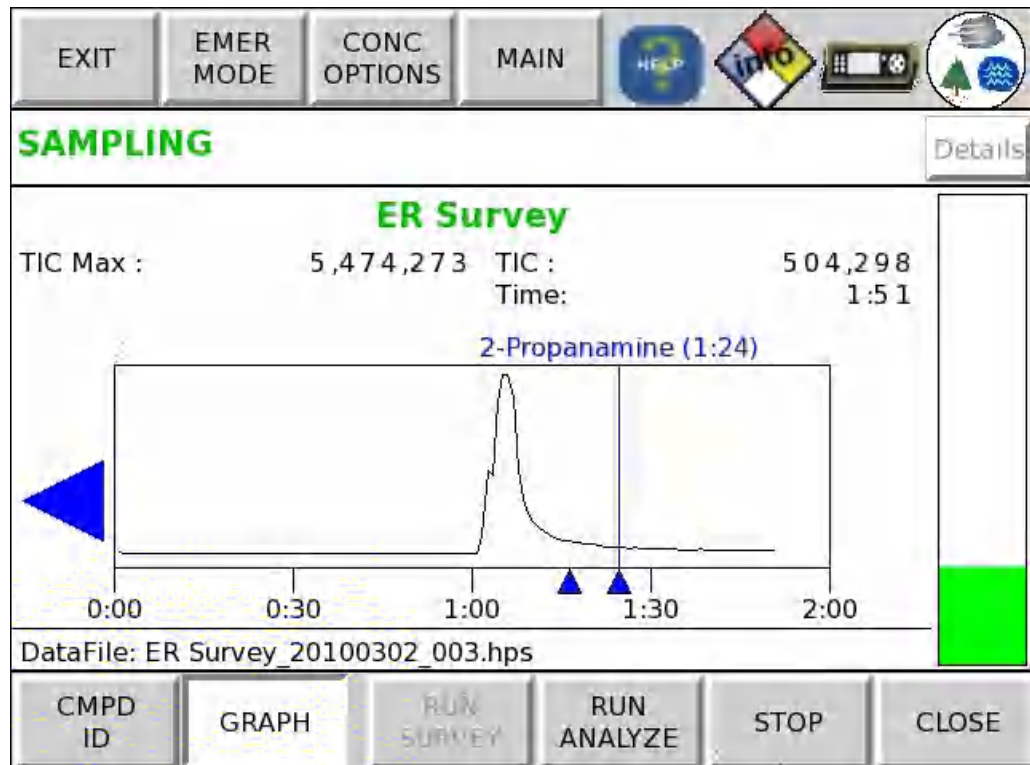


This screen states the TIC maximum, the current TIC, and the time the method has been running.



Touching the blue compound identification above the chromatogram will display Synonym and Exposure Limit information.

- 13 When the TIC begins to increase, move the probe away from the sample of interest. Continue the run until the TIC level returns to the initial background TIC level that was noted in Step 8.





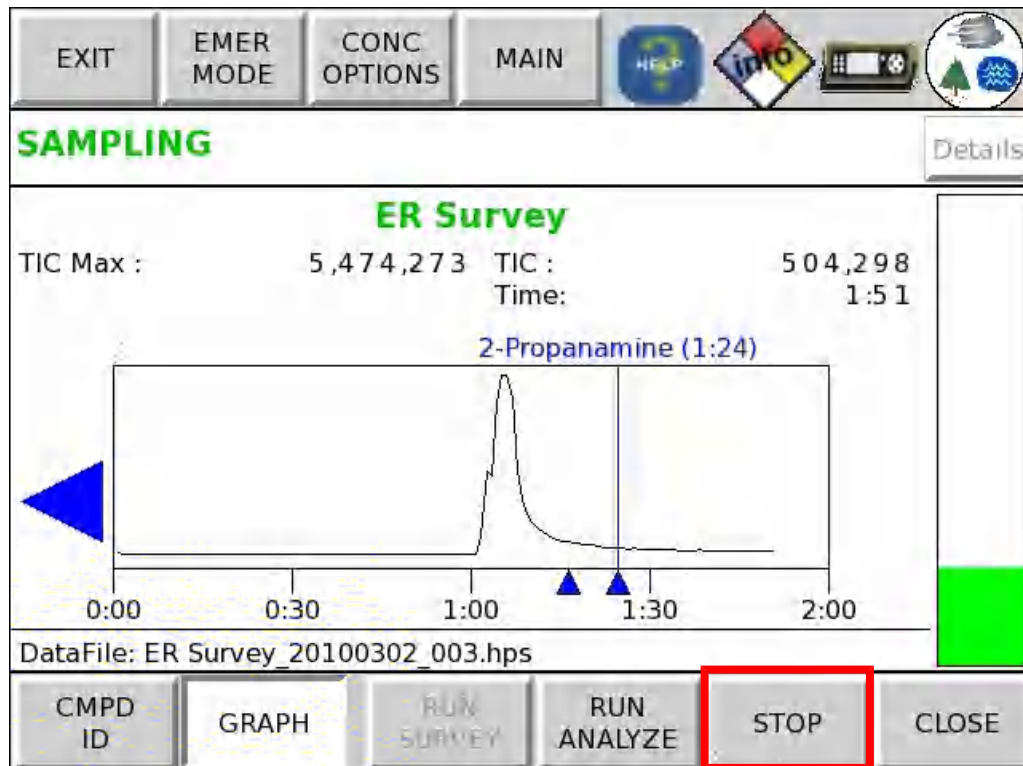
Monitor the side bar on the HAPSITE ER screen for guidance. The bar rises as the TIC increases and green signifies that the proper sampling distance is being maintained. To avoid saturation, remove the probe from the sample when the bar increases and turns yellow. If saturation occurs, the side bar turns red and the TIC is above 60 million.

- 14** To confirm the **Survey** results with a GC/MS run, **ANALYZE** can be touched or **ANALYZE RUN** can be pushed during the survey run.

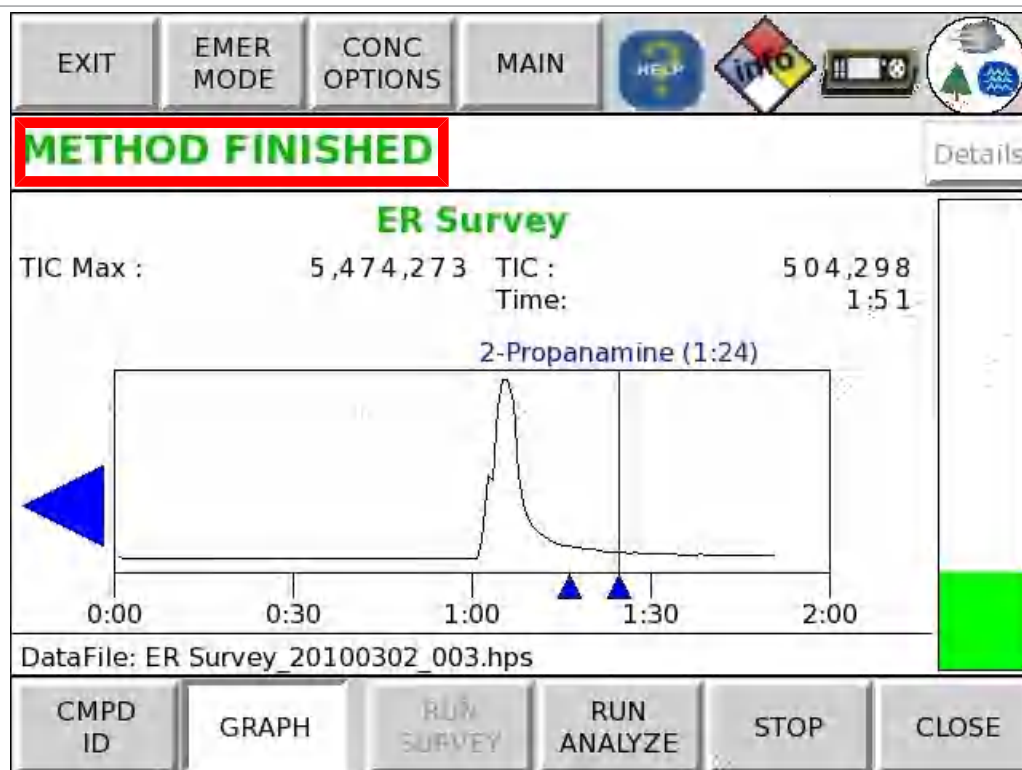


It is advised to begin an **Analyze** run either after a peak has been displayed and/or **Survey** has been run for the full two minutes.

- 15** If running an **Analyze** method is not desired, touch **STOP** to stop the sampling process and automatically save the data.



- 16** A **METHOD FINISHED** message appears when the survey method has ended.



The total time required for a **Survey** analysis is typically less than 3 minutes. If the **Survey** is not stopped manually, it automatically stops at 5 minutes.

### 9.3.1 Quick Reference SOP - Survey Method

- 1 If an **Analyze** (GC/MS) method is going to be run after **Survey**, verify that the appropriate configuration (concentrator) is installed and the proper **Analyze** method is displayed on the screen.
- 2 If powering on HAPSITE ER or exiting **Extended Standby**, HAPSITE ER automatically begins preparing **Survey**.
- 3 If needed, touch **PREPARE** on the touch screen. Alternately, using the arrow keys, highlight **PREPARE** and push **OK SEL**.
- 4 When prompted by the **SYSTEM IS READY** message, touch **RUN SURVEY** or push **SURVEY RUN**.
- 5 Monitor the background for one minute.
- 6 Hold the probe over the sample.
- 7 Move the probe away from the sample when the TIC begins to increase and a peak begins to form.
  - ⇒ If the TIC does not increase after a full minute of sampling, move the probe away from the sample.

- 8 To confirm data with an **Analyze** (GC/MS) run, touch **RUN ANALYZE** or press **ANALYZE RUN**.
- 9 A **METHOD FINISHED** message is displayed when the method has ended.

## 9.4 ANALYZE (GC/MS) Mode with the Concentrator

### 9.4.1 Tri-Bed Concentrator

The Tri-Bed concentrator is used for analyzing samples with concentration levels in the low part per million to high part per trillion range. Two default qualitative methods are ER\_Tri-Bed\_PPM\_Standard and ER\_Tri-Bed\_PPB Standard. Use the ER\_Tri-Bed\_PPM\_Standard method when a response is seen in Survey. If a compound is suspected but Survey does not show an increase in TIC (total ion count, which is a method of response), use the ER\_Tri-Bed\_PPB\_Standard method.



#### **CAUTION**

**The concentrator feature has increased sensitivity. Use the appropriate method to avoid saturating HAPSITE ER.**

### 9.4.2 Tenax Concentrator

This method is also used for analyzing samples with concentration levels in the low part per million to high part per trillion range. The Tenax concentrator's use is similar to that of the Tri-Bed concentrator. However, the Tenax concentrator is not designed to exhaustively concentrate volatile compounds with boiling points below 80°C.



#### **WARNING**

**The Tenax concentrator will not effectively concentrate compounds with boiling points below 80°C.**

### 9.4.3 Procedure for Running Concentrator Methods



Before an **Analyze** (GC/MS) concentrator method can be run, the concentrator must be installed. Once installed, the concentrator is automatically cleaned before sampling begins.

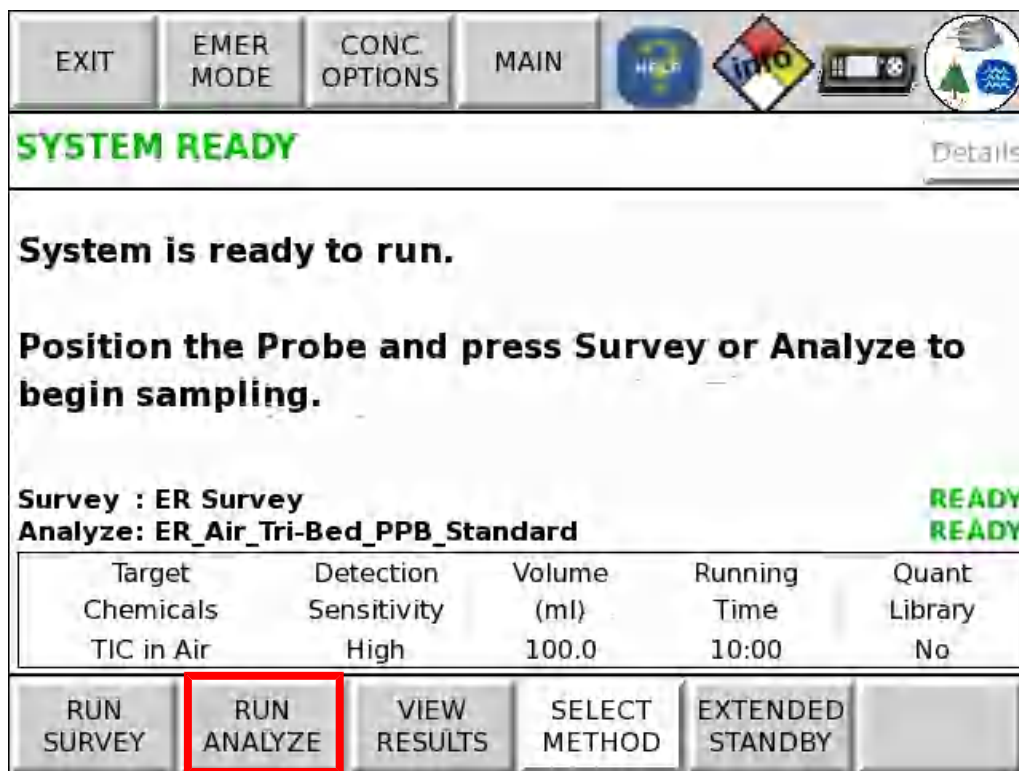
- ✓ Verify that the appropriate concentrator is installed.

- 1 The HAPSITE ER automatically starts preparing a concentrator method. If HAPSITE ER does not prepare the desired concentrator method, refer to Select a Different Method Using the SELECT METHOD Icon [▶ 71].
- 2 When the HAPSITE ER has finished preparing and the concentrator cleanout is successful, a **SYSTEM READY** message is displayed with a prompt to press **Survey** or **Analyze** to begin sampling.



A blank run is recommended before running a sample.

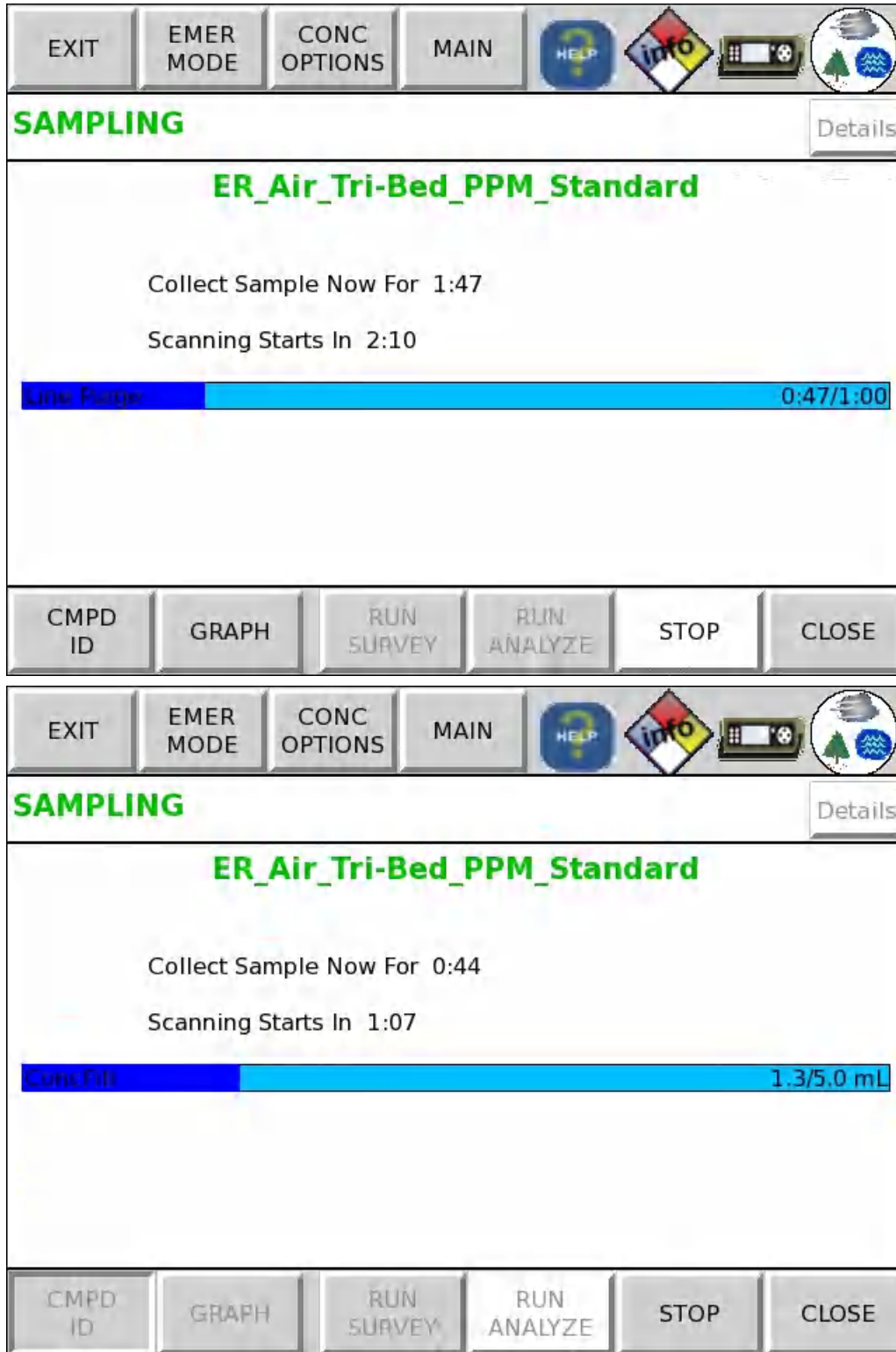
- 3 Using the touch screen, touch **RUN ANALYZE**.



- 4 Alternately, if using the push buttons, push **ANALYZE RUN**.



- When the screen prompts **Collect Sample Now**, hold the probe over the sample. Continue to collect the sample during both the **Line Purge** and the **ConcFill** screens.







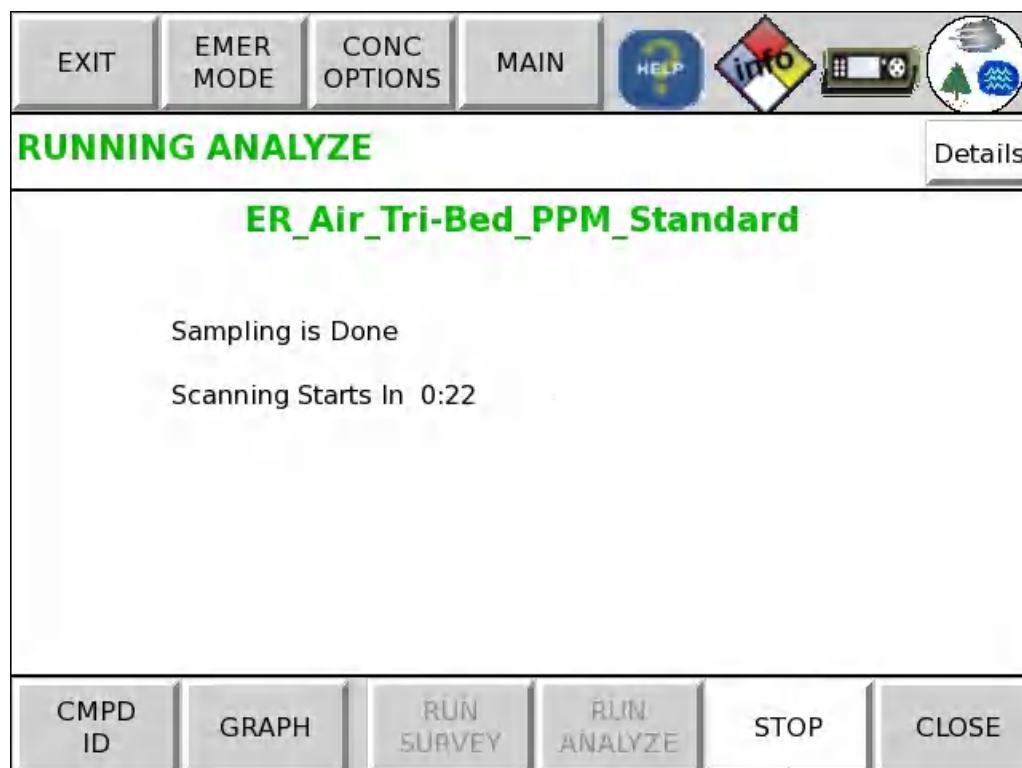
The **Line Purge** is based on time while the **ConcFill** is based on volume.



### ⚠ CAUTION

**Do not touch the sample with the probe. Do not allow liquids to enter the probe.**

- 6 Move the probe away from the sample when the screen prompts **Sampling is Done**.



- 7 By touching **CMPD ID**, a list of found compounds is displayed. This page displays for each compound:
  - ⇒ The CAS number
  - ⇒ The **Fit**
  - ⇒ The retention time
  - ⇒ TIC (Total Ion Count) Max
  - ⇒ The current TIC
  - ⇒ The time left until the run finishes

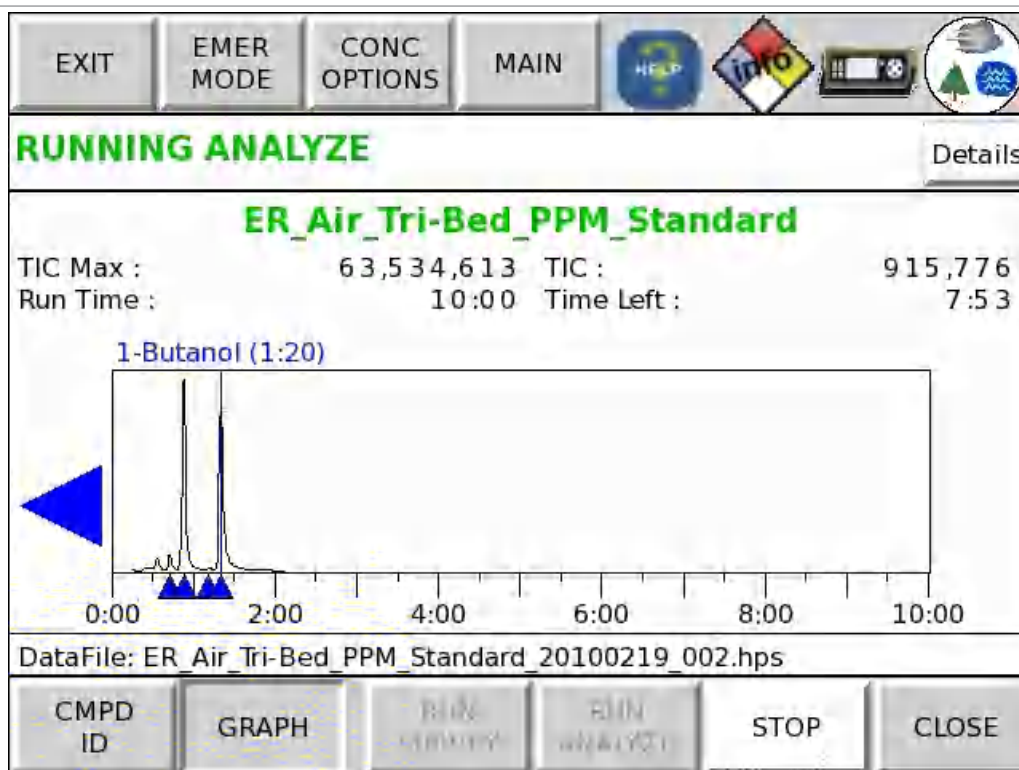


Touching a compound on the list will display Synonym and Exposure Limit information if it is contained in the NIOSH database.

- 8 The **CMPD ID** screen can also be accessed by using the arrow keys to highlight **CMPD ID** and pushing **OK SEL**.

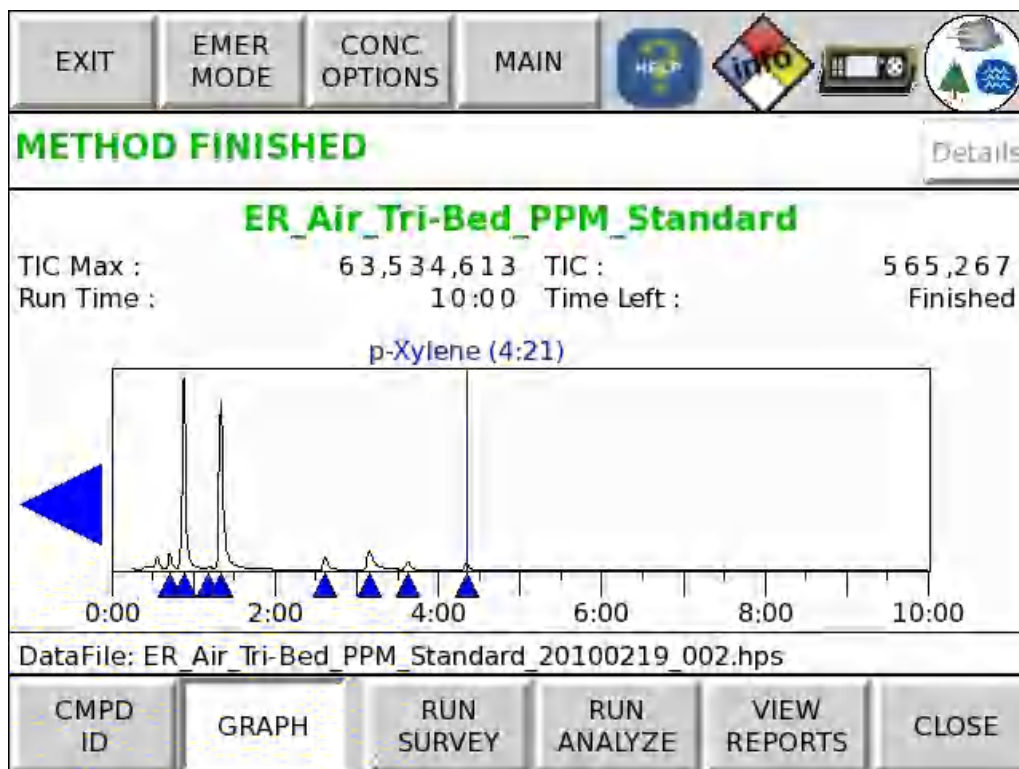
RUNNING ANALYZE				Details
<b>ER_Air_Tri-Bed_PPM_Standard</b>				
TIC Max :	63,534,613	TIC :	862,114	
Run Time :	10:00	Time Left :	7:45	
<b>1: Acetone</b>			RT: 0:42	
CAS#: 67-64-1	FIT: 88.0%			
<b>2: 1-Propanol</b>			RT: 0:53	
CAS#: 71-23-8	FIT: 96.0%			
<b>3: TRIS HAPSITE IS #1</b>			RT: 1:11	
CAS#: 729-81-7	FIT: 90.0%			
<b>4: 1-Butanol</b>			RT: 1:20	
CAS#: 71-36-3	FIT: 93.0%			
DataFile: ER_Air_Tri-Bed_PPM_Standard_20100219_002.hps				
CMPD ID	GRAPH	STOP	CLOSE	

- 9 To view the chromatogram while the method is running, touch **GRAPH**. Alternately, use the arrow keys to highlight **GRAPH** and push **OK SEL**. This screen displays:
- ⇒ The TIC Max
  - ⇒ The current TIC
  - ⇒ The time left until the run finishes



Touching the blue compound identification above the chromatogram will display Synonym and Exposure Limit information.

10 A **METHOD FINISHED** message is displayed when the **Analyze** method has ended.





Another **Analyze** (GC/MS) run can be started immediately after one has finished. Depending upon the temperature profile, the column may need to cool before another run may begin.

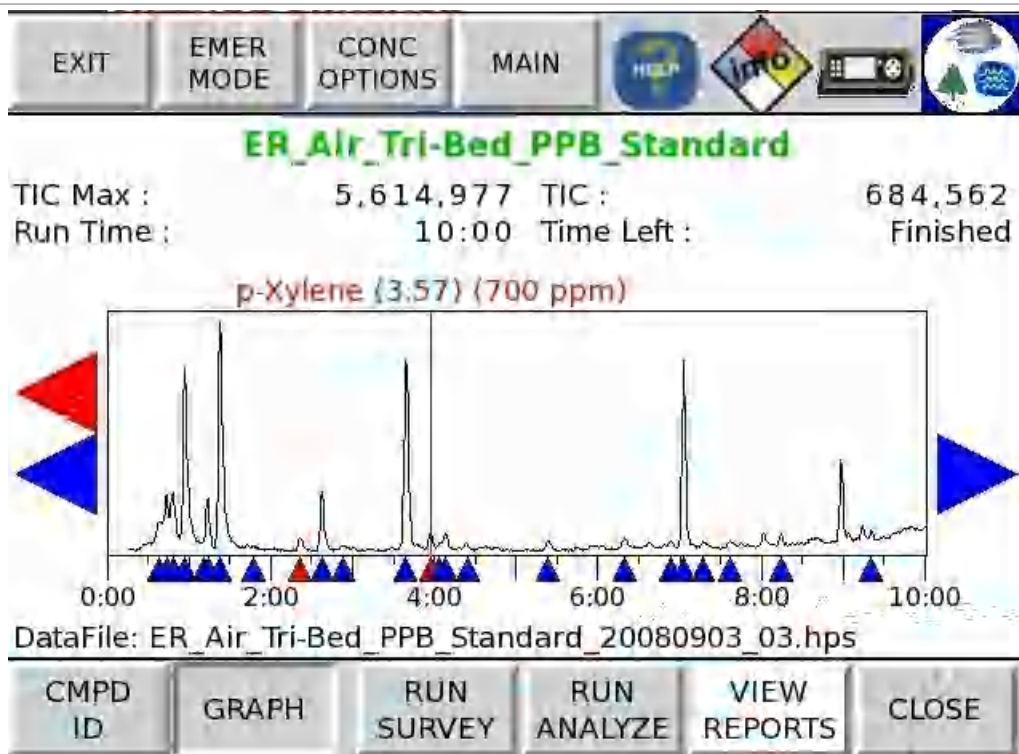
### 9.4.4 Quick Reference SOP - Concentrator Methods

- Verify that the concentrator is installed.
- Refer to Quick Reference SOP- Heat-up and Tune [▶ 71] for startup instructions.
- Verify that the desired method is displayed on the Analyze line.
  - 1 Touch **RUN ANALYZE** or push **ANALYZE RUN** when the **SYSTEM IS READY** screen is displayed.
  - 2 When the screen prompts **Collect Sample Now**, hold the probe over the sample until the screen prompts **Sampling is Done**.
  - 3 When the run is complete, a **Method Finished** prompt will be displayed.

## 9.5 Detecting Hazardous Chemicals

If the HAPSITE ER **Analyze** message turns red, the chemical's concentration is either approaching the IDLH limit or the chemical is a chemical warfare agent. In **CMPD ID** mode, the compound is highlighted in red and in **GRAPH** mode, the name of the compound is written in red. Red arrows on the side of the screen are displayed in **GRAPH** mode if there is more than one red compound.

EXIT	EMER MODE	CONC OPTIONS	MAIN	Info	Help
<b>ER_Air_Tri-Bed_PPB_Standard</b>					
TIC Max :	5,614,977	TIC :	684,562		
Run Time :	10:00	Time Left :	Finished		
1: Toluene					
2: p-Xylene					
2: Ethanol, 2-fluoro-					
CAS#: 371-62-0 FIT: 70.0% RT: 0:38					
2: Acetone					
CAS#: 67-64-1 FIT: 79.0% RT: 0:43					
DataFile: ER_Air_Tri-Bed_PPB_Standard_20080903_03.hps					
CMPD ID	GRAPH	RUN SURVEY	RUN ANALYZE	VIEW REPORTS	CLOSE



## 9.6 Help Icon

The **Help** icon is located on the front panel in the top right hand corner.

**SYSTEM READY** Details

**System is ready to run.**

**Position the Probe and press Survey or Analyze to begin sampling.**

**Survey : ER Survey** **READY**  
**Analyze: ER\_Air\_Tri-Bed\_PPB\_Standard** **READY**

Target	Detection Sensitivity	Volume (ml)	Running Time	Quant Library
TIC in Air	High	100.0	10:00	No

Navigation buttons: RUN SURVEY, RUN ANALYZE, VIEW RESULTS, SELECT METHOD, EXTENDED STANDBY

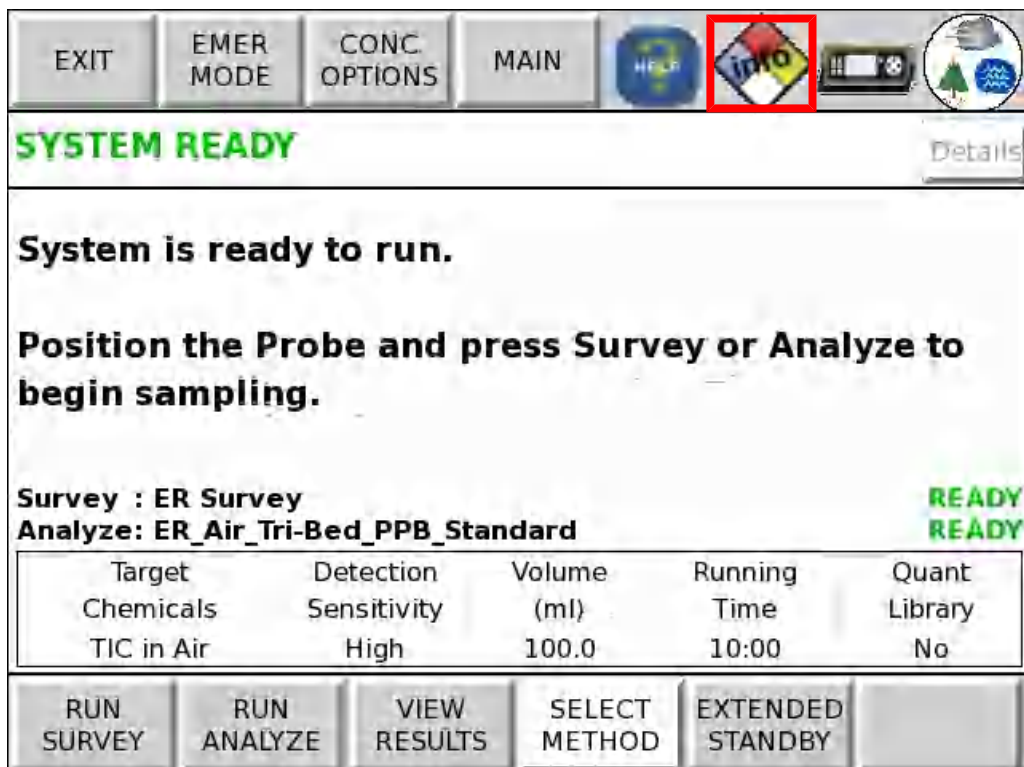
**Help** can be accessed by touching the Help icon or pushing the **HELP** button that is located on the front panel.



The main Help screen displayed will display a **Survey** link, an **Analyze** link, a **View Results** link, a **Select Method** link, and a **Go To Standby** link. Touching a link will provide instructions for performing the specified function. Touching **Simple Steps** at the bottom of the page will give a step-by-step outline of how to perform the desired function. The **Book** icon will give a more detailed summary of the function.

## 9.7 Info Icon

The **Info** icon is located next to the **Help** icon in the right corner of the HAPSITE ER screen. **Info** can be accessed by touching the **Info** icon, or by pushing the **STAT** key until the NIOSH database is displayed. When the **Info** page is displayed, the **Info** icon is highlighted in blue.



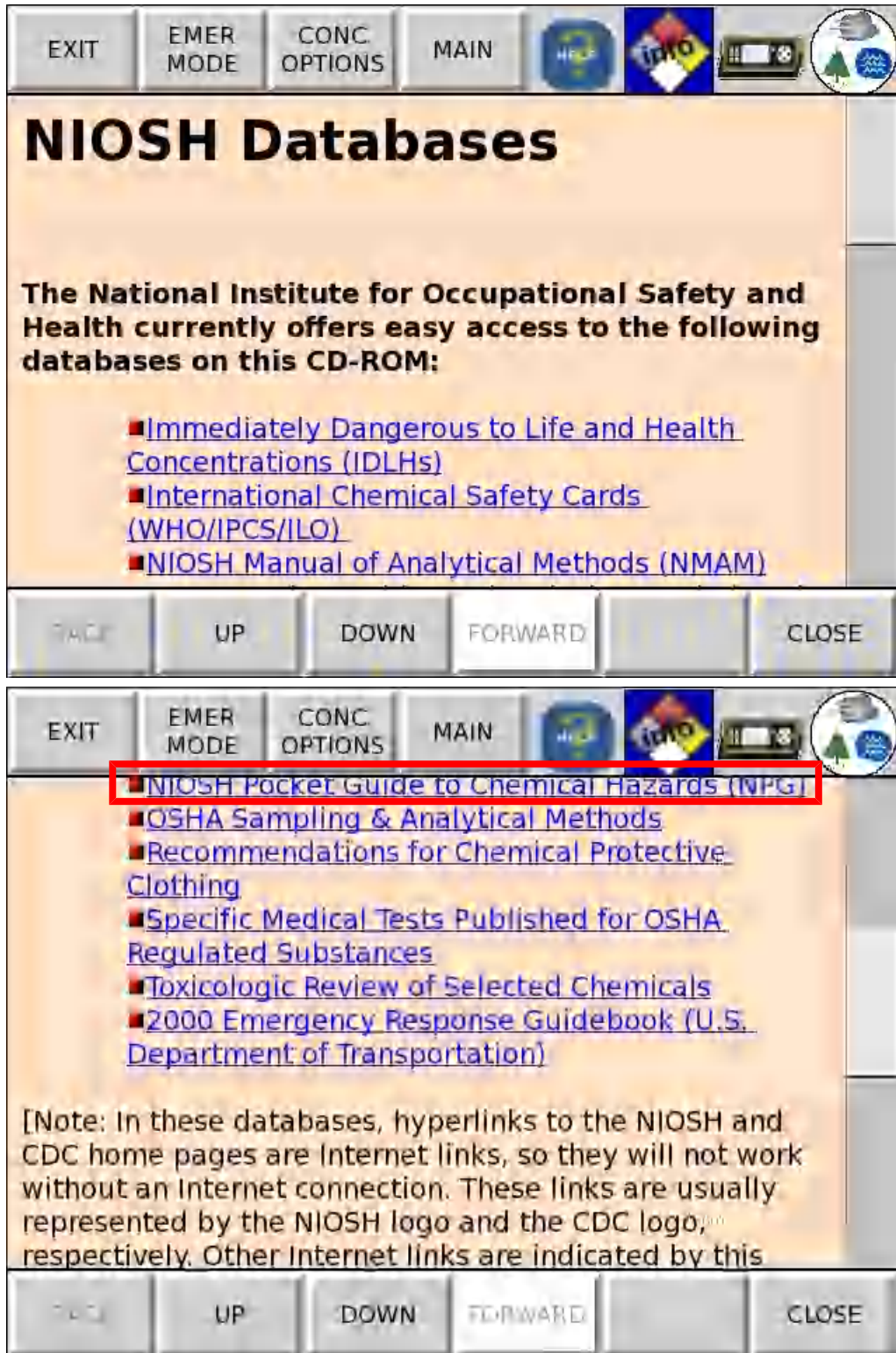
The NIOSH Database screen is displayed. This screen provides links to:

- Immediately Dangerous to Life and Health Concentrations (IDLHs)
- International Chemical Safety Cards, NMAM
- The NIOSH Pocket Guide to Chemical Hazards (NPG)
- OSHA Sampling and Analytical Methods
- Recommendations for Chemical Protective Clothing
- Specific Medical Tests Published for OSHA Regulated Substances
- Toxicologic Review of Selected Chemicals

These publications provide information on exposure limits, synonyms and detection limitations.

Scrolling to the bottom of the page accesses additional links.

- The **Conversion Calculator** converts concentration units
  - **Hazard ID's** accesses specific NIOSH studies about hazardous conditions
  - **PPE** recommends the proper equipment needed to withstand exposure to hazardous conditions
  - **Respiratory Protection** provides information on selecting the proper respirator
  - **Hazard Controls** accesses specific studies that have identified ways to reduce hazardous exposures
  - **Indoor Air Quality** includes selected publications from the EPA about improving air quality
  - The **Periodic Table**
  - **RTECS User Guide** was designed by NIOSH to provide synonyms, skin and eye irritation data, mutation data, and respiratory effects data for certain compounds. It stands for *The Registry of Toxic Effects of Chemical Substances*.
- 1** An important resource in this database is **The NIOSH Pocket Guide to Chemical Hazards**. To access the database, scroll to the fourth option on the list and touch **The NIOSH Pocket Guide to Chemical Hazards** link.

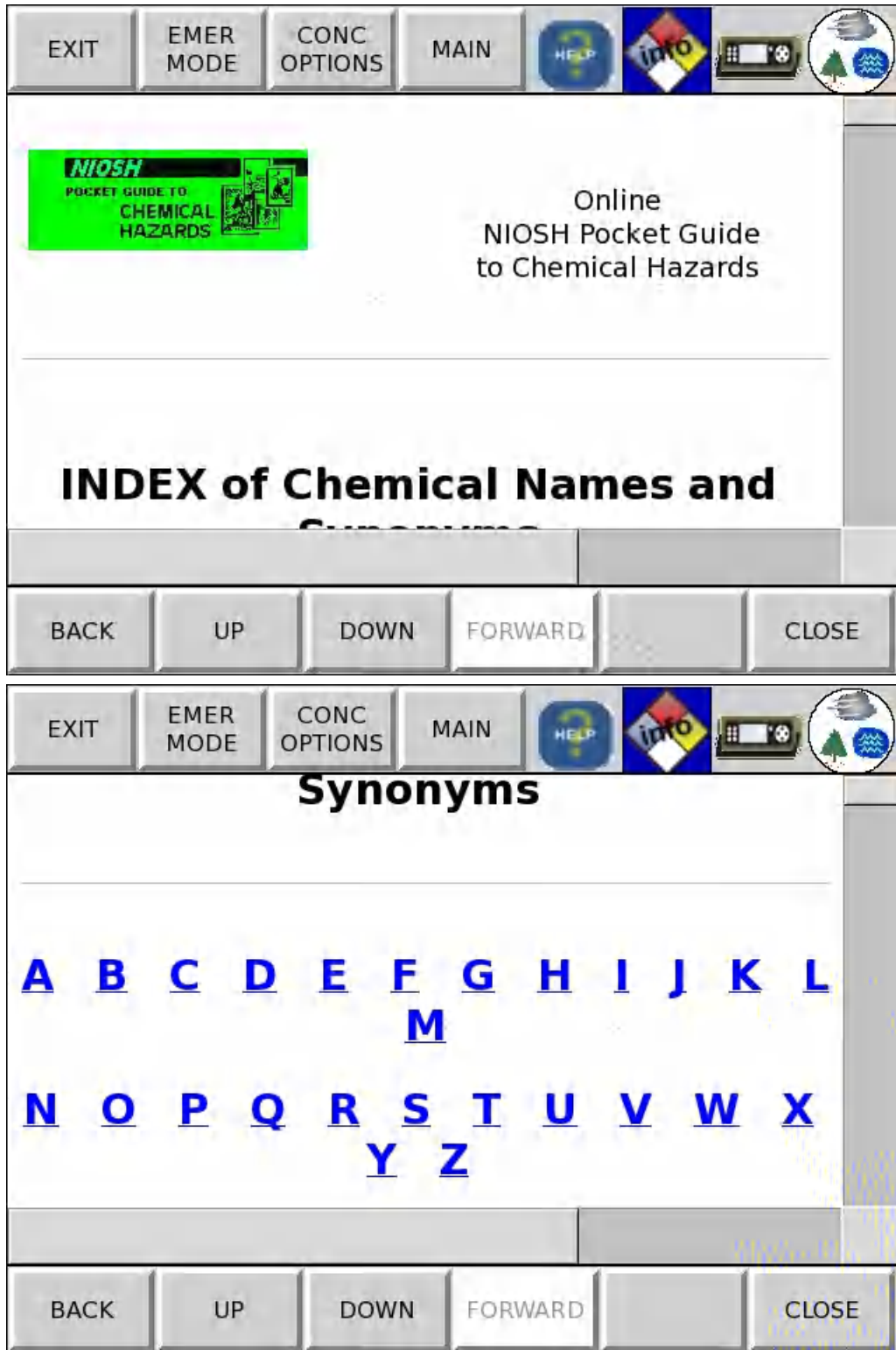


- 2 When the publication appears, touch **INDEX with CHEMICAL NAMES and SYNONYMS**.

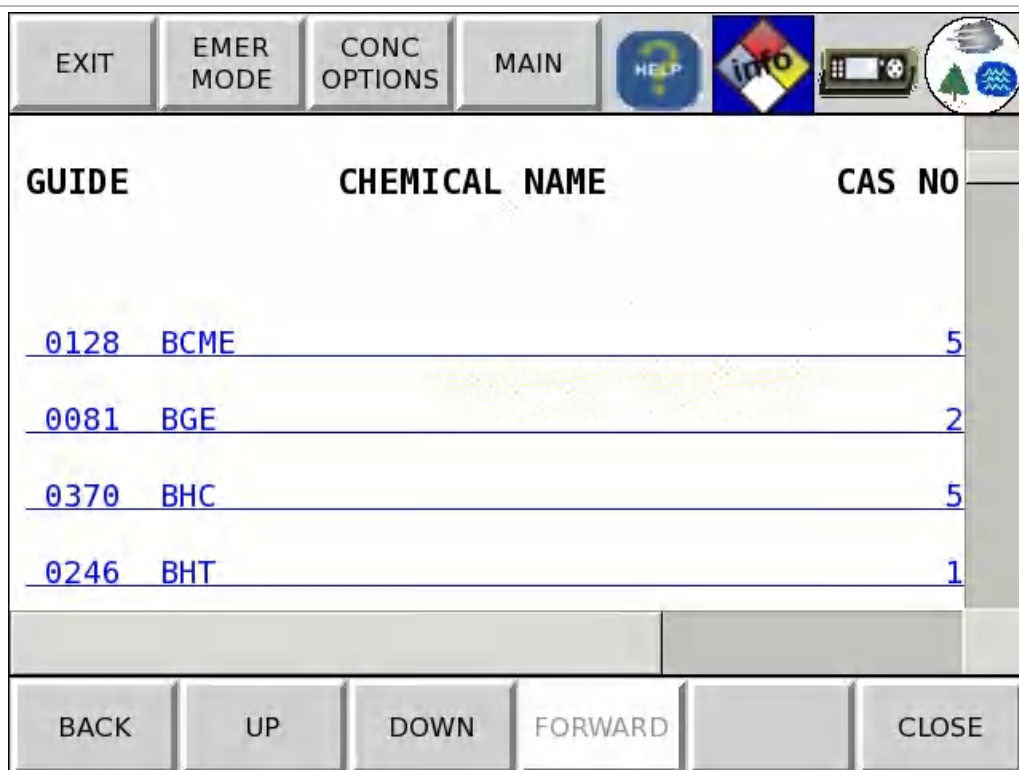




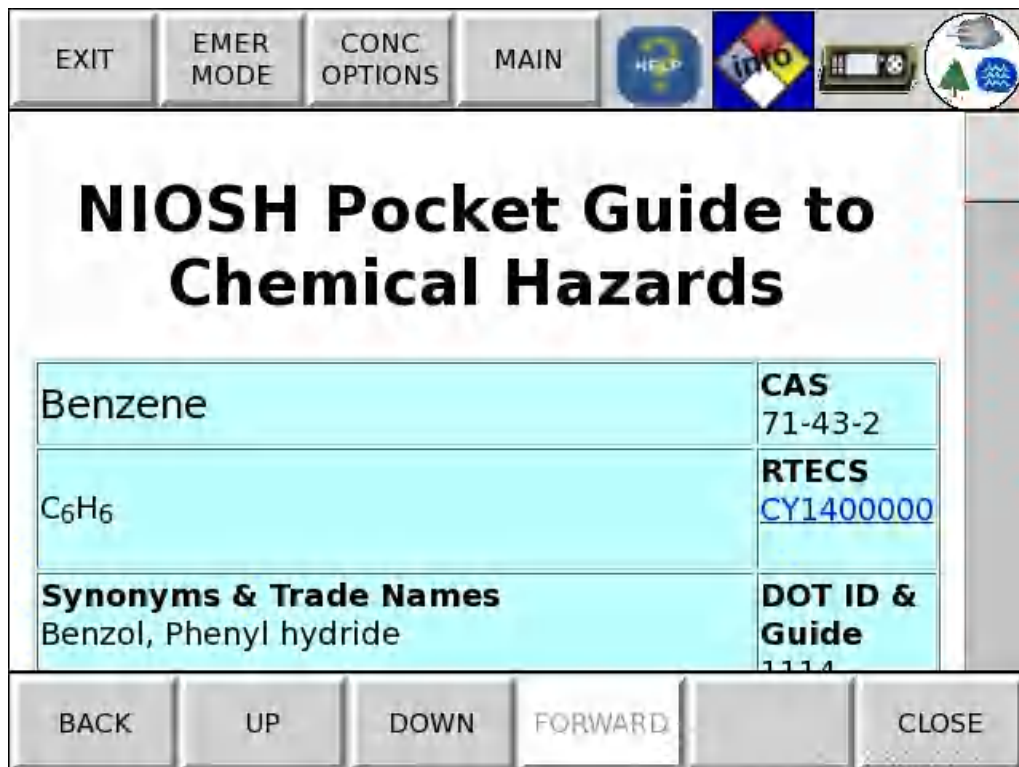
- 3 Scroll down to display an alphabet. Touch the first letter of the desired compound.



4 A list of the chemicals that start with the selected letter is displayed.



5 Touch the desired chemical. The **Pocket Guide** for this specific chemical is displayed.



6 Scrolling down displays information about the exposure limit and the boiling point of the chemical. Boiling point is one of the factors that determines if the chemical can be detected by HAPSITE ER. See Specifications [ 22] for boiling point recommendations.

The screenshot shows the 'Info' screen with the following content:

<b>Exposure Limits</b>	NIOSH REL: Ca TWA 0.1 ppm ST 1 ppm <a href="#">See Appendix A</a>
	OSHA PEL: [1910.1028] TWA 1 ppm ST 5 ppm <a href="#">See Appendix F</a>
<b>IDLH Ca [500 ppm] See: <a href="#">71432</a></b>	<b>Conversion</b> 1 ppm = 3.19 mg/m <sup>3</sup>
<b>Physical Description</b> Colorless to light-yellow liquid with an aromatic odor, [Note: A solid below 42°F.]	

At the bottom of the screen, there are navigation buttons: BACK, UP, DOWN, FORWARD, and CLOSE.

- 7 To access information regarding IDLHs, touch the first hyperlink on the **Info** screen.

The screenshot shows the 'NIOSH Databases' screen with the following content:

## NIOSH Databases

The National Institute for Occupational Safety and Health currently offers easy access to the following databases on this CD-ROM:

- [Immediately Dangerous to Life and Health Concentrations \(IDLHs\)](#)
- [International Chemical Safety Cards \(WHO/IPCS/ILO\)](#)
- [NIOSH Manual of Analytical Methods \(NMAM\)](#)

At the bottom of the screen, there are navigation buttons: BACK, UP, DOWN, FORWARD, and CLOSE.

- 8 Scroll down or touch **DOWN** until the **IDLH-Chemical listing and Documentation** link is displayed. Touch this link.

EXIT	EMER MODE	CONC OPTIONS	MAIN	HELP	INFO	RECYCLE	HOME
------	--------------	-----------------	------	------	------	---------	------

**NIOSH** Documentation for  
Immediately Dangerous  
to Life or Health  
Concentrations (**IDLHs**)\*

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U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES  
Public Health Service  
Centers for Disease Control and Prevention

BACK	UP	DOWN	FORWARD		CLOSE
------	----	------	---------	--	-------

EXIT	EMER MODE	CONC OPTIONS	MAIN	HELP	INFO	RECYCLE	HOME
------	--------------	-----------------	------	------	------	---------	------

REVISED CRITERIA FOR DETERMINING IDLHs  
References

[IDLHs--Chemical Listing and Documentation](#)

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**ACKNOWLEDGMENTS**

Special appreciation is extended to the following individuals from the Division of Standards Development and Technology Transfer: Crystal L. Ellison for locating the references and verifying the information used during the Standards Completion Program to determine the original

BACK	UP	DOWN	FORWARD		CLOSE
------	----	------	---------	--	-------

- 9 Scroll down, press **DOWN** or use the down arrow to find the desired compound. Press the link to view the compound's information.

EXIT
EMER MODE
CONC OPTIONS
MAIN

Documentation for  
Immediately Dangerous  
to Life or Health  
Concentrations (**IDLHs**)

NIOSH CHEMICAL LISTING  
AND DOCUMENTATION OF  
REVISED IDLH VALUES  
(AS OF 3/1/95)

BACK
UP
DOWN
FORWARD
CLOSE

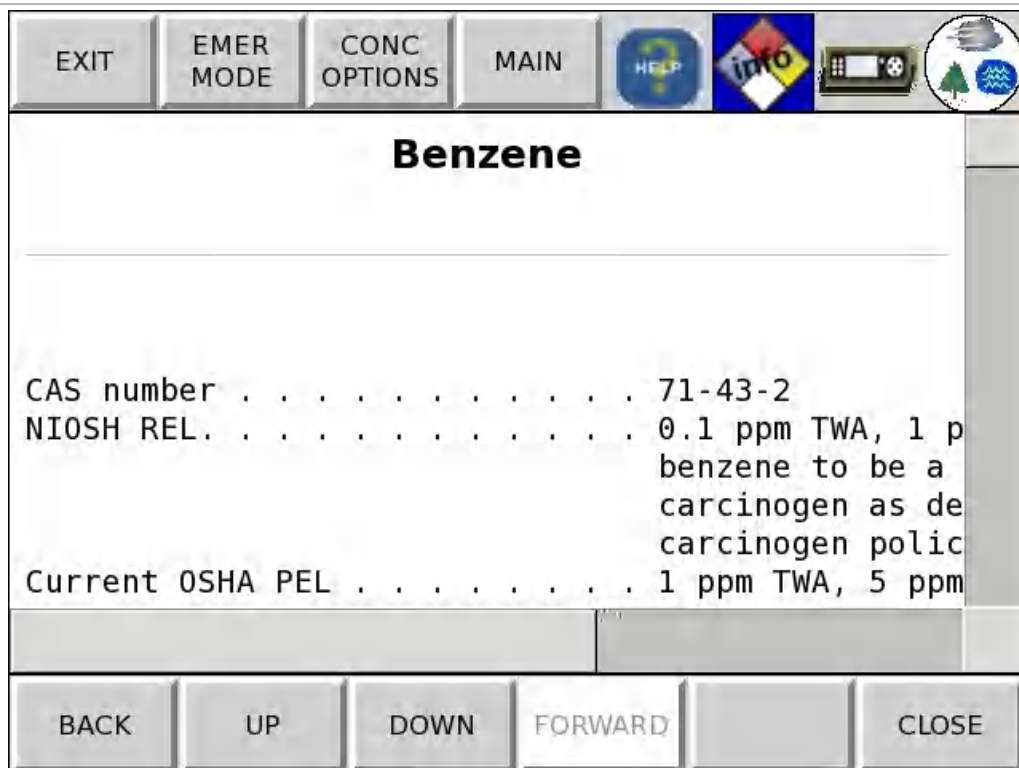
  

EXIT
EMER MODE
CONC OPTIONS
MAIN

<a href="#">Barium (soluble compounds, as Ba)</a>	1,100 mg Ba/m <sup>3</sup>	50 mg Ba/m <sup>3</sup>
<a href="#">Benzene</a>	3,000 ppm	500 ppm
<a href="#">Benzoyl peroxide</a>	7,000 mg/m <sup>3</sup>	1,500 mg/m <sup>3</sup>
<a href="#">Benzyl chloride</a>	10 ppm	10 ppm [Unch]
	10 mg	4 mg

BACK
UP
DOWN
FORWARD
CLOSE

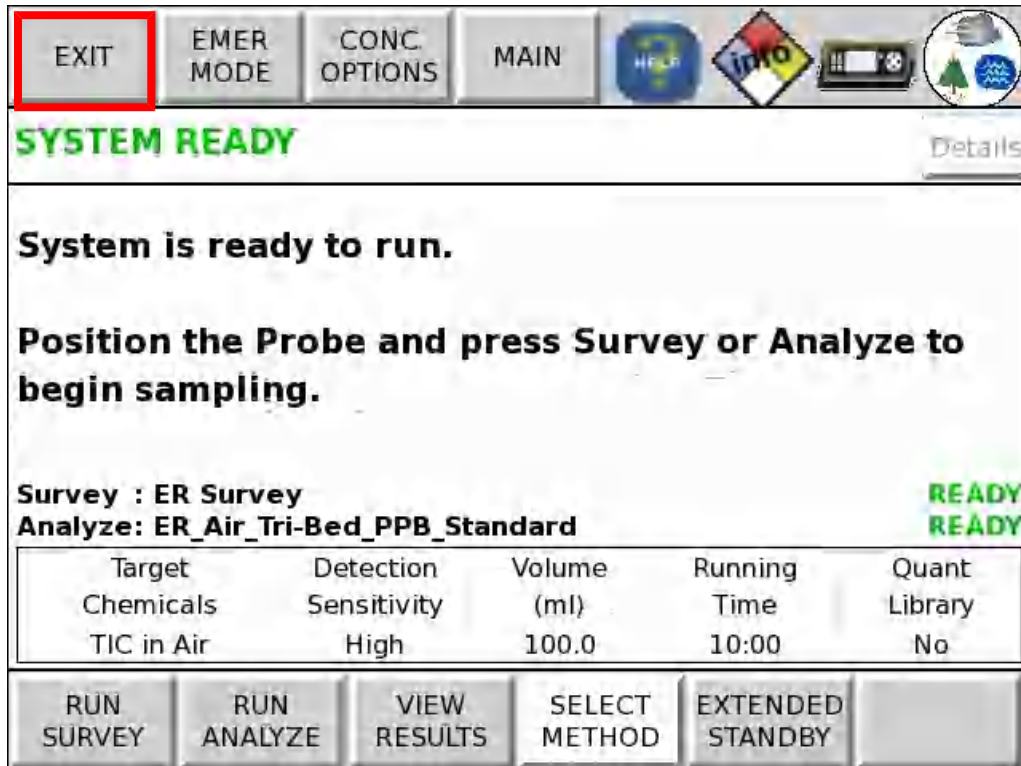
**10** Information regarding the compound's NIOSH REL, OSHA PEL, and toxicity data is displayed.



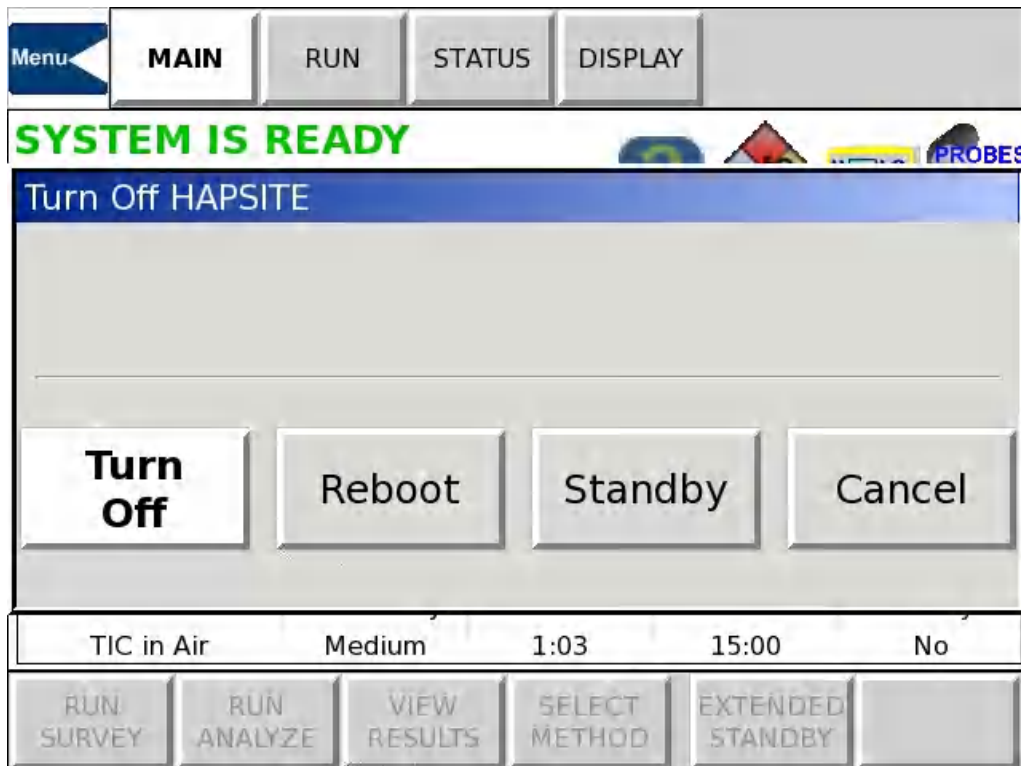
## 9.8 EXIT Menu

The **EXIT** menu is located on the top row of the front panel. This option will access **Turn Off**, **Reboot**, or **Standby**. **Turn Off** will shut down the HAPSITE ER power. **Reboot** will reset the microprocessor in HAPSITE ER and reload the drivers. It will also restart the operating system, HAPSITE ER program, and the front panel program. The **Standby** option will put the system into Extended Standby. Refer to Extended Standby [▶ 105] for Extended Standby instructions.

- 1 Touch **EXIT**. Alternately, use the arrow keys to highlight **EXIT** and push **OK SEL**.

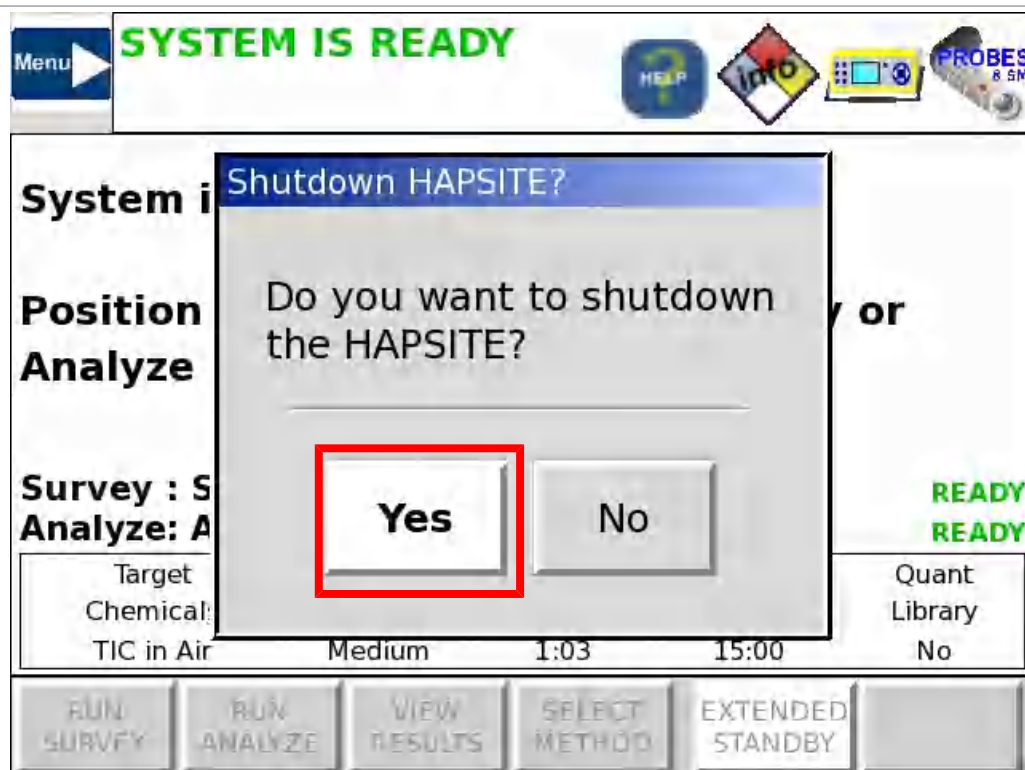


- 2 The three exit options will be displayed on the screen. There will also be a **Cancel** button. Either touch or use the arrow keys to highlight the desired choice on the screen. If using the push buttons, push **OK SEL**.



- 3 A prompt is displayed to confirm the selection. For example, if **Turn Off** is selected, a prompt **Do you want to shutdown the HAPSITE ER?** Touch **Yes** or select **Yes** and push **OK SEL** to continue.





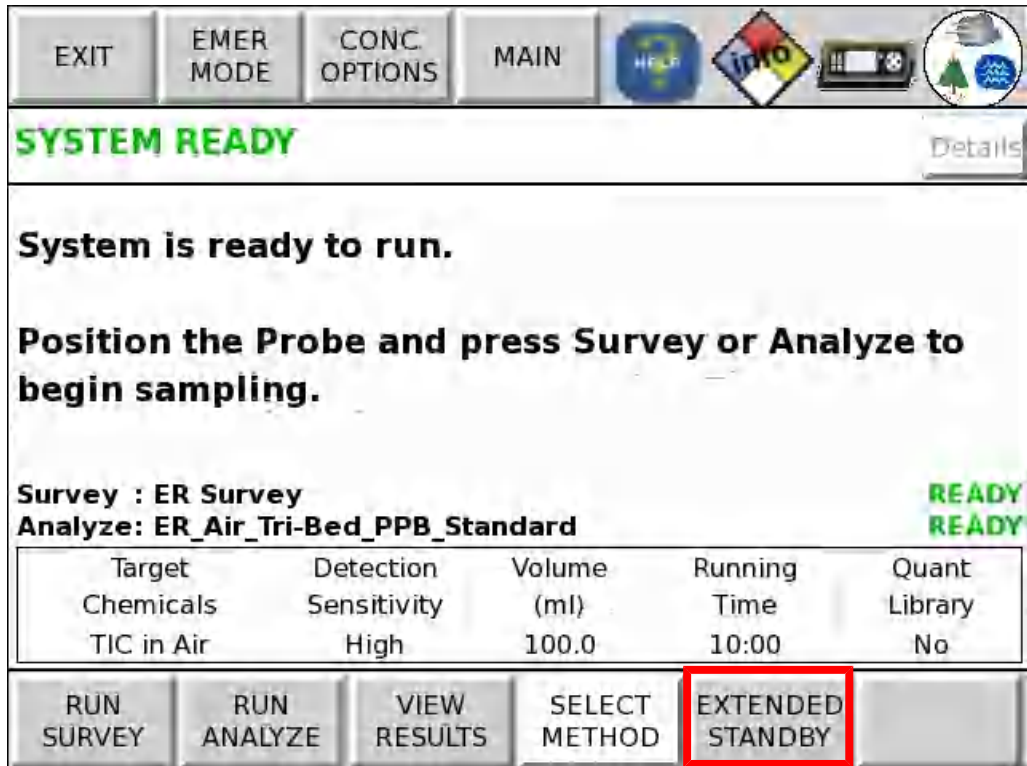
- 4 For **Turn Off**, the HAPSITE ER will turn off the power.
- 5 For **Reboot**, the screen will turn off and in approximately one minute, the screen will become active again. The preparation sequence will be restarted.
- 6 For **Standby**, the Extended Standby screen will be displayed. See Extended Standby [▶ 105].

### 9.8.1 Extended Standby

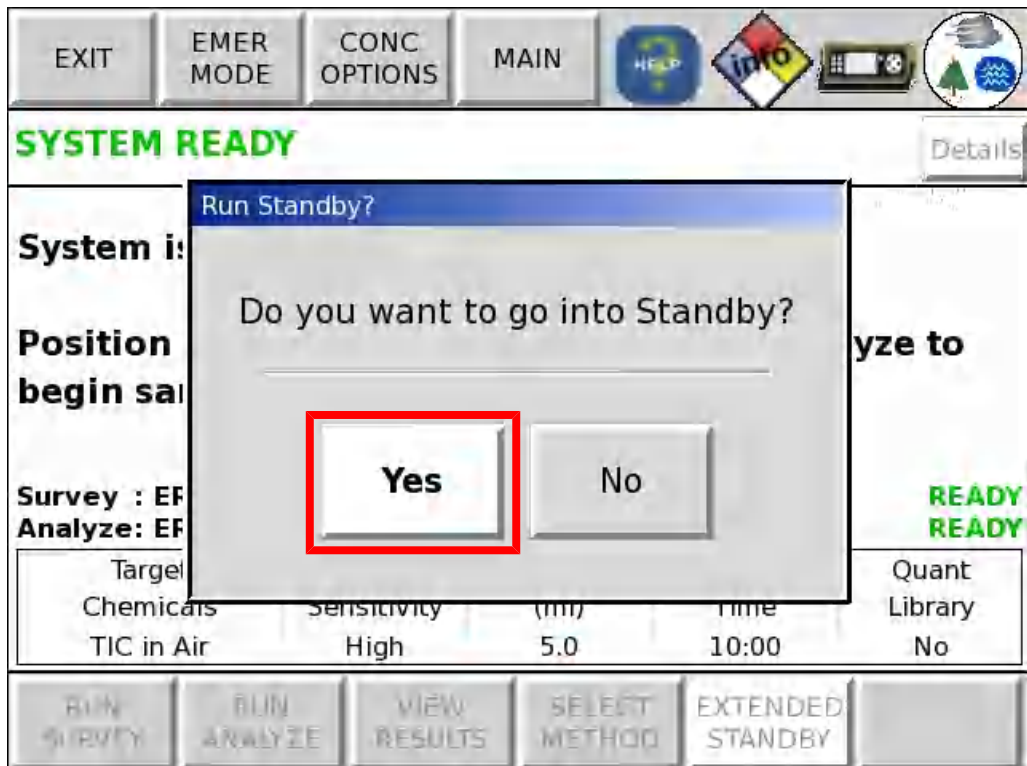
**Extended Standby** is the preferred storage mode. In this state, the NEG pump remains heated at 400°C and the ion pump continues pumping to maintain a vacuum in the mass spectrometer. HAPSITE ER turns off the heaters for all other components. When in **Extended Standby**, remove the gas canisters to avoid consumption.

**Extended Standby** extends NEG pump life and allows the system to prepare faster. Proceed as follows to place the system into **Extended Standby**.

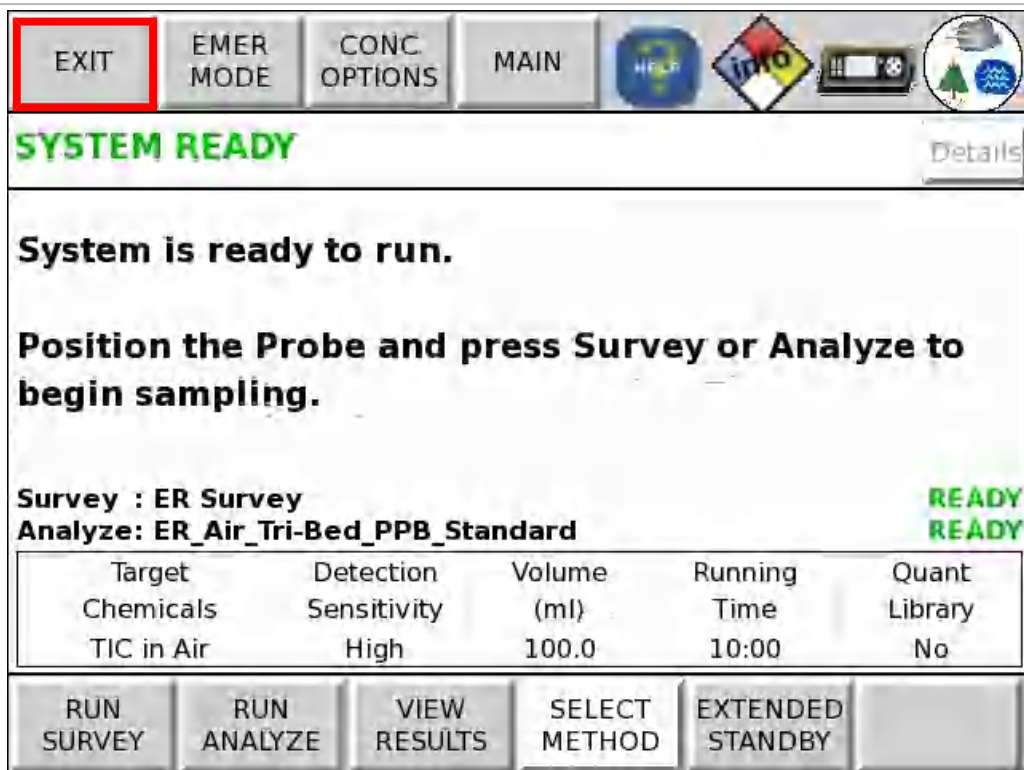
- 1 Touch **EXTENDED STANDBY**. Alternately, use the arrow keys to highlight **EXTENDED STANDBY** and push **OK SEL**.



- When the screen prompts, **Do you want to go into Standby?**, touch **Yes**. Alternately, use the arrow keys, highlight **Yes** and push **OK SEL**.



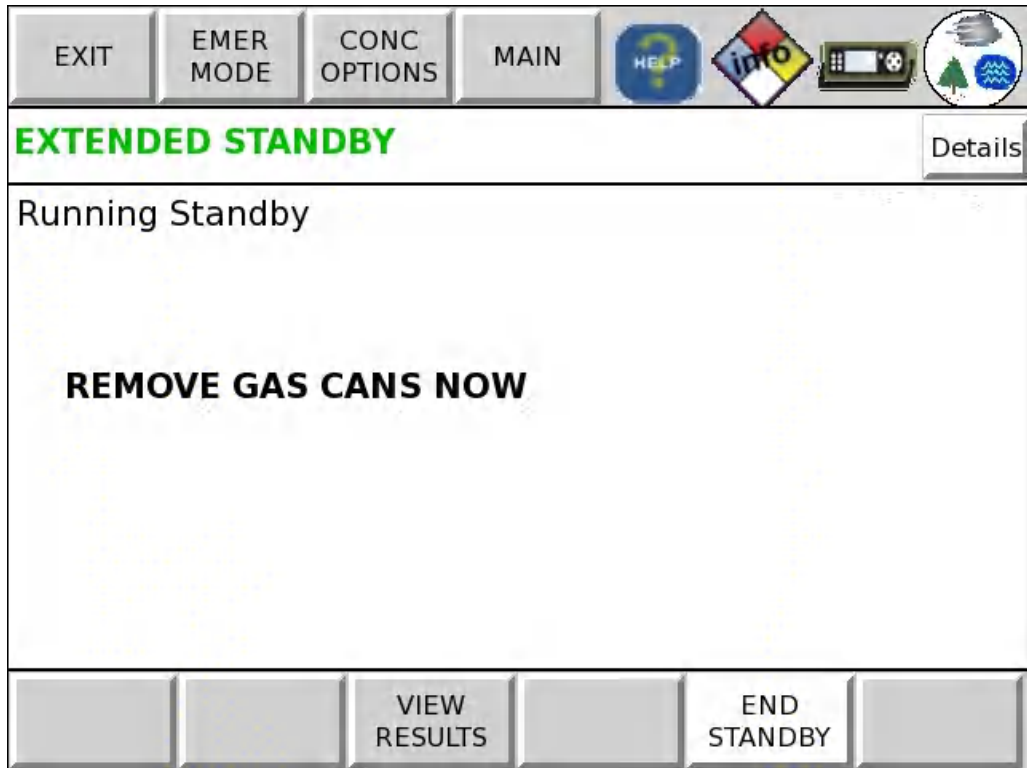
- Alternately, touch **EXIT** or use the arrow keys to highlight **EXIT**. Push **OK SEL**.



- 4 When the screen prompts, **Do you want to go into Standby?**, touch **Yes**. Alternately, use the arrow keys, highlight **Yes** and push **OK SEL**.

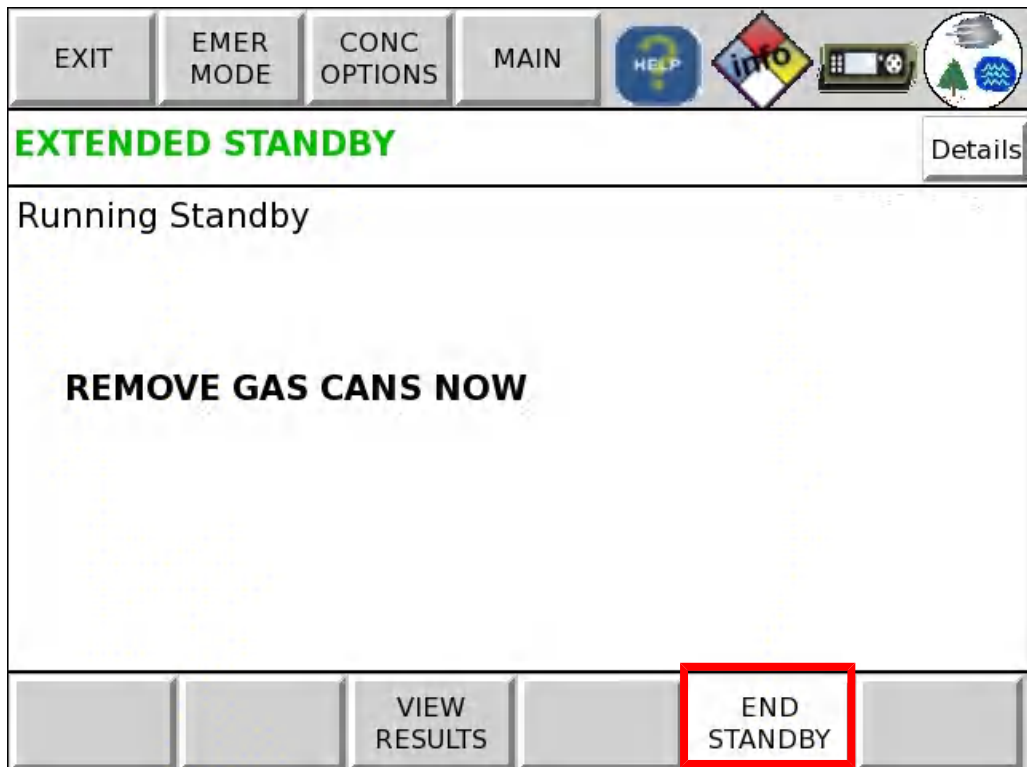


- 5 HAPSITE ER goes into **Extended Standby**. Remove the gas canisters.

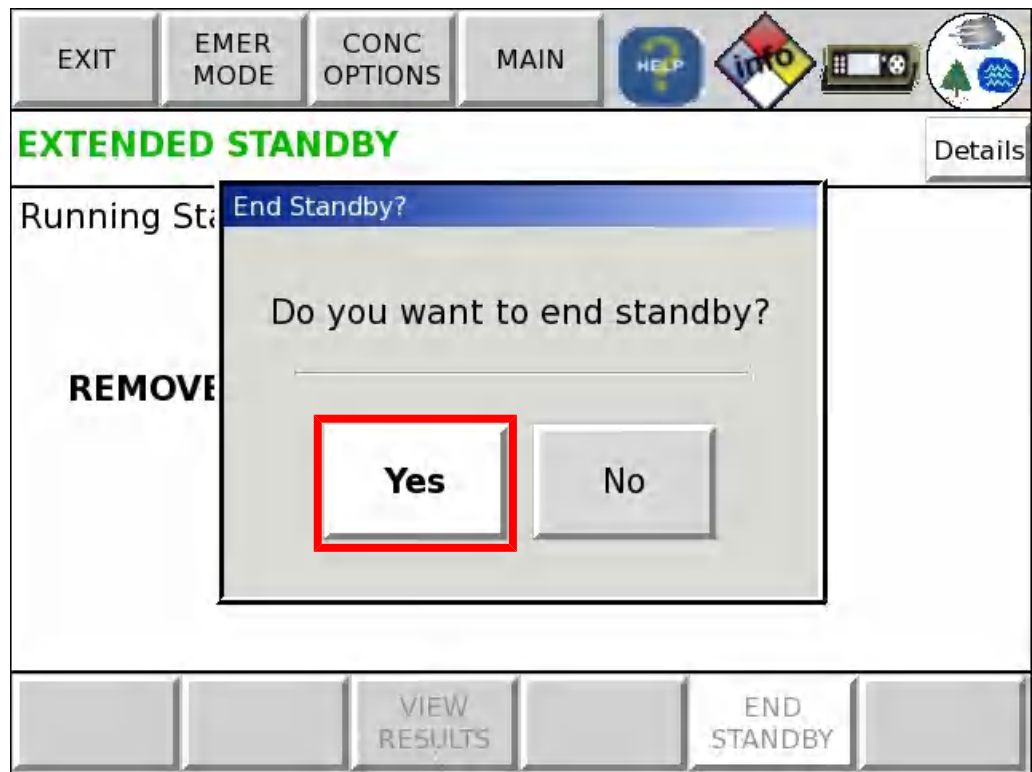


### 9.8.2 End Standby

- 1 To end standby, touch **END STANDBY** or using the arrow keys, highlight **END STANDBY** and push **OK SEL**.



- 2 When the system prompts, **Do you want to end standby?**, touch **Yes**.  
Alternately, highlight **Yes** using the arrow keys and push **OK SEL**.



# 10 Communications and Touch Screen Options

## 10.1 Communications

HAPSITE ER has two communication options: the cross-over cable and the wireless connection. The wireless settings will be configured with the laptop at the factory. Before connecting wirelessly, the wireless radio on HAPSITE ER and the wireless button on the laptop will have to be enabled. Follow the instructions below to turn on the radio. Refer to Connecting the Laptop [▶ 42] for instructions on attaching the laptop.

### 10.1.1 Wireless Range

HAPSITE ER is equipped with an 802.11 b/g wireless adapter. The typical range for a single is 300 ft. (100 m) with no obstructions. The following may degrade the signal:

- Metal buildings
- Concrete structures
- Electric devices in the area

### 10.1.2 Turning On the Radio

This procedure gives instructions for turning on the radio, which is necessary for wireless communication.



#### **DANGER**

**When the HAPSITE ER radio is on, even if wireless communication is not being used, a radio signal is being transmitted. The only way to eliminate the radio signal is to turn the radio off.**

- 1 Open the HAPSITE ER front panel.
- 2 Remove the cover from the power switch (for the wireless radio). It is located on the far left side. To remove, unscrew the cover by turning it counter-clockwise.



- 3 Press the power button until a click is heard. The green lights adjacent to **Radio** and **WLAN** should illuminate. When the green lights are illuminated, the wireless radio is being powered.



- 4 Replace the switch cover by placing it over the switch. Turn it clock-wise until finger tight.





### **⚠ DANGER**

HAPSITE ER contains a wireless transmitter/receiver that emits electromagnetic radiation (EMR). This radiation in a tactical or operational environment may potentially be used to locate the HAPSITE ER and its operators. This radiation also has the potential to detonate some types of unexploded ordnance (UXO), or improvised explosive devices (IEDs), or both, if HAPSITE ER is transmitting in the safety exclusion area around the device(s). Discussed below is a hardware switch to turn off the wireless radio so that HAPSITE ER may still be used in areas where these hazards are a concern. Consult applicable regulations and policies when using HAPSITE ER with the wireless device active in such environments.

## 10.1.3 Wireless Module Indicator Lights

Located on the Wireless Module inside the HAPSITE ER front cover are four indicator lights:

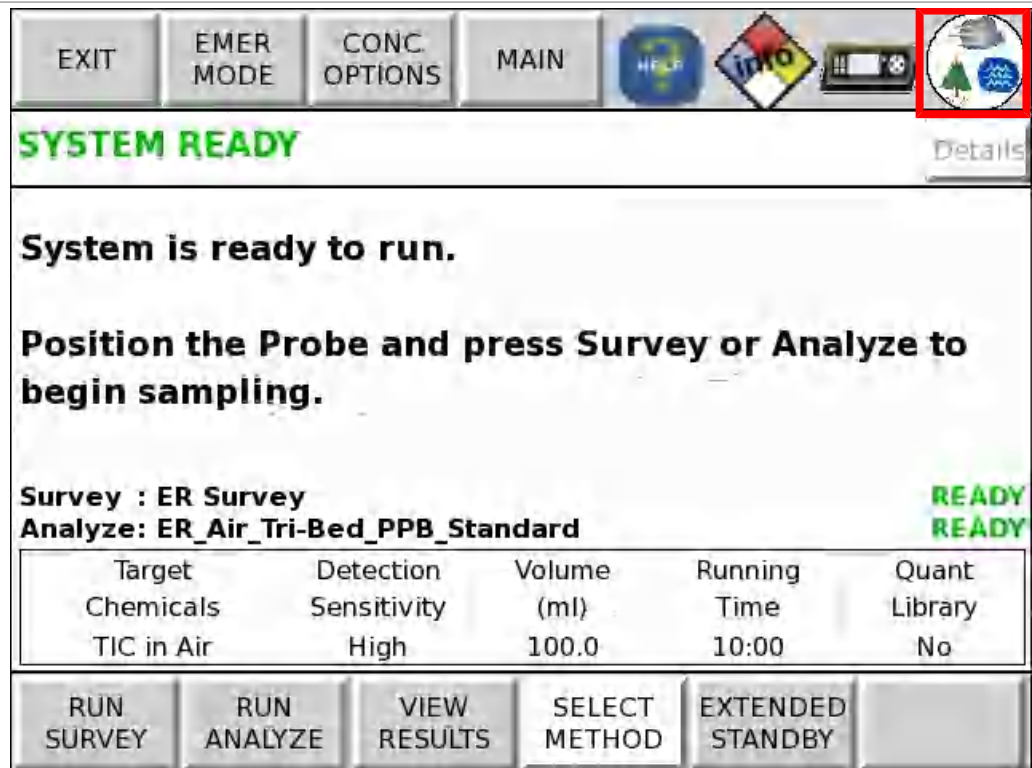
RADIO	When illuminated, the radio is enabled.
WLAN	When illuminated, the wireless connection is linked to the laptop. The indicator blinks when transmitting or receiving data.
LAN	When illuminated, the HAPSITE ER is connected via a crossover cable to the laptop. The indicator blinks when transmitting or receiving data. The indicator will be extinguished if the crossover cable is disconnected.
586	When illuminated, the HAPSITE ER 586 processor is linked to a wired or wireless connection.

## 10.2 Setting Up Communications

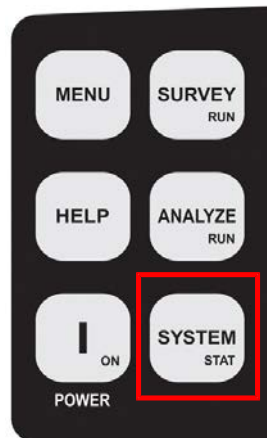
**Setting up communications is an Advanced user function.**

- 1 To locate the HAPSITE ER number on the front panel, touch the HAPSITE ER icon.

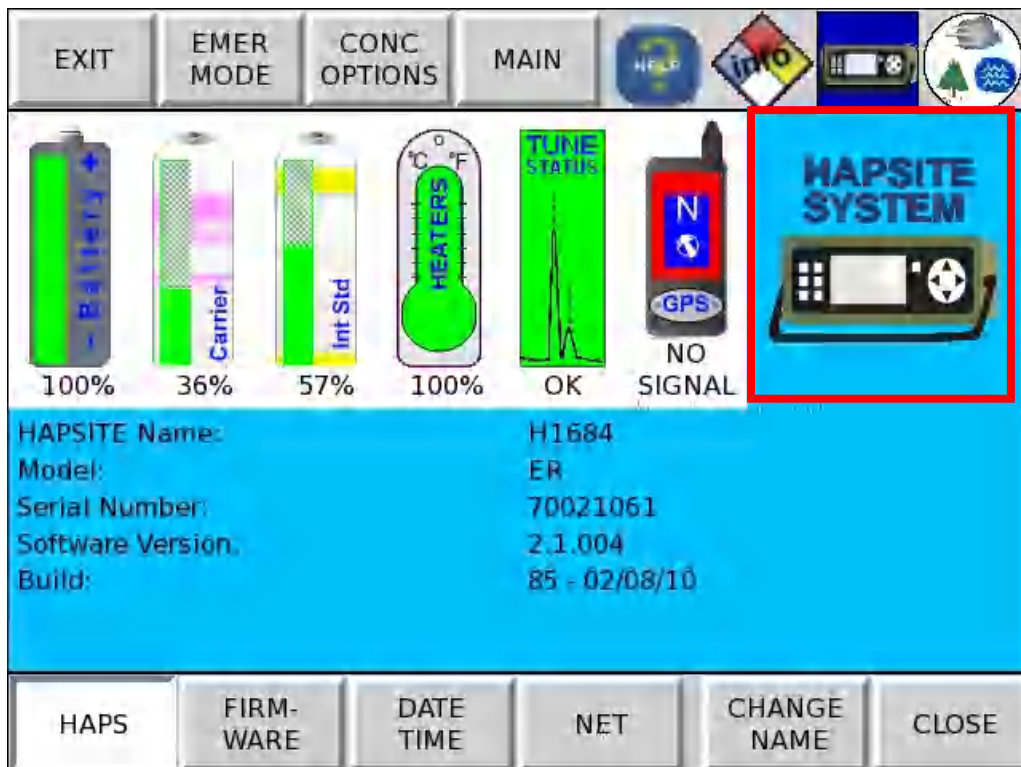




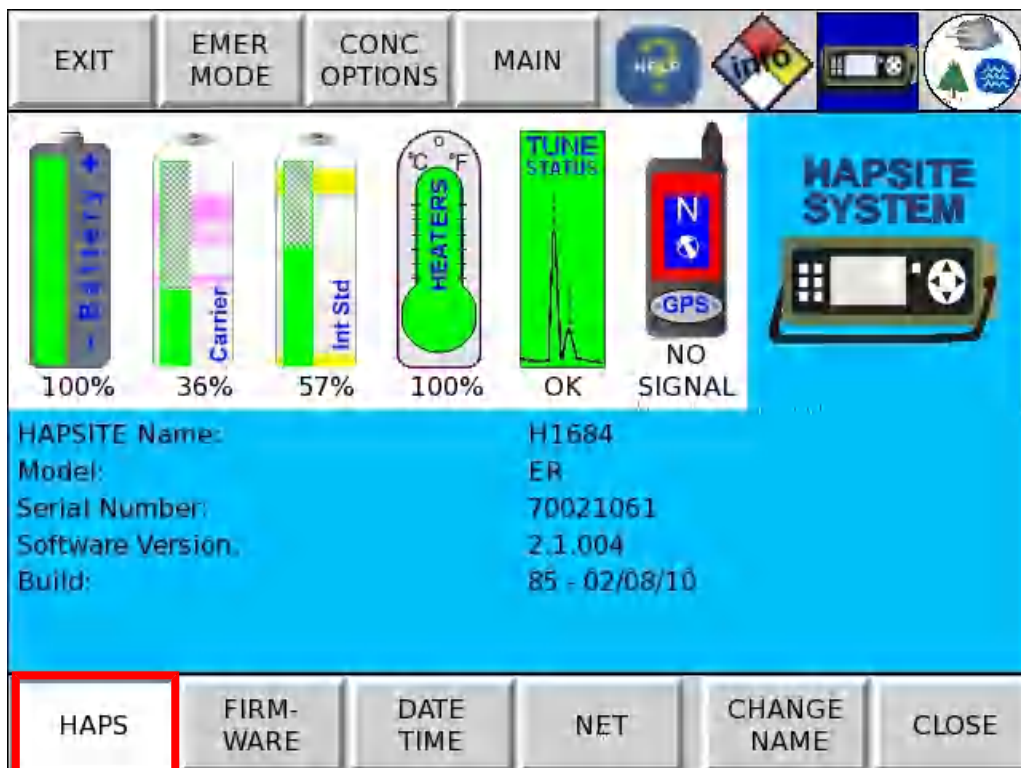
2 Alternately, push the **STAT** button until the HAPSITE ER icon is highlighted.



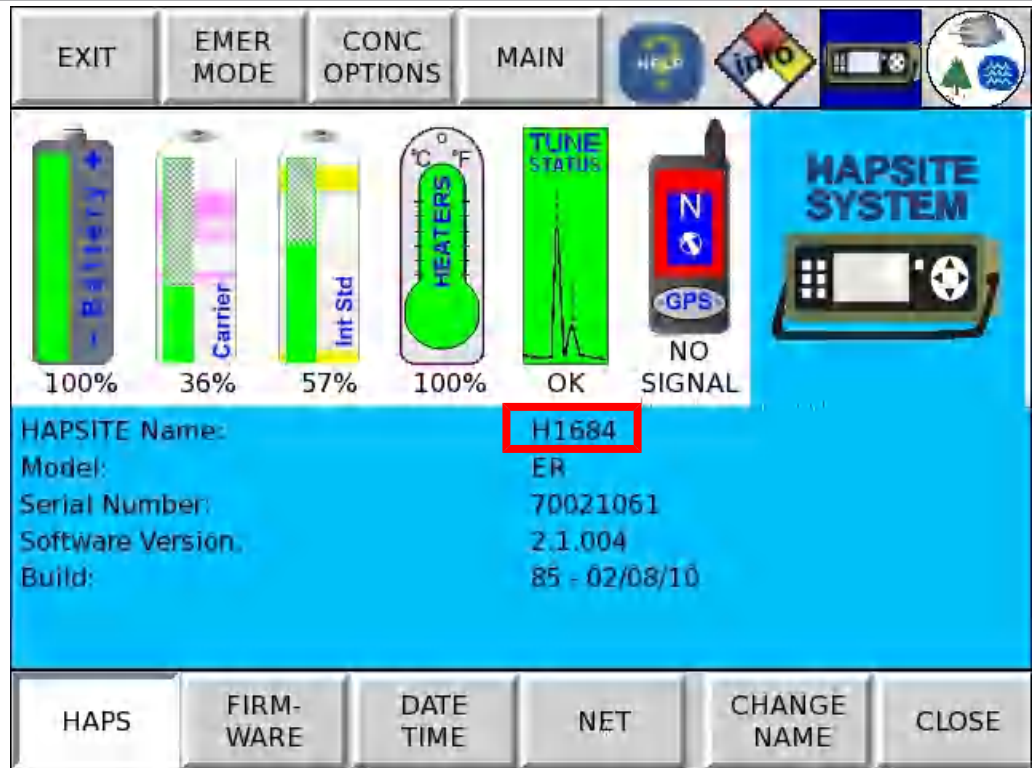
3 Touch the **HAPSITE System** icon.



- 4 Touch the **HAPS** button or use the arrow keys to highlight the **HAPS** button and push **OK SEL**.



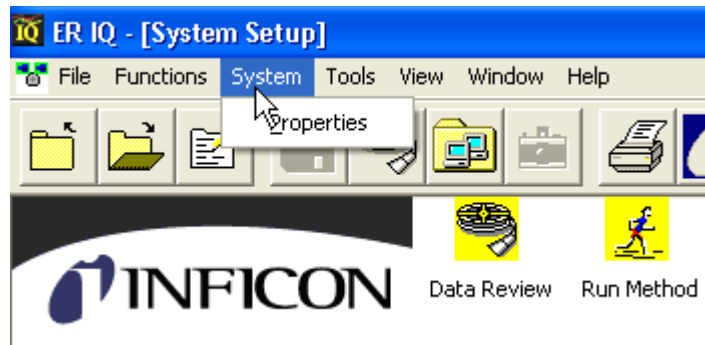
- 5 Locate and note the HAPSITE ER name.



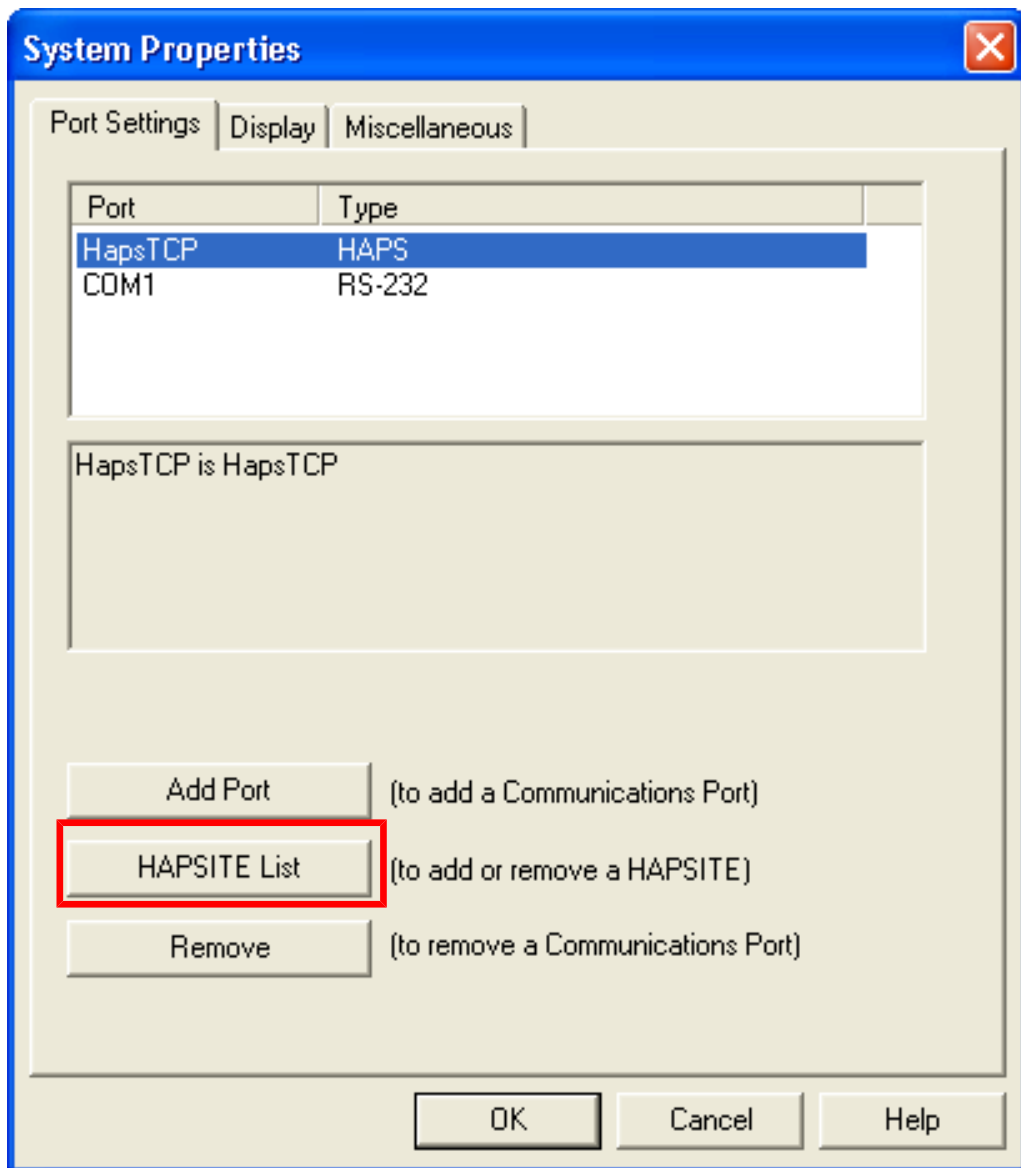
6 Open **ER IQ** Software.



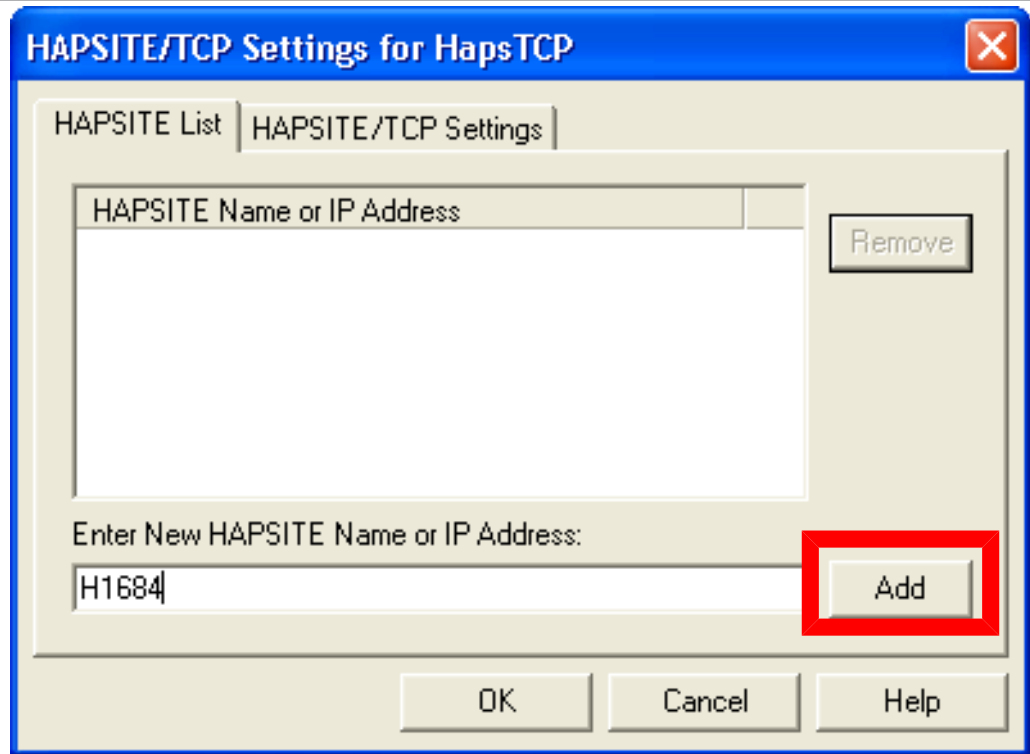
7 From the **System** drop-down menu, select **Properties**.



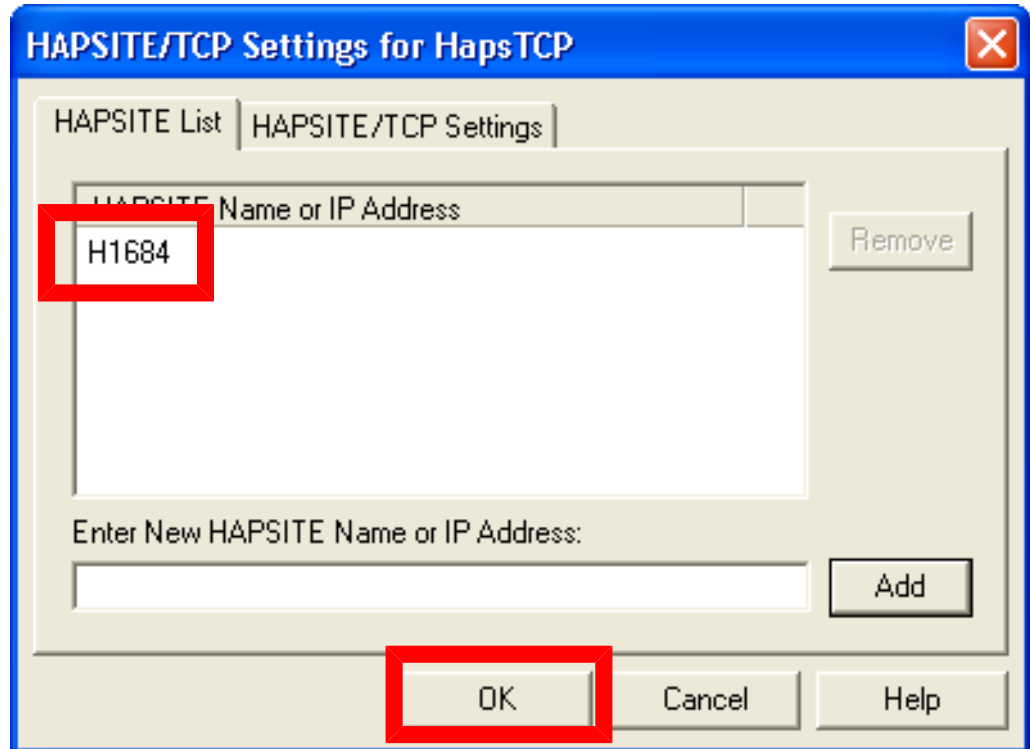
8 Click the **HAPSITE List** button.



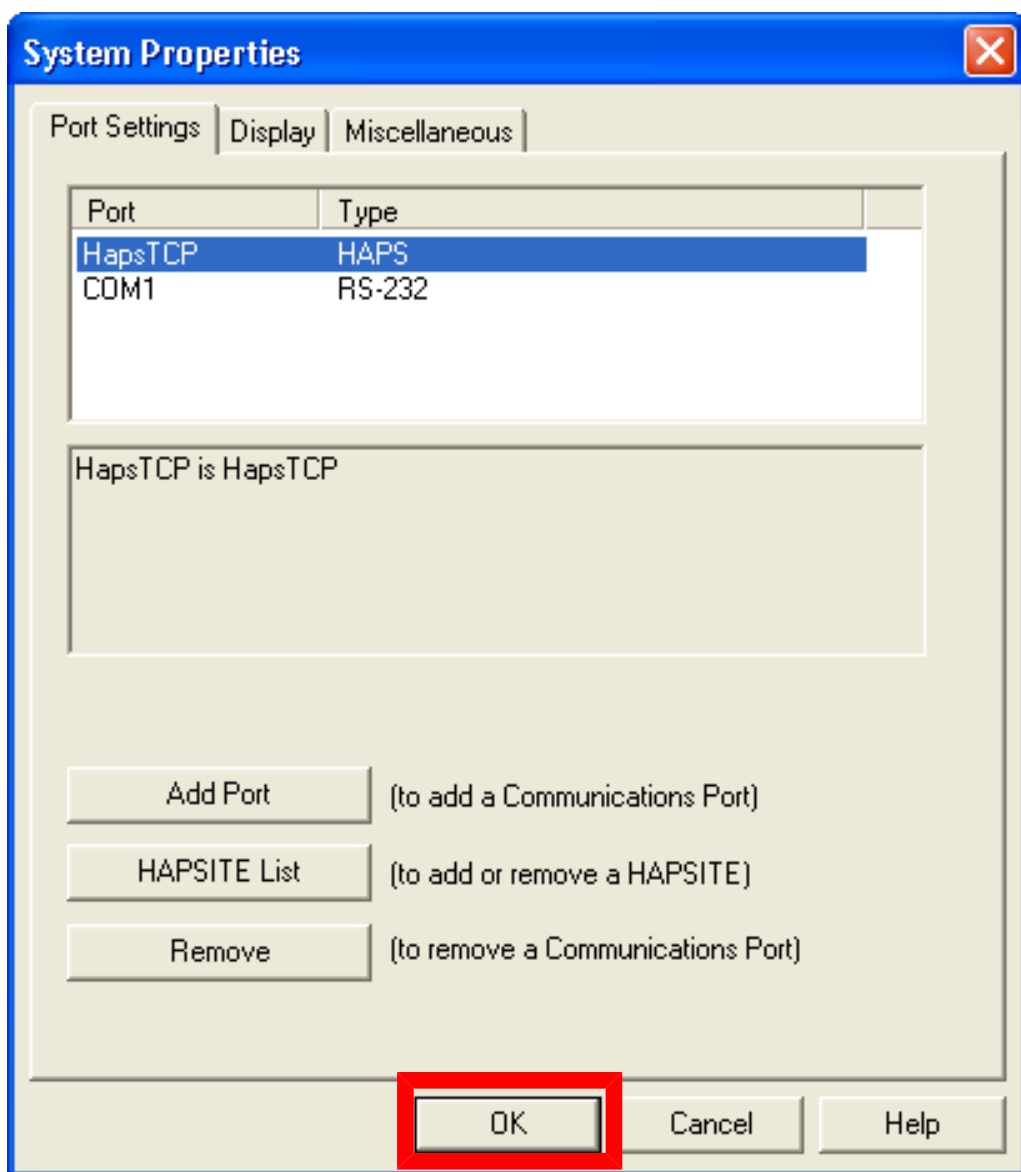
- 9 Enter the **H Number** into the **Enter New HAPSITE Name or IP Address**. Click **Add**.



10 The newly added HAPSITE ER will appear in the HAPSITE List. Press **OK**.



11 Press **OK** on the **System Properties** window.



- 12** The newly added HAPSITE ER icon will now appear at the bottom of the **System Setup** screen. If HAPSITE ER is displayed, as seen below, then communications have been established.



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- 13** If the HAPSITE ER icon is overlaid with a gray "X," HAPSITE ER is not trying to communicate with the computer.



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- 14 If the HAPSITE ER icon is overlaid with a red "X," HAPSITE ER is not properly communicating with the laptop. For example, the cross-over cable is disconnected.



- 15 If the HAPSITE ER icon is overlaid with a blue "X," communication has not been fully established. Continue with Configuring HAPSITE ER for Communications, see Configuring the Instrument for Communications [▶ 119].



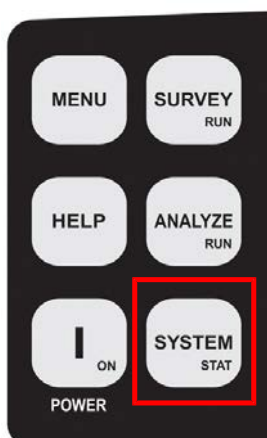
### 10.3 Configuring the Instrument for Communications

If communication between HAPSITE ER and the laptop could not be established using Setting Up Communications [▶ 112], continue as follows.

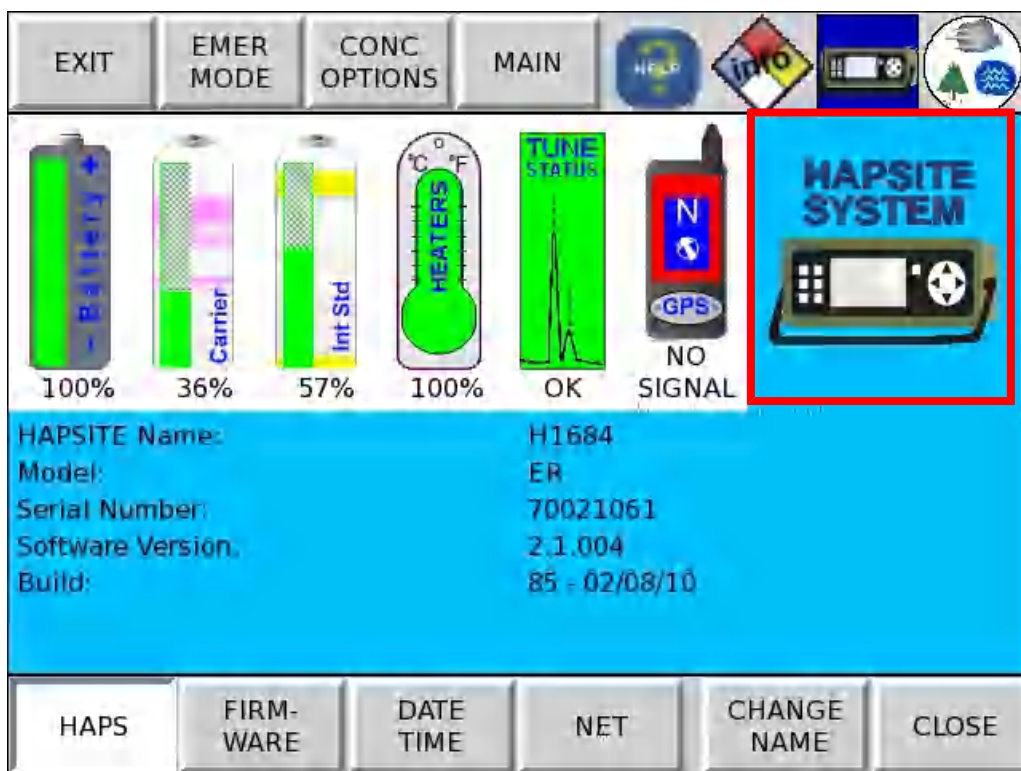
- 1 To locate the HAPSITE ER number on the front panel, touch the HAPSITE ER icon.

Target	Detection Sensitivity	Volume (ml)	Running Time	Quant Library
Chemicals	High	100.0	10:00	No

- Alternately, push the **STAT** button until the HAPSITE ER icon is highlighted.

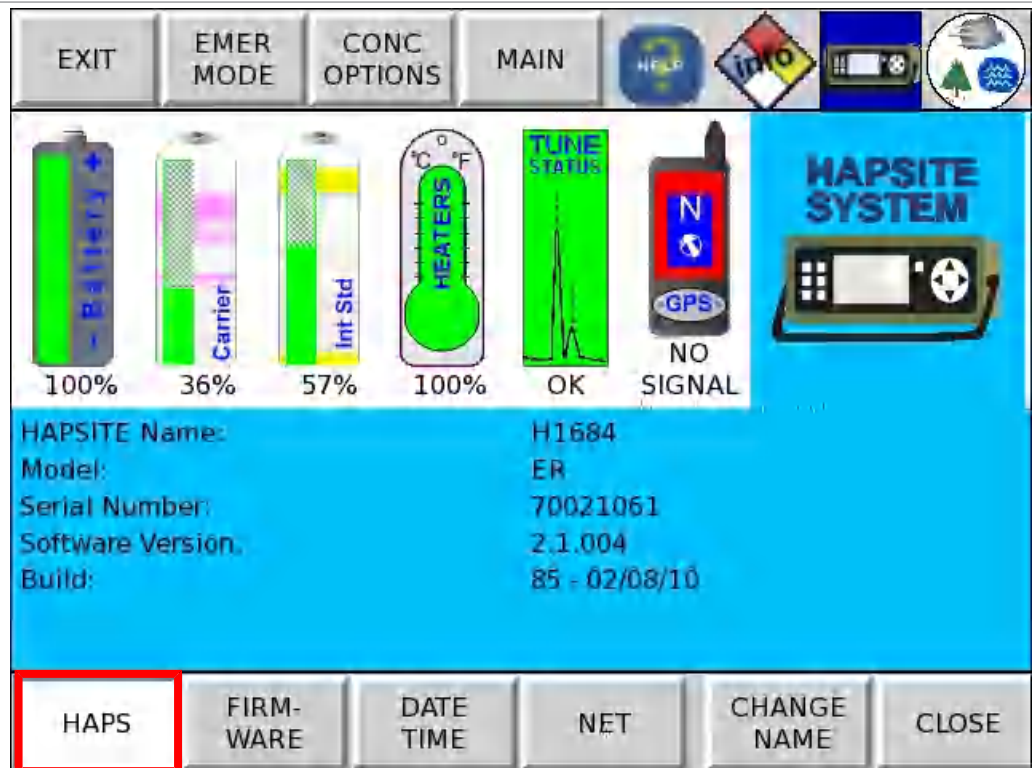


- Touch the **HAPSITE System** icon.

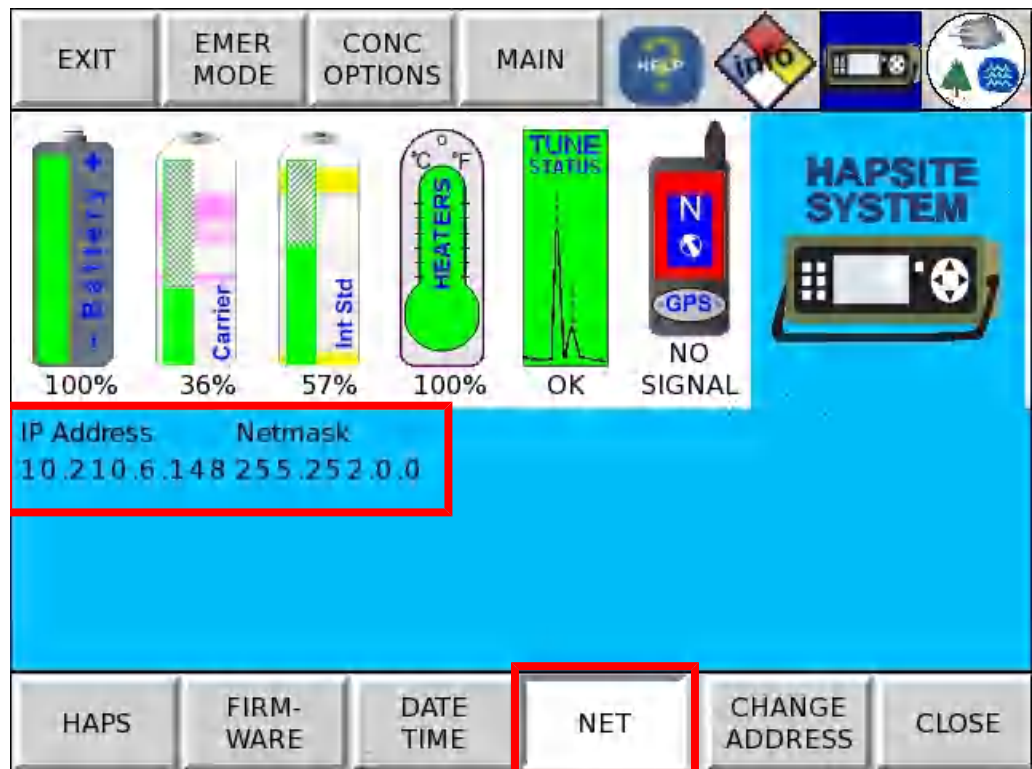


- Touch the **HAPS** button or use the arrow keys to highlight the **HAPS** button and push **OK SEL**.



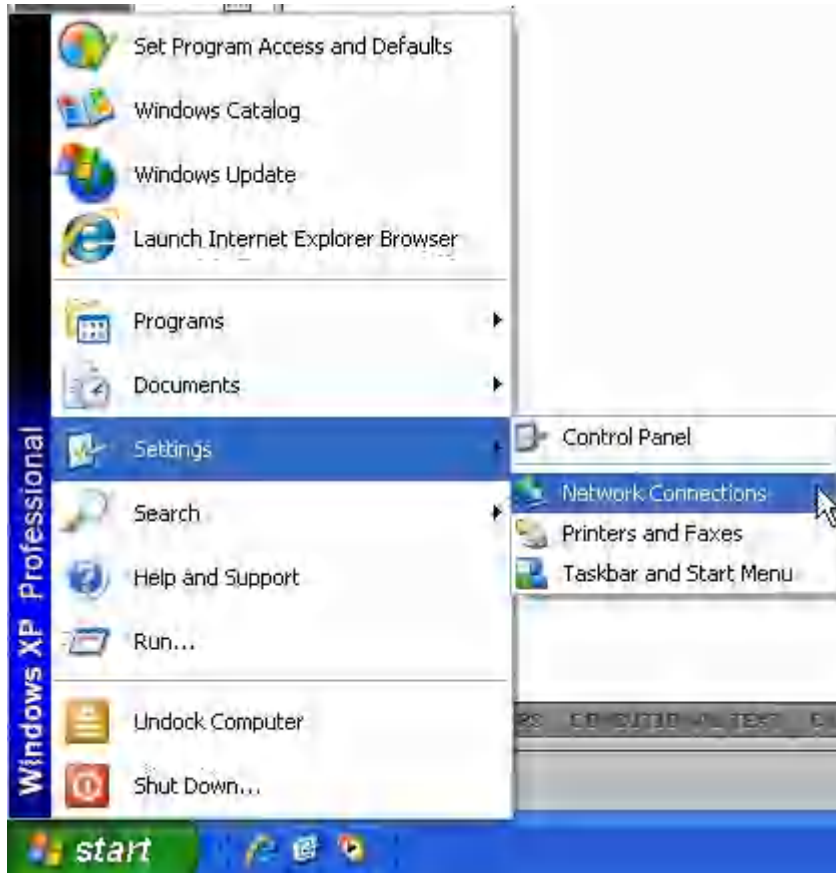


5 Touch the **NET** button or use the arrow keys to highlight the **NET** button and push **OK SEL**.

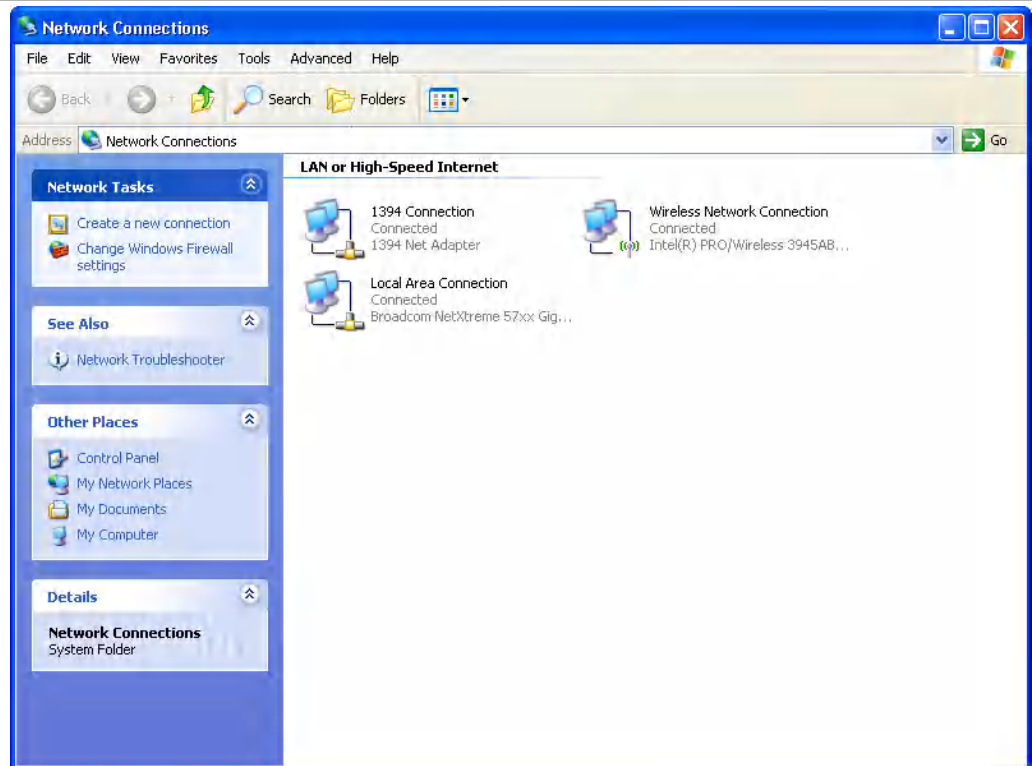


6 The **IP Adress** and the **Netmask** of HAPSITE ER is displayed. For example: 10.210.6.1.148/255.252.0.0. Each HAPSITE ER has a unique **IP Address**.

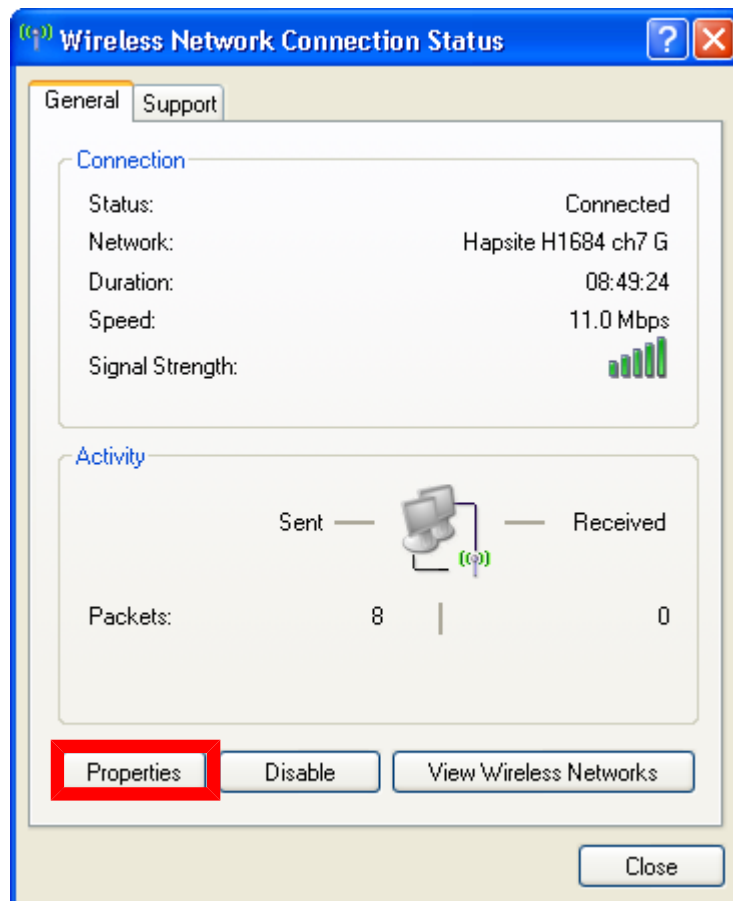
- 7 On the laptop, click the **Start** button on Microsoft Windows. Mouse over the **Settings** option and click **Network Connections**.



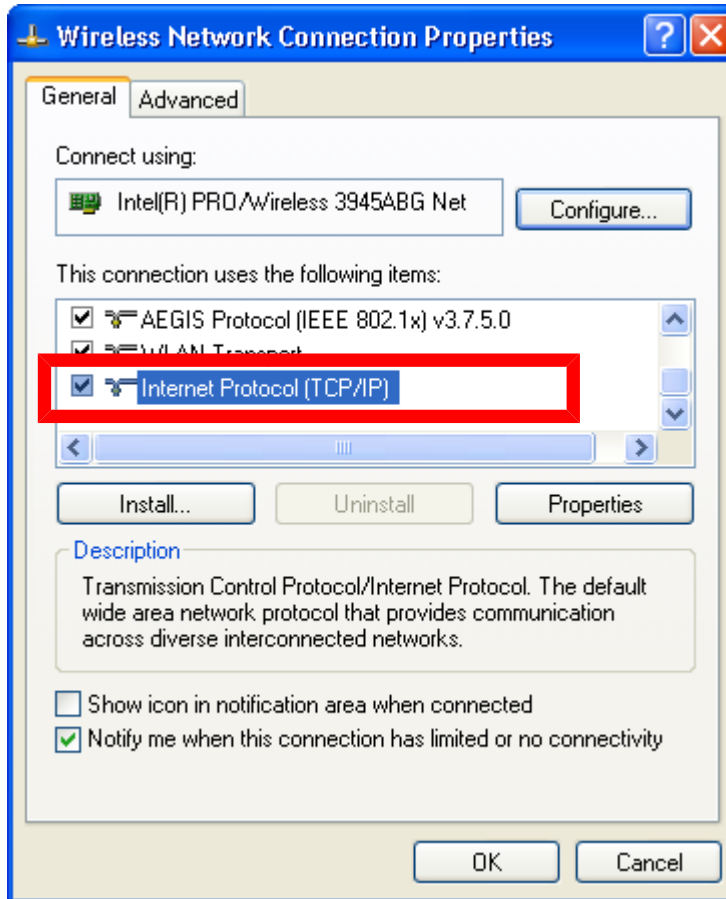
- 8 The following window is displayed. Double-click on the desired connection. Choose local area connection to troubleshoot a crossover cable. Choose **Wireless Connection** to connect wirelessly.



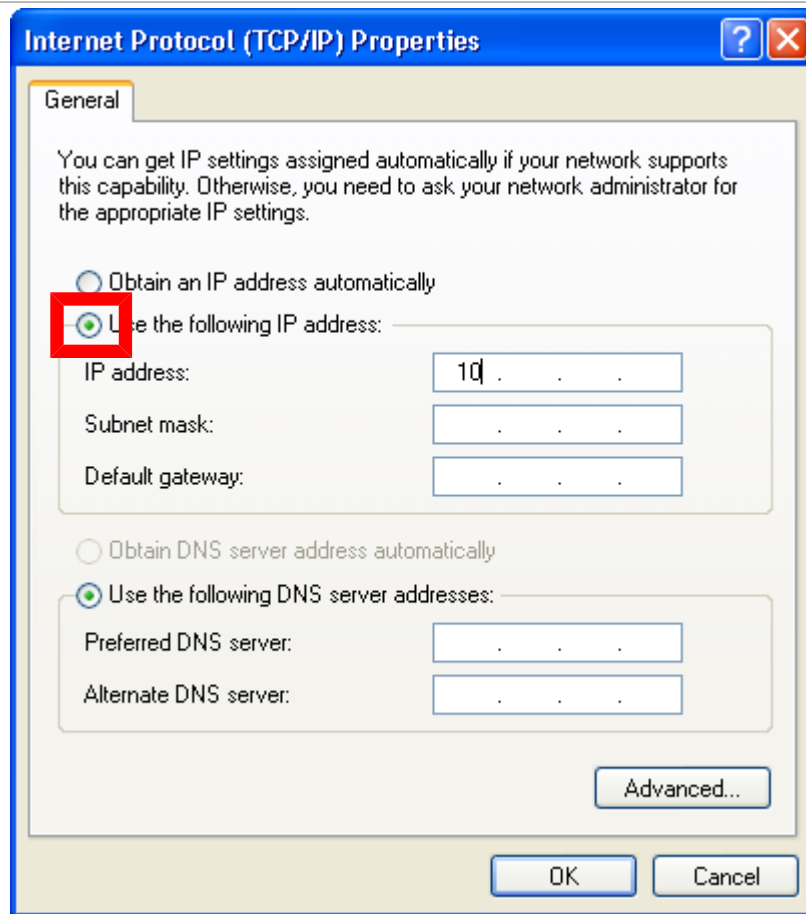
9 The **Connection Status** window opens. Click **Properties**.



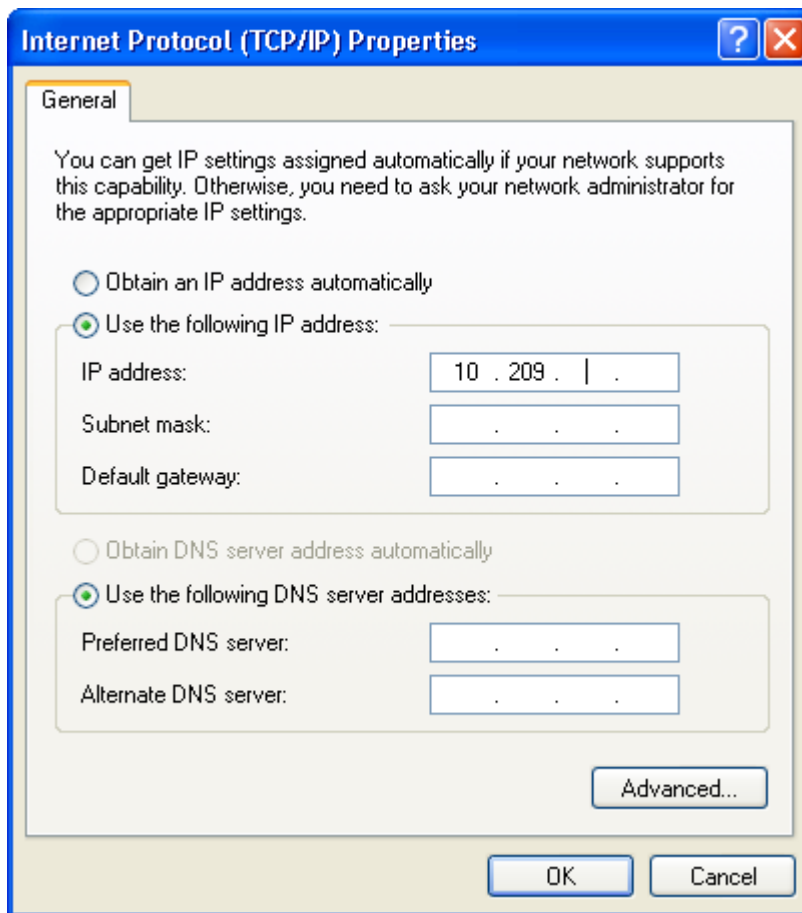
- 10 In the **General** tab, scroll down and highlight **Internet Protocol (TCP/IP)** and click **Properties**.



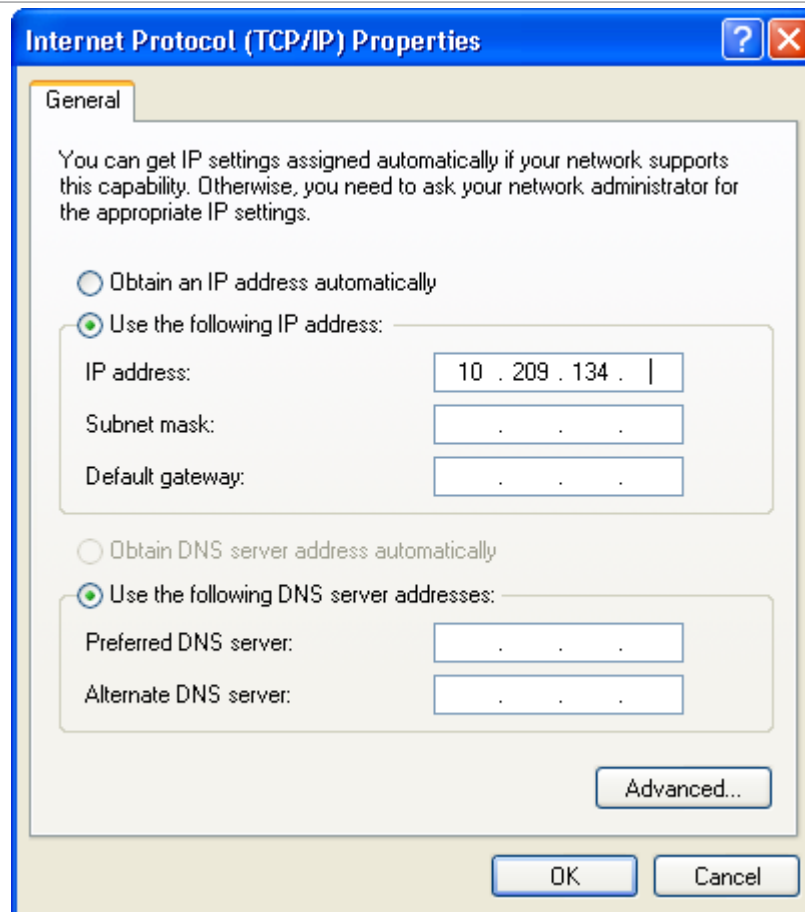
- 11 Select **Use the following IP address**. Enter the first number of the IP address into the first slot. For example, if the IP Address is **10.210.6.148**, enter **10** into the first slot.



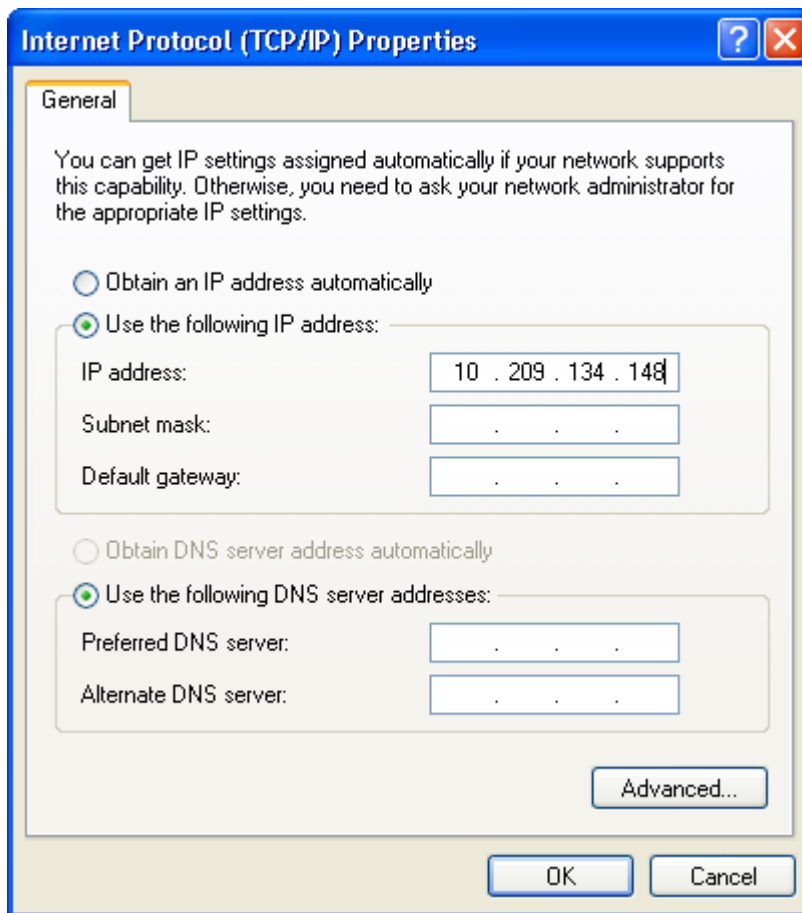
**12** For the second number of the **IP Address**, enter **210** if connecting with the cable and **209** if connecting with the wireless radio into the second slot.



- 13** For the third number of the **IP Address**, add **128** to the number in the IP address. In this example, adding **128** to **6** equals **134**, so **134** is entered into the third slot.

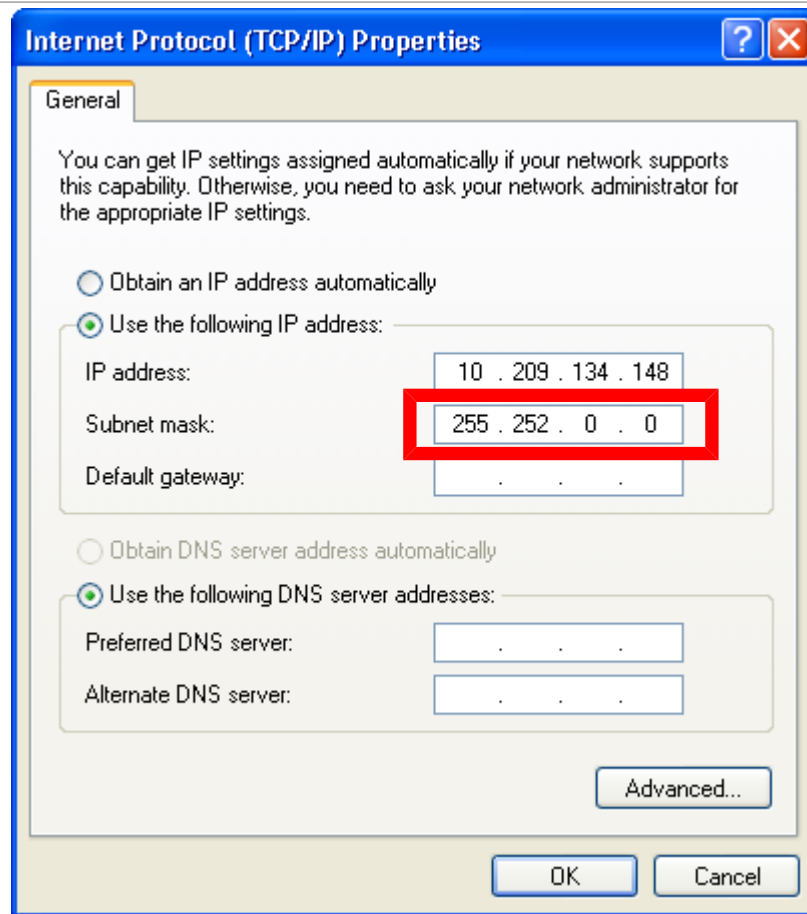


- 14** The fourth number of the **IP Address** is entered into the fourth slot without modification. Therefore, in this example, **148** would be entered into the fourth slot.

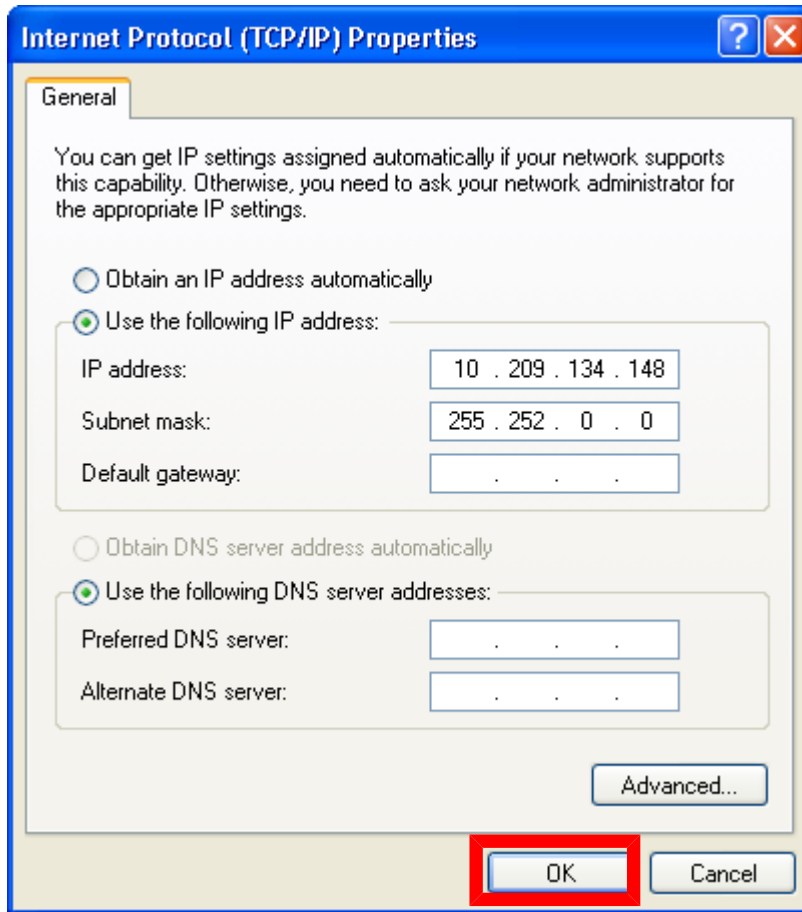


**15** Enter in the **Subnet mask** exactly as displayed.





**16** Click **OK** in the **Internet Protocol Properties** window to close it.



- 17 Communication between HAPSITE ER and the laptop is now established as indicated by the absence of an "X" over the HAPSITE ER **Sensor Icon** in the **System Setup** screen.



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### 10.3.1 Turning Off the Radio

See the following procedure for instructions for turning off the radio when wireless communication is not desired.

When the HAPSITE ER radio is on, even if the wireless communication is not being used, a radio signal is being transmitted. The only way to eliminate the radio signal is to turn off the radio.



#### **⚠ DANGER**

**HAPSITE ER contains a wireless transmitter/receiver that emits electromagnetic radiation (EMR). This radiation in a tactical or operational environment may potentially be used to locate the HAPSITE**

ER and its operators. This radiation also has the potential to detonate some types of unexploded ordnance (UXO), or improvised explosive devices (IEDs), or both, if HAPSITE ER is transmitting in the safety exclusion area around the device(s). Discussed below is a hardware switch to turn off the wireless radio so that HAPSITE ER may still be used in areas where these hazards are a concern. Consult applicable regulations and policies when using HAPSITE ER with the wireless device active in such environments.

- 1 Open the front panel of HAPSITE ER.
- 2 Remove the cover from the power switch (for the wireless radio). It is located on the far left hand side. To remove, unscrew the cover by turning it counter-clockwise.



- 3 Press the button until a click is heard. The green lights adjacent to **Radio** and **WLAN** should extinguish. When the green lights are extinguished, the power to the wireless radio is off.



- 4 Replace the switch cover by placing it over the switch. Turn it clock-wise until finger-tight.



## 10.4 Wireless Information



### **⚠ DANGER**

HAPSITE ER contains a wireless transmitter/receiver that emits electromagnetic radiation (EMR). This radiation in a tactical or operational environment may potentially be used to locate the HAPSITE ER and its operators. This radiation also has the potential to detonate some types of unexploded ordnance (UXO), or improvised explosive devices (IEDs), or both, if HAPSITE ER is transmitting in the safety exclusion area around the device(s). Discussed below is a hardware switch to turn off the wireless radio so that HAPSITE ER may still be used in areas where these hazards are a concern. Consult applicable regulations and policies when using HAPSITE ER with the wireless device active in such environments.

### 10.4.1 Regulatory Compliance Information for UNITED STATES Users

This section of the Operating Manual lists FCC compliance information for the HAPSITE ER system that contains the wireless communication option.



This equipment contains an OEM Embedded Wireless Bridge (Ethernet to Wireless LAN) Module from Quatech Inc.

#### **FCC ID: F4AWLNG1**

This device complies with Part 15 of the FCC rules and is subject to the following two conditions:

- 1 This device may not cause harmful interference, and
- 2 This device must accept any interference received, including interference that may cause undesired operation.



### CAUTION

To maintain compliance with FCC standards and regulations and to ensure the proper operation of the wireless communication system used within the HAPSITE ER instrument, **ONLY** use the antenna that was originally supplied with the instrument. If damage occurs to the original antenna, please contact the INFICON service department for a replacement antenna (see Customer Support [▶ 19] for contact information).

#### 10.4.1.1 FCC Statement

This equipment has been tested and found to comply with the limits for a Class B digital device, pursuant to Part 15 of the FCC Rules. These limits are designed to provide reasonable protection against harmful interference in a residential installation. This equipment generates, uses and can radiate radio frequency energy and if not installed and used in accordance with the instructions, may cause harmful interference to radio communications. However, there is no guarantee that interference will not occur in a particular installation. If this equipment does cause harmful interference to radio or television reception, which can be determined by turning the equipment off and on, the user is encouraged to try to correct the interference by one or more of the following measures:

- Reorient or relocate the receiving antenna
- Increase the separation between the equipment and receiver
- Connect the equipment into an outlet on a circuit different from that to which the receiver is connected
- Consult the dealer or an experienced radio/TV technician for assistance

#### 10.4.1.2 FCC RF Exposure Statement



### WARNING

To satisfy RF exposure requirements, this device and its antenna must operate with a separation distance of at least 20 cm from all persons and must not be co-located or operating in conjunction with any other antenna or transmitter.

## 10.4.2 Regulatory Compliance Information for CANADIAN Users

This section of the Operating Manual lists Industry Canada (IC) compliance information for the HAPSITE ER system that contains the wireless communication option.



This equipment contains an OEM Embedded Wireless Bridge (Ethernet to Wireless LAN) Module from Quatech Inc.

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### IC: 3913A-WLNG1

This device complies with RSS-210 of Industry Canada (IC) and is subject to the following two conditions:

- 1 This device may not cause harmful interference, and
- 2 This device must accept any interference received, including interference that may cause undesired operation.

### 10.4.2.1 Industry Canada (IC) Notes

This equipment complies with Canadian RSS-210.



#### CAUTION

**This device has been designed to operate with an antenna having a maximum gain of 5.0 dB. An antenna having a higher gain is strictly prohibited per regulations of Industry Canada (IC). The required antenna impedance is 50 ohms.**

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To reduce the potential radio interference to other users, the antenna type and gain should be so chosen that the equivalent isotropically radiated power (EIRP) is not more than required for successful communications.

## 10.4.3 Regulatory Compliance Information for EUROPEAN Users

This section of the Operating Manual lists R&TTE compliance information for the HAPSITE ER system that contains the wireless communication option.

HAPSITE ER is marked with the following symbol:



This symbol indicates compliance with the essential requirements of Directive 73//23/EEC and the essential requirements of articles 3.1(b), 3.2, and 3.3 of Directive 1999/5/EC. Such marking is indicative that this equipment meets or exceeds the following technical standards:

- EN 300 328-2 – Electromagnetic compatibility and Radio Spectrum Matters (ERM); Wideband Transmission systems; data transmission equipment operating in the 2.4 GHz ISM band and using spread spectrum modulation techniques.
- EN 301 489-17 – Electromagnetic compatibility and Radio Spectrum Matters (ERM); Electromagnetic Compatibility (EMC) standard for radio equipment and services; Part 17: Specific conditions for 2.4 GHz wideband transmission systems and 5 GHz high performance RLAN equipment.
- EN 61010-1 – Safety requirements for electrical equipment for measurement, control, and laboratory use.

#### 10.4.3.1 European Usage Restrictions



#### CAUTION

**European usage restrictions apply to this equipment. The end user must comply with the usage restrictions noted in the table below when operating this equipment in the countries that have restrictions.**

HAPSITE ER is marked with the following symbol:



This symbol indicates that usage restrictions apply to this equipment. Such marking indicates that the end user must comply with the following statements about usage restrictions:

- To ensure compliance with local regulations, be sure to select the country in which the access point is installed.
- This instrument can be used as shown in the table below :

Countries	Restrictions
France	Outdoor use limited to 10mW e.i.r.p. within the band 2454 ro 2483.5 MHz
Italy	If used outside of own premises, general authorization is required.
Luxembourg	General authorization is required for public service.
Romania	On a secondary basis. Individual license required.
Austria, Denmark, Finland, Germany, Greece, Iceland, Ireland, Liechtenstein, Netherlands, Norway, Portugal, Spain, Sweden, Switzerland, United Kingdom	None.

### 10.4.3.2 European EMC Compliance Statement

English	Hereby, INFICON Inc. declares that this HAPSITE ER Portable GC/MS is in compliance with the essential requirements and other relevant provisions of Directive 1999/5/EC.
Finnish	INFICON Inc. vakuuttaa täten että HAPSITE ER Portable GC/MS tyyppinen laite on direktiivin 1999/5/EY oleellisten vaatimusten ja sitä koskevien direktiivin muiden ehtojen mukainen.
Dutch	Hierbij verklaart INFICON Inc. dat het toestel HAPSITE ER Portable GC/MS in overeenstemming is met de essentiële eisen en de andere relevante bepalingen van richtlijn 1999/5/EG



Dutch	Bij deze verklaart INFICON Inc. dat deze HAPSITE ER Portable GC/MS voldoet aan de essentiële eisen en aan de overige relevante bepalingen van Richtlijn 1999/5/EC.
French	Par la présente INFICON Inc. déclare que l'appareil HAPSITE ER Portable GC/MS est conforme aux exigences essentielles et aux autres dispositions pertinentes de la directive 1999/5/CE.
Danish	Undertegnede INFICON Inc. erklærer herved, at følgende udstyr HAPSITE ER Portable GC/MS overholder de væsentlige krav og øvrige relevante krav i direktiv 1999/5/EF.
German	Hiermit erklärt INFICON Inc. dass sich dieser HAPSITE ER Portable GC/MS in Übereinstimmung mit den grundlegenden Anforderungen und den anderen relevanten Vorschriften der Richtlinie 1999/5/EG befindet". (BMWi)
German	Hiermit erklärt INFICON Inc. die Übereinstimmung des Gerätes HAPSITE ER Portable GC/MS mit den grundlegenden Anforderungen und den anderen relevanten Festlegungen der Richtlinie 1999/5/EG. (Wien)
Swedish	Härmed intygar INFICON Inc. att denna HAPSITE ER Portable GC/MS står i överensstämmelse med de väsentliga egenskapskrav och övriga relevanta bestämmelser som framgår av direktiv 1999/5/EG.
Greek	ΜΕ ΤΗΝ ΠΑΡΟΥΣΑ INFICON Inc. ΔΗΛΩΝΕΙ ΟΤΙ Η HAPSITE ER Portable GC/MS ΣΥΜΜΟΡΦΩΝΕΤΑΙ ΠΡΟΣ ΤΙΣ ΟΥΣΙΩΔΕΙΣ ΑΠΑΙΤΗΣΕΙΣ ΚΑΙ ΤΙΣ ΛΟΙΠΕΣ ΣΧΕΤΙΚΕΣ ΔΙΑΤΑΞΕΙΣ ΤΗΣ ΟΔΗΓΙΑΣ 1999/5/EK
Italian	Con la presente INFICON Inc. dichiara che questo HAPSITE ER Portable GC/MS è conforme ai requisiti essenziali ed alle altre disposizioni pertinenti stabilite dalla direttiva 1999/5/CE.
Spanish	Por medio de la presente INFICON Inc. declara que el HAPSITE ER Portable GC/MS cumple con los requisitos esenciales y cualesquiera otras disposiciones aplicables o exigibles de la Directiva 1999/5/CE.
Portuguese	INFICON Inc. declara que este HAPSITE ER Portable GC/MS está conforme com os requisitos essenciais e outras disposições da Directiva 1999/5/CE.

### 10.4.3.3 European Safety Compliance Statement

This device has been tested and certified according to the safety standard EN 61010-1: 2010 and is intended to be used in accordance with the information provided in this manual. For additional information concerning the directives and standards that this instrument complies with, please refer to the Declaration of Conformity [▶ 12] that is located in the front of this manual.

# 11 Laptop Operation

## 11.1 Laptop Operation



See ER IQ Software [▶ 152] for additional information on the **ER IQ** software installed on the laptop computer.

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### 11.1.1 Sampling Procedure

✓ For assembly instructions, refer to Basic Assembly [▶ 30].

- 1 Press the **POWER** button on the front panel to turn on HAPSITE ER. HAPSITE ER takes 1-2 minutes to boot.



If desired and equipped, HAPSITE ER can be used with the laptop computer via the wireless connection. Refer to Communications and Touch Screen Options [▶ 110] for additional information on set-up and usage.

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- 2 Locate the power cord and mouse (optional). Plug them into the appropriate ports on the computer. Open the laptop and press the power button.

## 11.2 Survey Mode

Survey mode is used for quick analysis and tentative results. It is generally two minutes long and detects compounds with a concentration greater than 1 ppm.



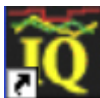
### ⚠ CAUTION

**Do not touch the sample with the probe.**

**Do not allow liquids to enter the probe.**

## 11.2.1 Sampling Procedure

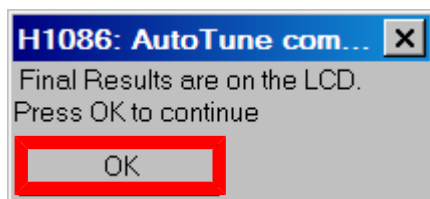
- 1 Open the **ER IQ** software by double-clicking on the ER IQ icon.



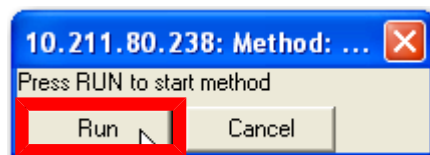
- 2 If the probe is attached, HAPSITE ER will begin preparing a Survey method. If this method is not the desired one, see [Selecting a New Method](#) [▶ 149].
  - ⇒ The following message will be displayed while HAPSITE ER prepares for sampling. No action is required from the user.



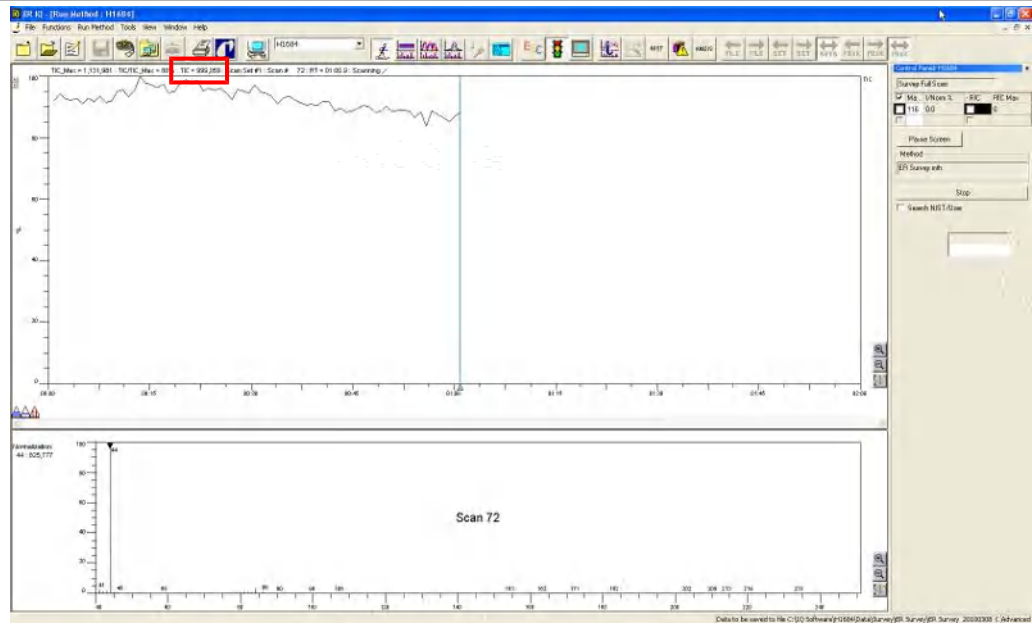
- 3 As part of the preparation, an AutoTune will run. If the Autotune is successful, the following message will display. Click **OK**. If AutoTune fails, see [Performing Manual Tune](#) [▶ 283].



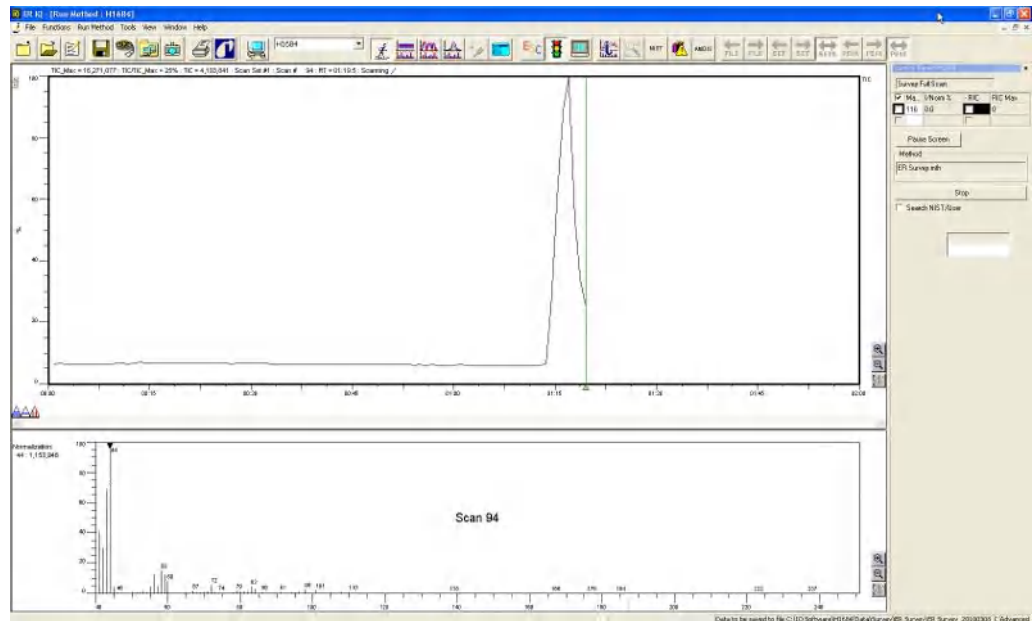
- 4 HAPSITE ER will check pressures and automatically heat all necessary components to the setpoint temperatures. Progress will be indicated by a bar graph. Once all components have reached their setpoint temperatures, a prompt will be displayed to **Press RUN to start method**.
- 5 Click the **RUN** button on the pop-up window or from the **Control Panel** on the screen.



- 6 Sample the background for one minute and note the TIC (the total ion count, which is a measure of response.)

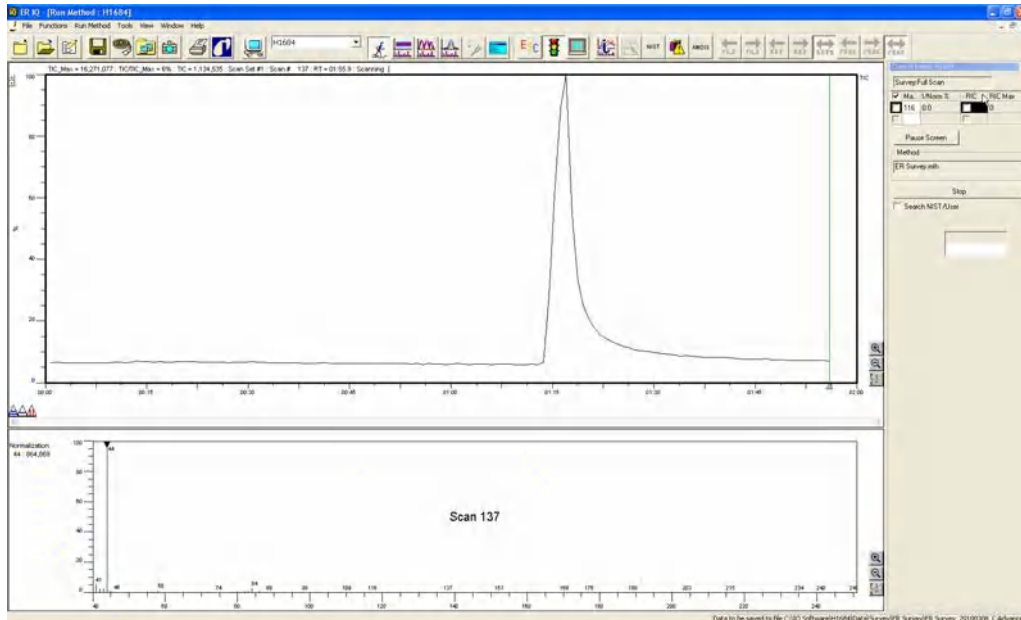


- 7 When the TIC increases 2 to 3 times the baseline level, move the probe away from the sample. A peak may appear if the compound concentration is greater than 1 ppm. A compound identification may also be present on the HAPSITE ER screen.

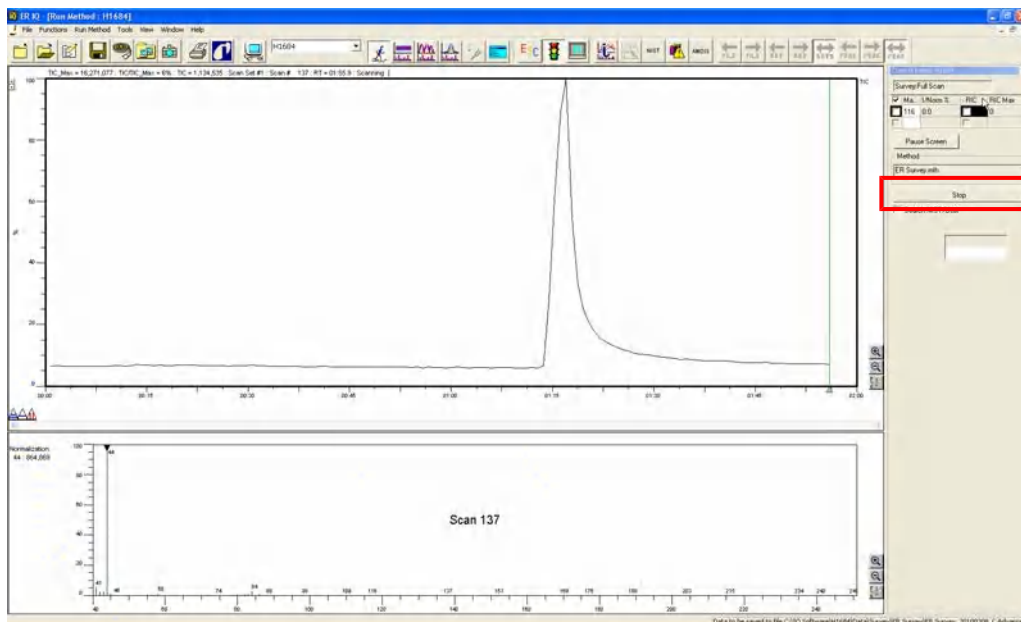


- ⇒ No response may indicate either the compound present is less than the detection limit, or that no detectable compound is present.
- 8 Monitor the TIC for guidance. If the TIC approaches 60 million, move the probe away from the sample to avoid saturation. If the system is saturated, there will also be red lines in the peak on the laptop.
- 9 If the TIC does not increase, hold the probe over the sample of interest for up to a minute. If the TIC does not increase after a full minute, move the probe away from the sample.

- 10** Monitor the TIC until it decreases to the initial background level that was noted in Step 6.



- 11** Click the **Stop** button, in the center of the **Control Panel** on the right side of the screen, to stop the sampling process. If it has not already been stopped manually, the survey run will stop automatically when the run time has reached five minutes.



- ⇒ Survey is a tentative identification. To confirm results, run an **Analyze** (GC/MS) Method.
- 12** Record the data file name to reference for later review. See Data Review [ 203] for instructions on recalling data.

## 11.2.2 Quick Reference SOP - Running Survey Mode

- 1 Double-click the **ER IQ** software icon.
- 2 Double-click the **Run Method** icon.
- 3 Wait for heaters to reach the setpoint temperatures.
- 4 Click the **RUN** button in the pop-up window.
- 5 Sample background for one minute and note the TIC.
- 6 Hold the probe over the sample until a response that is 2 to 3 times the baseline is observed. If the TIC does not increase, sample for a full minute.
- 7 Press **STOP** to stop the method.
  - ⇒ This is a tentative identification. To confirm results, run an **Analyze (GC/MS) Method**.



### CAUTION

**Do not touch the sample with the probe.**

**Do not allow liquids to enter the probe.**

## 11.3 ANALYZE (GC/MS) Mode with the Concentrator

### 11.3.1 Tri-Bed Concentrator

The Tri-Bed concentrator is used for analyzing samples with concentrations in the part per million to high part per trillion range. Two default qualitative methods are ER\_Tri-Bed\_PPM\_Standard and ER\_Tri-Bed\_PPB Standard. Use the ER\_Tri-Bed\_PPM\_Standard method when a response is seen in Survey. If a compound is suspected, but Survey does not show an increase in TIC (total ion count, which is a measure of response), use the ER\_Tri-Bed\_PPB\_Standard method.



### CAUTION

**The concentrator feature has increased sensitivity. Use the appropriate method to avoid saturating HAPSITE ER.**

## 11.3.2 Tenax Concentrator

The Tenax concentrator is also used for analyzing samples with concentration levels in the low part per million to high part per trillion range. The Tenax concentrator will not effectively concentrate compounds with boiling points below 80°C, but may be more effective at concentrating compounds with higher boiling points.



### **WARNING**

**The Tenax concentrator will not effectively concentrate compounds with boiling points below 80°C.**

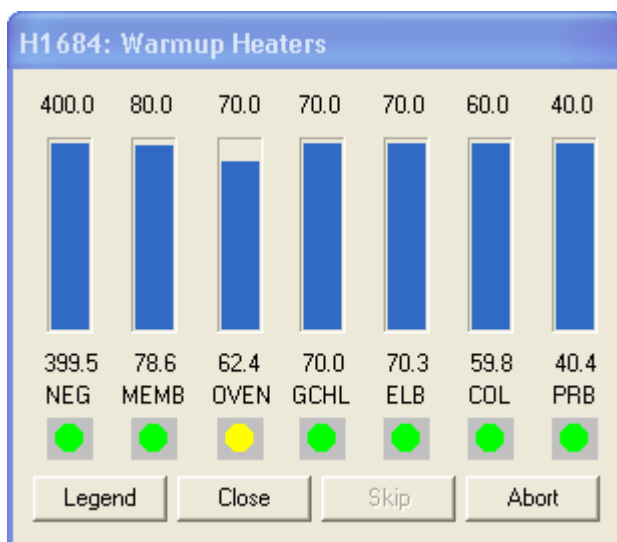
Once installed, the concentrator must be cleaned before sampling begins.

✓ Verify that the concentrator is installed.

- 1 When powered on (refer to Operate the Instrument in Portable Mode [▶ 51]) or taken out of **Extended Standby** (refer to Extended Standby [▶ 105]), HAPSITE ER will automatically start preparing a concentrator method. If the method that HAPSITE ER begins preparing is not the desired one, refer to Selecting a New Method [▶ 149].
- 2 Power on the laptop by pushing the **POWER** button. Open **ER IQ** Software by double-clicking on the **ER IQ** icon.

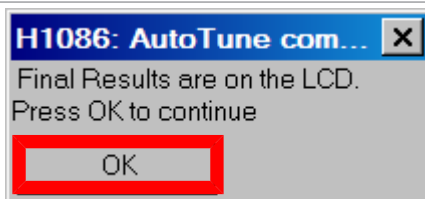


- 3 HAPSITE ER will begin preparing to run the default concentrator method. It will heat all necessary components, check pressures, and run an AutoTune, if necessary. Progress of the heaters is indicated by a bar graph on the laptop screen.



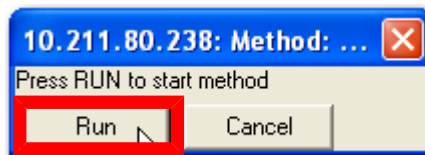
- 4 When the AutoTune is finished, the following message will be displayed. Click **OK**.





⇒ If AutoTune fails, refer to Performing Manual Tune [▶ 283].

- 5 A concentrator cleanout will also be run as part of the preparation of HAPSITE ER. Hold the probe in a clean environment for the duration of the cleanout. If the cleanout is successful, a **SYSTEM IS READY** message will be displayed on the front panel. The TIC on the chromatogram will be less than 5 million.
  - ⇒ If the cleanout is unsuccessful, refer to Concentrator Cleanout Failure.
  - ⇒ If this method is not the desired method, refer to Select a Different Method Using the SELECT METHOD Icon [▶ 71].
- 6 Once all temperature zones have reached their setpoints, a prompt will be displayed to **Press RUN to start method**.
- 7 Click the **RUN** button on the pop-up window or from the **Control Panel** on the screen.



- 8 When the HAPSITE ER screen prompts **Collect Sample Now**, place the probe over the sample for the entire specified sampling time. Be sure to keep the probe over the sample for both the Line Purge and ConcFill events.
  - ⇒ The Line Purge event is collected by time and the ConcFill is collected by volume.

EXIT
EMER MODE
CONC OPTIONS
MAIN
HELP
info

## SAMPLING

Details

### ER\_Air\_Tri-Bed\_PPM\_Standard

Collect Sample Now For 1:47

Scanning Starts In 2:10

Time Elapsed
0:47/1:00

CMPD ID
GRAPH
RUN SURVEY
RUN ANALYZE
STOP
CLOSE

EXIT
EMER MODE
CONC OPTIONS
MAIN
HELP
info

## SAMPLING

Details

### ER\_Air\_Tri-Bed\_PPM\_Standard

Collect Sample Now For 0:44

Scanning Starts In 1:07

Conc Fill
1.3/5.0 mL

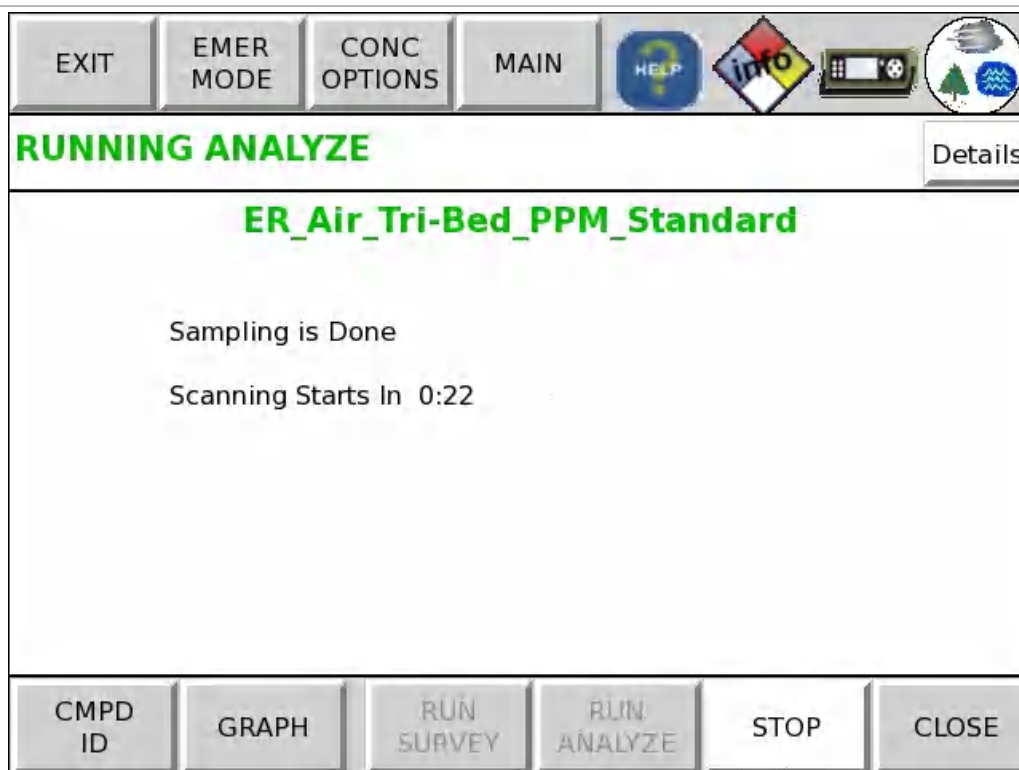
CMPD ID
GRAPH
RUN SURVEY
RUN ANALYZE
STOP
CLOSE



**⚠ CAUTION**

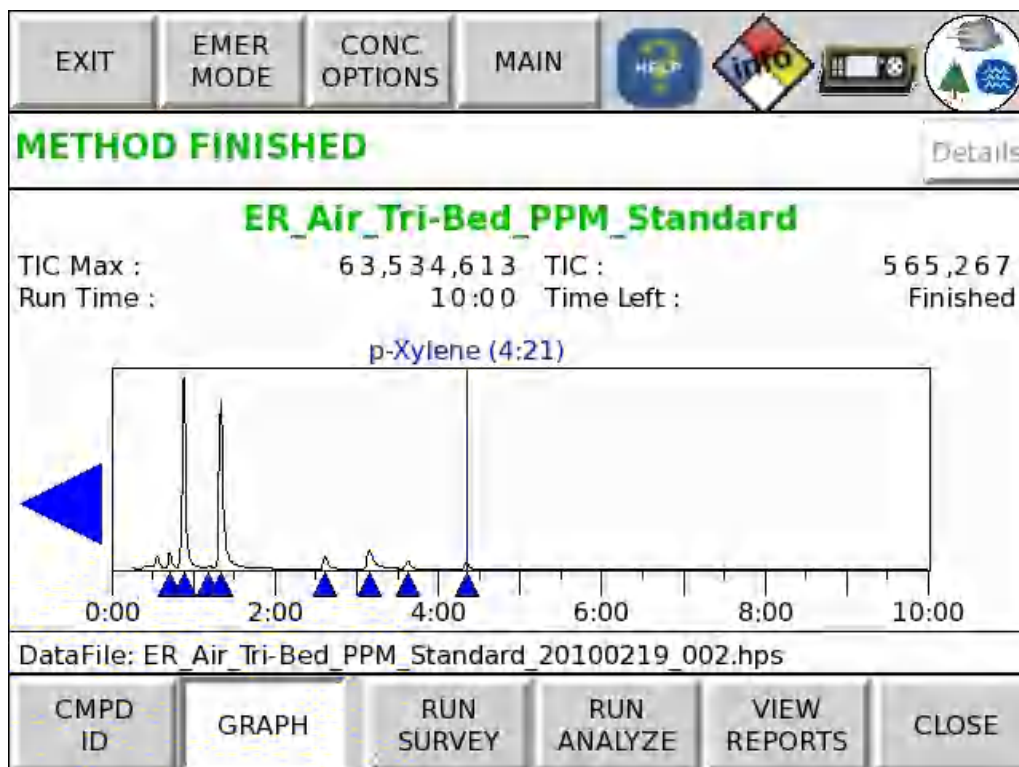
**Do not place the sample probe in liquids while sampling.**

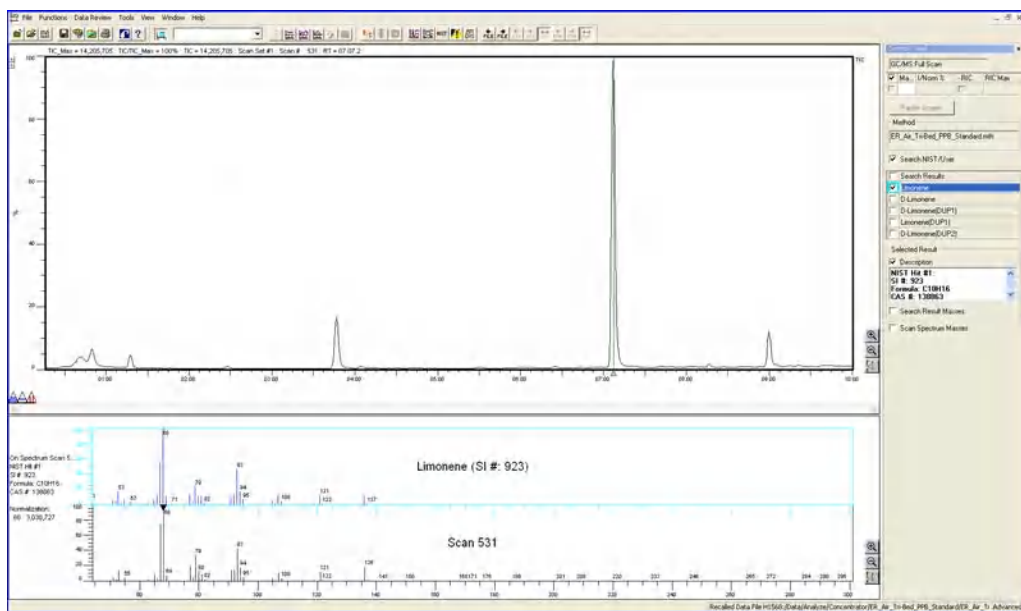
- 9 When prompted **Sampling is Done** on the HAPSITE ER screen, remove the probe from the sample source.



10 As the method runs, the chromatogram will begin to appear on the laptop screen.

11 The message **METHOD FINISHED** will appear on the HAPSITE ER screen when the run is complete. An example of a completed chromatogram on the laptop is shown below.





- 12** Review results at the end of the run. If red lines appear on the chromatogram, saturation has occurred. To clear saturation, run blank runs until the saturation has cleared.



### **CAUTION**

The concentrator feature has increased sensitivity. Take care to avoid saturating HAPSITE ER.

## 11.3.3 Quick Reference SOP - Tri-Bed Concentrator Method

- ✓ Verify that the concentrator is installed.
  - 1** If the system is shut down or in **Extended Standby**, either power on HAPSITE ER or take the system out of **Extended Standby**. HAPSITE ER begins preparing a concentrator method.
  - 2** When HAPSITE ER has finished preparing, a prompt to press **Run** is displayed on the laptop screen.
  - 3** When the screen prompts **Collect Sample Now For**, hold the probe over the sample until the screen prompts **Sampling is Done**
  - 4** When the run is complete, a **Method Finished** prompt is displayed.
    - ⇒ See View Results/ View Reports or Data Review [▶ 203] for information on data review.

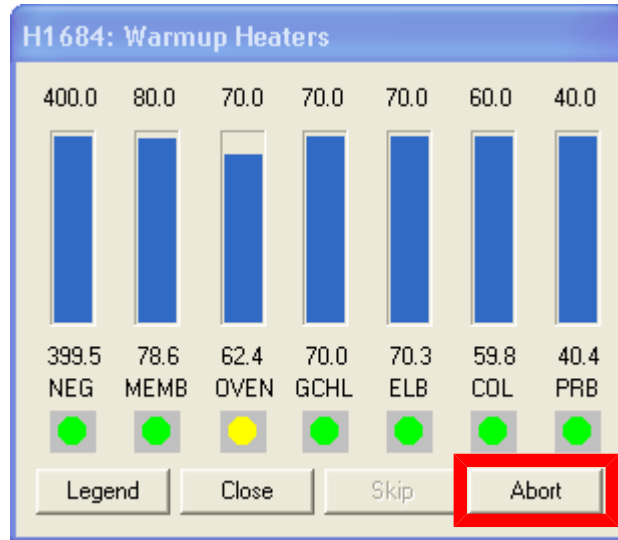


### **CAUTION**

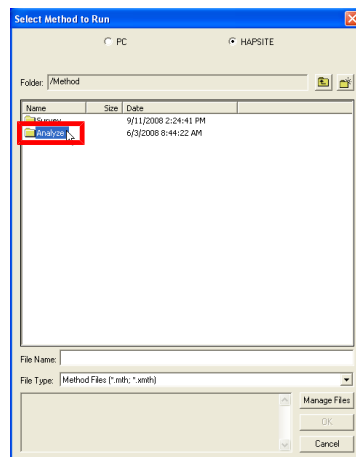
Do not place the sample probe in liquids while sampling.

## 11.4 Selecting a New Method

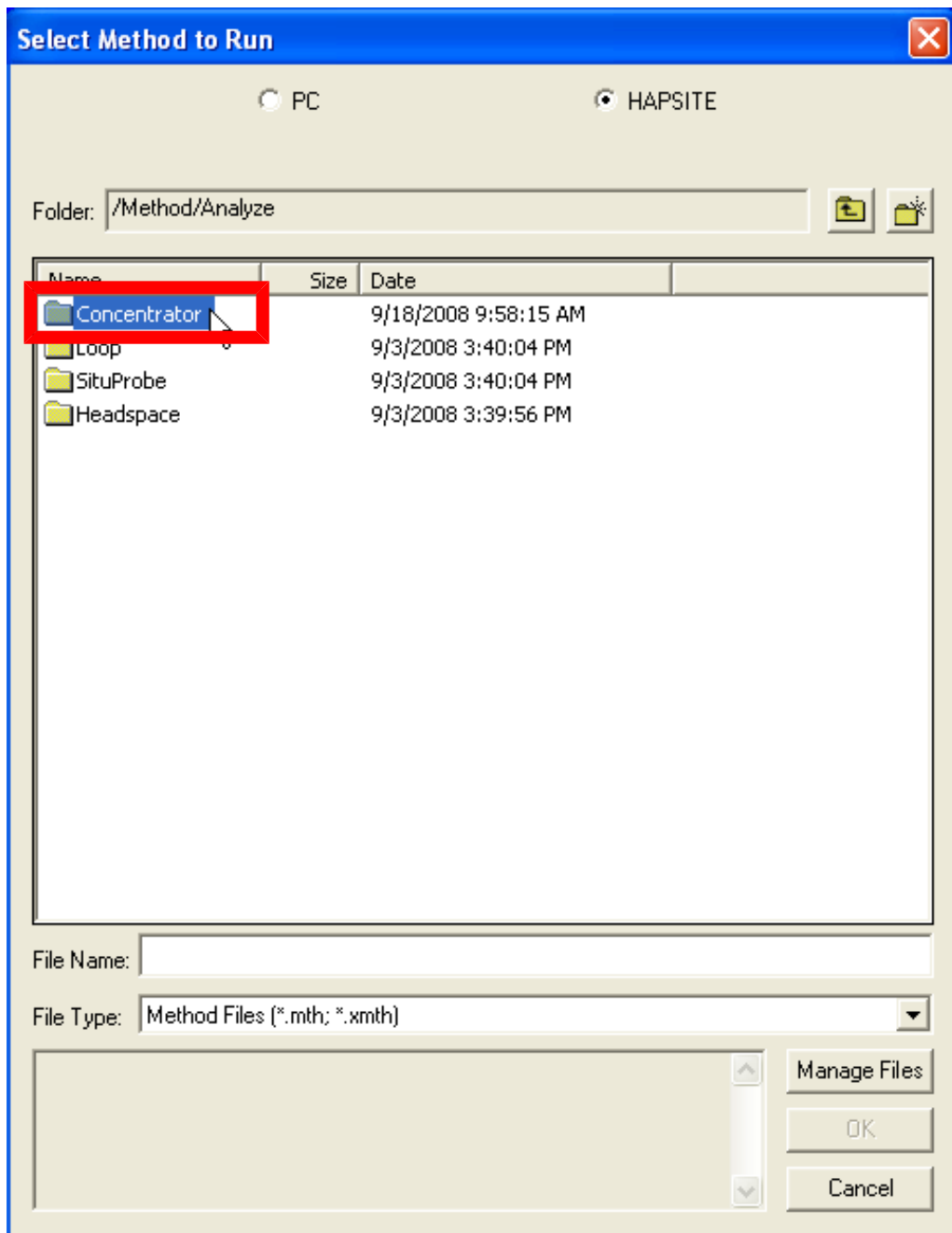
- 1 Click the **Abort** button.



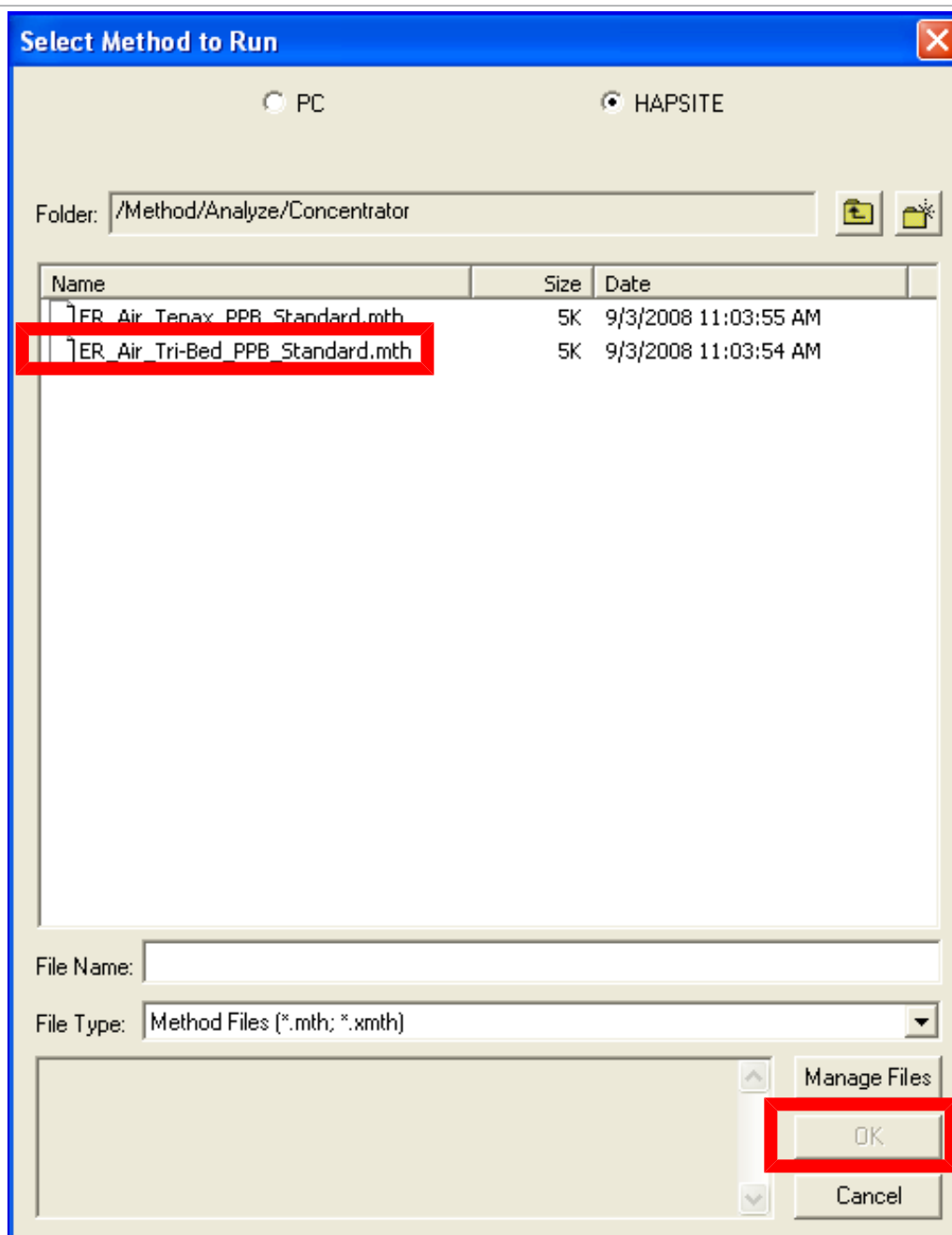
- 2 Double-click on the **Run Method** icon. A dialog is displayed for selecting the desired method. In the example below, **ER\_Air\_Tri-Bed\_PPB\_Standard** will be selected.
- 3 Double-click the **Analyze** folder.
  - ⇒ Use the buttons at the top of the dialog box to choose the methods on HAPSITE ER.



- 4 Choose a folder that matches the sampling configuration of HAPSITE ER. The concentrator folder refers to the Probe accessory. In this example, the probe is installed. Double-click the **Concentrator** folder.



- 5 Click the desired method and then click **OK**. This example shows the **ER\_Air\_Tri-Bed\_PPB\_Standard.mth** method.



- 6 The software will check the pressure in the gas canisters, heat up all necessary components, and run an AutoTune (if required). A concentrator cleanout will also be run if needed.
- 7 When it is finished heating, a prompt will appear to indicate HAPSITE ER is ready to run a sample. Click **RUN**. For detailed instructions, refer to ANALYZE (GC/MS) Mode with the Concentrator [▶ 86].



### CAUTION

**Do not place the sample probe in liquids while sampling.**

## 12 ER IQ Software

### 12.1 HAPSITE Software - ER IQ

ER IQ software is the laptop software that controls instrument operation, runs analyses, manages files and creates reports. Data collected with HAPSITE ER is viewed and interpreted using ER IQ. This software allows for use of the entire NIST mass spectral library. This section provides instructions on Data Review and analysis. The Data Review section of the ER IQ laptop software allows access to previously acquired data for review and analysis, or to view data that is being acquired in real time. ER IQ software operates with Microsoft Windows on the laptop.

#### 12.1.1 Computer System Requirements

The following is the minimum recommended laptop computer system for communication with one HAPSITE ER:

Processor	Pentium III 550 MHz or greater
RAM	512 MB or greater
Hard Disk Space to load ER IQ	20 Mb
Hard Disk Space for storage	10 GB
Monitor	14 in., SVGA or greater
Monitor Resolution	1920 x 1080 or greater
Communications	Ethernet port
Operating System	Windows

### 12.2 Software Installation

The software is loaded onto the laptop at the factory. If reinstallation is necessary, the software installation instructions are located on the **ER IQ** software CD or can be downloaded off the INFICON website.

#### 12.2.1 System Setup Screen

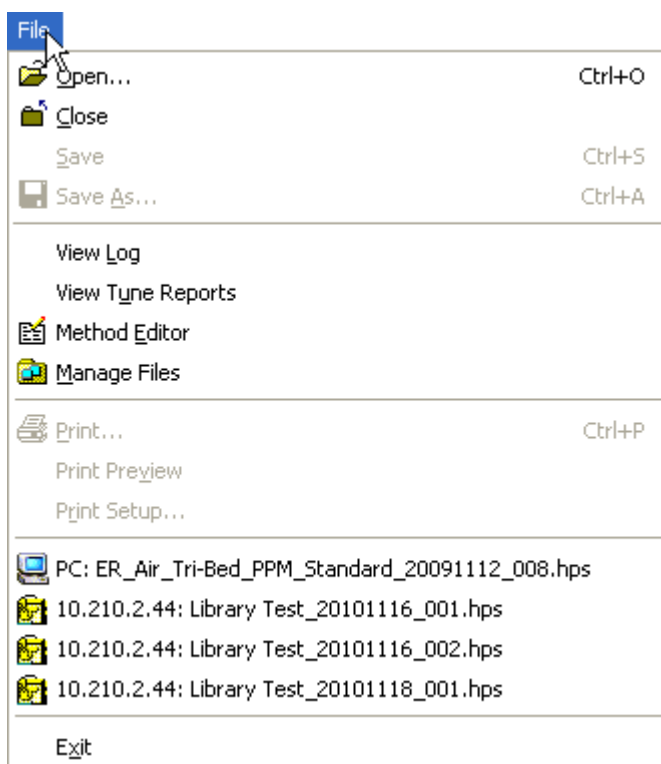
- 1 Double-click the **ER IQ** icon to open the **ER IQ** software.



- 2 To connect to a HAPSITE ER, see Setting Up Communications [▶ 112]. When opening **ER IQ**, the main window of the software is the **System Setup** screen.







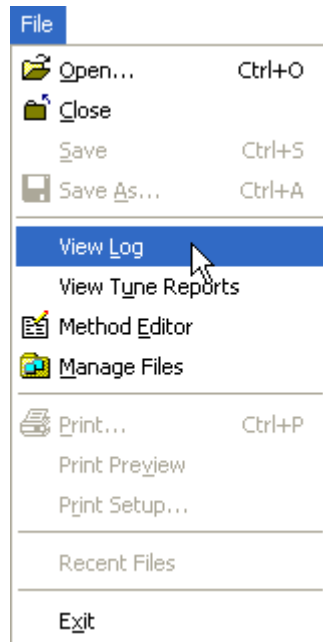
- **Open** opens a data file from either **ER IQ** or the laptop.
- **Close** closes the data file.
- **Save** is grayed out when in the **System Setup Screen**. However, when a data file is opened, a new screen, the **Data Review Screen**, will be displayed. The **Save** option will be activated in the **Data Review Screen** and changes to the data file can be saved.
- **Save As** is grayed out in the **System Setup** screen. However, when a data file is opened, a new screen, the **Data Review** screen, will be displayed. The **Data Review** screen will have the **Save As** option activated. The data file can be saved with a different name and/or to a different location.
- **View Log** allows for event log files (.evt) to be opened. Examples of files logged are warnings, errors and run history.  
**View Tune Reports** allows for tune reports (.tun) to be opened. For more information on tune reports, see Viewing a Tune Report [▶ 277].
- **Method Editor** opens the **Method Editor** function. It performs the same function as the **Method Editor icon**. See Method Editor [▶ 301] for further instructions.
- **Manage Files** opens the **Manage Files** function. It performs the same function as the Manage Files icon. See Safety Database [▶ 172].
- **Print** will print files and is active on the **Data Review** screen.
- **Print Preview** will display an example of the final printing layout and is active on the **Data Review** screen.
- **Print Setup** accesses the printer setup options.

- **Recently Accessed Files** are displayed below **Print Setup**. Double-click on a file name to open it in the **Data Review** screen.
- **Exit** closes **ER IQ**.

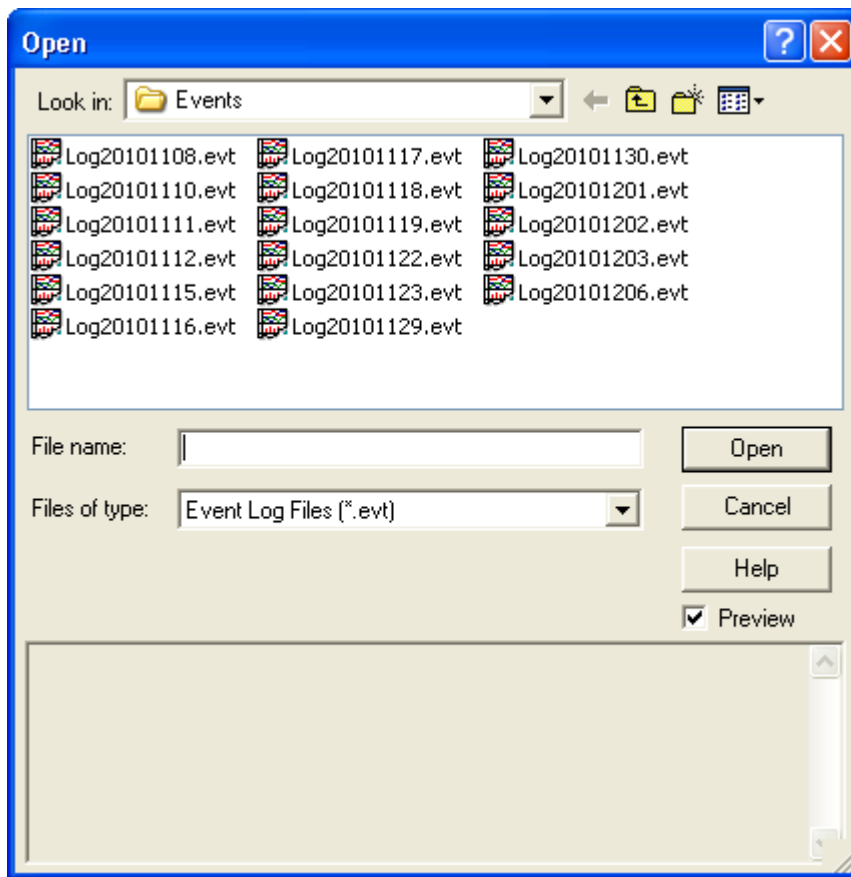
### 12.3.1.1.1 View Log

HAPSITE ER will log errors, warnings, and events, if desired. See Parameters [▶ 196] for information on enabling this function. A warning signifies there is a problem with the unit, such as high pressure. If the warning is ignored, it will become an error. An example of an event is the system coming online or going offline.

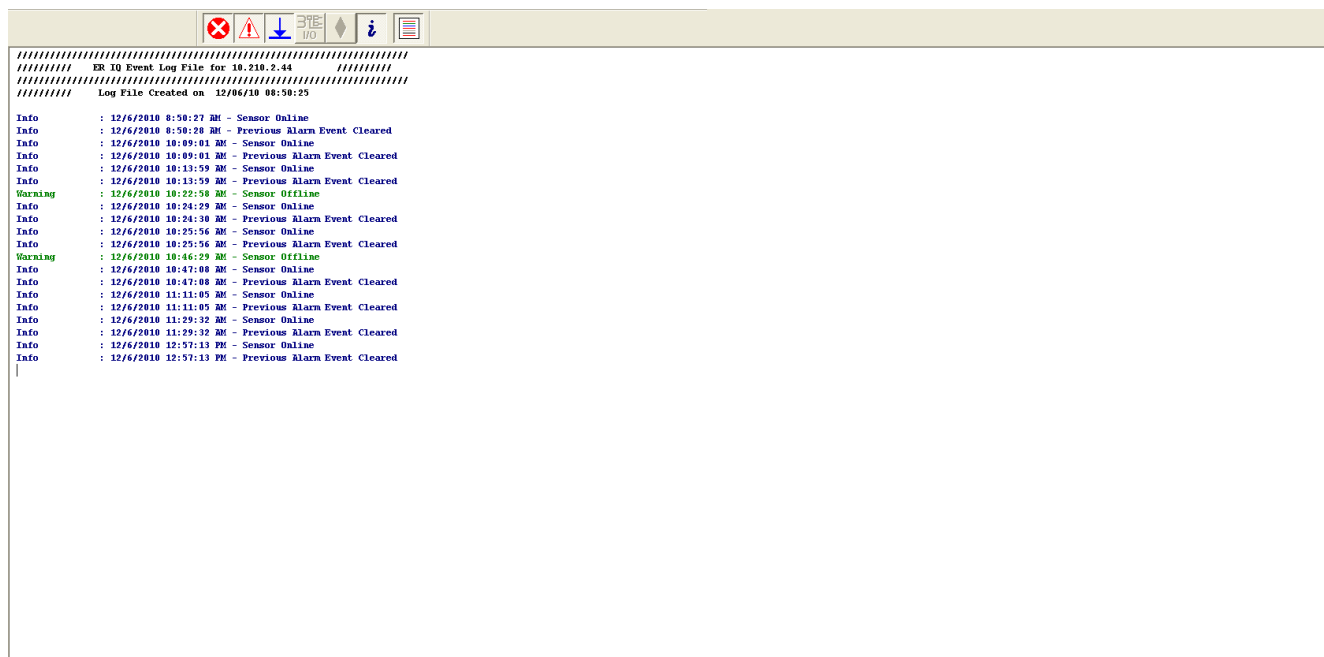
- 1 Select **View Log** from the **File** menu.



- 2 Double-click the desired log file.








3 The log file will be displayed.



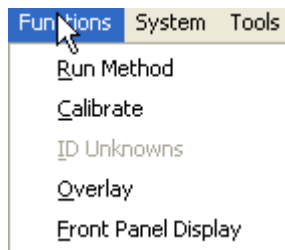
### 12.3.1.1.2 Log File Toolbar

The following icons will be displayed on the **Log File Toolbar**.

Icon	Function
	Displays the logged warning
	Displays the logged errors
	Displays the logged events
	Displays all logged files
	Color codes the warnings, errors, and events.

### 12.3.2 Functions Menu

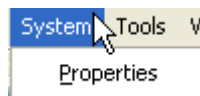
The **Functions** menu is shown below.



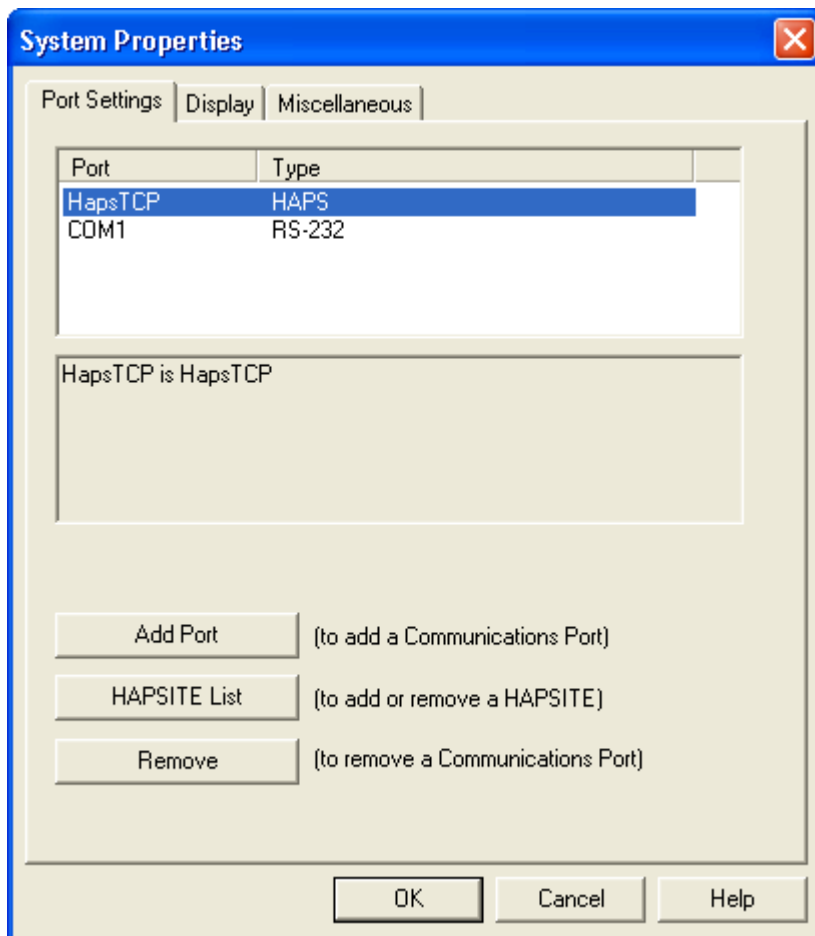
The **Run Method**, **Calibrate**, **Overlay**, and **Front Panel Display** options function identically to the icons of the same name.

### 12.3.3 System

The **System** menu is shown below.



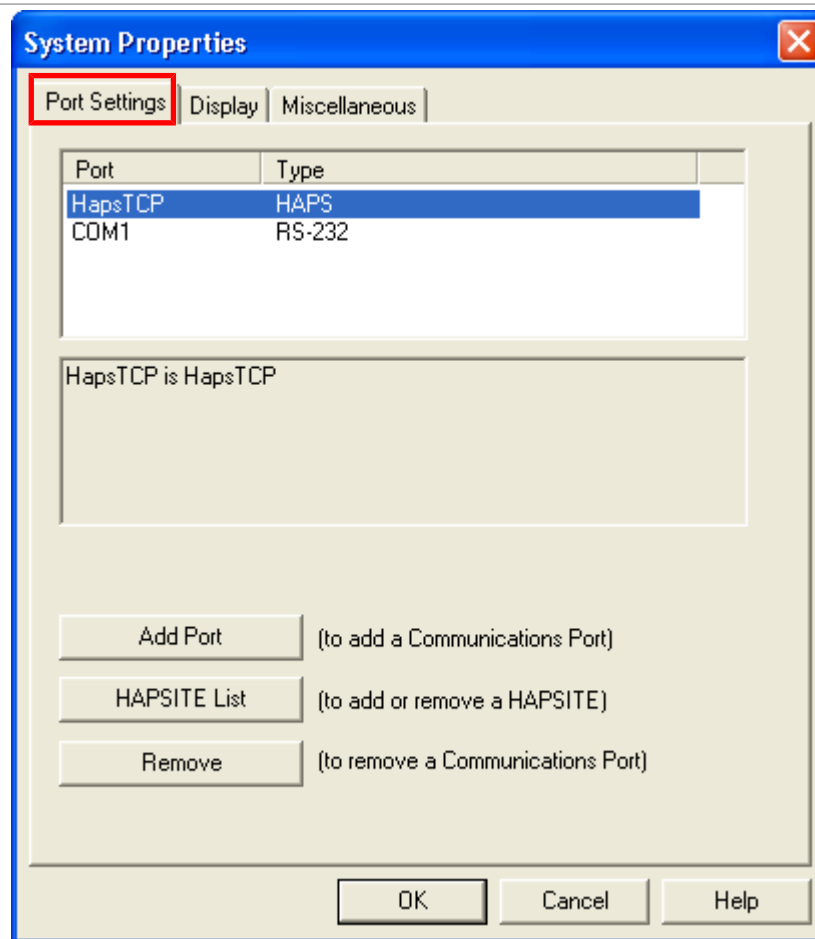
Clicking **Properties** will open the **System Properties** window.



### 12.3.3.1 Port Setting Tab

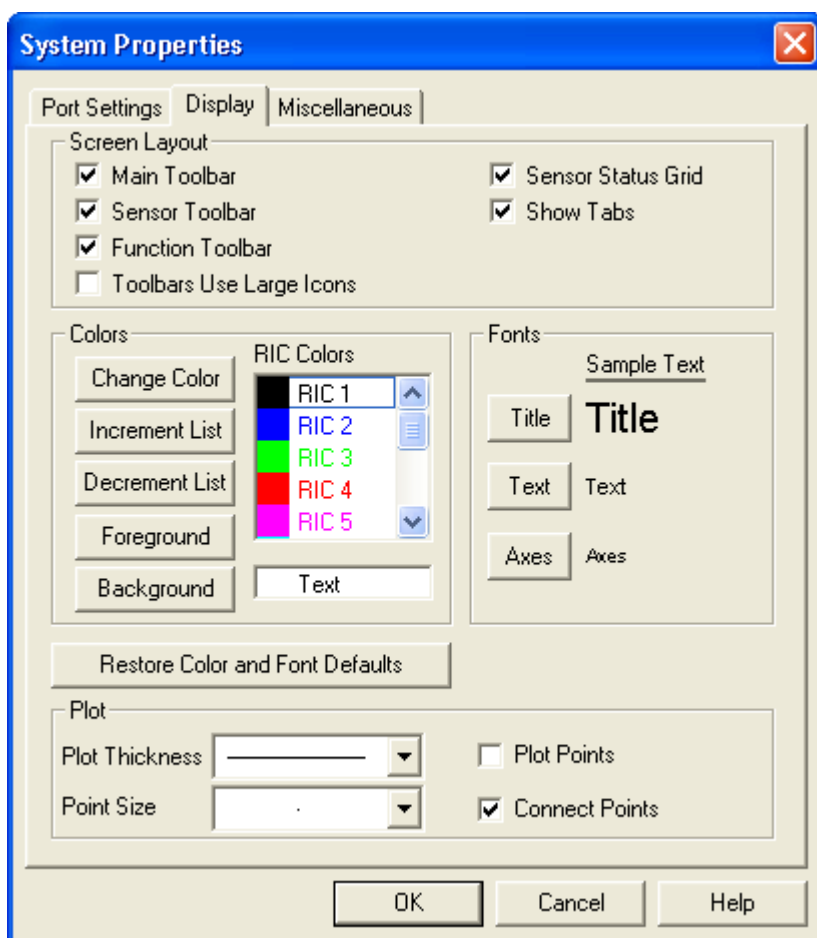
**Port Settings** is the default tab in the **System Properties** window.

HAPSITE ER is configured at the factory to connect to the laptop. However, the HAPSITE ER option allows the user to add a different HAPSITE ER to the laptop or connect a HAPSITE ER to a new laptop.



### 12.3.3.2 Display Tab

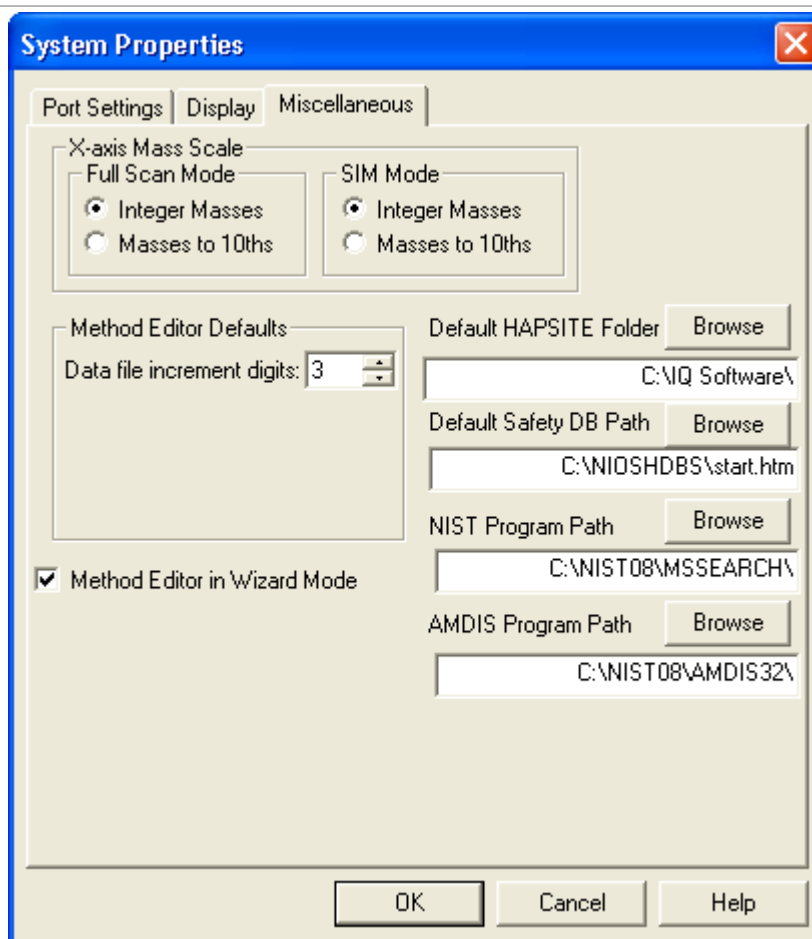
The **Display** tab is used to change the appearance of the **ER IQ** settings, including the thickness of the chromatogram line, the fonts used, and the screen layout.



### 12.3.3.3 Miscellaneous Tab

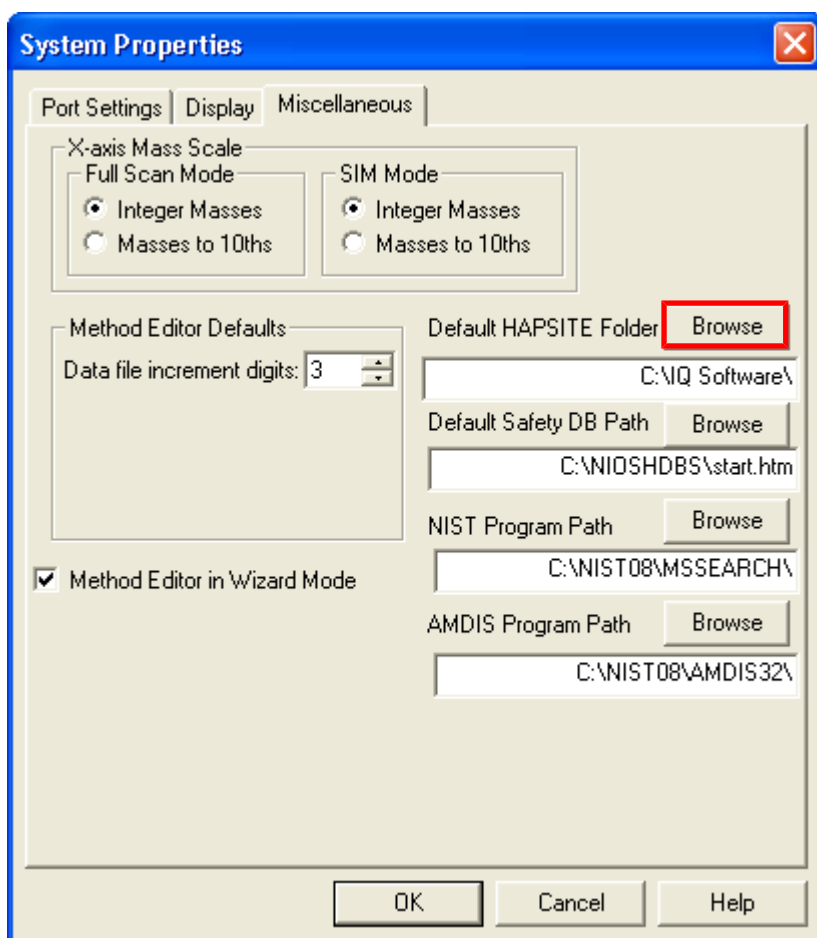
The **Miscellaneous** tab displays the default pathways, the data file increment digits, the software, safety and library pathways, the scaling preferences for the chromatogram, and the option to select **Wizard Mode** for **Method Editor**.



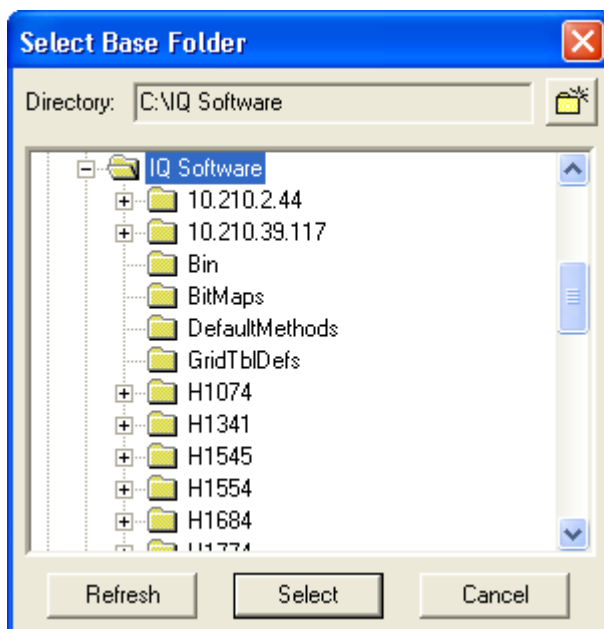


Four default software pathways are displayed. The **Browse** buttons access folders to reset the pathways, if necessary. However, the software installation should properly select these options. If a pathway requires resetting, follow the instructions below.

- 1 Click **Browse** for the **Default HAPSITE Folder**.

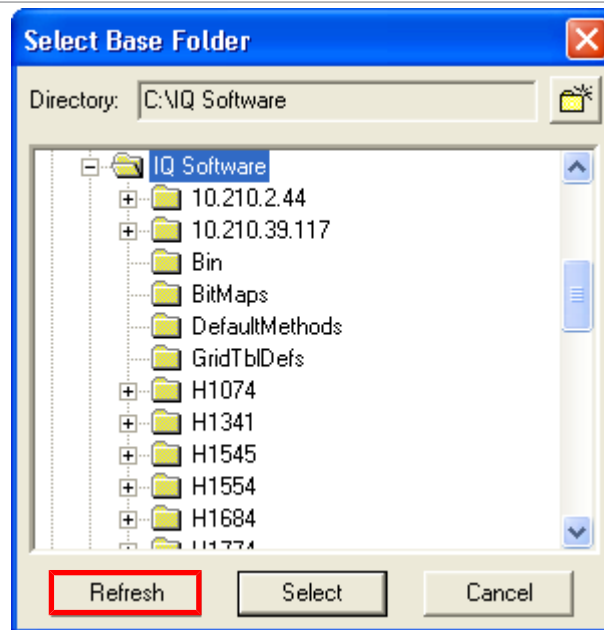


2 The **Select Base Folder** window will open.

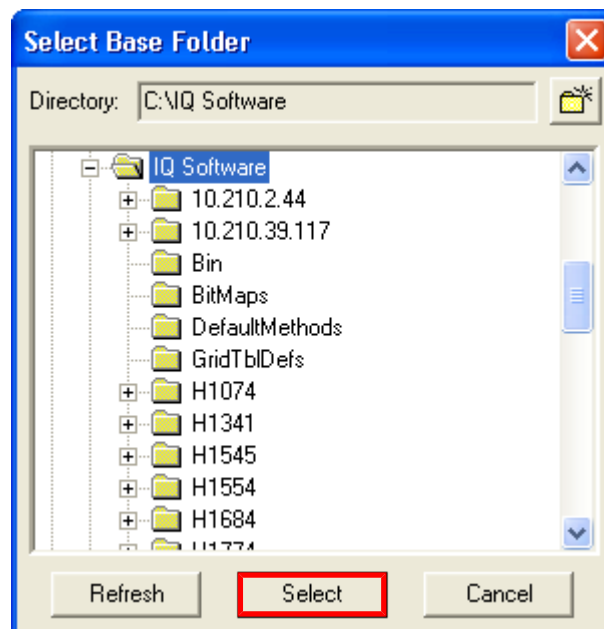


3 Click to highlight the desired folder.

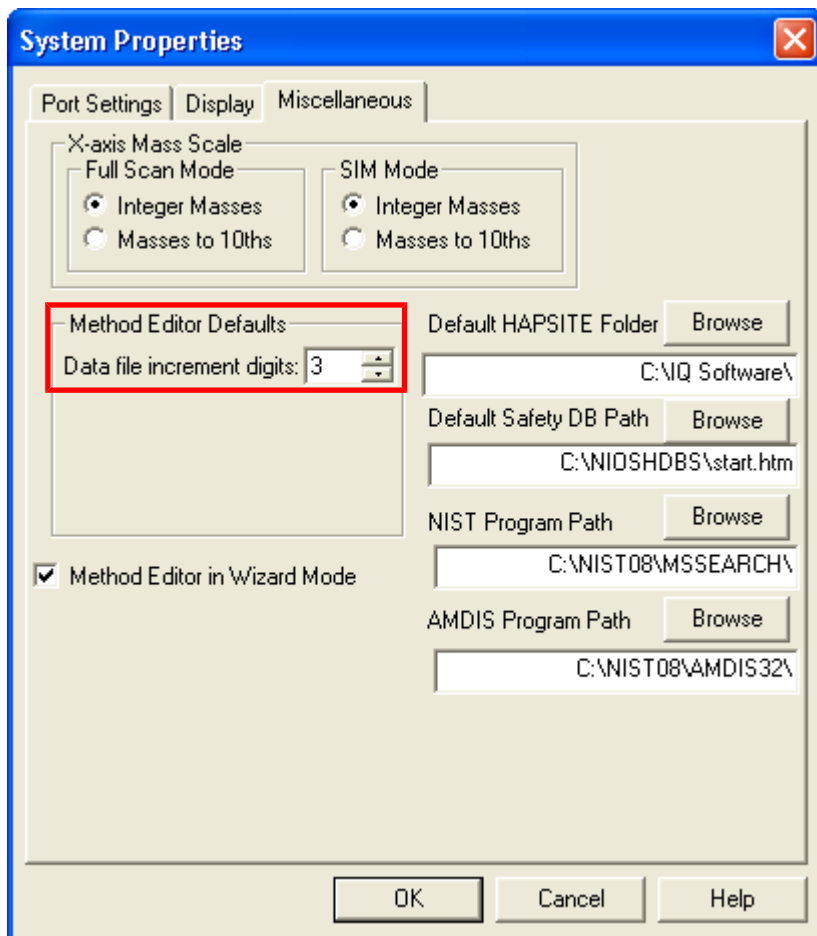
⇒ Click **Refresh** to update the displayed folders if the desired folder is not displayed.



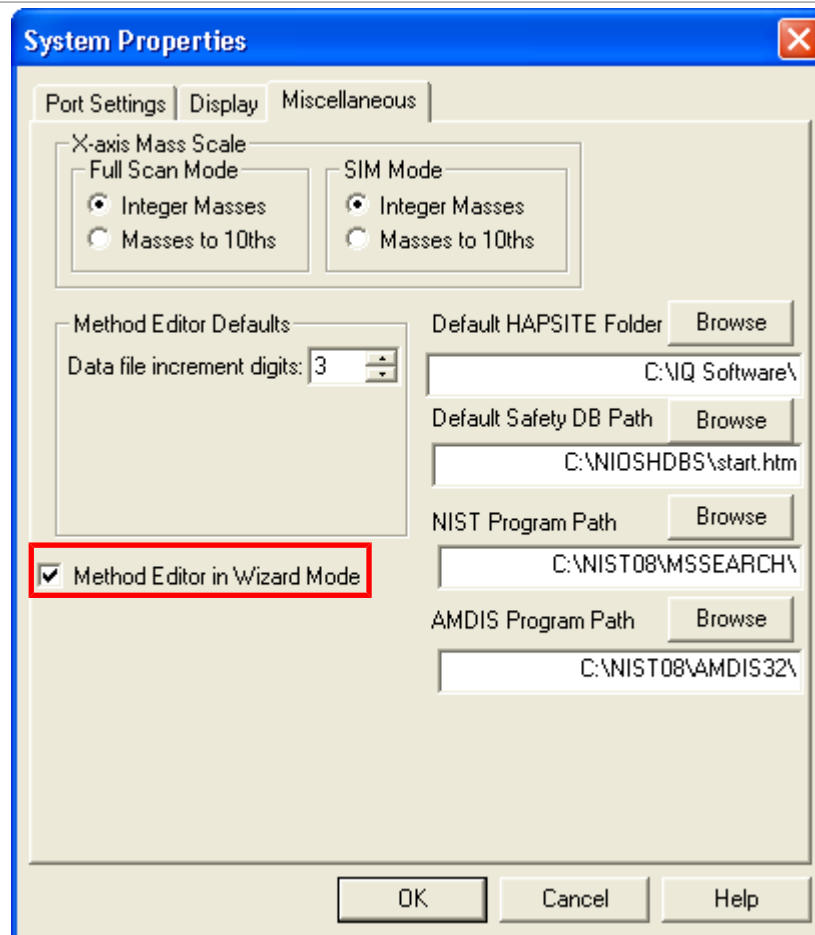
- 4 Once the desired file is highlighted, click **Select**. Once **Select** is clicked, the window will close.



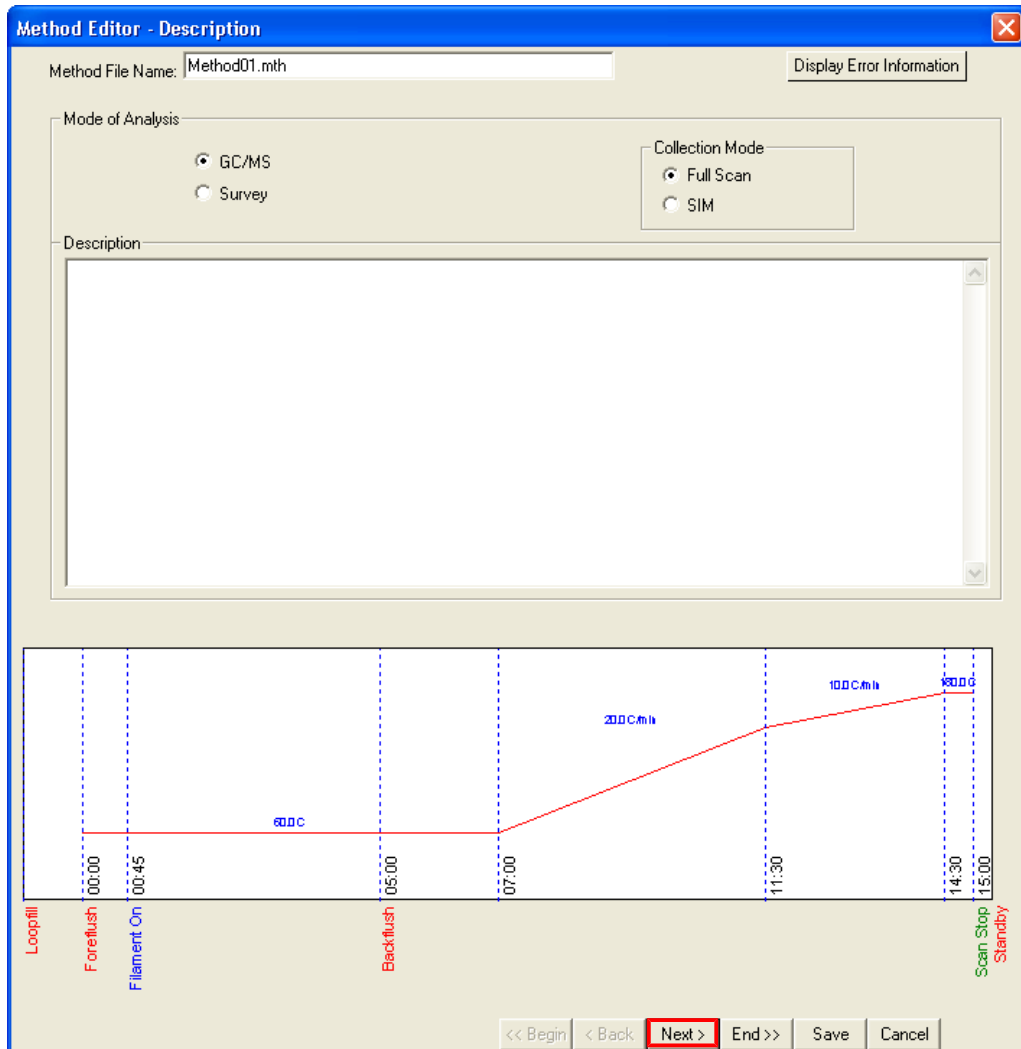
The **Data file increment digits** is used to select the number of digits that are to be appended to a data file. For example, if 2 is selected, the file name would read Method\_yearmonthday\_01. If 3 is selected, the file name would read Method\_yearmonthday\_001. The data file increment digits can also be selected in Method Editor. See Data File Information [▶ 362] for instructions.



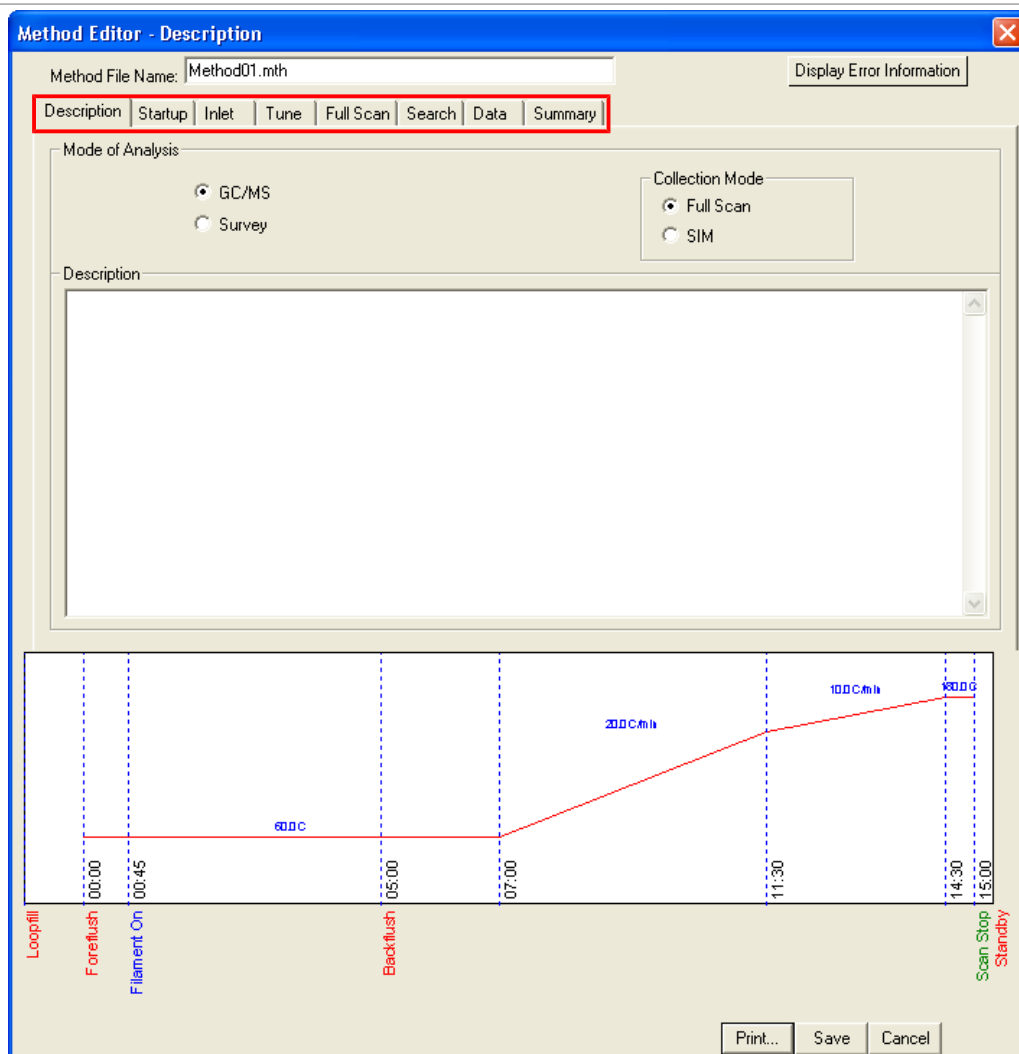
The **Method Editor in Wizard Mode** checkbox is the next option.



The Wizard Mode will guide the user through the Method Editor software by using **Next >** and **< Back** buttons at the bottom of the screen.

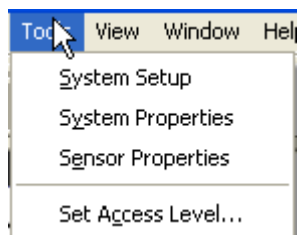


If the **Method Editor in Wizard Mode** box is not checked, tabs must be clicked at the top of the Method Editor screen to access method writing options.



### 12.3.4 Tools Menu

The **Tools** menu is shown below.



**System Setup** closes the **System Setup** screen.

**System Properties** functions identically to the **System Properties** option in the System menu. Refer to System [▶ 157] for further information.

**Sensor Properties** functions identically to the **Properties** option in the System Menu. Refer to System [▶ 157] for further information.

### 12.3.4.1 Set Access Level

In the **Set Access Level** option there are two user levels which can be set in **ER IQ**, **Normal** and **Advanced**. Neither access level has a factory set password.

**Normal** level allows users to run samples, view results, and perform basic operations with HAPSITE ER.

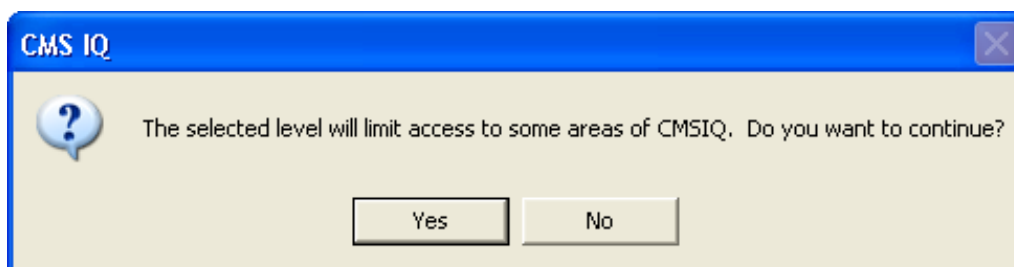
**Advanced** allows access to all user operations. This includes all normal user functions plus method creation and editing, file deletion, changing alarm parameters, and changing network settings.

To restrict access to advanced functions, an advanced user password can be set. Once the password is set, it must be entered each time the **ER IQ** program is opened, or whenever the access level is changed from normal to advanced. See [Setting or Changing the Access Level Password \[▶ 169\]](#).

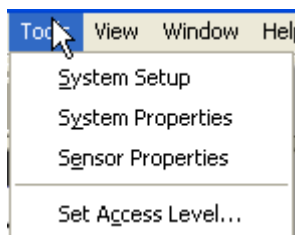
#### 12.3.4.1.1 Changing Access Levels



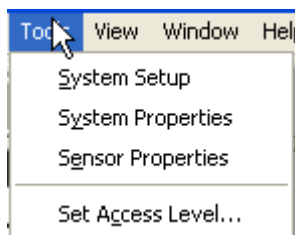
When the **Normal** access level is selected, a prompt will be displayed stating that some areas of the **ER IQ** will have restricted access. Click **Yes** if continuing is desired.



- 1 To change the access level, click on the **Tools** menu on the System Setup Screen.

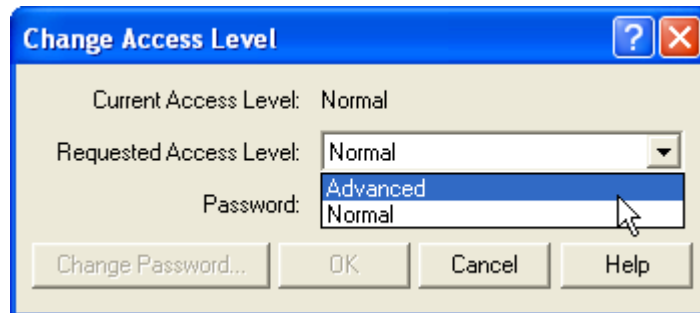


- 2 Select **Set Access Level...**

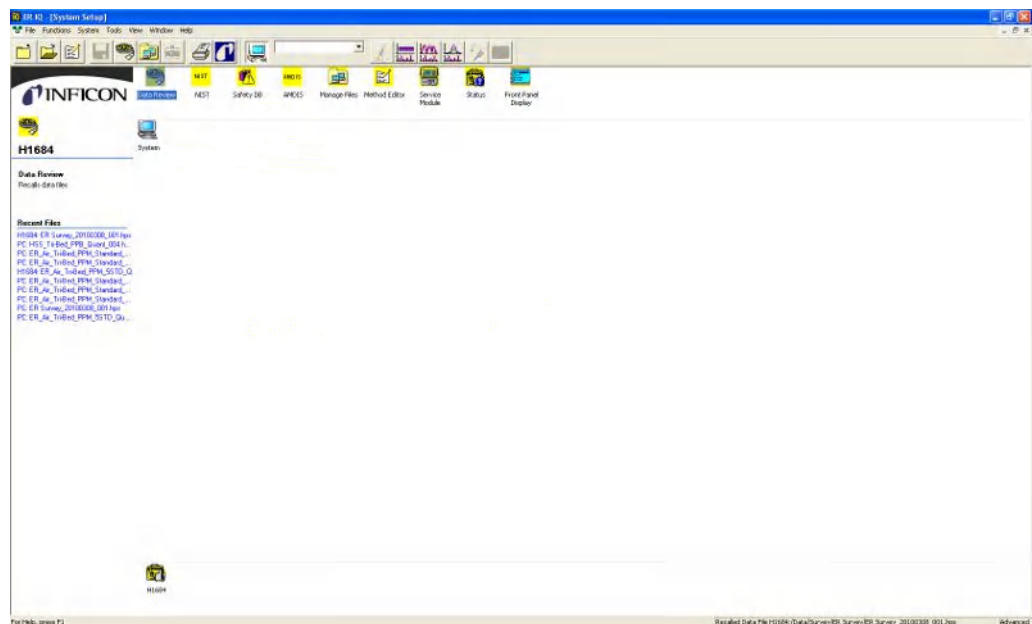




- To select advanced access, click on **Requested Access Level** drop-down menu and select **Advanced**. If a password has been set, it will need to be entered in the password box before pressing **OK**.

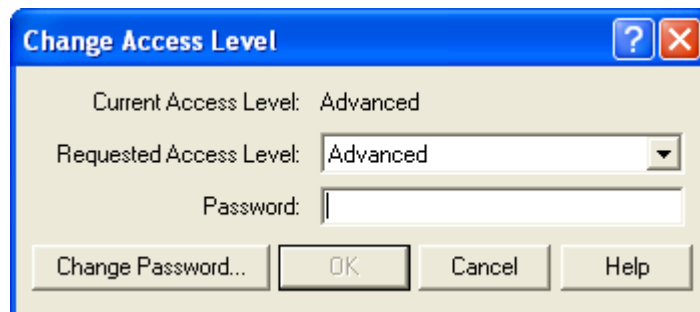


- The current access level of the system is displayed at the bottom right corner of the **ER IQ** program, in the **Status Bar**.



### 12.3.4.1.2 Setting or Changing the Access Level Password

- To change the Advanced password, first enter advanced mode.
- Press the **Change Password** button.



- The window shown below will be displayed.



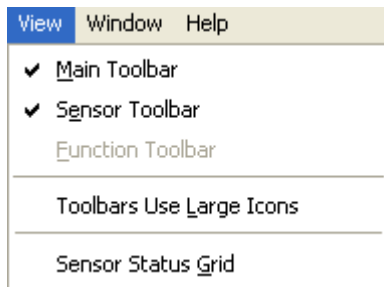
- 4 In order to change the password, the correct current password must be entered in the **Old Password** box. The Old Password box must be left blank if entering a password for the first time. The new password must be entered in both the **New Password** and **Verify New Password** boxes. Press **OK** to set the new password, or press cancel to exit without resetting the password.
- 5 Click **OK** to close the **Change Access Level** window.



**ER IQ** remembers the last access level when closed. Upon re-opening the program, the system will default to the last access level utilized. If a password has been set, the user will be required to enter the correct password for advanced access. If the password is not known, the user can select normal access and continue.

## 12.3.5 View Menu

The **View** menu is shown below. It is used to select the desired toolbars.



The **Main Toolbar** is shown below. See HAPSITE Icons [▶ 201] for icon descriptions.



The **Sensor Toolbar** is shown below. See HAPSITE Icons [▶ 201] for icon descriptions.



Fig. 1: Sensor toolbar

The **Function Toolbar** is only available when the **Data Review** screen is open. See Introduction [▶ 205] for icon descriptions.



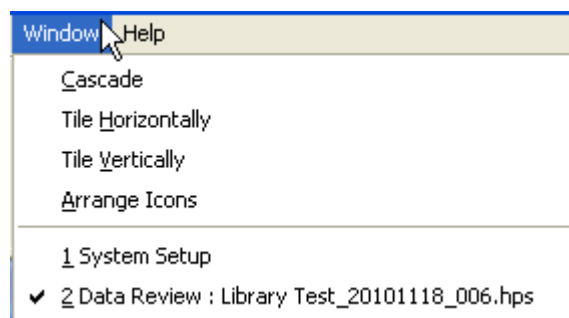
**Toolbars Use Large Icons** increases the size of the toolbar icons.

**Sensor Status Grid** will open the **Sensor Status Grid** which shows the current condition of various components.

Sensor Status												
Sensor	Status	Process	Process Status	SampleLoopPowerSetting	ConcPreDesorbPowerSetting	ConcPreDesorbTimeSetting	NEGPowerSetting	ProbePowerSetting	NEGControlMode	ProbeControlMode	ConcDesorbPowerSetting	ConcDes
10.210.2.44	Online	None		100	1	12:00:01 AM	400	40	0	0	1	12:00:01
HT1684	Offline	None		0	0		0	0	0	0	0	

### 12.3.6 Window Menu

The **Window** menu is shown below.



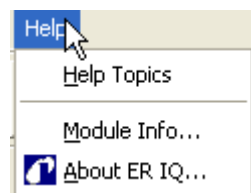
The first three options, **Cascade**, **Tile Horizontally**, and **Tile Vertically**, determine the arrangement of open windows on the screen.

**Arrange Icons** aligns the icons along the top row.

The last options are **System Setup** and **Data Review**. The current view is the one that is checked. Select the unchecked option to switch views.

### 12.3.7 Help Menu

The **Help** menu is displayed below.



**Help Topics** is not available at this time.

**Module Info** shows the build version of various files and product number of the installed software.

**About ER IQ** shows the installed software version.

## 12.4 Safety Database

The **Safety DB** icon accesses the NIOSH Safety Database which is used to locate NIOSH REL, OSHA PEL, CAS Numbers, synonyms, IDLH's, and safety recommendations. Follow the procedure below to access the Safety FB.

- 1 Double-click the **Safety DB** icon.



- 2 The following screen is displayed.

NIOSH Publication No. 2005-151:  
**NIOSH Pocket Guide to Chemical Hazards and Other Databases**

**NIOSH Pocket Guide to Chemical Hazards**  
 Exposure limits, Respirator Recommendations, First Aid, more...  
 The Pocket Guide is a source of general occupational hygiene information on several hundred chemical classes found in the work environment. Key data provided for each chemical substance includes name (including synonyms/ trade names), structural formula, CAS/ RTECS Numbers, DOT ID, conversion factors, exposure limits, IDLH, chemical and physical properties, measurement methods, personal protection, respirator recommendations, symptoms, and first aid.

**Other Databases**  
 The following selected NIOSH databases are also available on this CD-ROM:

- Immediately Dangerous to Life and Health Concentrations (IDLHs)
- International Chemical Safety Cards (ICSC/IPC/SILO)
- NIOSH Manual of Analytical Methods (NMAM)
- OSHA Sampling & Analytical Methods
- Recommendations for Chemical Protective Clothing
- Chemicals Cited by RCSC and NPG - MSD, RTECS
- Specific Medical Tests Published for OSHA-Regulated Substances
- Toxicologic Review of Selected Chemicals
- 2004 Emergency Response Guidebook (U.S. Department of Transportation)
- more...

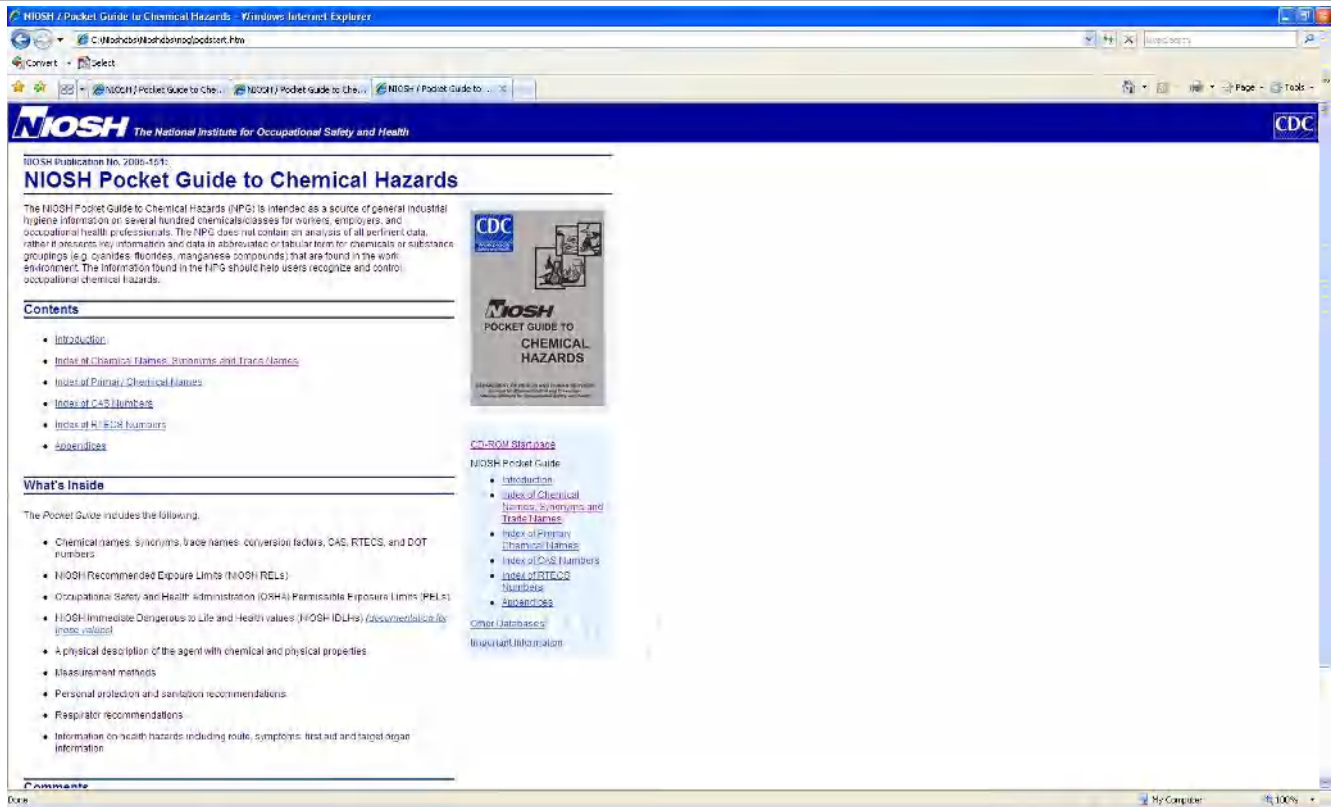
Many files on this CD-ROM require the Adobe Acrobat Reader. To download this software, click the appropriate file below:

- [Adobe Acrobat Reader 4.0.5](#) for Win 9x, 2000, XP
- [Adobe Acrobat Reader 4.0.5](#) for Win 95
- [Adobe Acrobat Reader 4.0.5](#) for Win 2000
- [Adobe Acrobat Reader 4.0.5](#) for Mac OS X

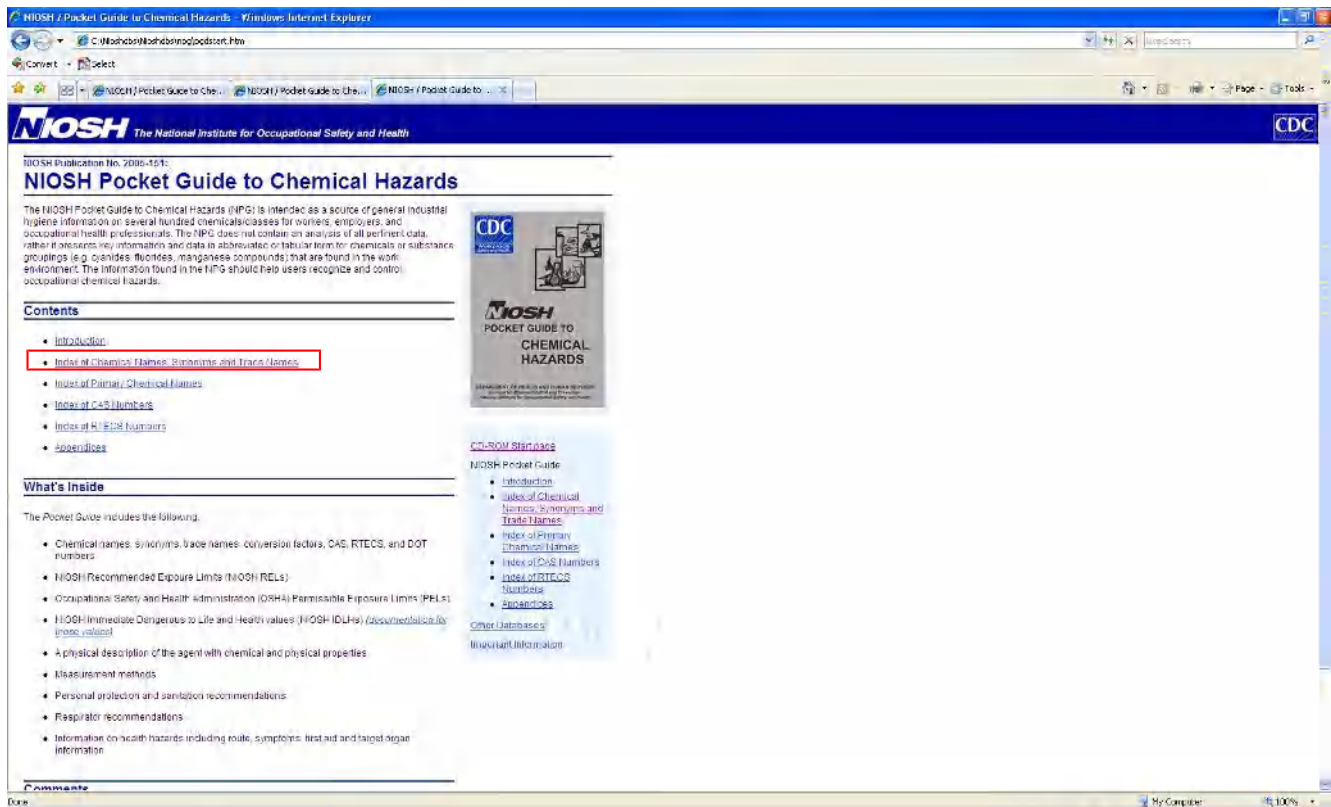
More information about the software available on this CD-ROM is available in the [user manual](#).

- 3 Click the **NIOSH Pocket Guide to Chemical Hazards** link or the link to the desired database.

- 4 If clicking the **NIOSH Pocket Guide to Chemical Hazards** link, the following screen is displayed.



5 This screen displays the following options: **Introduction, Index of Chemical Names, Synonyms and Trade Names, Index of Primary Chemical Names, Index of CAS Numbers, Index of RTECS Numbers and Appendices.** Click the **Index of Chemical Names, Synonyms, and Trade Names** link.



6 This screen displays an alphabetized list compounds in the database.

The screenshot shows the NIOSH Pocket Guide to Chemical Hazards website. The page title is "INDEX of Chemical Names, Synonyms and Trade Names" with a navigation bar for letters A through Z. The letter 'A' is selected, displaying a table of chemical compounds. To the right of the table is a sidebar with a "CDC" logo, a "NIOSH POCKET GUIDE TO CHEMICAL HAZARDS" book cover, and a list of navigation links including "Introduction", "Index of Chemical Names, Synonyms and Trade Names", "Index of Priority Chemical Names", "Index of CAS Numbers", "Index of RTECS Hazards", and "Appendices".

SEQ	CHEMICAL NAME	CAS No.	RTECS No.
0007	AA	107-16-6	BA5075000
0007	2-AAP	53-96-3	AB9450000
0007	AAP	53-96-3	AB9450000
0008	AbetaD	3363-63-6	TF6090000
0009	Acetaldehyde	75-07-0	AB1925000
0009	2-Acetaminofluorene	53-96-3	AB9450000
0009	Acetic acid	64-19-7	AT1225000
0009	Acetic acid anhydride	108-24-7	AK1825000
0009	Acetic acid (90-99-9)	54-19-7	AT1225000
0009	Acetic anhydride	75-07-0	AB1925000
0009	Acetic anhydride	108-24-7	AK1825000
0009	Acetic ester	141-76-8	AH4425000
0009	Acetic ester	141-76-8	AH4425000
0009	Acetic oxide	106-24-7	AK1825000
0009	Acetone	67-64-1	NL3150000
0009	Acetone cyanohydrin	75-36-0	OD9270000
0009	Acetanilide	75-05-9	AL7730000
0009	3-(alpha-Acetoxy)-benzo[1,4]-hydroquinazolin	81-81-2	QB4560000
0010	2-Acetobenzonic acid	50-78-2	VO0700000
0010	p-Acetobenzonic acid	50-78-2	VO0700000
0009	1-Acetoxyethane	108-85-4	AK3870000
0007	2-Acetaminofluorene	53-96-3	AB9450000
0007	N-Acetyl-2-aminoethanone	53-96-3	AB9450000
0007	Acetylene	74-86-2	AQ6500000
0102	Acetylene black	1332-63-4	FF6000000

7 To search specific compounds by chemical name, synonyms, and trade names, click on the first letter of the compound of interest.

The screenshot shows the NIOSH Pocket Guide to Chemical Hazards website with the letter 'B' selected in the navigation bar. The table displays a list of chemical compounds starting with 'B'. The sidebar navigation links are visible on the right side of the page.

SEQ	CHEMICAL NAME	CAS No.	RTECS No.
0072	Bacillus subtilis	1395-21-7	CO9450000
0072	Bacillus subtilis BPH	1395-21-7	CO9450000
0072	Bacillus subtilis Carlsberg	1395-21-7	CO9450000
0047	Banana oil	123-82-2	NS9800000
0047	Barte	7727-43-7	CR0600000
0045	Barium chloride (as Ba)	10381-37-2	CO8750000
0045	Barium dichloride	10381-37-2	CO8750000
0045	Barium dinitrate	10022-31-8	CO9525000
0048	Barium(II) nitrate (1:2)	10022-31-8	CO9525000
0045	Barium nitrate (as Ba)	10022-31-8	CO9525000
0045	Barium salt of nitric acid	10022-31-8	CO9525000
0047	Barium salt of sulfuric acid	7727-43-7	CR0600000
0047	Barium sulfate	7727-43-7	CR0600000
0047	Barites (natural)	7727-43-7	CR0600000
0103	Baxudint	333-41-5	TF3320000
0077	Battery acid	7664-93-8	VB5500000
0086	Baxter	65-38-9	TF9825000
0103	BCME	542-88-1	KN1575000
0074	Beech sugar	67-60-1	VH8500000
0086	Benomyl	17804-35-2	DD6475000
0072	Benzenamine	52-53-3	BW6550000
0080	Benzene	71-43-2	CY1400000
0121	Benzene chloride	108-90-7	CZ0175000
0085	1,4-Benzendiamine	105-50-3	SB8050000
0085	1,3-Benzendicarbonyl	626-17-6	CZ1900000
0085	1,2-Benzendicarbonyl anhydride	85-44-9	TJ3150000
0071	1,3-Benzendiamine	1477-55-0	FF8970000
0109	1,2-Benzendiol	126-80-9	LX1050000
0085	1,3-Benzendiol	108-45-3	VG9525000
0138	1,4-Benzendiol	123-31-9	MX3800000
0085	m-Benzendiol	108-45-3	VG9525000

- 8 To display information about a specific compound, click the **SEQ** number, the database entry number, which is located to the left of the compound name.

**NIOSH Pocket Guide to Chemical Hazards**

**Benzene** CAS 71-43-2

$C_6H_6$  RTECS CV1400000

Synonyms & Trade Names: Benzol, Phenylhydride, DOT ID & Guide 1114-100

**Exposure Limits**  
 NIOSH REL: Ca TWA 0.1 ppm ST 1 ppm See Appendix A  
 OSHA PEL (1010,1026) TWA 1 ppm ST 5 ppm See Appendix F  
 IDLH Ca (500 ppm) See 114-100 Conversion 1 ppm = 3.10 mg/m<sup>3</sup>

**Physical Description**  
 Colorless to light-yellow liquid with an aromatic odor. (Note: A solid below 42°F)  
 MW: 78.1 BP: 175°F FRZ: 42°F Sol: 0.07%  
 VP: 75 mmHg IP: 0.24 eU Sp Gr: 0.88  
 FLP: 12°F UEL: 7.3% LEL: 1.2%

Class B Flammable Liquid (F+ below 73°F and BP at or above 100°F)

**Incompatibilities & Reactivities**  
 Strong oxidizers, many fluorides & perchlorates, nitric acid

**Measurement Methods**  
 NIOSH 1500, 1501, 2700, 2800, OSHA 10, 1005  
 See: [MFM](#) or [OSHA Methods](#)

**Personal Protection & Sanitation** (See [appendix I](#))  
 Skin: Prevent skin contact  
 Eyes: Prevent eye contact  
 Wash skin when contaminated  
 Remove: When wet (flammable)  
 Change: No recommendation  
 Provide: Eyewash, quick drench

**First Aid** (See [appendix J](#))  
 Eye: Irrigate immediately  
 Skin: Soap wash immediately  
 Breathing: Respiratory support  
 Swallow: Medical attention immediately

**Respirator Recommendations** (See [appendix E](#)) NIOSH  
 All concentrations above the NIOSH REL, or where there is no REL, at any detectable concentration  
 (APF = 10,000) Any self-contained breathing apparatus that has a full facepiece and is operated in a pressure-demand or other positive-pressure mode  
 (APF = 10,000) Any supplied-air respirator that has a full facepiece and is operated in a pressure-demand or other positive-pressure mode in combination with an auxiliary self-contained positive-pressure breathing apparatus

**Escape**  
 (APF = 50) Any air-purifying, full-facepiece respirator (gas mask) with a chin-style, front- or back-mounted organic vapor canister/lin. acropolymer escape-type, self-contained breathing apparatus

**Exposure Routes** Inhalation, skin absorption, ingestion, skin and/or eye contact

**Symptoms** Irritation (eyes, skin, nose, respiratory system), dizziness, headache, nausea, staggered gait, anemia, lassitude (weakness, exhaustion), dermatitis, bone marrow depression, [potential occupational carcinogen]

**Target Organs** Eyes, skin, respiratory system, blood, central nervous system, bone marrow

**Cancer Site** (Leukemia)  
 See also: [INTRODUCTION](#), See [ICSC CARD, 0316](#), See [MEDICAL TESTS, 0022](#)

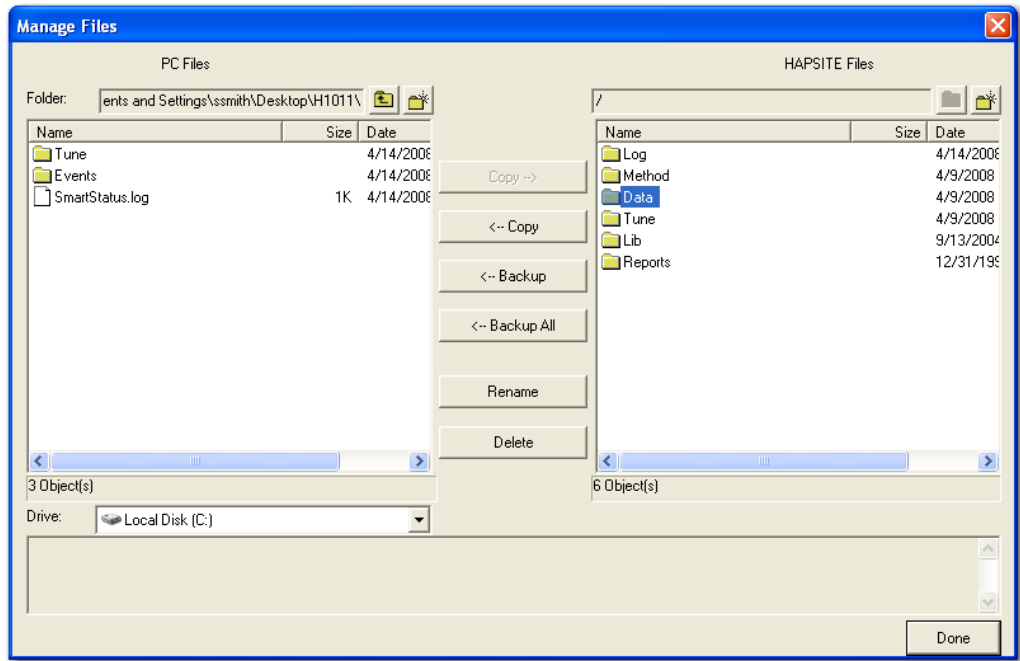
## 12.5 Manage File

The **Manage Files** function transfers files between HAPSITE ER and the laptop.



Manage Files

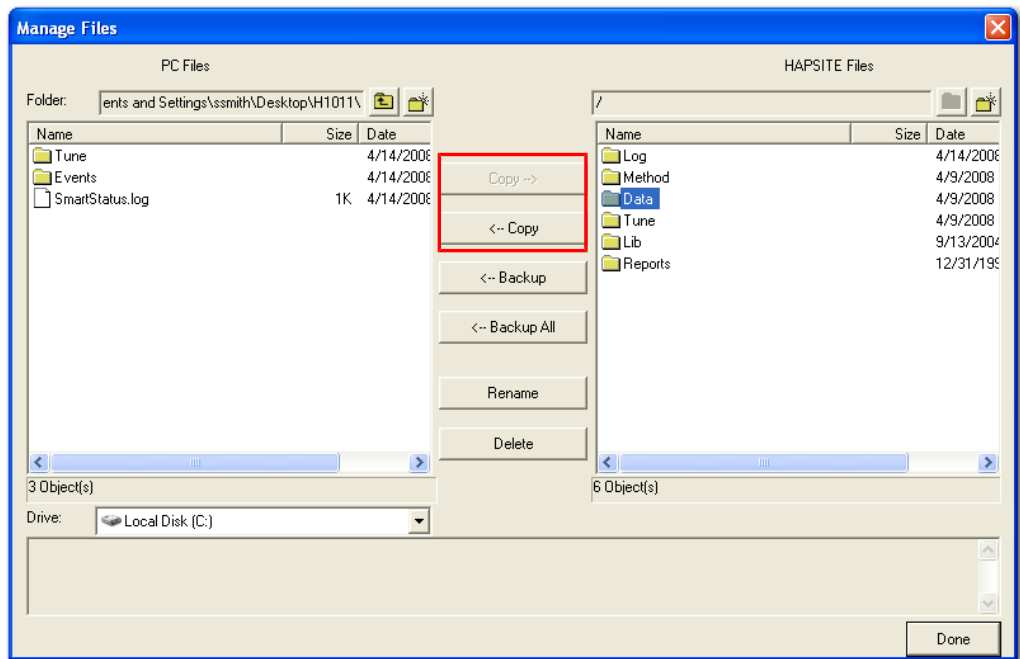
Double-clicking this icon opens the window shown below.



The **Copy -->** option allows methods only to be copied from the laptop to HAPSITE ER. The **<-- Copy** option allows methods and data files to be copied from HAPSITE ER to the laptop.

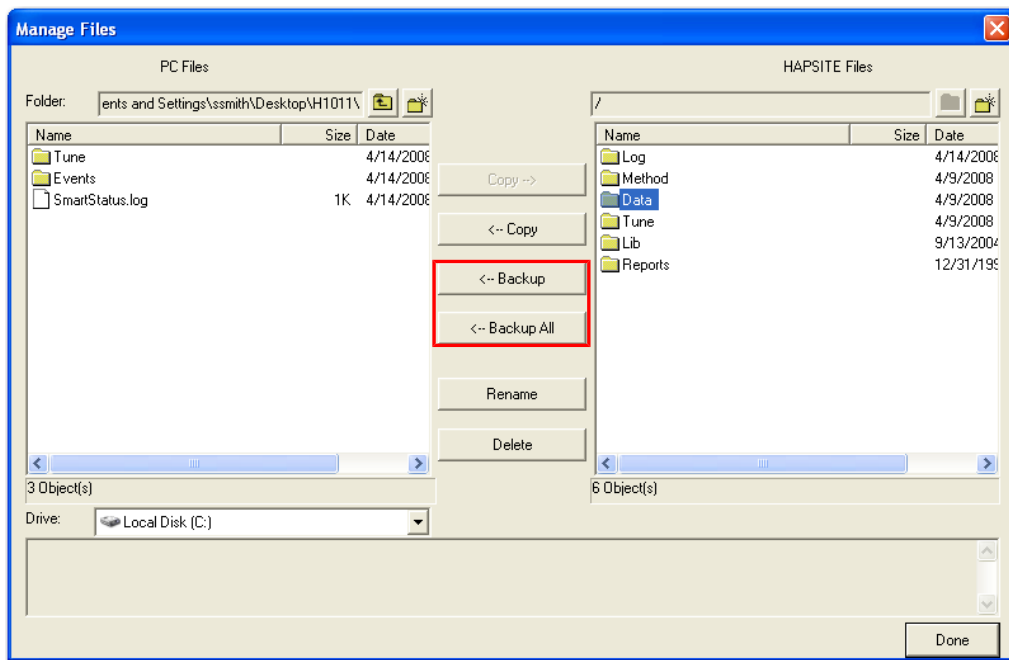


**Data files can only be transferred from the ER IQ to the laptop, they cannot be transferred from the laptop to HAPSITE ER. Method files can be transferred both from HAPSITE ER to the laptop and from the laptop to HAPSITE ER.**



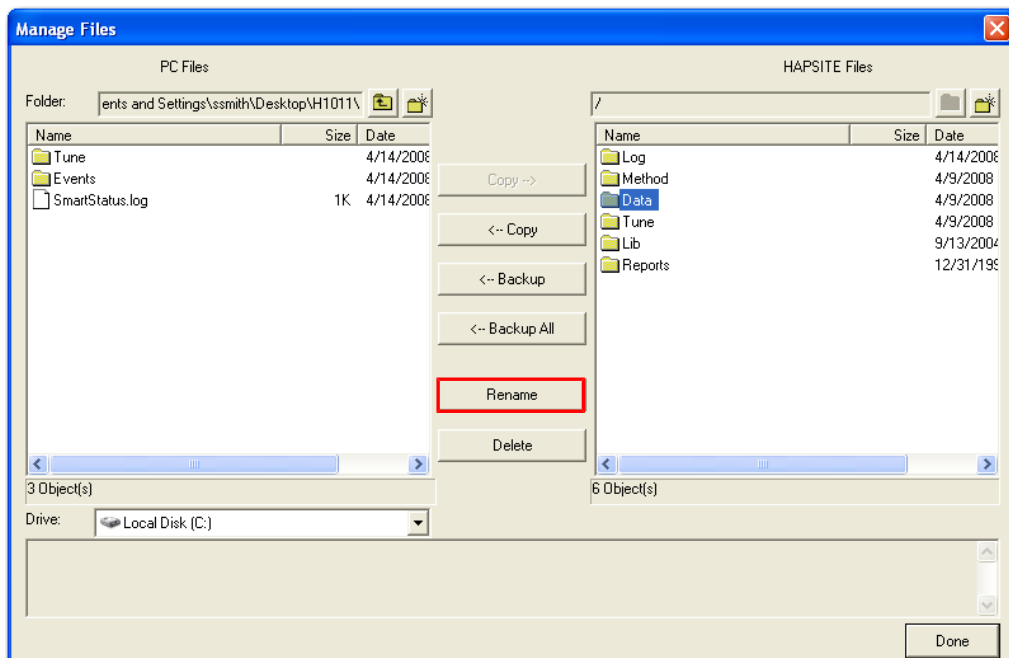


The <-- **Backup** option will backup the desired files from HAPSITE ER onto the laptop. The <-- **Backup All** option will backup all of the files found on HAPSITE ER onto the laptop. The **Backup** options will copy the files with a .tgz extension, while the **Copy** option maintains the .hps or .mth file extensions.

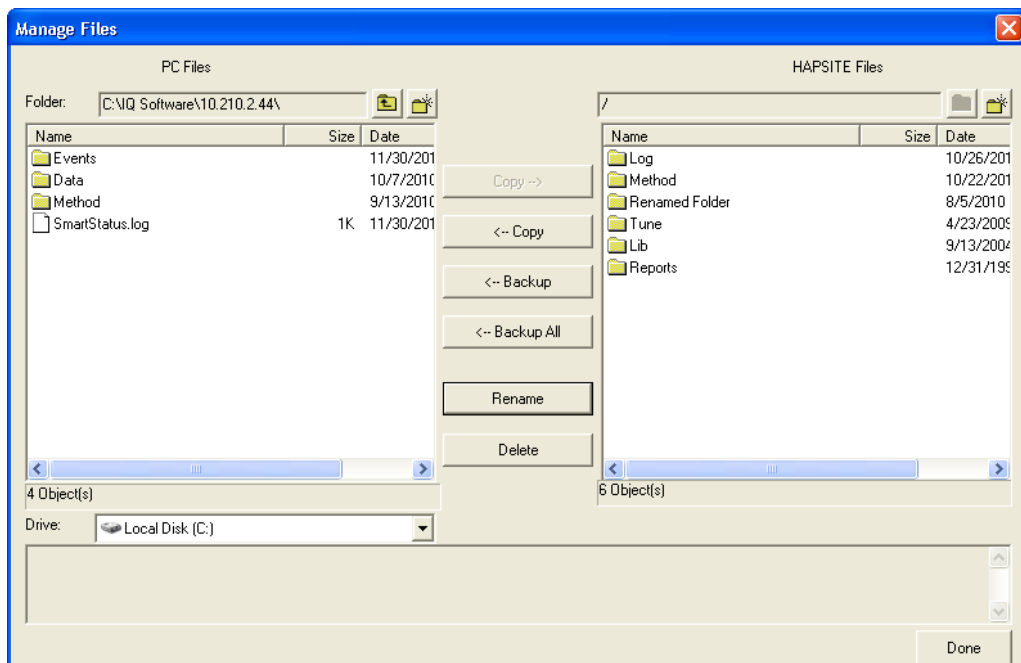
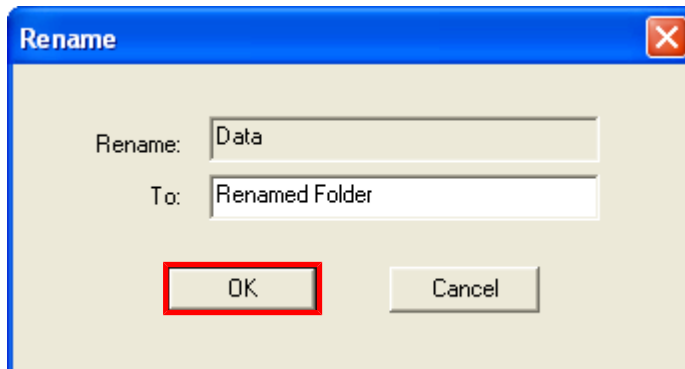


Renaming and/or deleting files are advanced user functions.

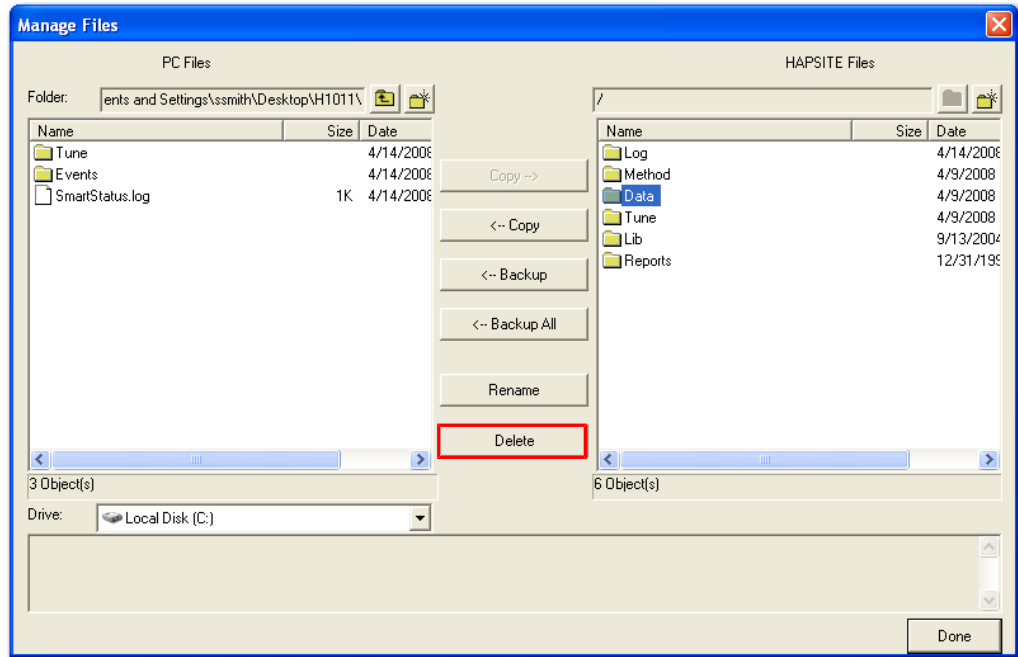
1 To rename a folder or file, click on the desired file and click **Rename**.



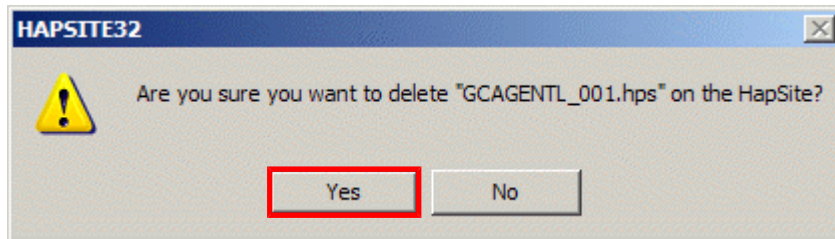
- 2 A new window is displayed. The former name will be displayed on top and a box typing in for the new name will be displayed beneath it. Type in the new name and click **OK**.



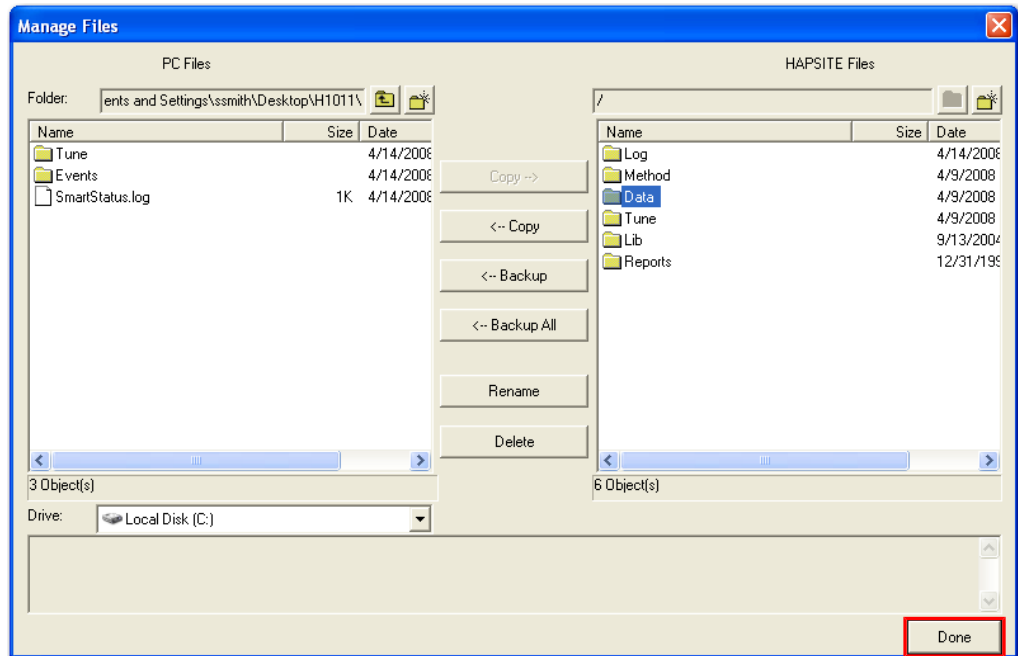
- 3 The **Delete** option removes folders or files. To delete folders or files, highlight the desired folder or file and click **Delete**.



4 After **Delete** is clicked, a confirmation window is displayed. Click **Yes** to delete the folder or file.



5 To exit the screen, click **Done**.



## 12.6 Status Icon

The **Status** icon provides the status of various system parameters. Options, such as the time, data settings, NEG and ion pump status, and pressure flows can also be set by selecting the **Status** icon.



Status

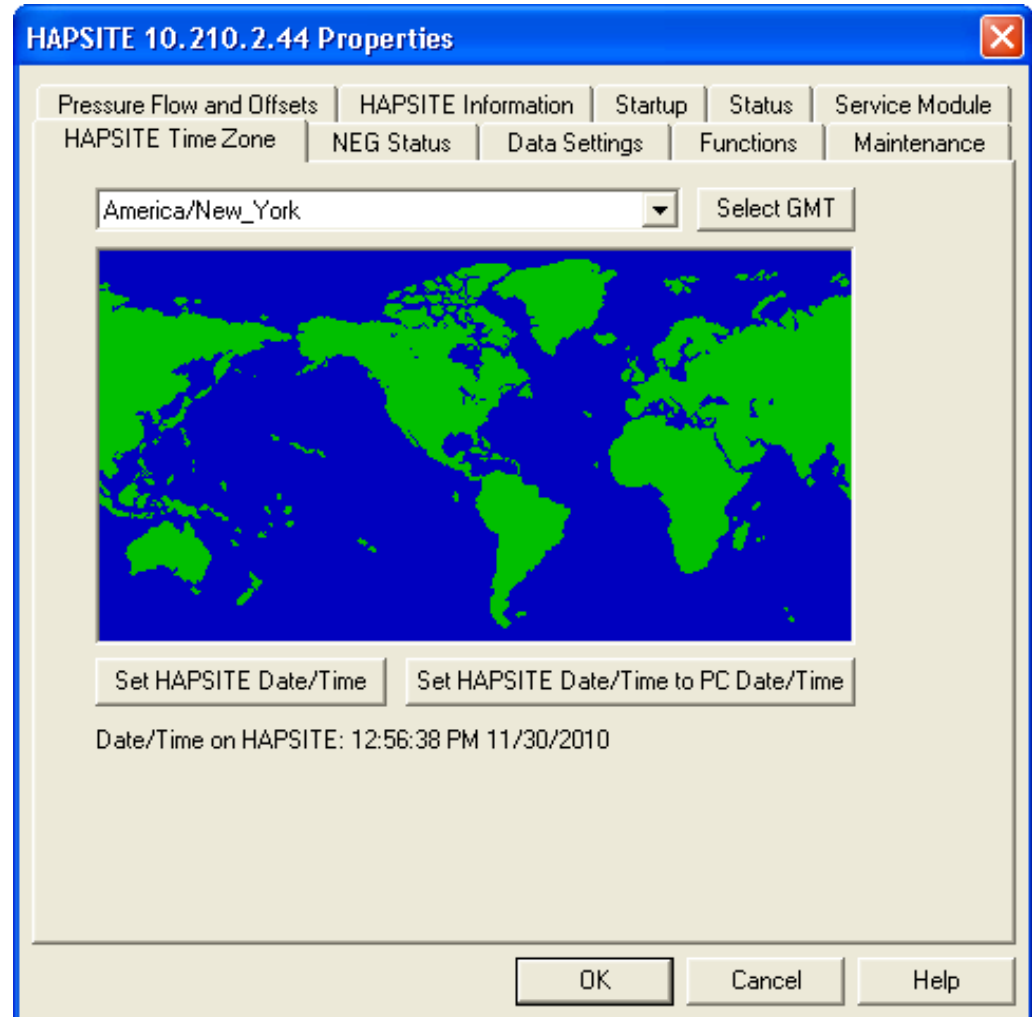
### 12.6.1 Status Properties

After double-clicking the **Status** icon, the first window displayed is the **Status** window. This screen displays the current temperatures and pressures of the key components in HAPSITE ER. The battery status and internal standard canister status is also displayed. Additionally, the sample input device, for example, probe, is shown.

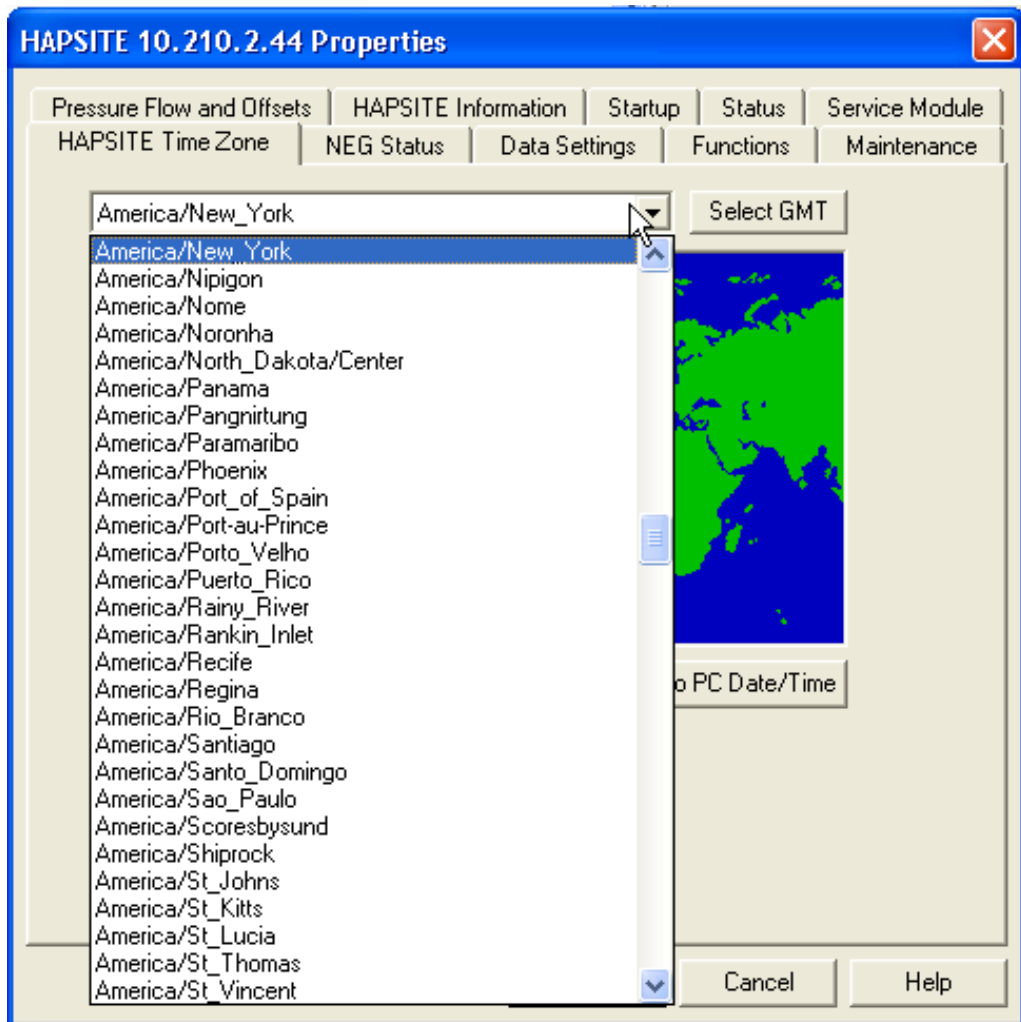
HAPSITE 10.210.2.44 Properties			
HAPSITE Time Zone	NEG Status	Data Settings	Functions
Pressure Flow and Offsets	HAPSITE Information	Startup	Status
Maintenance		Service Module	
Current Temperatures (C)		Current Pressures	
Column:	41.7	IS Supply (kPa):	48
Membrane:	60.0	Carrier Supply (kPa):	721
ValveOver:	60.0	GC Col. (kPa):	40
NEG:	Not Installed	Reservoir (kPa):	753
ConcElbow:	27.4	Total MS Pressure(Pa):	Below Gauge Range
Heated Lines:	60.0		
IS Canister		Batteries	
Fill Date:	11/12/08	HAPSITE Voltage:	N/A
Expiration Date:	12/12/09	HAPSITE Charge (%):	N/A
TRIS Conc. (ppm):	10.64	SM Voltage:	23.002
BPFb Conc. (ppm):	5.28	SM Charge (%):	100.0
Sample Input Device			
Type:	Not Installed		
Pressure (kPa):	N/A		
OK		Cancel	Help

## 12.6.2 HAPSITE Time Zone

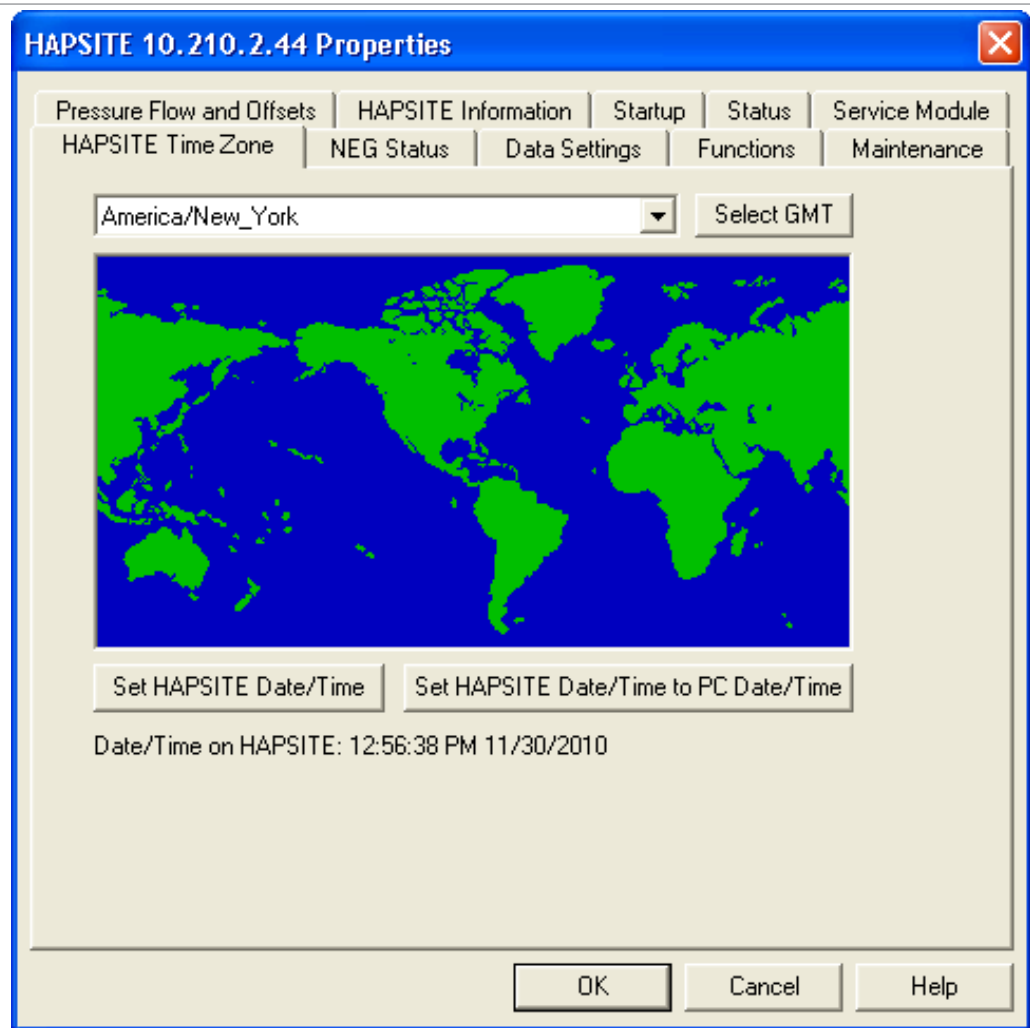
The HAPSITE ER **Time Zone** tab allows the user to set the time on the HAPSITE ER. Setting this parameter ensures that the data files are stamped with the proper date and time.



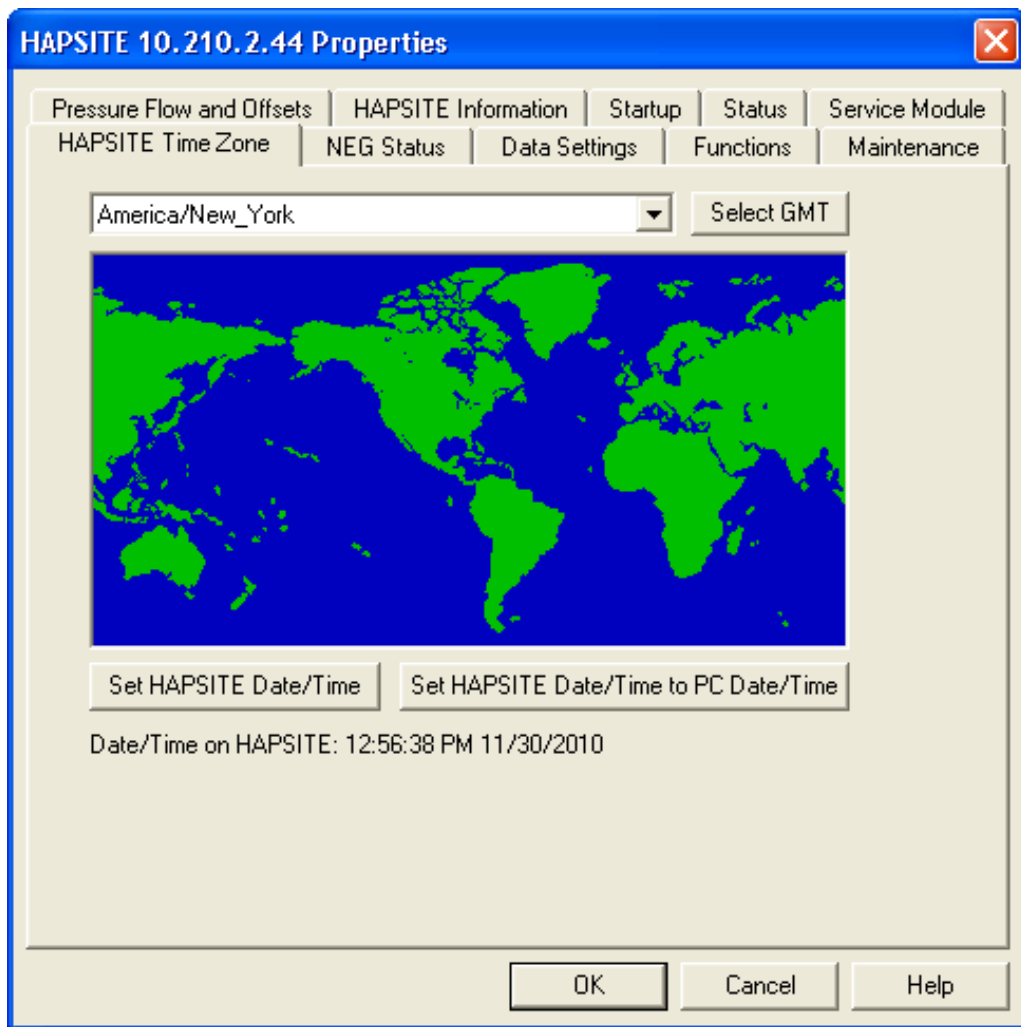
- 1 To set the time, select the desired time zone from the drop down menu.
  - ⇒ Click **Select GMT** if Greenwich Mean Time is desired.



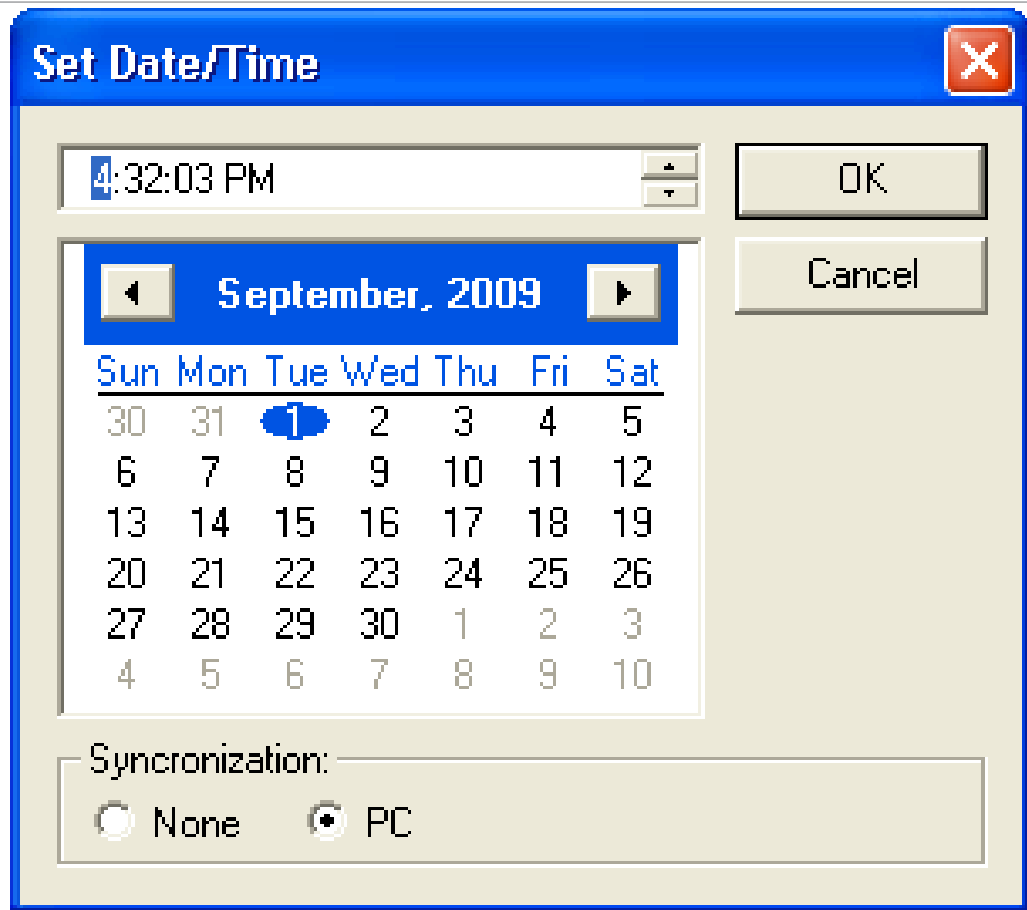
- 2 Clicking **Set HAPSITE Date/Time to PC Date/Time** automatically synchronizes HAPSITE ER to the laptop date and time.



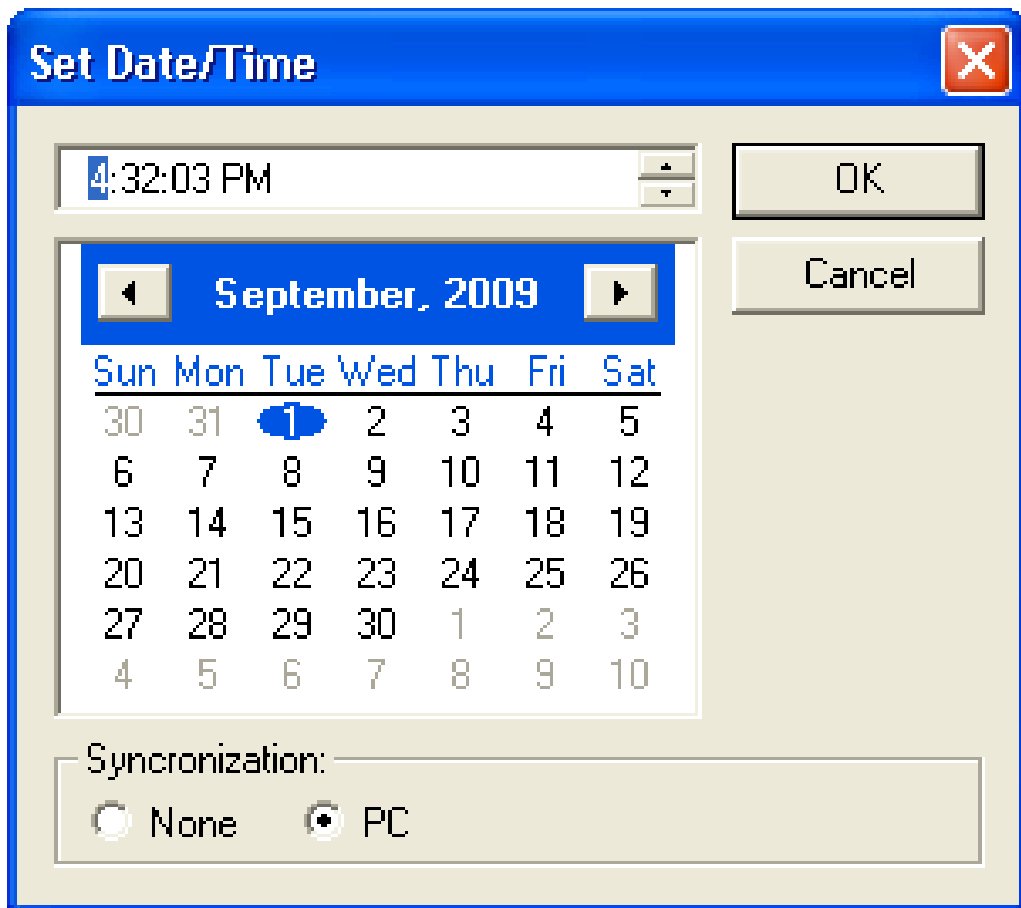
- 3 Clicking the **Set HAPSITE Date/Time** button displays a date/time window.



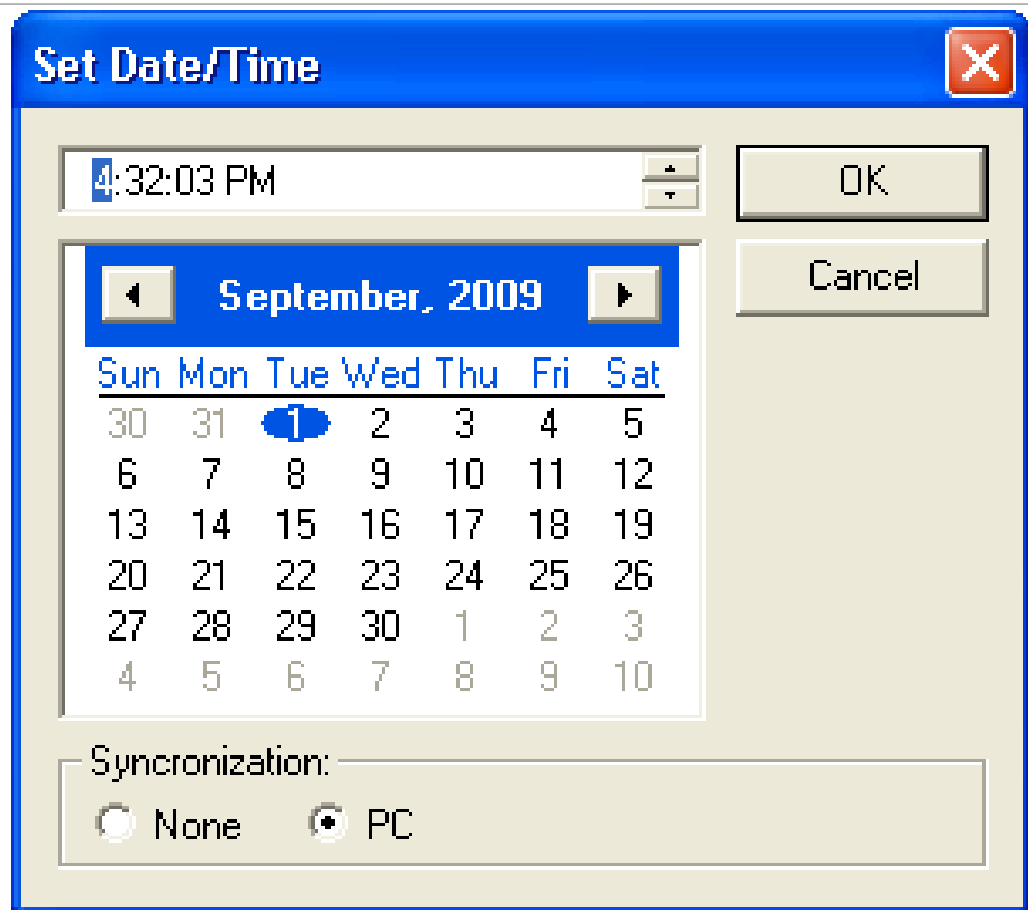




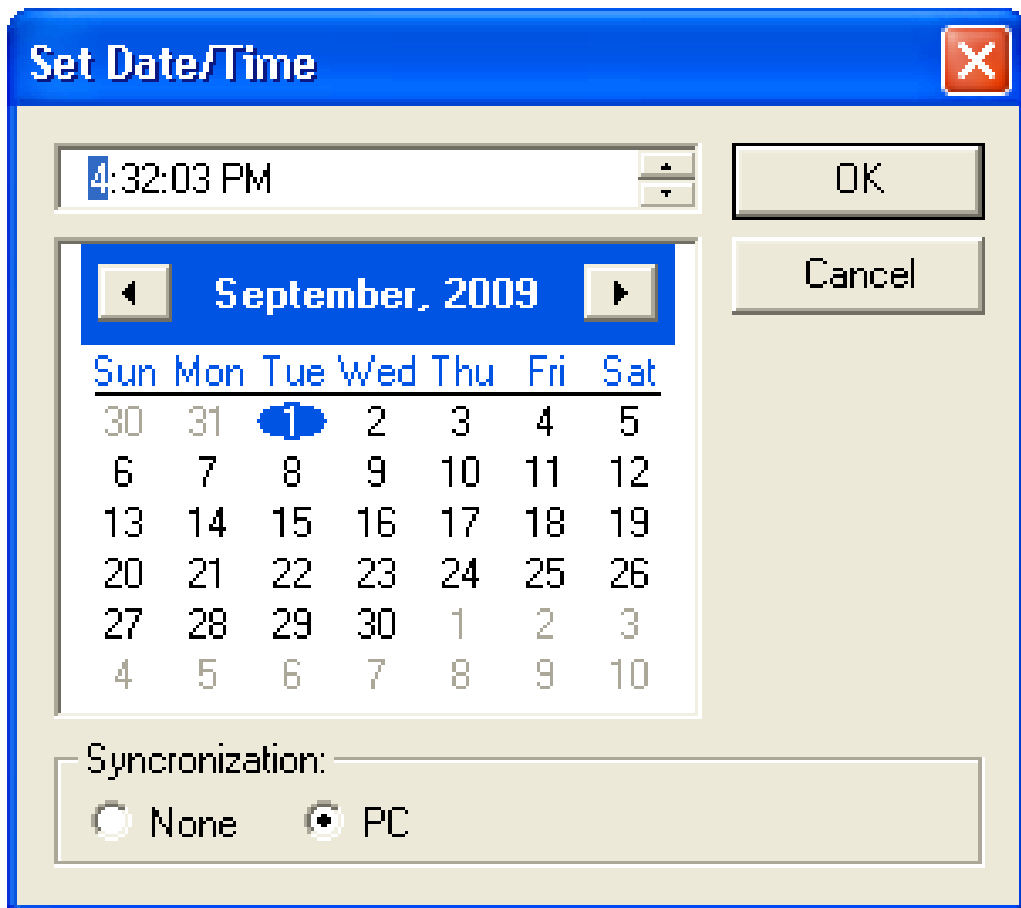
- 4 Use the top arrow keys to select the correct time.



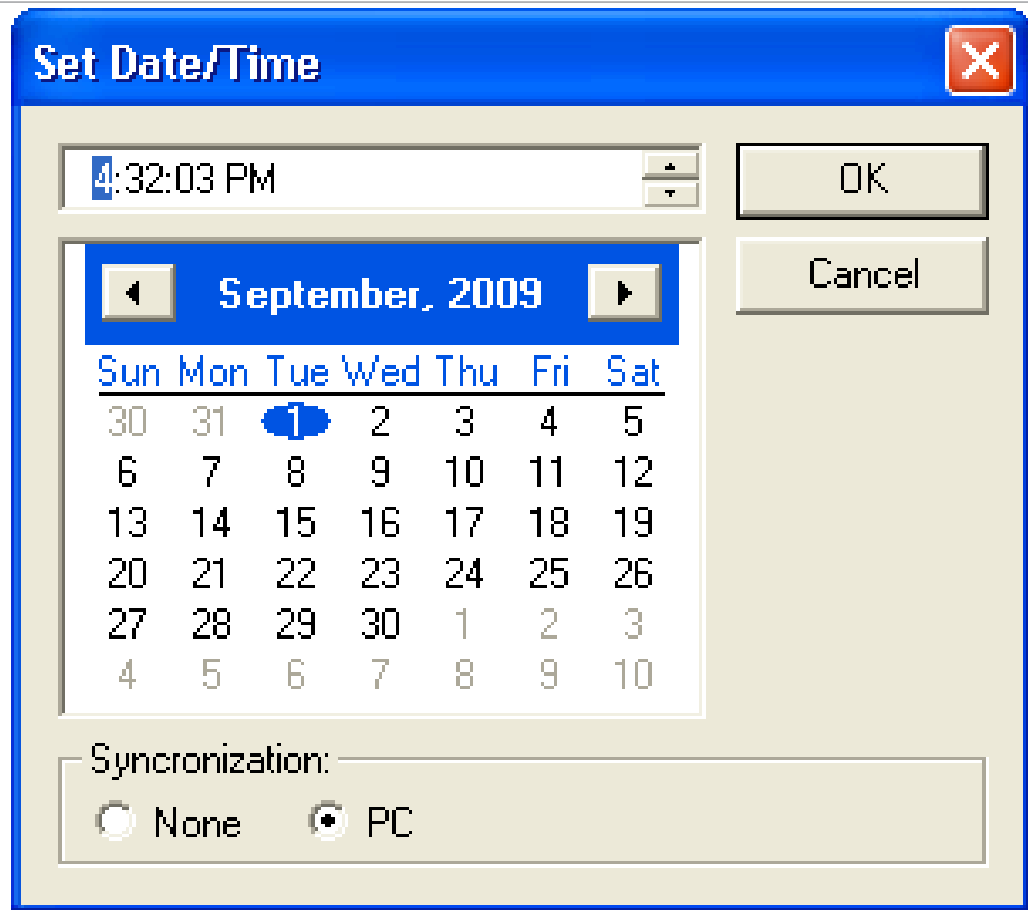
- 5 To select the proper date, use the arrow keys below the time to scroll to the current month. Click on the current date.



- 6 The **Synchronization** option synchronizes the time on the HAPSITE ER to the PC, GPS, or both. If synchronization is not required, click **None**.

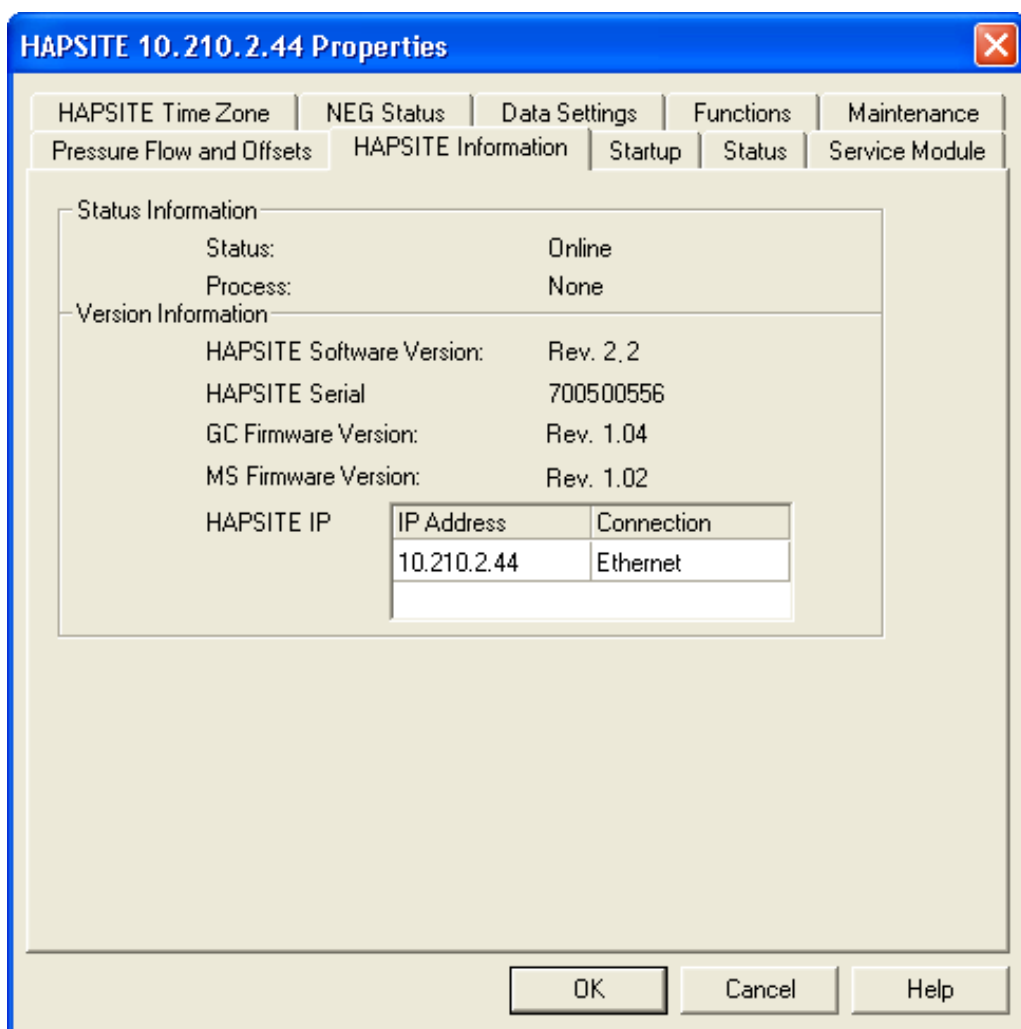


- 7 When all the parameters have been set, click **OK**.



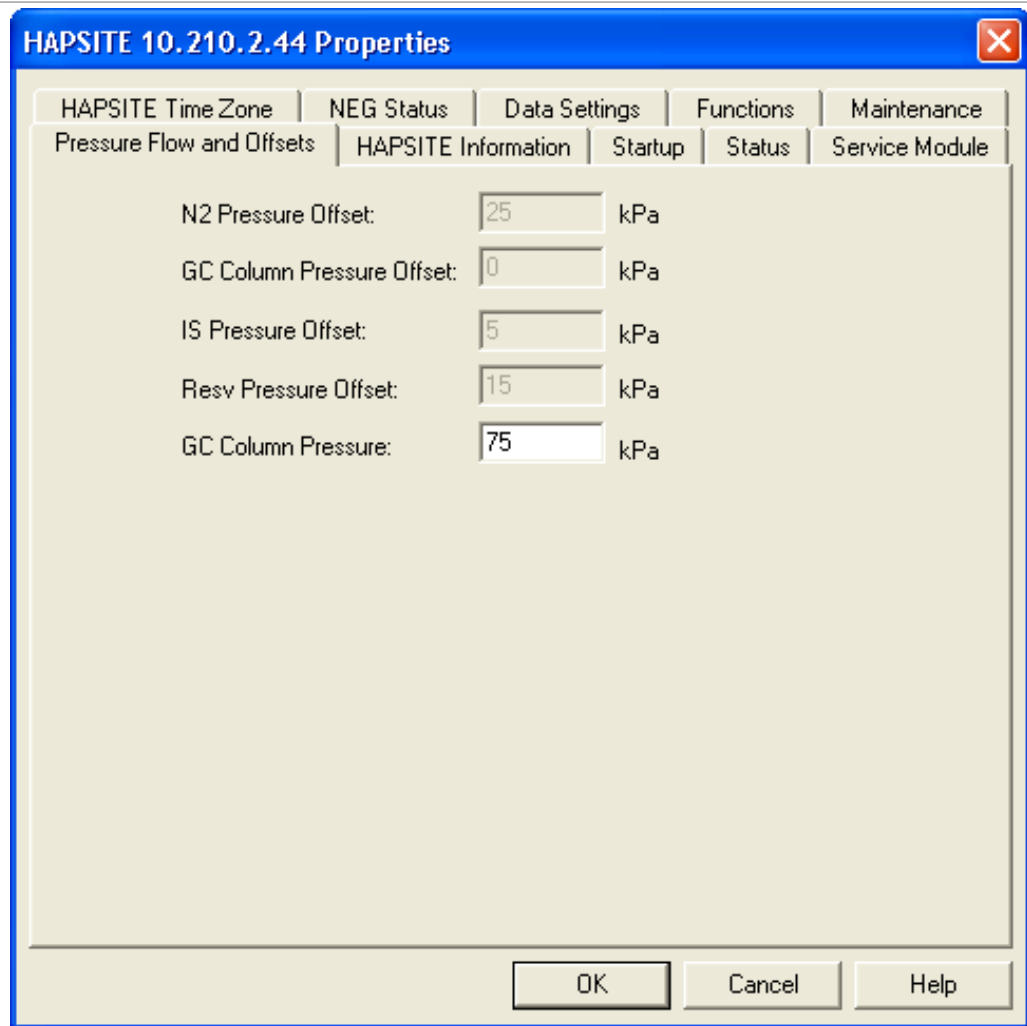
### 12.6.3 HAPSITE Information

The **HAPSITE Information** tab provides general information regarding the HAPSITE ER system. The top portion, **Status Information**, provides verification that the system is online. It will also notify the user when a method is running. The **Version Information** box provides the **HAPSITE Software Version**, **HAPSITE Serial Number**, the **GC Firmware Version**, the **MS Firmware Version**, the **HAPSITE IP Address**, and the **Connection** type.



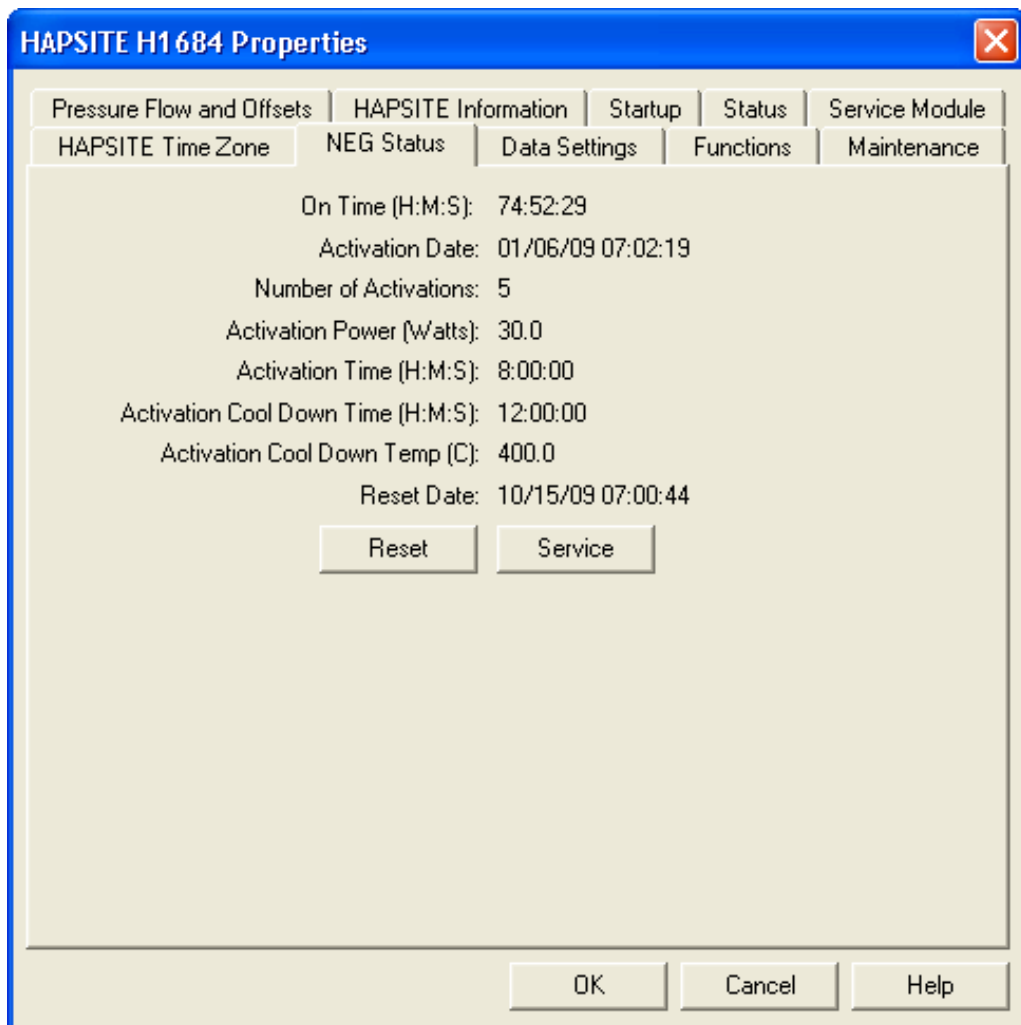
## 12.6.4 Pressure Flows and Temperatures

The **Pressure Flows and Temperatures** tab displays various pressures that have been set by the factory. The only pressure that can be changed by a user is the **GC Column Pressure**. When using HAPSITE ER, the BPF internal standard should elute from the column between 3:40 and 3:50, with 3:45 being the optimal elution time. If the standard elutes outside of this range, the pressure can be adjusted. To increase the retention time by approximately three seconds, decrease the **GC Column Pressure** by 1 kPa. To decrease the retention by approximately three seconds, increase the **GC Column Pressure** by 1 kPa. After adjusting the retention time, it is recommended that the user run another blank to verify that the BPF retention time is within range.



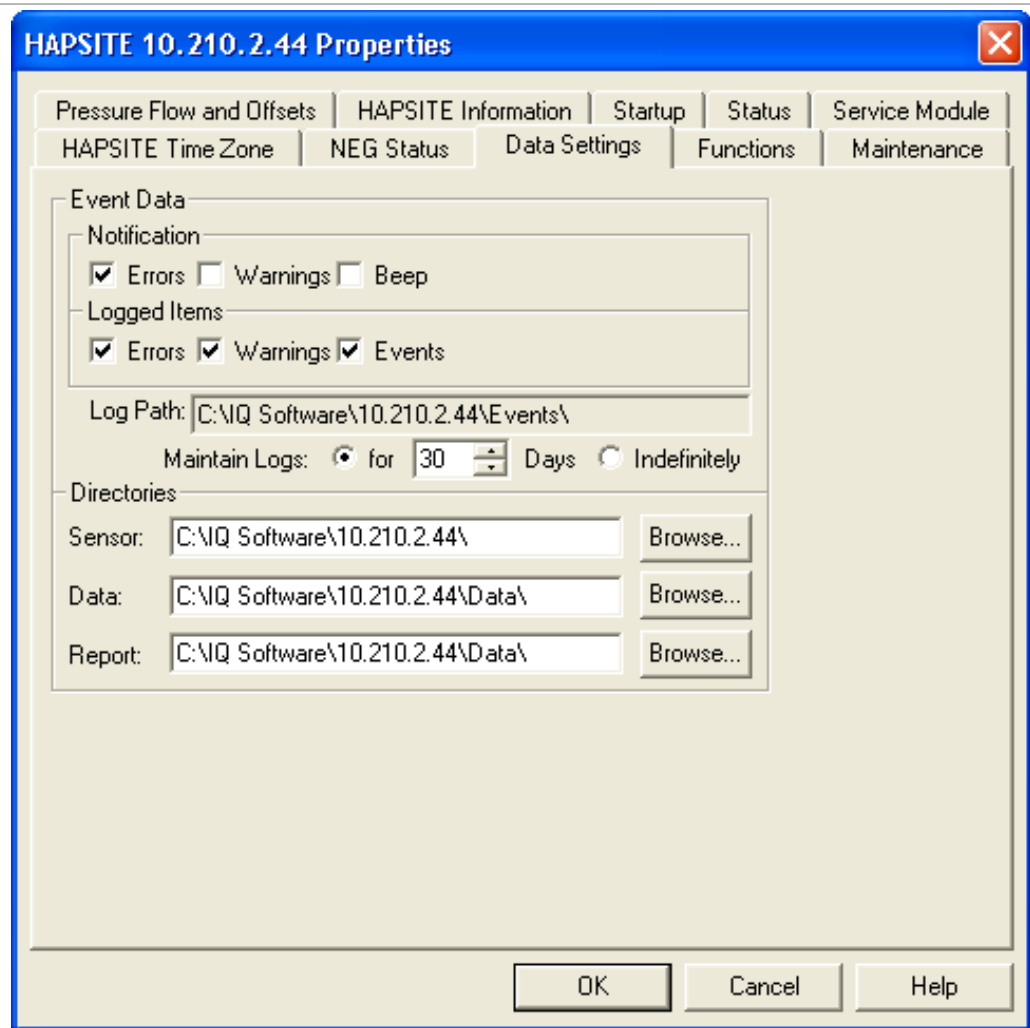
### 12.6.5 NEG Status

The NEG is a consumable item. **NEG Status** reports the number of hours that have been consumed. See NEG Troubleshooting [▶ 405].

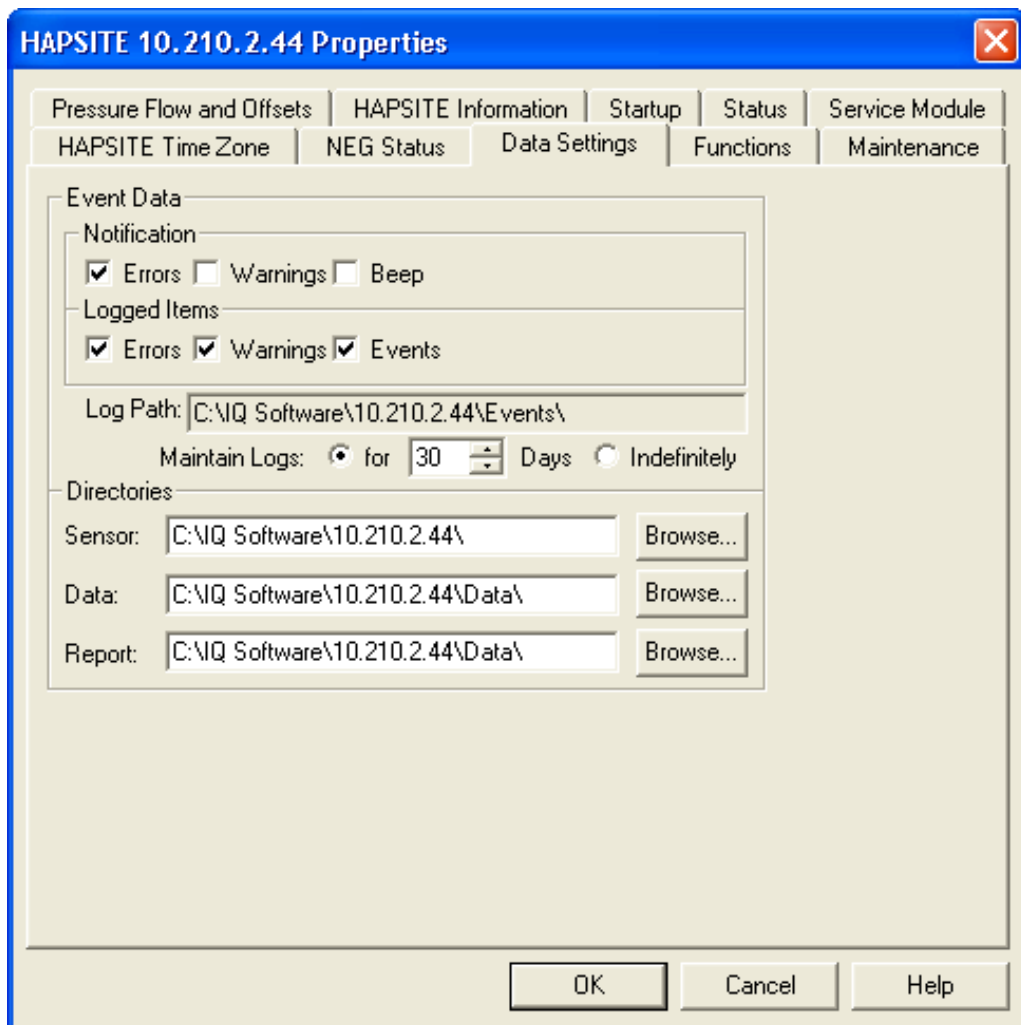


The **Data Settings** window displays the **Event Data** and the **Directories**. The **Event Data** allows the user to set the type of **Notifications** that will be displayed on the HAPSITE ER front panel and laptop. An error occurs when a warning has been displayed, but the warning has been ignored. If **Error** is checked, an error message is displayed. If **Warning** is checked, a warning message is displayed, when a problem, such as high pressure, arises. If **Beep** is checked, HAPSITE ER beeps when an error or a warning occurs.

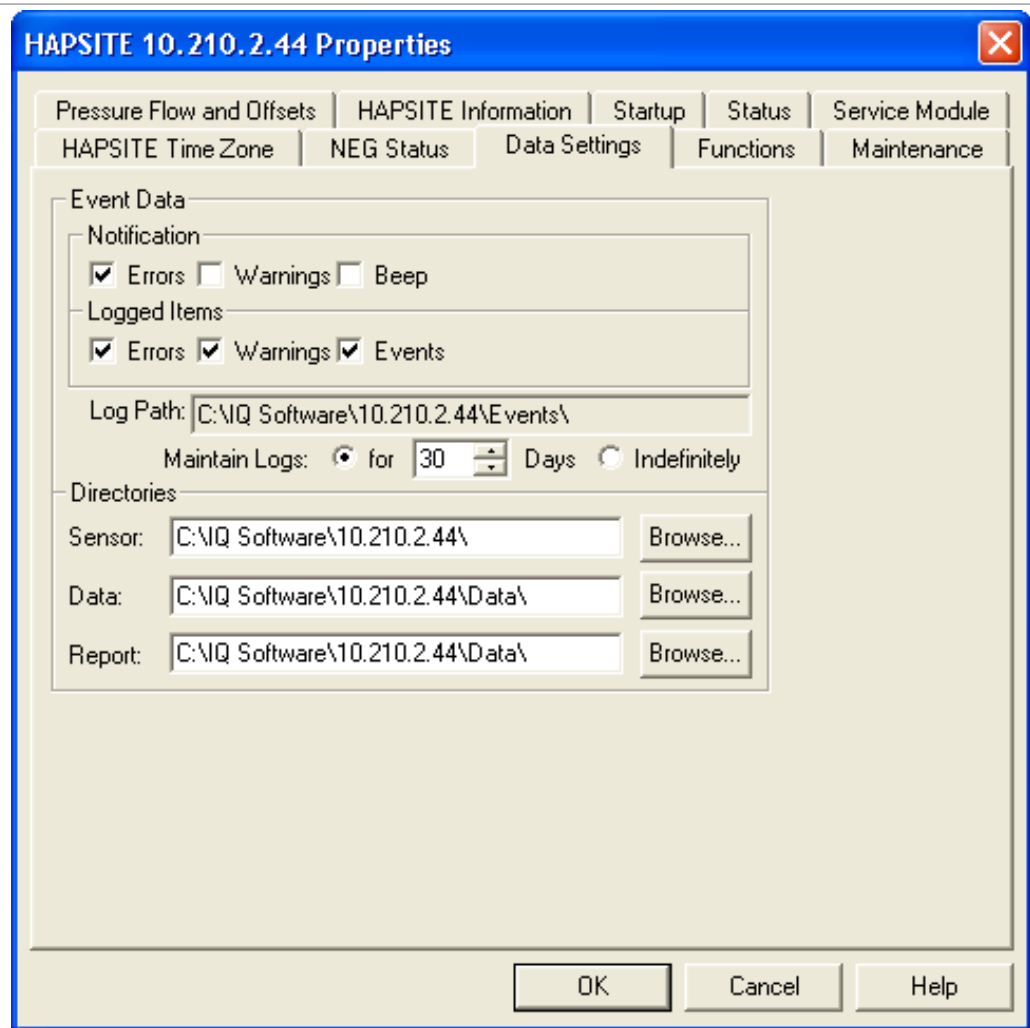




When an error, warning or event occurs, HAPSITE ER stores information about the occurrence and date it occurred. The pathway where this data is stored is displayed. The desired number of days for log storage can be set or the logs can be stored indefinitely.

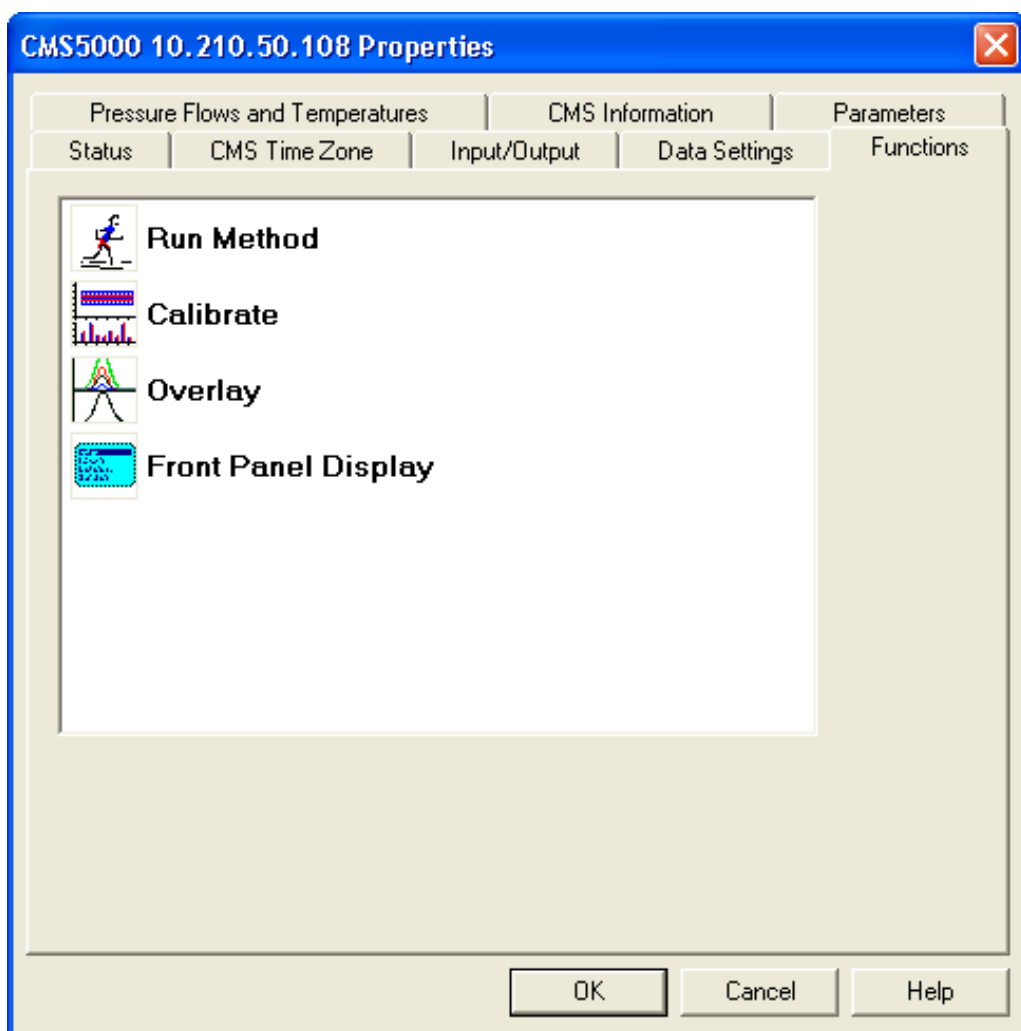


The **Directories** folder allows the file pathway for HAPSITE ER to be set. All data and information that has been created by HAPSITE ER is stored in the folder that has been selected in the **Sensor** pathway. All data files that have been created by HAPSITE ER are stored in the folder that was selected by the **Data** pathway. All report files which are text files of the quantitative, qualitative and summary report are stored in this folder.



## 12.6.6 Functions

The icons shown on the **Functions** tab perform the same functions as the icons displayed in the **System Setup** screen. To activate a function, highlight the icon and press **OK**.



For information on the **Run Method** function, refer to Laptop Operation [▶ 139].

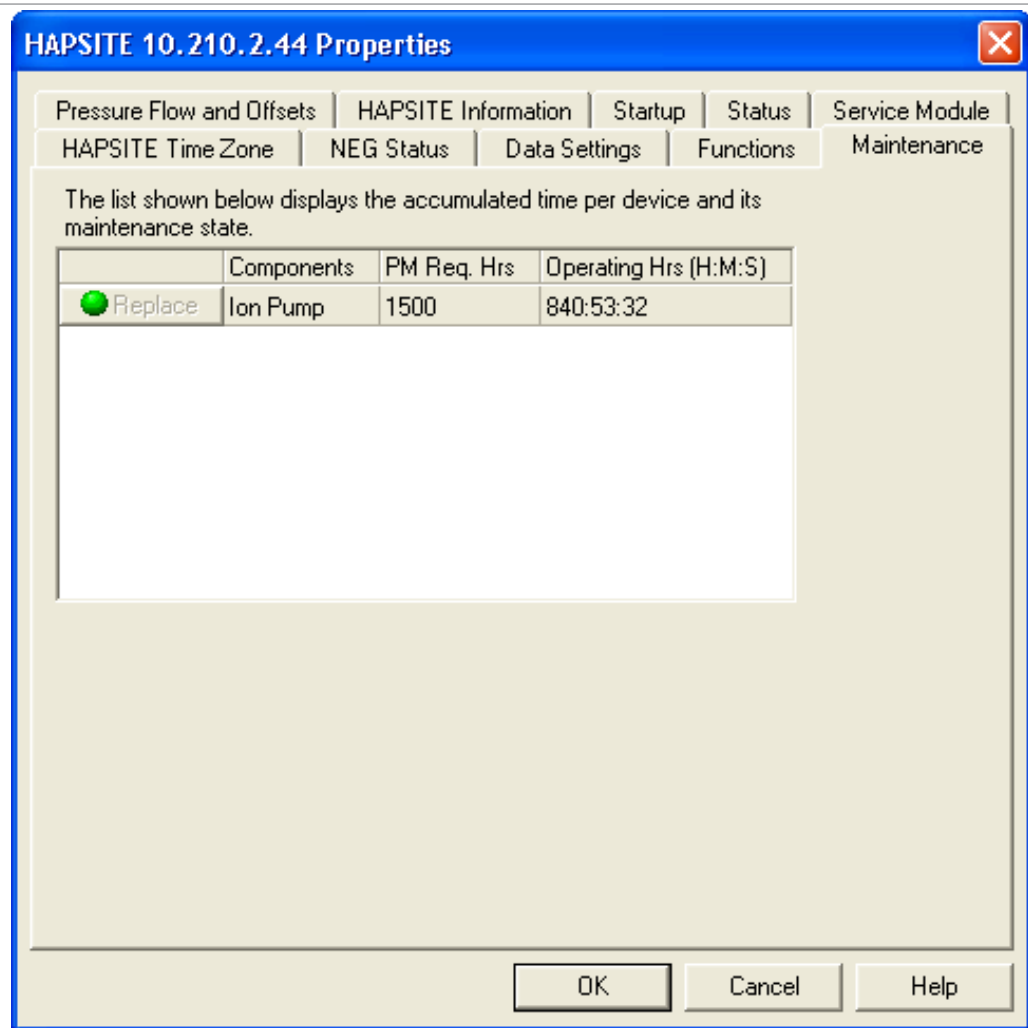
For information on the **Calibrate** function, see Calibration [▶ 370].

For information on the **Overlay** function, see Displaying Reconstructed Ion Chromatograms (RIC) [▶ 259].

For information on the **Front Panel Display** function, refer to Front Panel Display Icon [▶ 198].

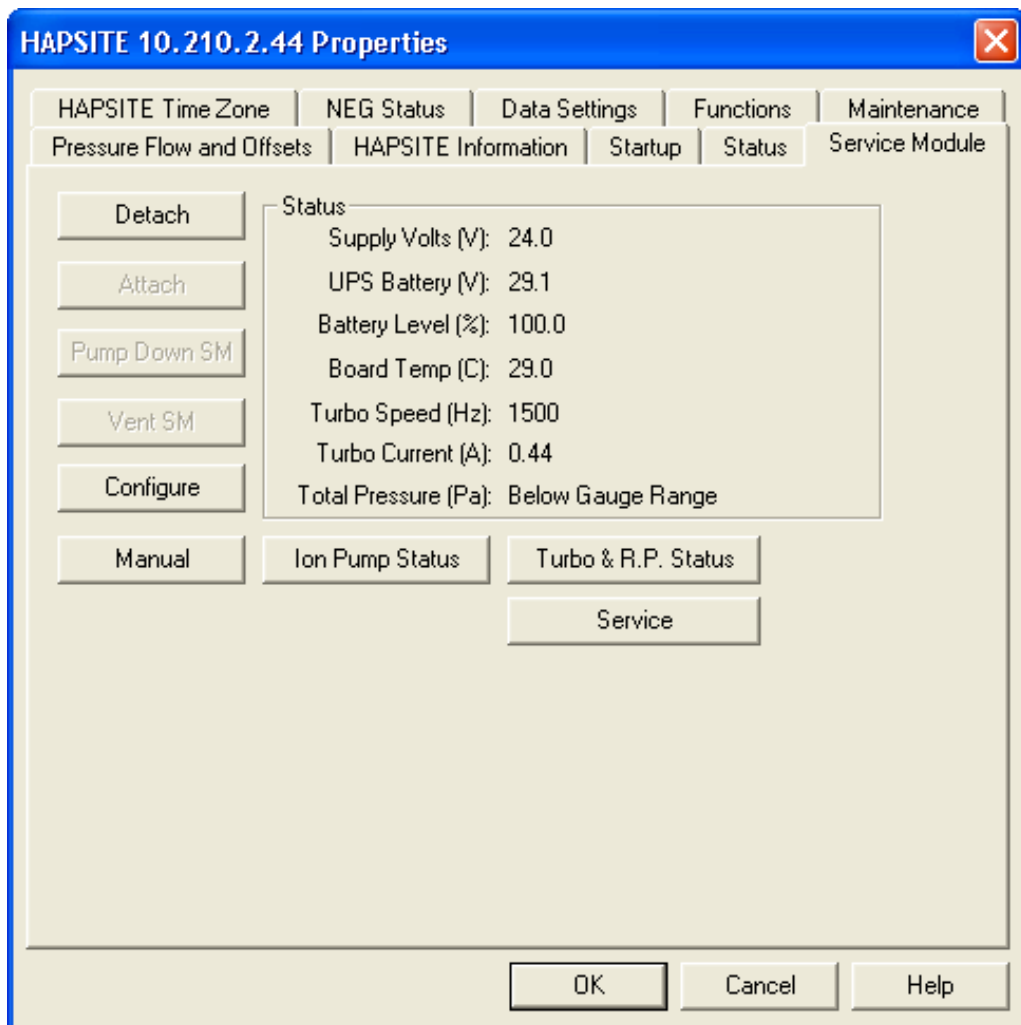
## 12.6.7 Parameters

The **Maintenance** tab will display the number of hours that the ion pump has been running. It will also display the recommended preventive maintenance guideline of 1500 hours. If it needs to be replaced, the **Replace** button will activate. See information on contacting customer support for service.



### 12.6.8 Service Module

The Service Module can be used as an alternate vacuum source or as a troubleshooting accessory. For more information on using the Service Module, see Maintenance [▶ 402] or refer to the *Service Module Operating Manual*.



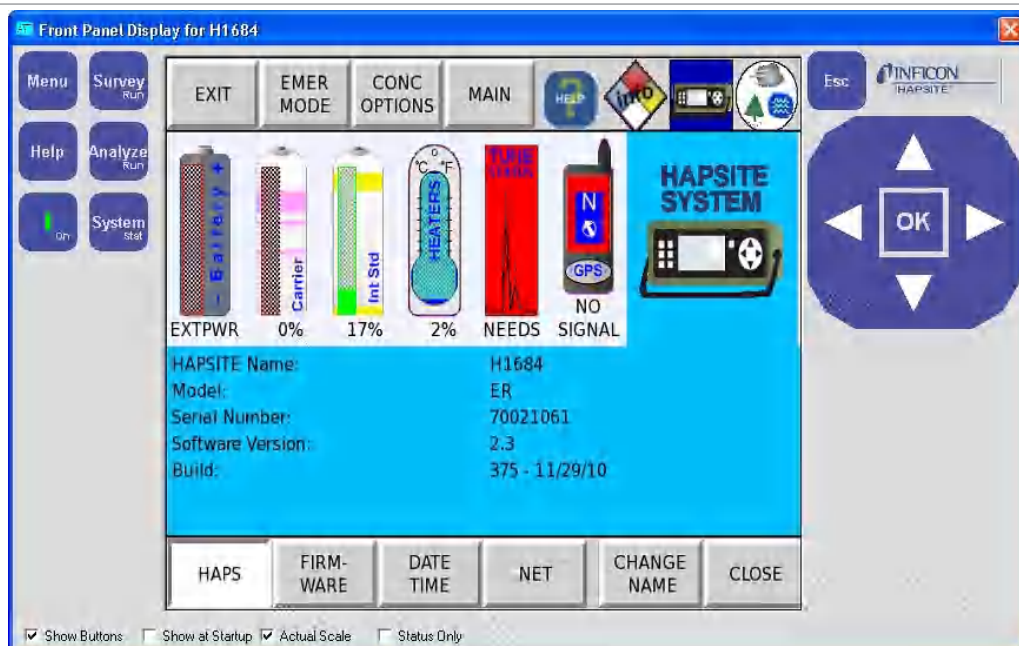
## 12.7 Front Panel Display Icon

Double-clicking on the **Front Panel Display** icon reveals an emulation on the laptop of the HAPSITE ER front panel screen, which can be used to control the front panel.



**Front Panel**

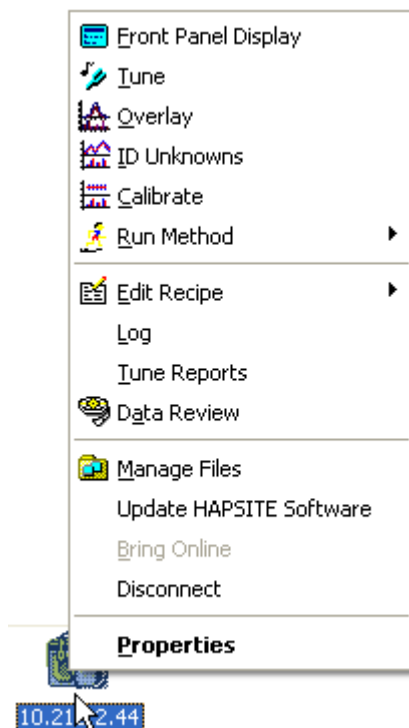
Double-click the **Front Panel Display** icon to open the emulation.



All of the buttons on the emulation operate identically to their front panel counterparts. To utilize the emulation, click on the desired button.

## 12.8 HAPSITE Sensor Icon

Right-clicking on the HAPSITE ER **Sensor Status** icon displays the following menu.



The first five options perform the same functions as their counterpart located in the System Setup screen. The **Edit Recipe** option performs the same functions as Method Editor. Refer to HAPSITE Icons [▶ 201] for more information.

The **Log** and **Tune Report** options can also be accessed through the **File** menu. Refer to File Menu [▶ 153] for more details.

The **Data Review** and **Manage Files** options perform the same functions as their icon counterpart located on the System Setup Screen. Refer to HAPSITE Icons [▶ 201] for more information.

## 12.8.1 Update HAPSITE Software

Periodically, a software update for HAPSITE ER may be available. Clicking the **Update HAPSITE Software** option, allows the user to select the software update file. Once selected, the update will be loaded onto the analytical module and the analytical module will restart. For complete installation instructions, refer to the Software Installation Instructions that are located on the update CD, as instructions for each update may vary.

**All update files will have the .upd extension.**

Latest versions of the HAPSITE software, along with instructions for loading these onto the unit, can be downloaded from the INFICON website, Software Downloads page: <https://www.inficon.com/en/downloads/software-downloads/>.

## 12.8.2 Bring Online

If HAPSITE ER is not communicating when connecting through the Ethernet cable, clicking on the **Bring Online** option will attempt to re-establish communication. If the connection has been manually disabled, clicking **Bring Online** will re-enable the connection. When the connection is active, the **HAPSITE Sensor** icon will not be overlaid with an “X.”

### 12.8.2.1 Communication Messages

If the laptop is not communicating with HAPSITE, there are three types of “X’s” that may be displayed.

The red “X” signifies that communication was suddenly lost. For example, an Ethernet cable was disconnected.

The blue “X” signifies that communication has yet to be established.

The gray “X” signifies that communication has been disabled through ER IQ by using the **Disconnect** option.



## 12.8.3 Disconnect


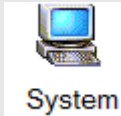

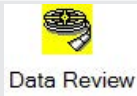
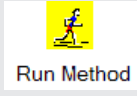



The **Disconnect** option will manually disconnect the laptop from HAPSITE ER and will remain disconnected until **Bring Online** is selected.


















### ⚠ CAUTION

The Laptop and HAPSITE ER should always have the most current version of the software installed. Verify that the unit software and ER IQ software have the same version number. Do not try to run incompatible versions of software together. (For example ER IQ 1.05 and HAPSITE ER Analytical Module software 1.16)

## 12.9 HAPSITE Icons

Icon	Description
	Start ER IQ Software from the desktop.
	System properties (Communications, Display, Miscellaneous).
	HAPSITE ER sensor. Right-click to access menu.
	Accesses all saved data files.
	Accesses methods to initiate a run.
	Accesses the NIST software and library.
	Accesses the NIOSH database.
	Accesses the AMDIS software and library.

Icon	Description
 Manage Files	Allows transfer of files between HAPSITE ER and laptop.
 Method Editor	Allows editing and creating methods.
 Service Module	Accesses the Service Module when attached.
 Status	Accesses HAPSITE ER properties.
 Tune	Accesses the HAPSITE ER tune program.
 Front Panel	Opens the HAPSITE ER front panel display on the laptop screen.
	Accesses Data File information.
	Returns the current screen to the System Setup screen.
	Displays the software version of <b>ER IQ</b> software that is installed on the laptop.
	Accesses the Calibrate function.
	Accesses the ID Unknowns function.
	Accesses <b>Chromatogram Overlay</b> function.
	Navigates through files in <b>Data Review</b> .
	Navigates through peaks in “search for peaks.”
	Returns to the complete full chromatogram (TIC) display in “search for peaks.”

# 13 Data Review

## 13.1 Chromatogram Overlay

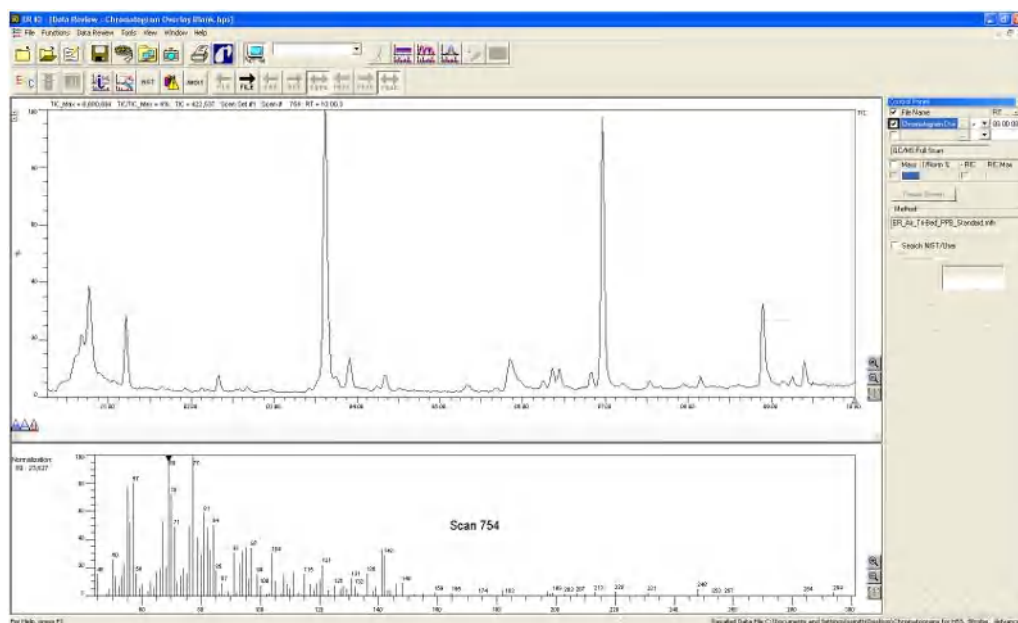
In order to compare multiple chromatograms, **Chromatogram Overlay** allows chromatograms to be superimposed in the same window. Follow the instructions below to overlay chromatograms.

- 1 Click on the **Chromatogram Overlay** icon.

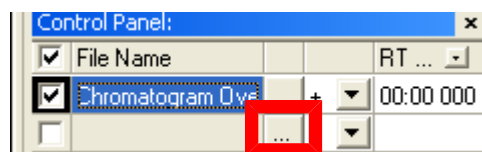


- 2 Follow the **Data Review** icon instructions in order to locate the desired file. Refer to Introduction [▶ 205].

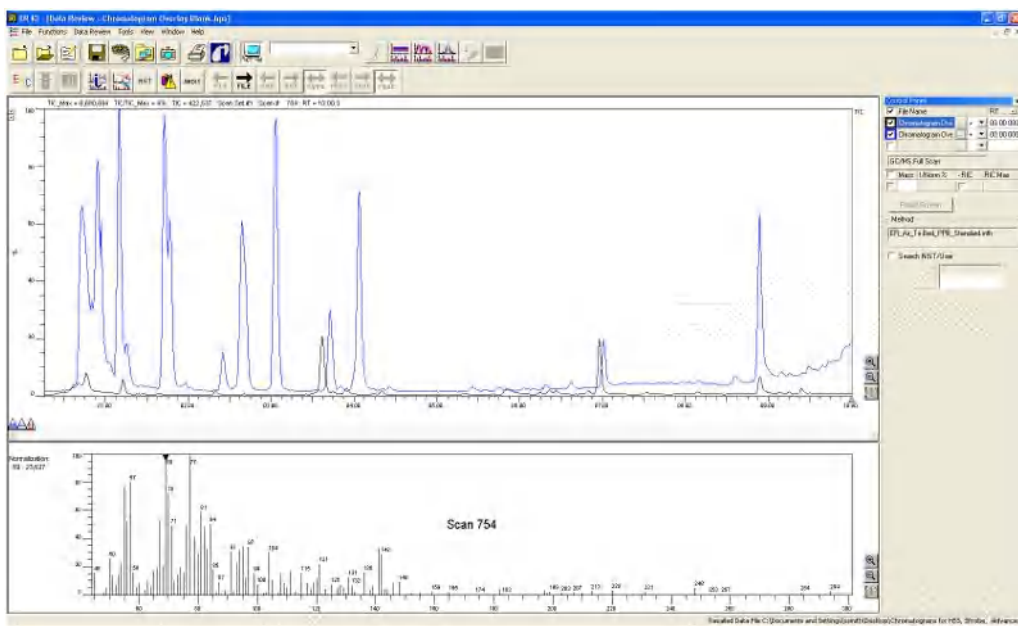
⇒ The data file is displayed in the **Control Panel**.



- 3 Click the icon displayed below in the row below the data file.



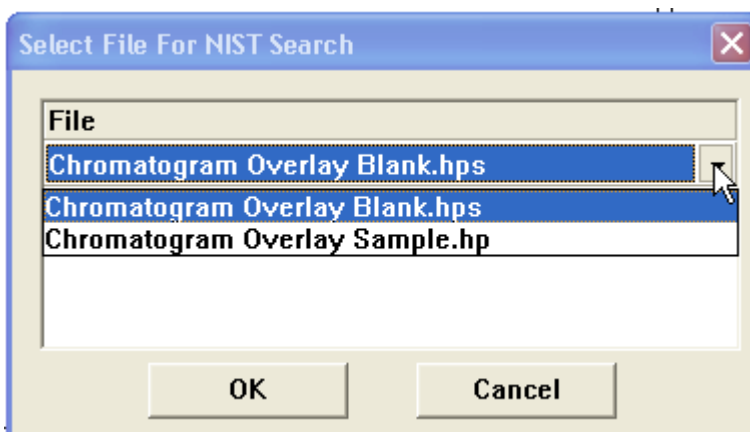
- 4 Follow the file selection procedure that was used in Step 2.
- 5 Both chromatograms are displayed in the chromatogram window. The color displayed in the check box correlates with the color of the chromatogram.



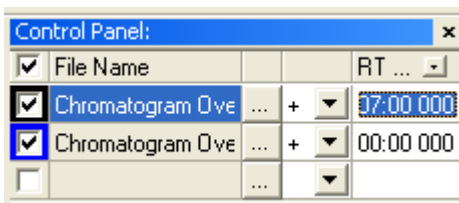
The mass spectrum is displayed for the highlighted file.



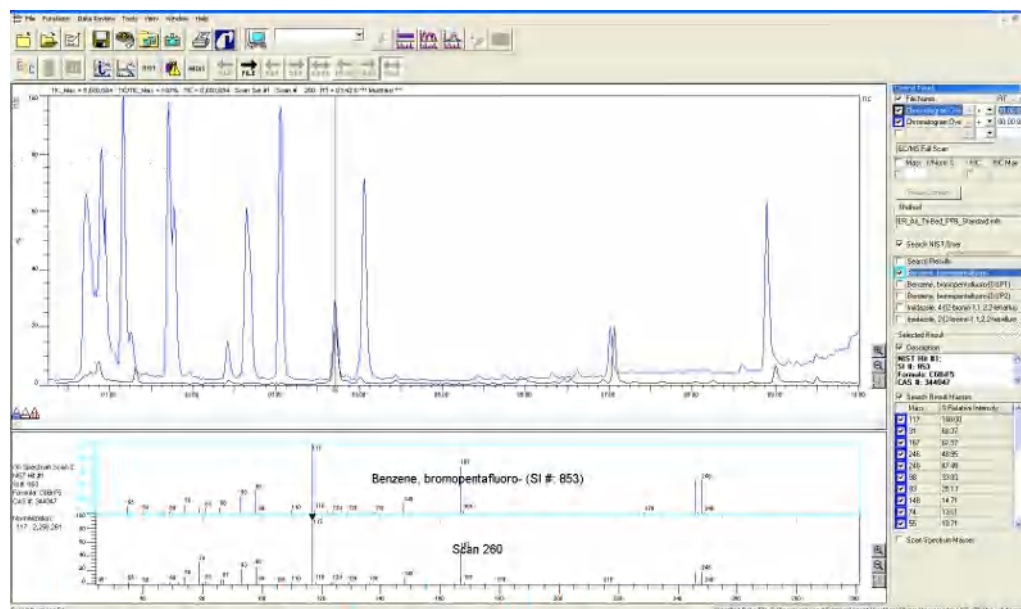
A NIST search can be performed on either chromatogram. **Select Search NIST/User** (refer to NIST Library Searches [▶ 230] for instructions) and select the desired file from the drop-down menu. The NIST identification is displayed for the highlighted file.



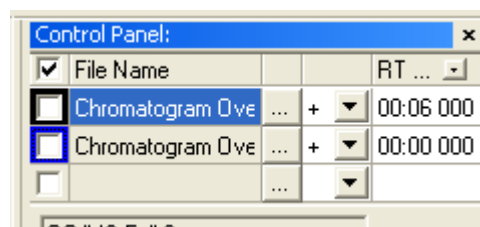
- Peaks can be aligned by retention time for further comparison. Determine the time difference between the peaks being compared. The chromatogram is shifted the desired amount of time by selecting + or - and typing in the time difference.



7 Press **Enter**. The chromatogram will shift by the time selected.



8 To close the **Chromatogram Overlay** feature, uncheck the box located to the left of the data file's name.



## 13.2 Introduction





This chapter provides information regarding the analysis of data samples. Topics include opening data files, compound identification using the AMDIS and NIST Libraries, overviews of all data review menus, **Background Subtract** and **Chromatogram Overlay**.

## 13.3 \*Data Review Toolbar

The **Data Review** toolbar is shown in the figure below.



	Aborts a running method.
	Start/stops a method.
	Pauses the data updates to the laptop during a run. This does not pause the analysis of the data by the HAPSITE ER.

	Accesses the <b>Data File Information</b> window.
	Views <b>Search Reports</b> for this data file.
	Open the <b>NIST</b> program.
	Opens the <b>NIOOSH</b> database.
	Opens the <b>AMIDS</b> program.
	Opens the previous file in the current directory.
	Opens the next file in the current directory.
	Opens the previous <b>SIM</b> Set.
	Opens the next <b>SIM</b> Set.
	Opens all <b>SIM</b> Sets.
	Select the previous peak when using the <b>Search for Peaks</b> function.
	Selects the next peak when using the <b>Search for Peaks</b> function.
	Returns to the full chromatogram display.

## 13.4 Accessing the Data Review Feature

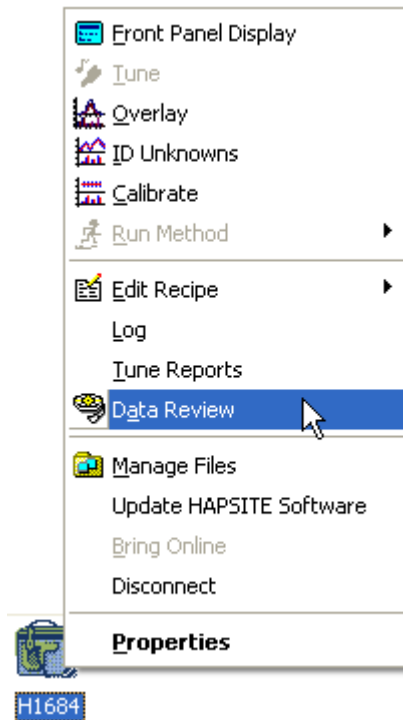
The **Data Review** feature can be accessed as follows:

- 1 Double-click the **Data Review** icon.

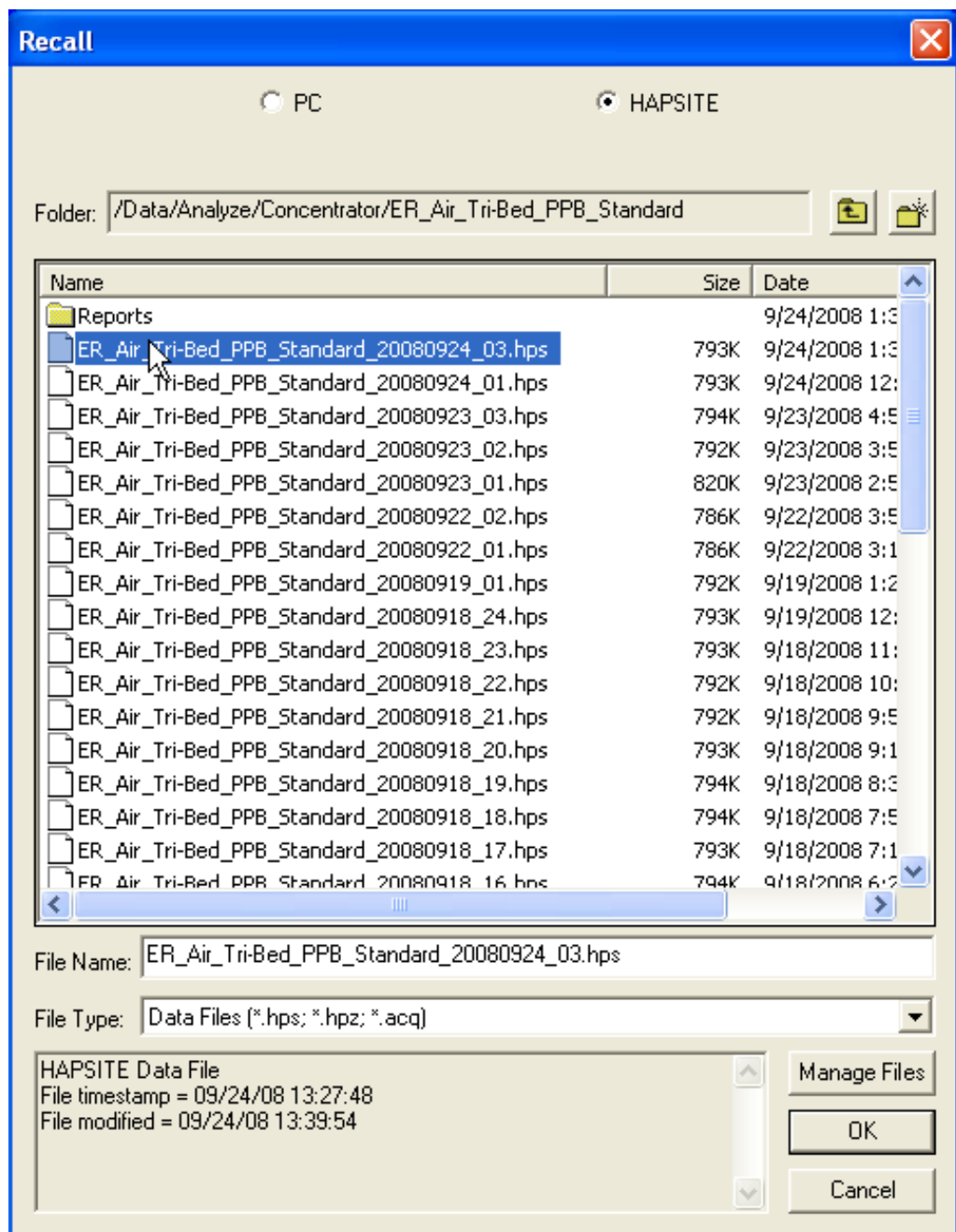


**Data Review**

- 2 Alternately, right-click the **HAPSITE Sensor** icon. The menu shown in the figure below is displayed. Click **Data Review**.

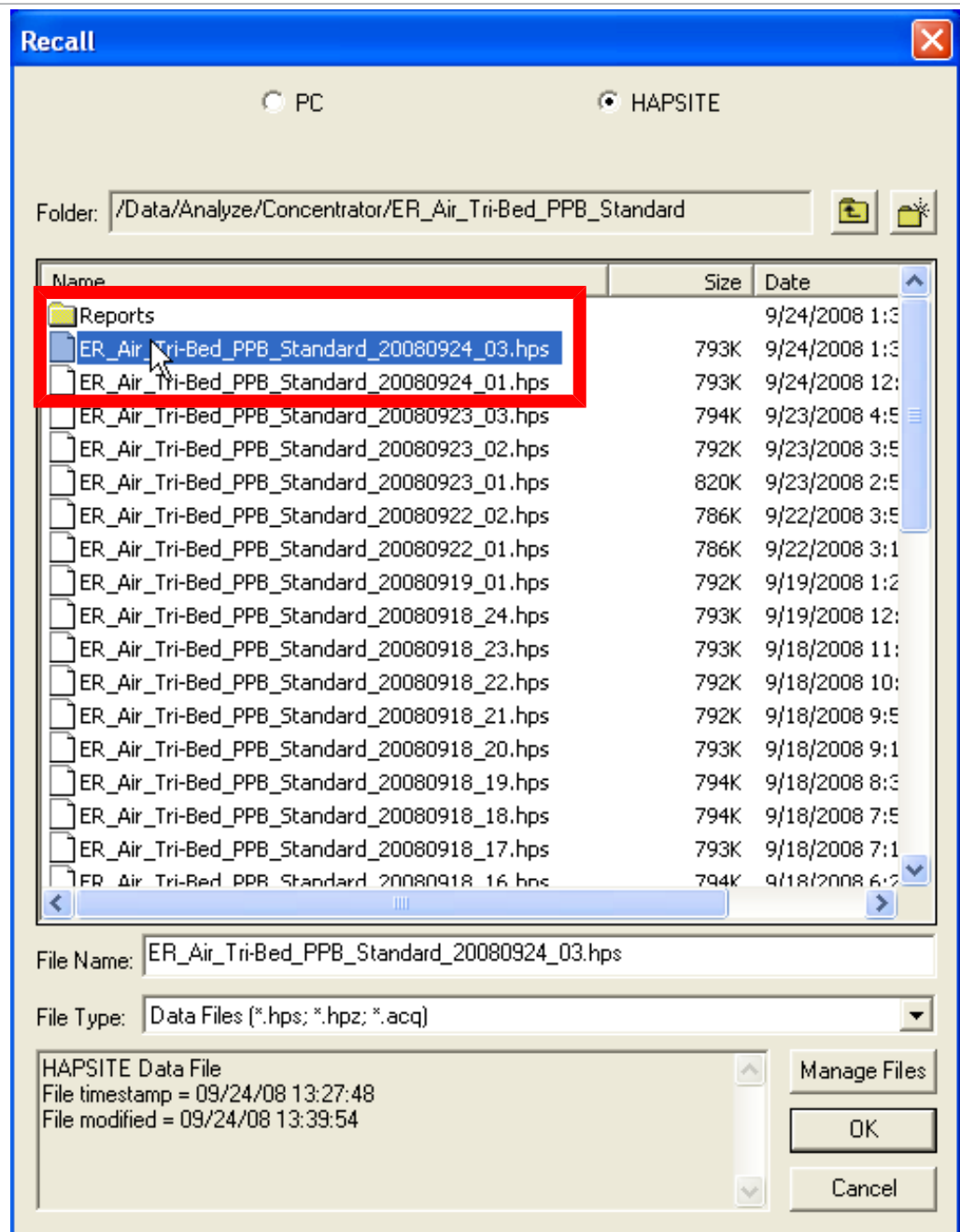


- 3 The **Recall** window will be displayed. Select **PC** if the file was run using the laptop. Select **HAPSITE** if the file was run using the HAPSITE ER front panel and the laptop was not connected at the time of sample collection.



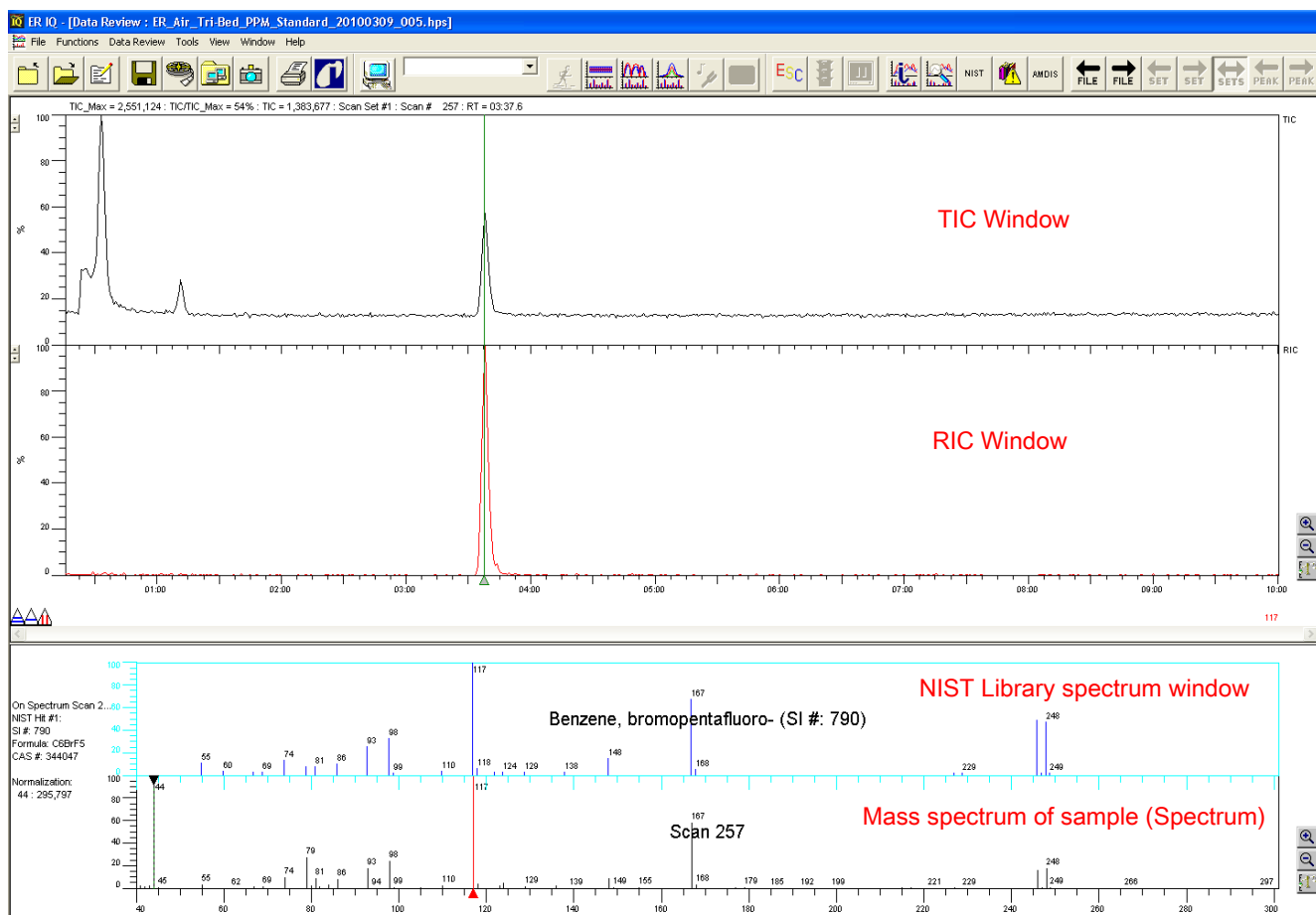
4 Double-click on the desired data file.





⇒ HAPSITE ER data file extensions end in .hps.

- 5 The **Data Review** screen with the selected data file will be displayed. The **Data Review** screen is divided into four sections, as shown below.

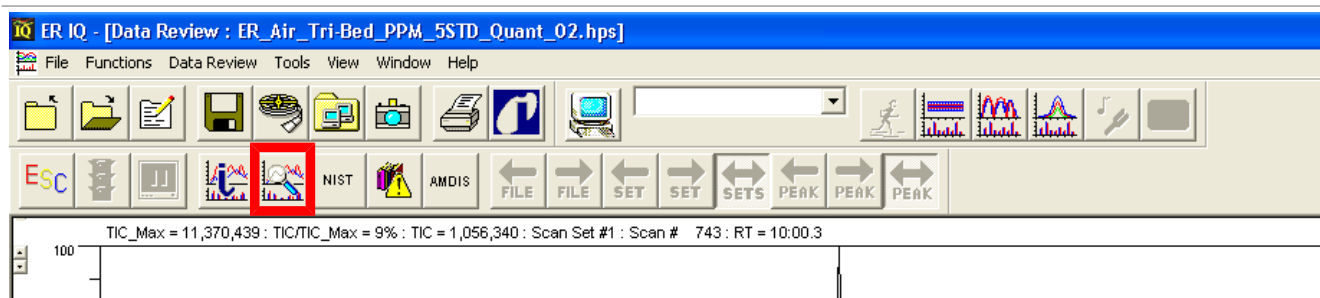


TIC Window	The total ion chromatogram, which is the total intensity of the mass fragments, is plotted in this screen. Basic data analysis, such as background subtraction and peak identification, is also conducted here.
RIC Window	The intensity of a specific mass fragment is plotted in this screen.
NIST Library spectrum	This window will display NIST matches if <b>Search NIST/User</b> is checked in the <b>Control Panel</b> .
Mass spectrum of sample (Spectrum)	The mass spectrum generated from the sample is displayed in this window.

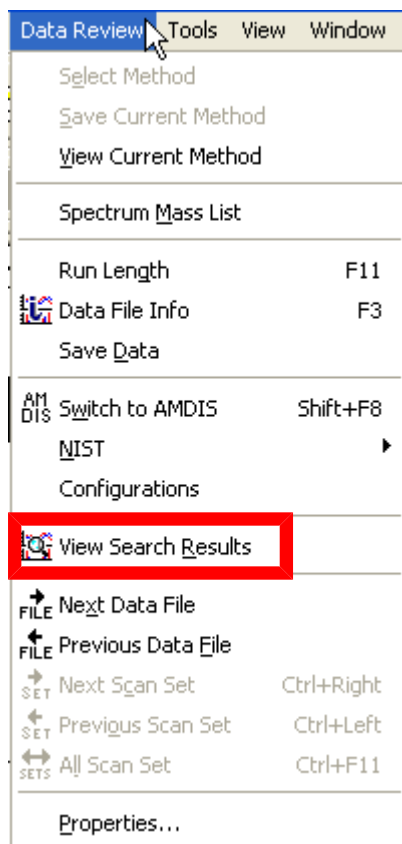
## 13.5 Reports

- 1 To access data reports, double-click the **View Search Results** icon on the **Data Review** screen.





- 2 Alternately, **View Search Results** may be accessed from **Data Review** drop-down menu.

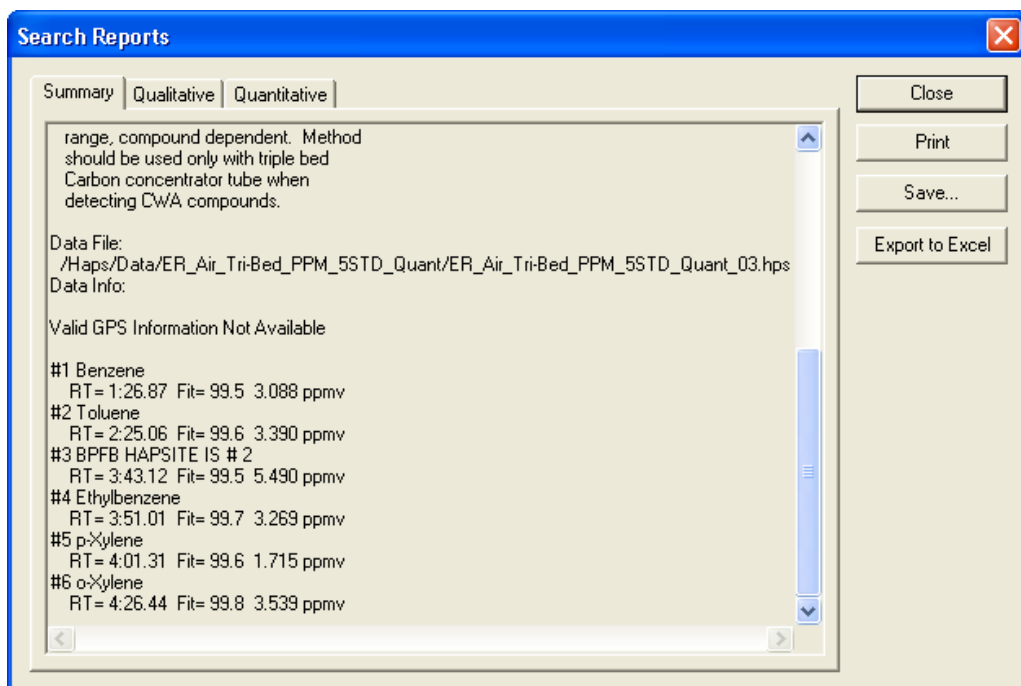


- 3 There are a maximum of three reports available, depending on how the method was configured.
- ⇒ The **Summary** report provides an overview of the **Qualitative** and/or **Quantitative** reports.
- 4 The **Quantitative** report can be exported to Excel for further analysis by clicking on the **Export to Excel** button.

The **Summary** report includes:

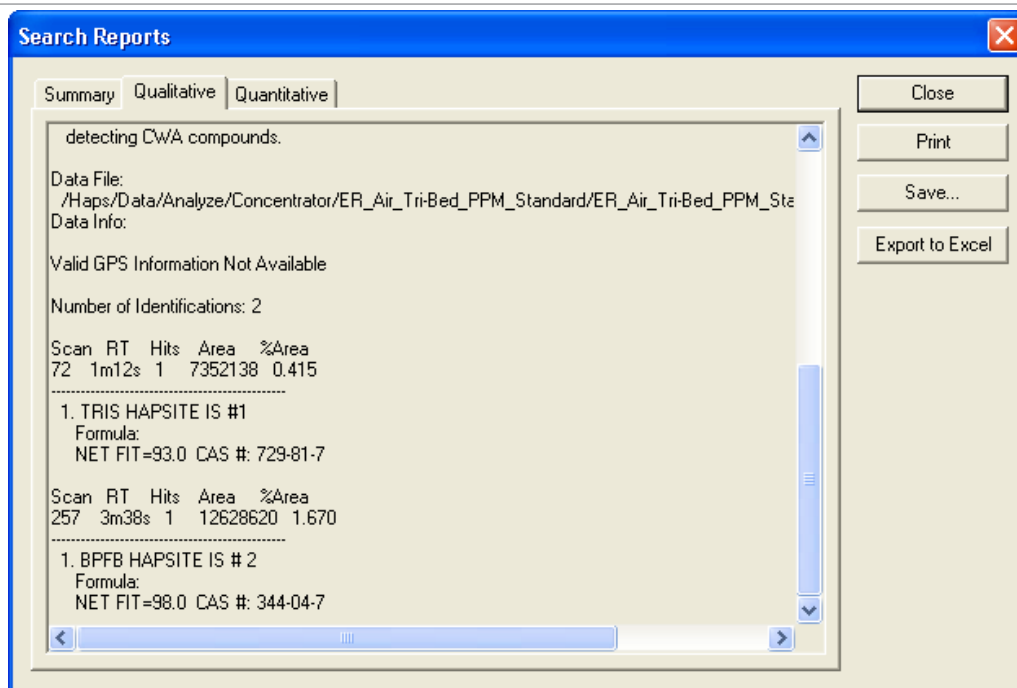
- date
- time
- method name
- method description

- GPS info
- analyte identification
- retention time
- fit (see Analyzing Data Using AMDIS [▶ 222])
- concentration



The **Qualitative** report includes:

- date
- time
- method name
- method description
- GPS info
- scan number
- retention time
- number of hits (possible identifications)
- area
- percent area
- analyte identification
- formula
- fit (see Analyzing Data Using AMDIS [▶ 222])
- CAS number



The **Quantitative** report includes:

- date
- time
- method name
- method description
- GPS info
- target library
- date of the last library calibration
- peak search parameters
- target ion
- predicted retention time
- actual retention time
- scan number
- internal standard
- retention time
- number of hits (possible identifications)
- area
- percent area
- analyte identification
- formula
- fit (see Analyzing Data Using AMDIS [▶ 222])

- purity
- CAS number
- concentration with units
- RFC
- The flag, which provides the reason that the compound was not identified.

### Search Reports

Summary
Qualitative
Quantitative

Peak Search Parameters:

Search Window: 0.30.00

Window Expand Factor: 0.050

Peak Resolution: 5

Noise Level Multiplier: 2.000

Minimum Area: 50000

Minimum Width: 7

Maximum Width: 70

Minimum Fit: 0.750

Minimum Purity: 0.750

REC NO.	Target	Pred. RT	Internal Standard Name
1	213	1:18.42	TRIS HAPSITE IS #1
2	117	3:43.92	BPFH HAPSITE IS # 2

REC NO.	Target	RT	Fit	Purity	Area	ppmv	RFC	Flag
1	213	1:15.87	0.9902	0.6515	610630	N/A	-6.78	Purity too low
2	117	3:43.12	0.9952	0.8576	6114424	5.490	4.00	

REC NO.	Target	Pred RT	Analyte Name
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Microsoft Excel - tmp\_report.qrt

File Edit View Insert Format Tools Data Window Help

Unknown Identification Report

Q-ION	Pred_RT	Int.Std	Nar	Act_RT	fit	purity	area	ppmv	RFC	Flag
47	213	01:18.4	TRIS HAP	01:15.9	0.99	0.651	610630		-6.78	Purity too low
48	117	03:43.9	BPFH HAF	03:43.1	0.995	0.858	6114424	5.49	4	

O-ION	Pred_RT	Analyte	Nr	Act_RT	fit	purity	area	ppmv	Flag
52	78	01:29.2	Benzene	01:26.9	0.995	0.968	10275394	3.088	
53	91	02:26.8	Toluene	02:25.1	0.996	0.97	11239442	3.39	
54	91	03:52.4	Ethylbenz	03:51.0	0.997	0.982	19314334	3.269	
55	91	04:02.4	p-Xylene	04:01.3	0.996	0.979	18308996	1.715	

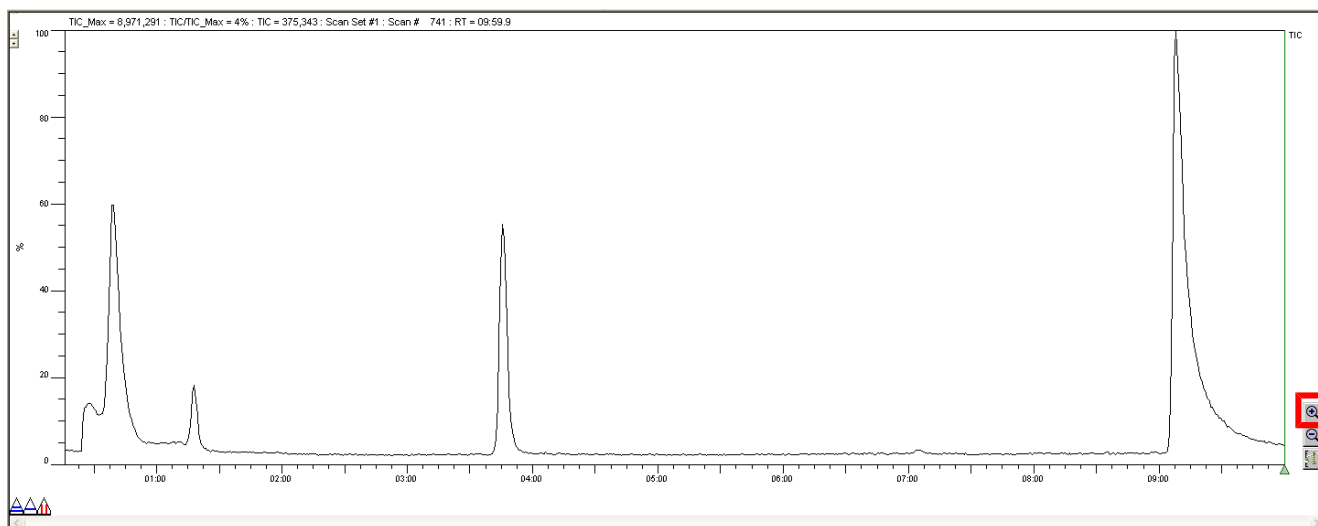


If the method does not contain a calibrated library, the Quantitative lab will display No Report.

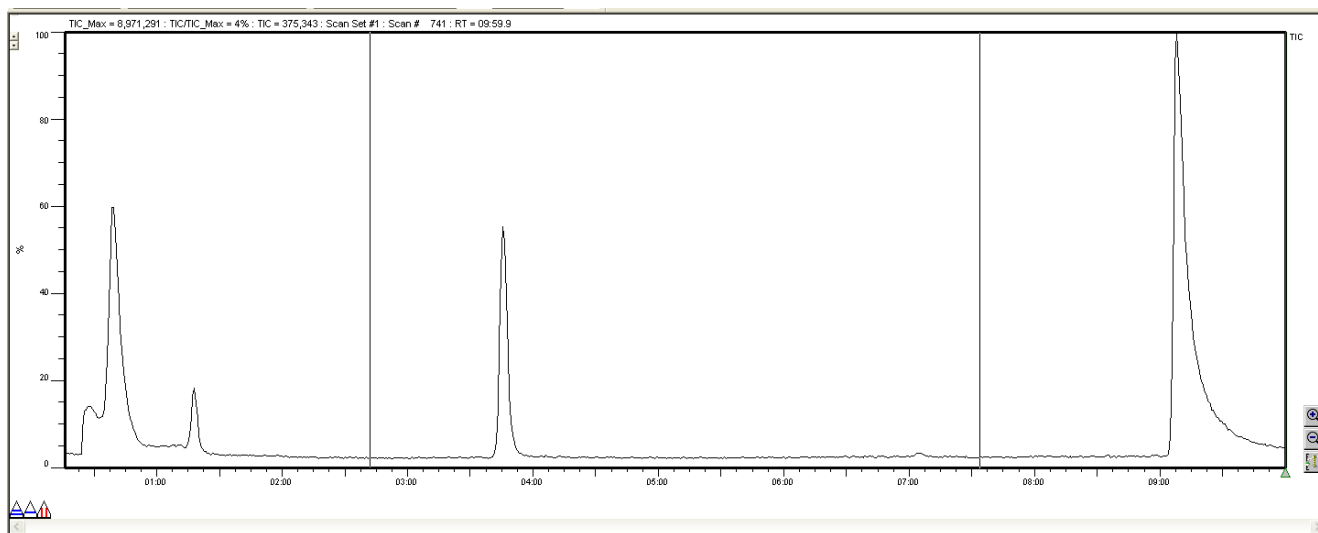
### 13.5.1 Using the Zoom Function in the TIC/RIC Window

In order to magnify the peaks, **ER IQ** has a zoom capability.

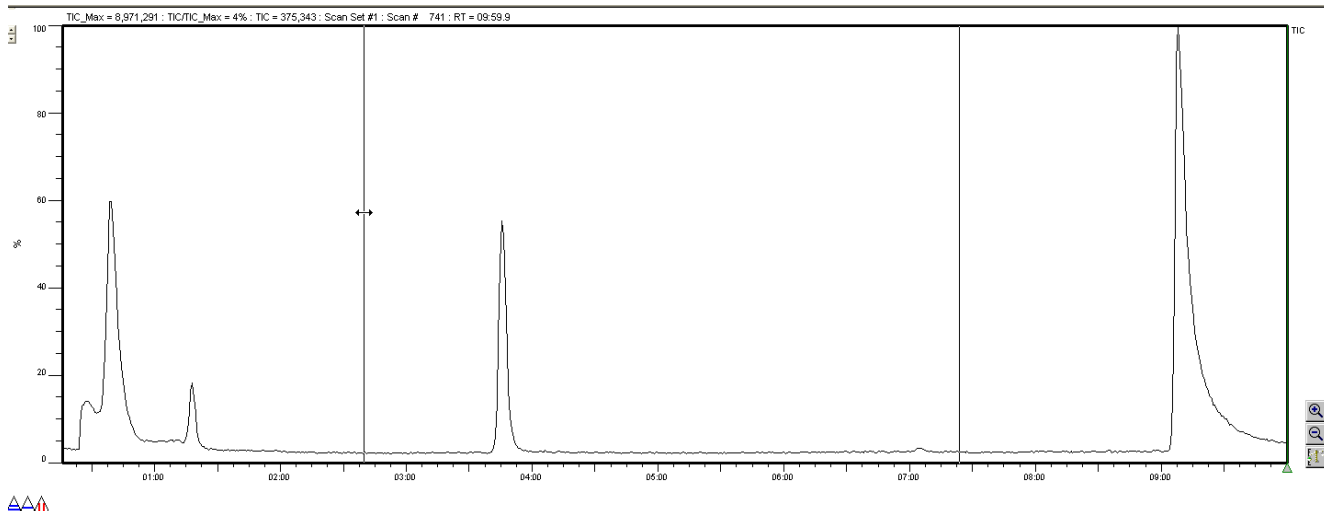
**1** Click the **Zoom** icon.



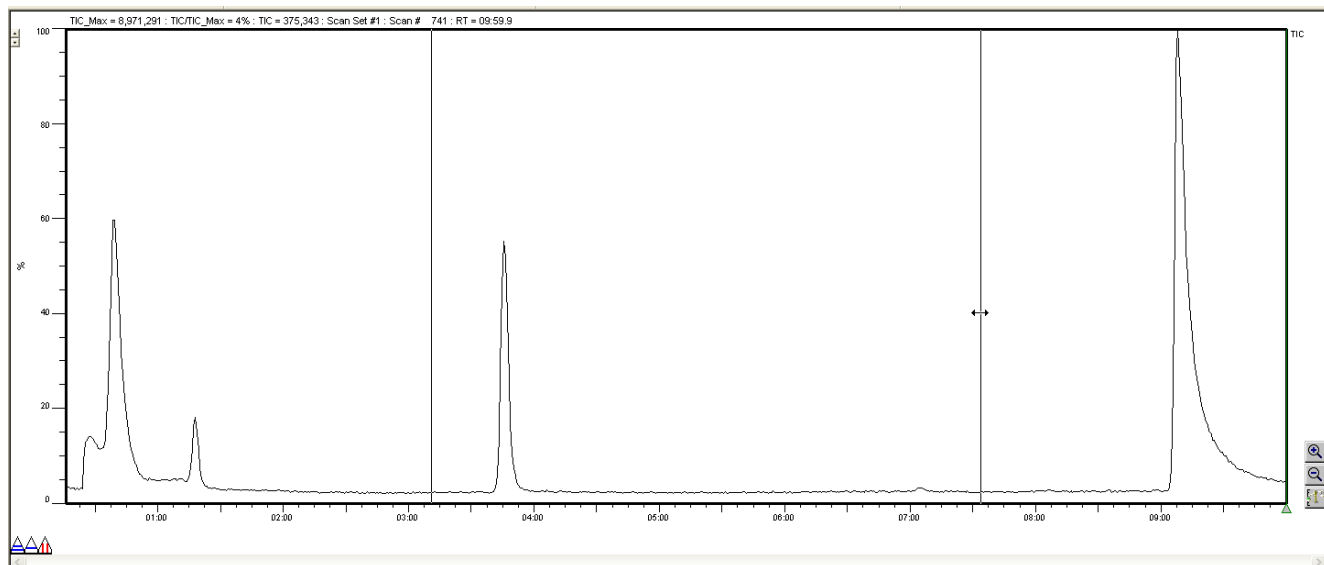
**2** Two vertical lines are displayed.



**3** Mouse over one of the lines. The cursor becomes a double-sided arrow. Move the line to the desired point.

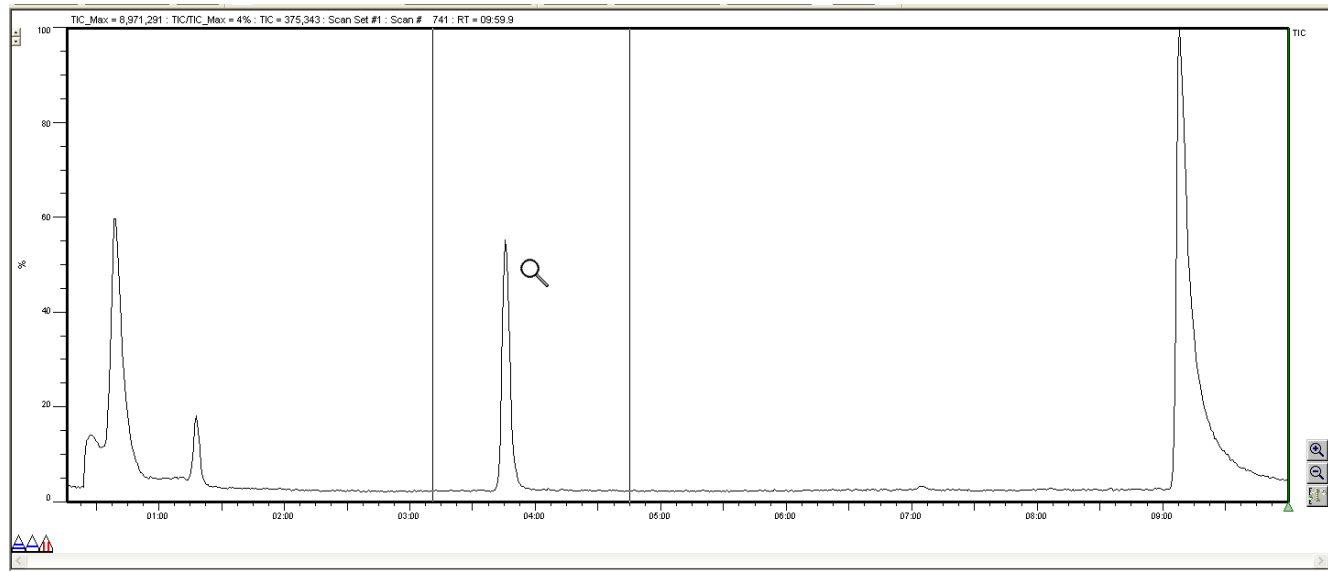


- 4 Mouse over the other line. The cursor will again become a double-sided arrow. Move the line to the desired point.

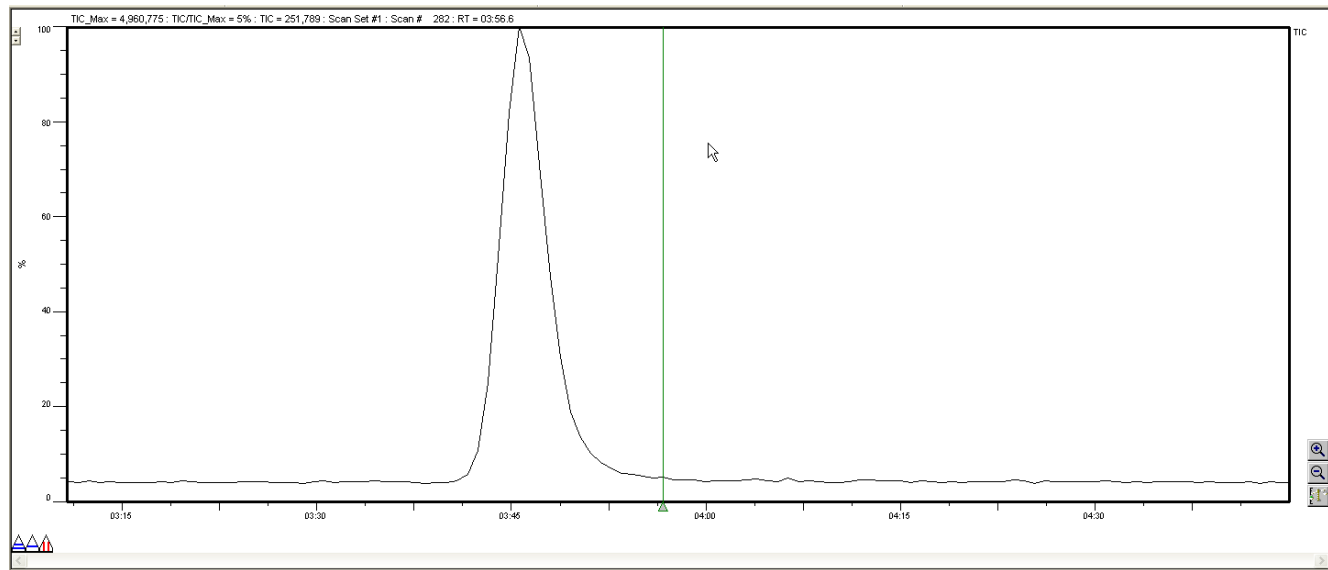


- 5 Move the cursor between the two vertical lines. The cursor will become a magnifying glass.

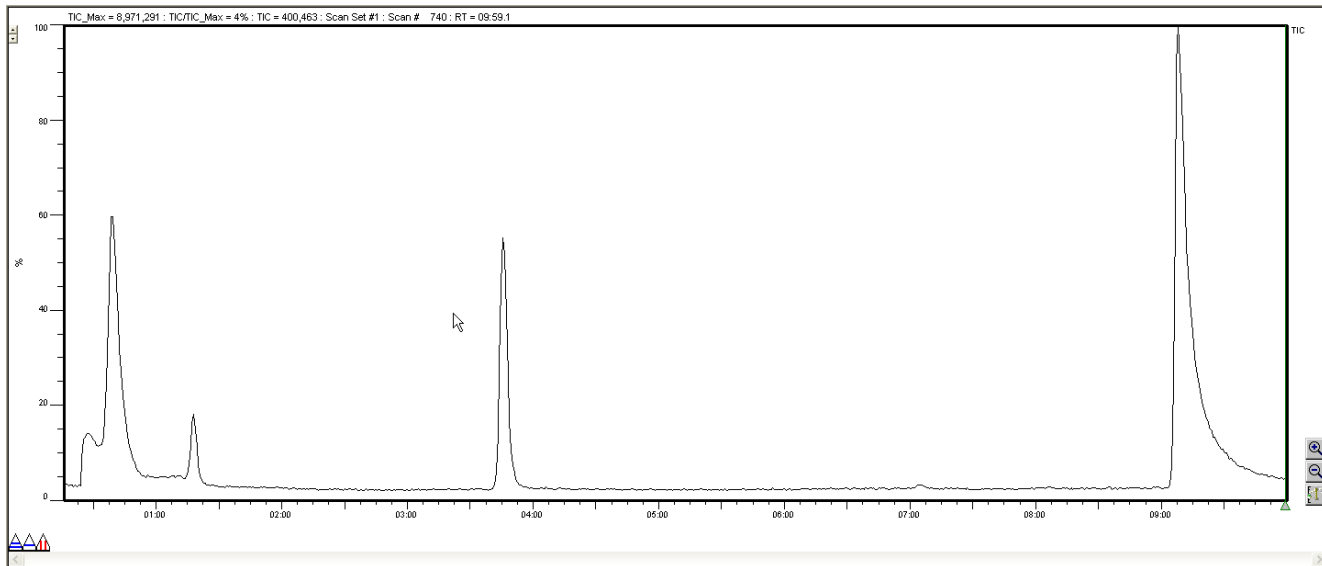




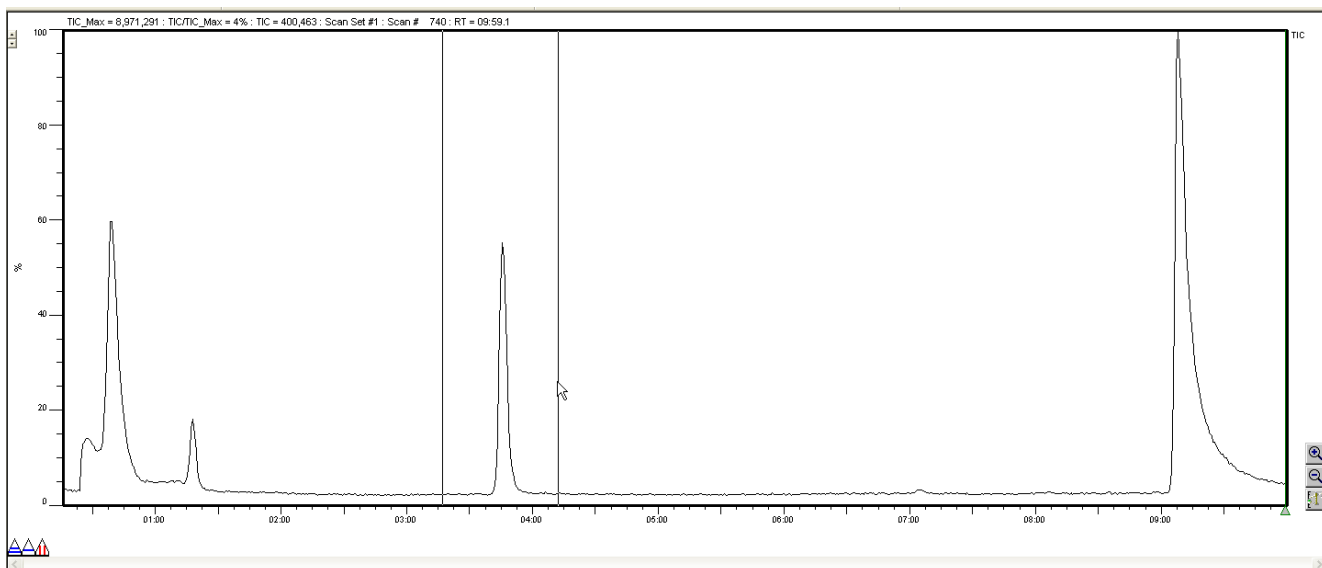
**6** Click between the two lines to zoom.



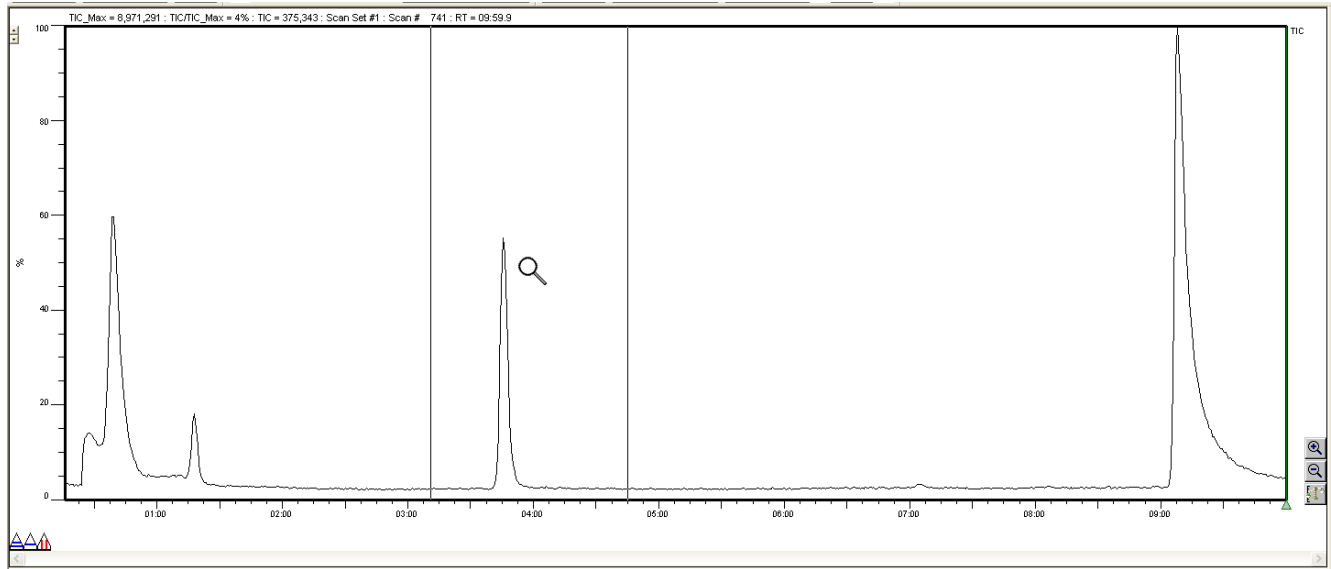
**7** Alternately, a zoom can be completed by clicking and holding the left mouse button at the desired zoom starting point.



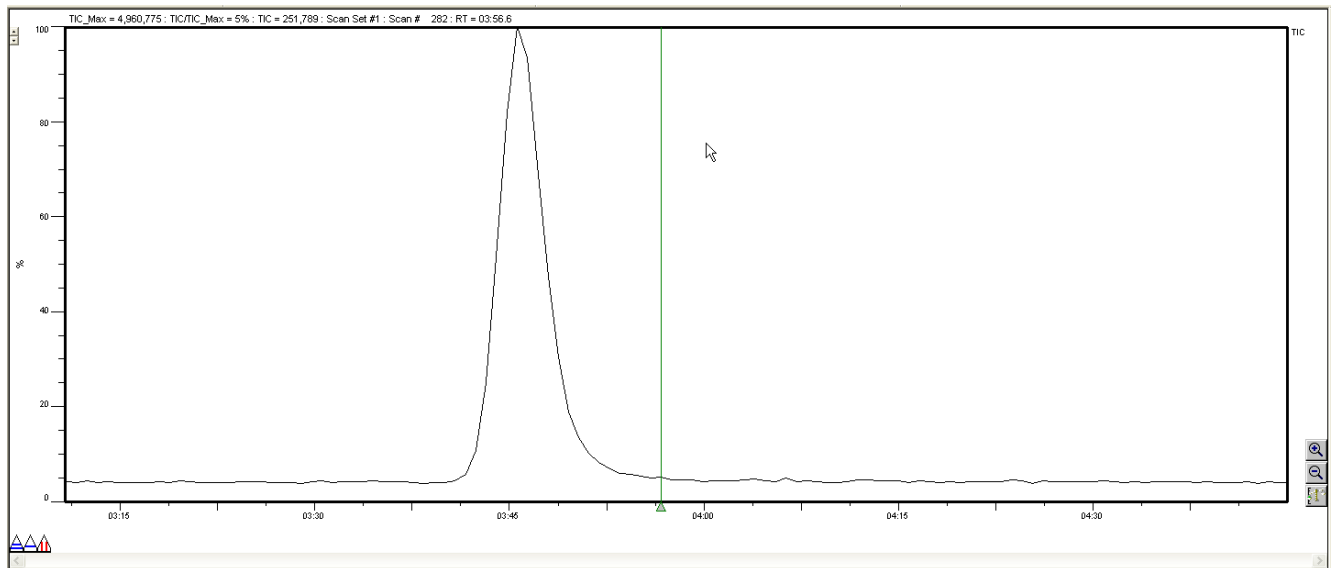
- 8** Continue to hold the left mouse and drag the mouse to the desired zoom ending point. Two vertical lines are displayed.



- 9** Release the left mouse button. Move the cursor in between the two vertical lines. The cursor becomes a magnifying glass.

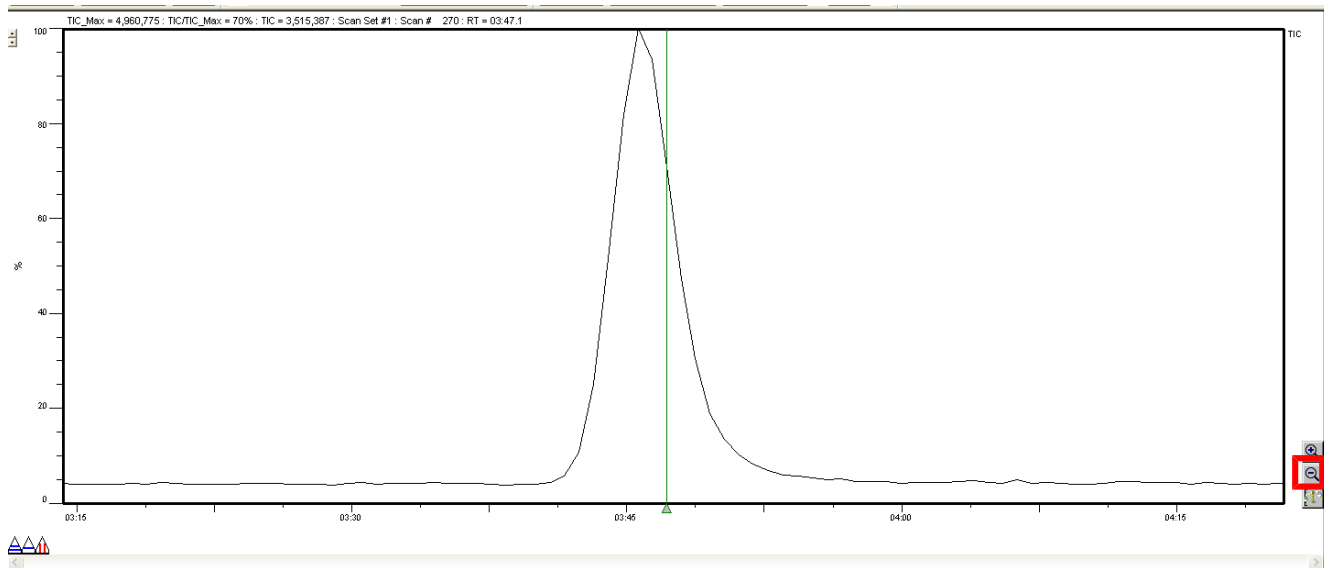


10 Click between the lines to zoom.

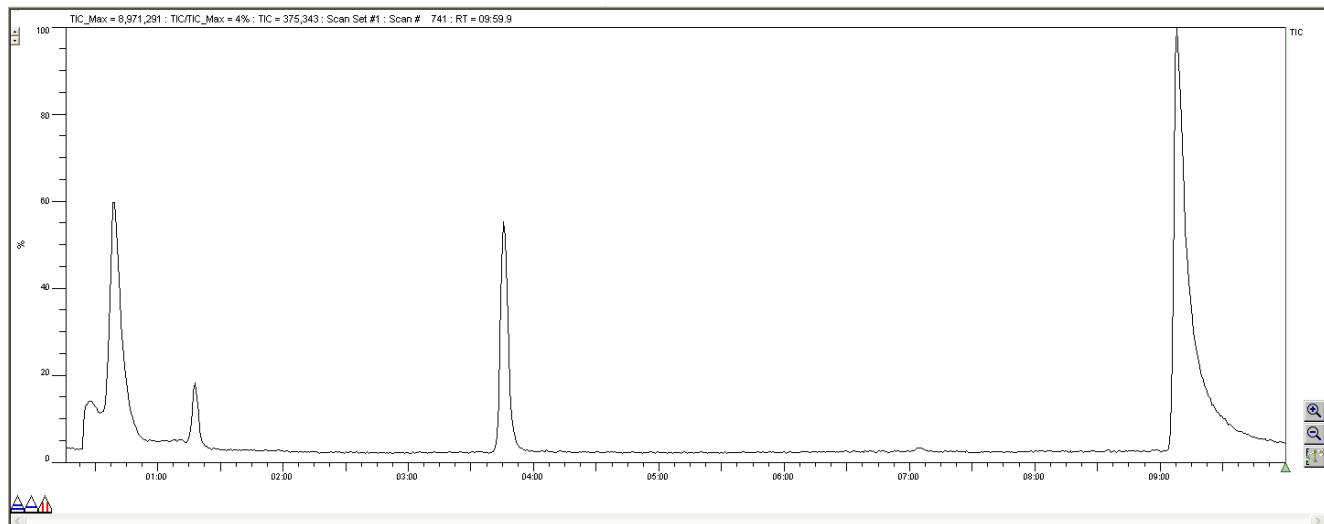


### 13.5.2 Zooming Out

1 Click on the **Zoom Out** icon.



2 The screen will return to the expanded view.

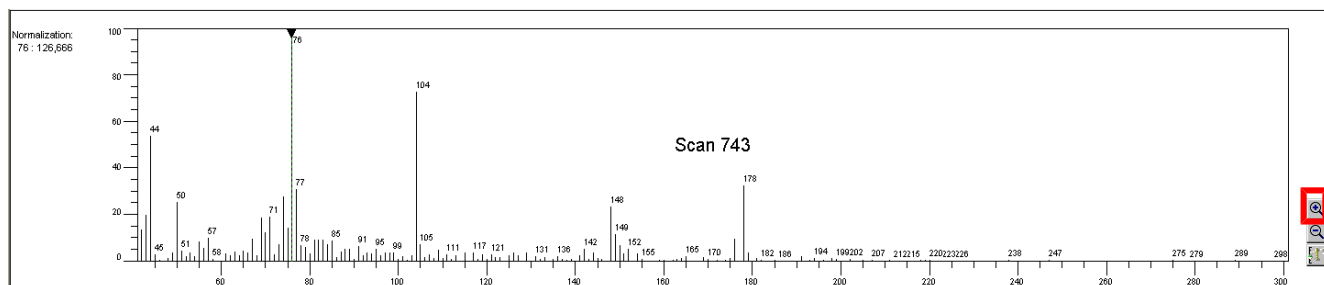


3 Alternately, click F11 to return to the expanded view.

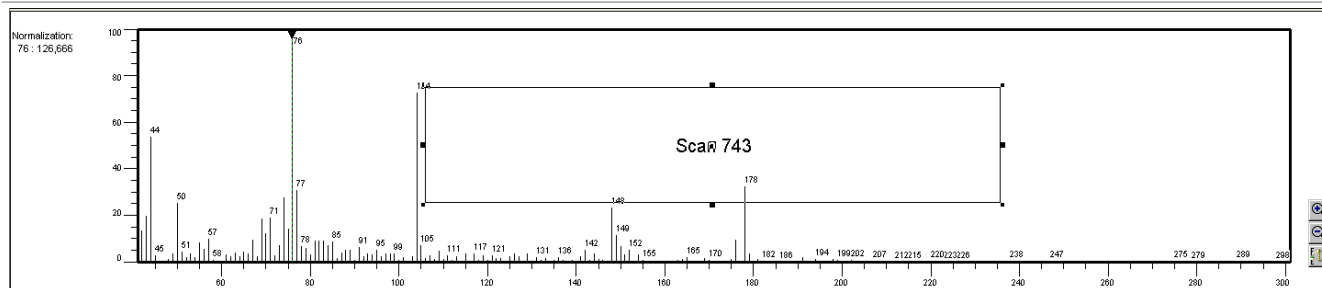
### 13.5.3 Using the Zoom Spectrum Function

The **Spectrum** window has a zoom function to magnify the spectra.

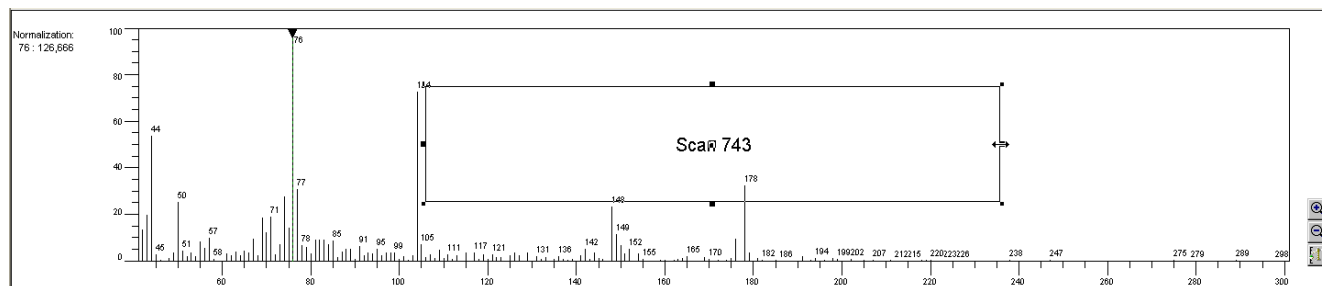
1 Click the **Zoom** icon.



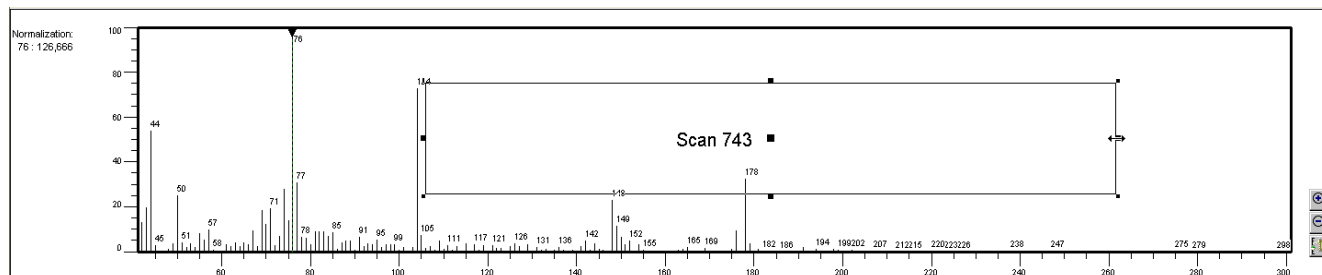
2 A rectangle is displayed in the **Spectrum** window.



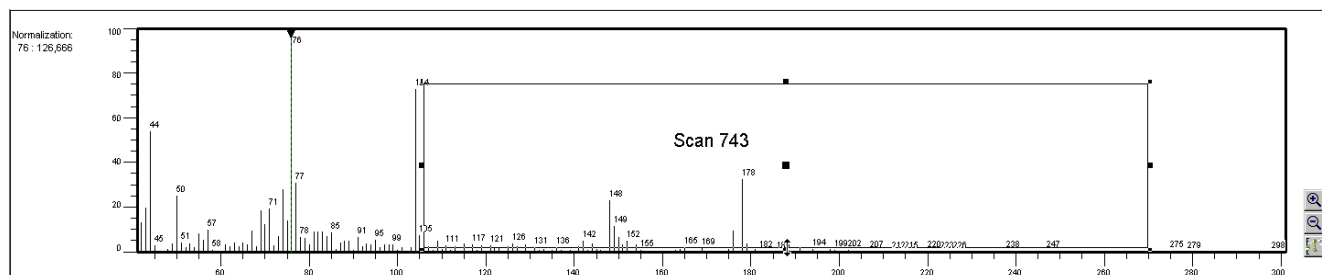
3 Mouse over a side of the rectangle. The cursor becomes a double-sided arrow.



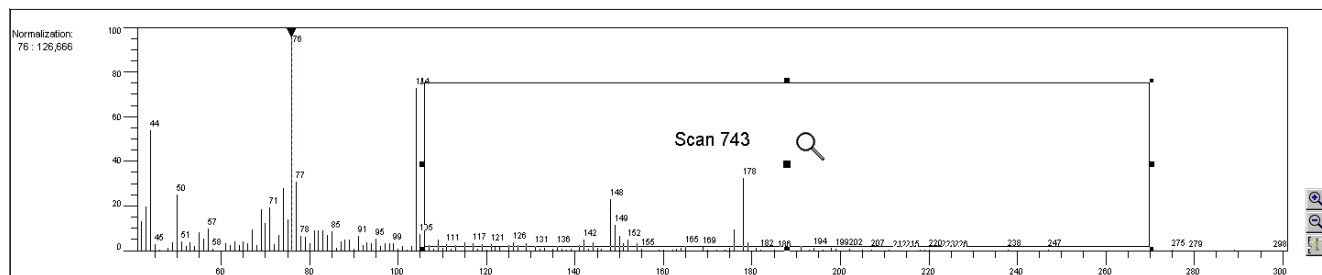
4 Drag the side to the desired end zoom point.



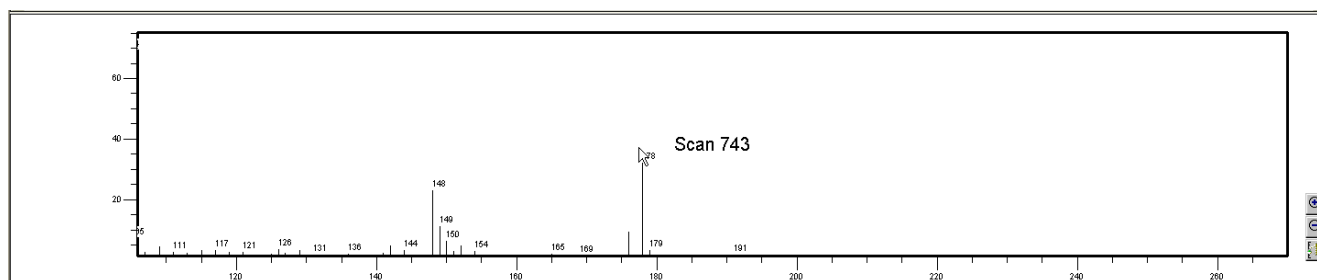
5 If necessary, repeat with the other sides of the rectangle in order to adjust the desired zoom area.



6 Move the cursor into the center of the rectangle. The cursor becomes a magnifying glass.



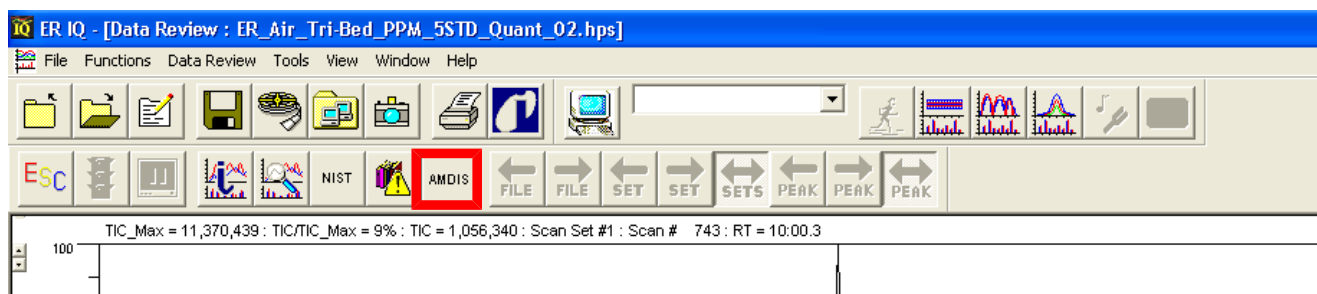
7 Click inside the rectangle to zoom.



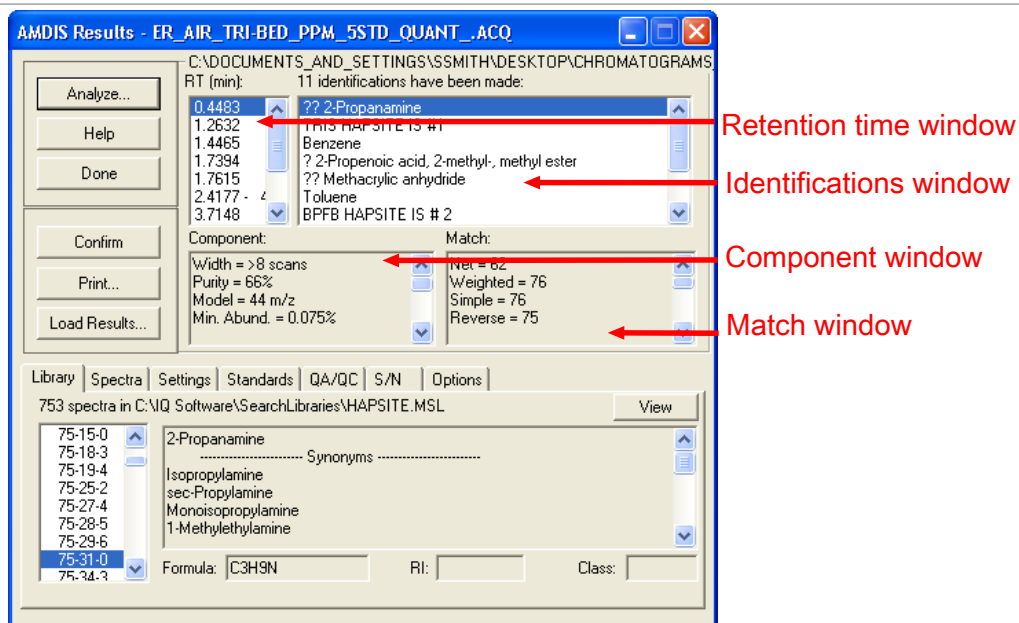
## 13.6 Analyzing Data Using AMDIS

AMDIS is an acronym for Automated Mass Spectrum Deconvolution and Identification System, a tool which was developed by the National Institute of Science and Technology. HAPSITE ER utilizes an on-board library, **HAPSITE.msl**, and the AMDIS deconvolution algorithm to make identifications. This library contains approximately 750 chemicals including chemical warfare agents and is able to identify complex mixtures, including co-eluting chemicals. The on-board library can be updated to include several thousand compounds. The laptop AMDIS software can be accessed through ER IQ, enhancing the quality of data analysis by including access to the NIST mass spectral library.

- ▶ Double-click on the **AMDIS** icon.



⇒ The following window is displayed.



The results screen includes:

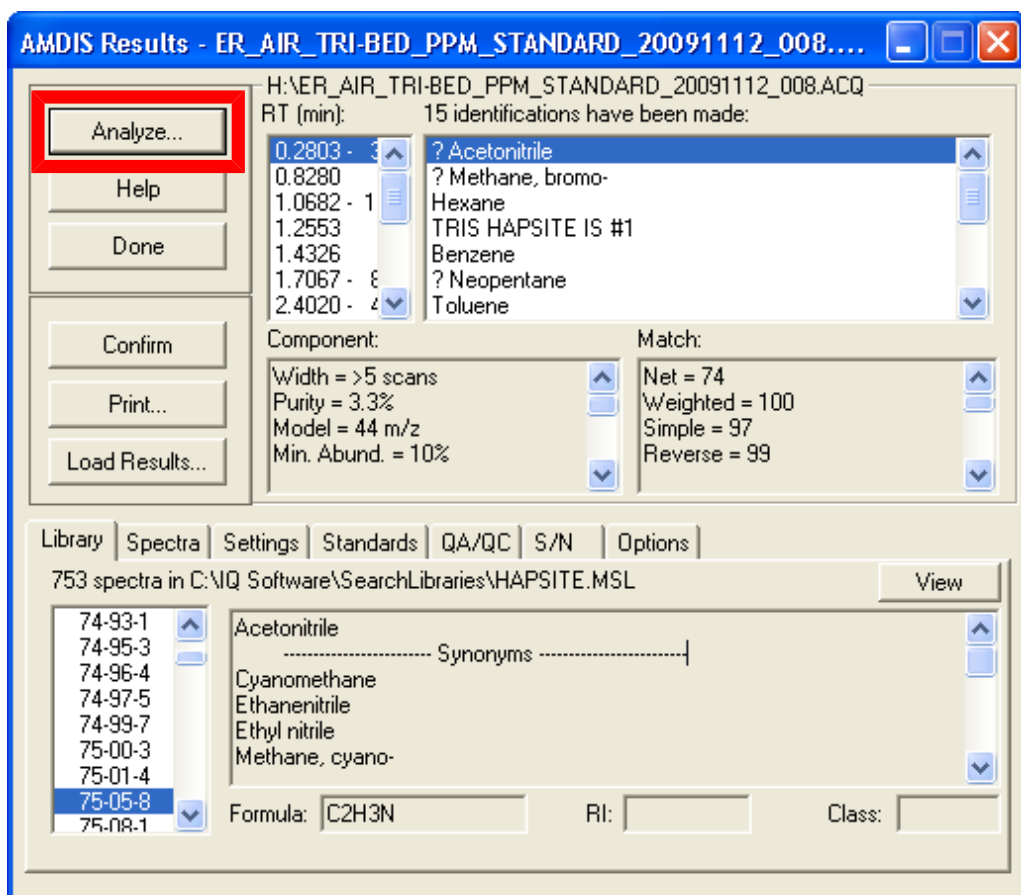
Retention time window	AMDIS uses a decimal time format. Multiply the numbers after the decimal point to convert to a seconds format.
Identifications window	Lists the identifications in order of retention time. If a question mark is displayed before the identification, the match is between 70-79. If two question marks are displayed, the fit is between 60-69, and if three question marks are displayed, the fit is less than 60.
Component window	Displays the width of the peak in terms of scans, the purity of the peak and the min. abund (minimum abundance). This is the abundance of the smallest observable mass spectral peak and model, which is the m/z value or TIC used to determine the peak shape. It is generally the ion that rises and falls the fastest.
Match window	Displays the quality of the spectral match. If the Net is greater than 70, the identification is considered to be a good match. If the Net is greater than 80, the identification is considered to be a very good match. If the Net is greater than 90, the identification is considered to be an excellent match.
Library Tab	Displays the search library, CAS number, synonyms and formula for the compound that is highlighted in the identifications box.
Analyze Button	Sets the library pathway, which may be necessary when reloading the <b>ER IQ</b> program. See Setting the AMDIS Pathway [ 224].
Help	Detailed <b>Help</b> instructions about AMDIS.

Done	Closes the AMDIS screen.
Confirm	Labels the peaks in the chromatogram that were not identified by AMDIS and allows the peaks to be exported to NIST for further identification. See Confirm Screen in AMDIS [ 228] for further information.
Print	Prints the AMDIS data in a report format.
Load Results	Allows for the analyst to select a different data file and perform an AMDIS search on the newly selected file.
View	Allows the analyst to view the library components. See View Function in AMDIS [ 227].

### 13.6.1 Setting the AMDIS Pathway

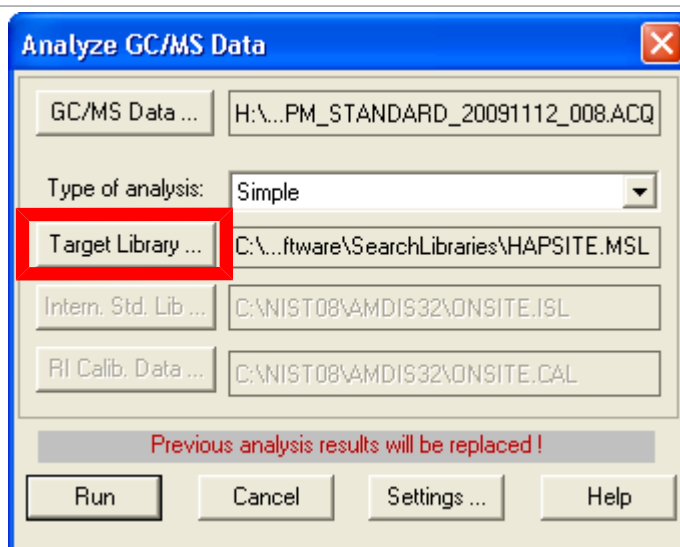
If AMDIS is reloaded onto the laptop, the library pathway may need to be reset. To reset the pathway:

- 1 Double-click on **Analyze...**

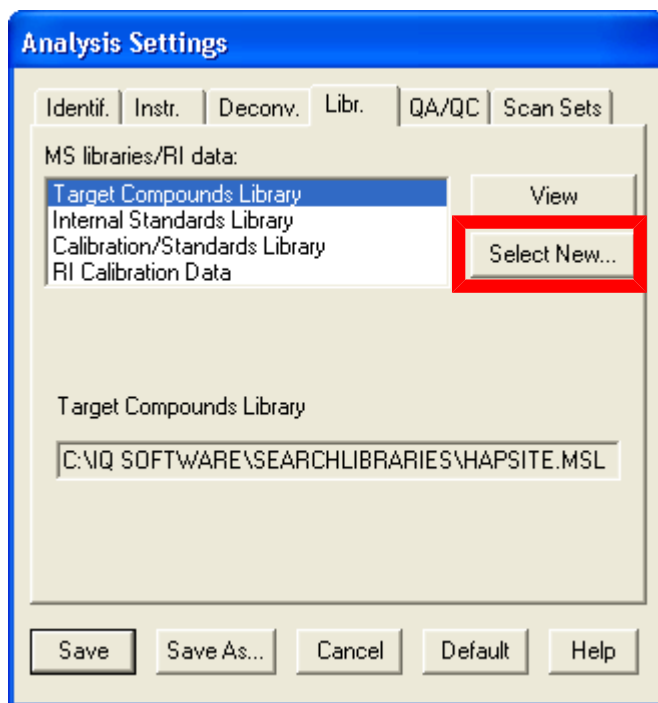


- 2 Double-click on **Target Library**.

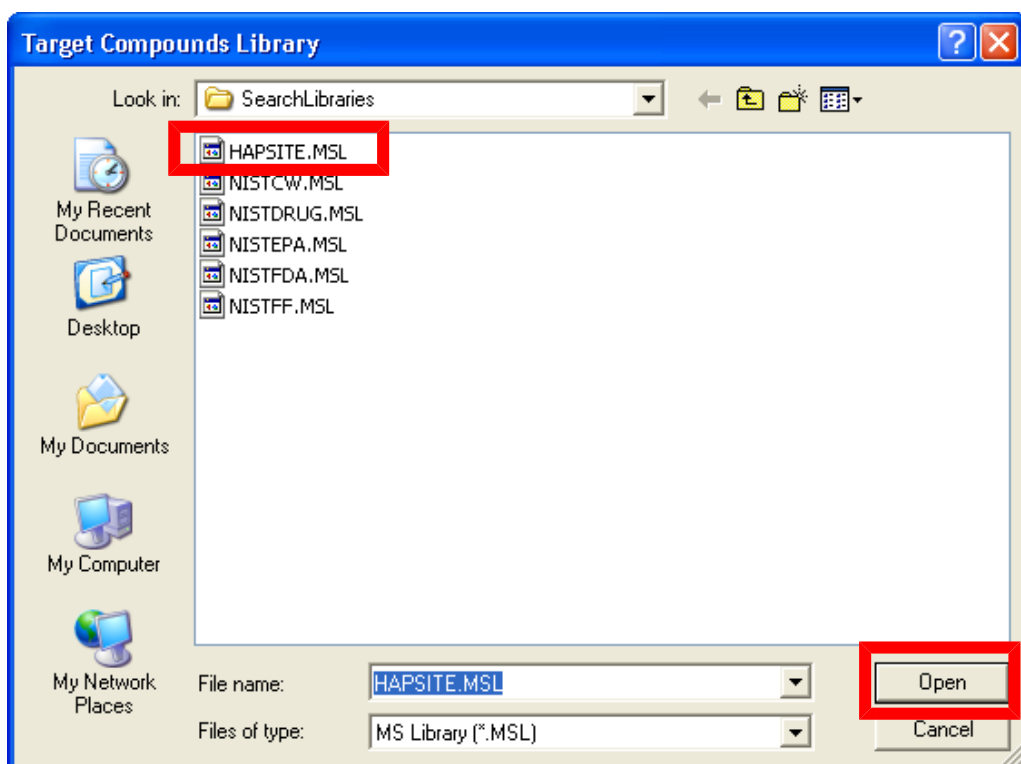




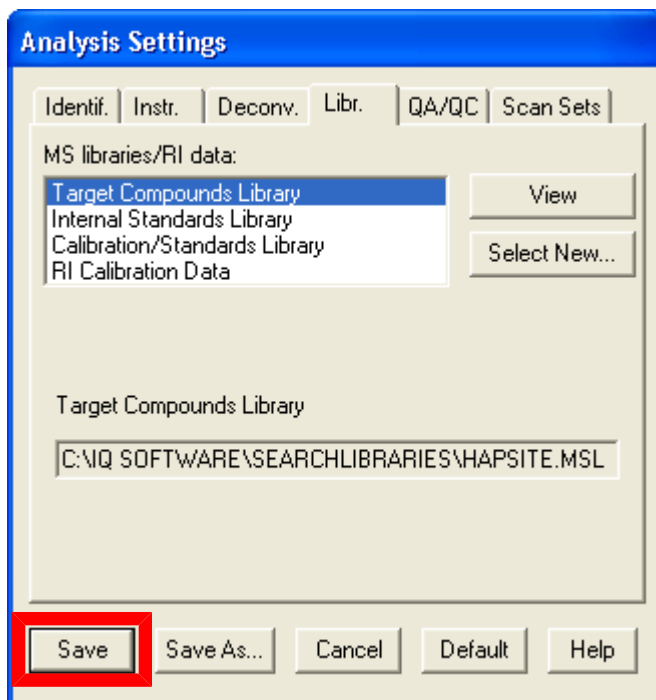
- 3 Click **Select New** to change the library pathway.



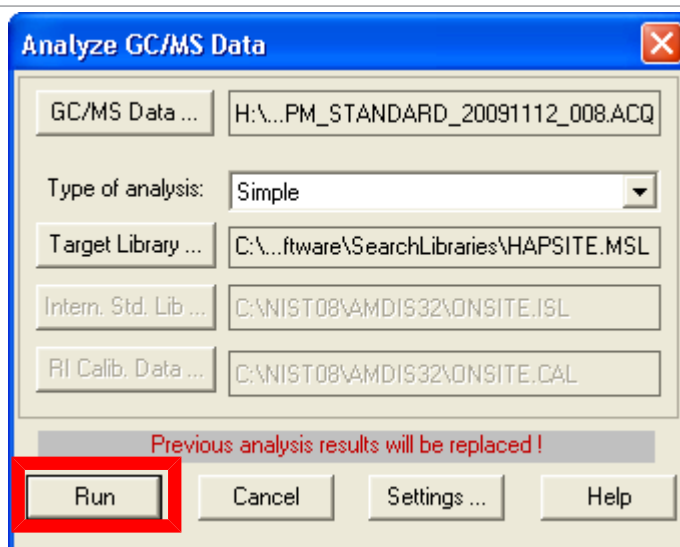
- 4 The **HAPSITE.msl** is located at the following pathway: C:\NQ Software\SearchLibraries. If custom libraries are used, they must be located in this directory. Highlight the library and click **Open**.



5 Click **Save**.

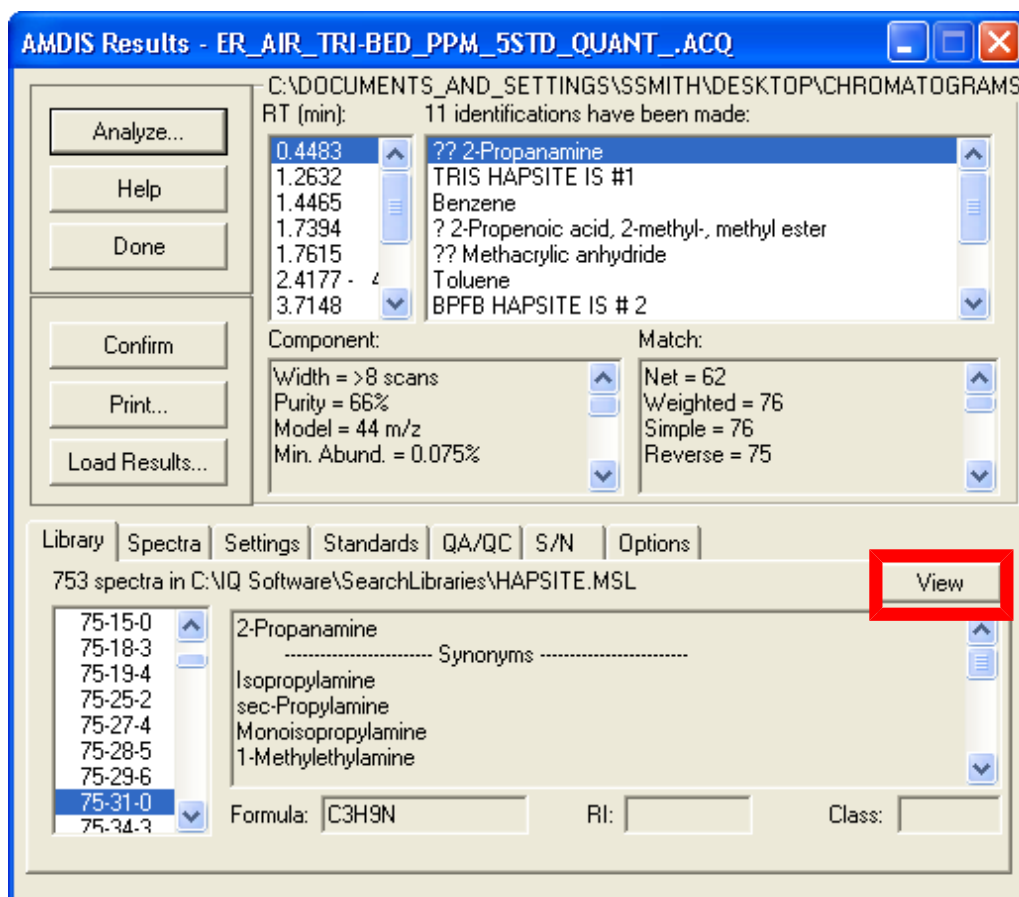


6 Click **Run**.

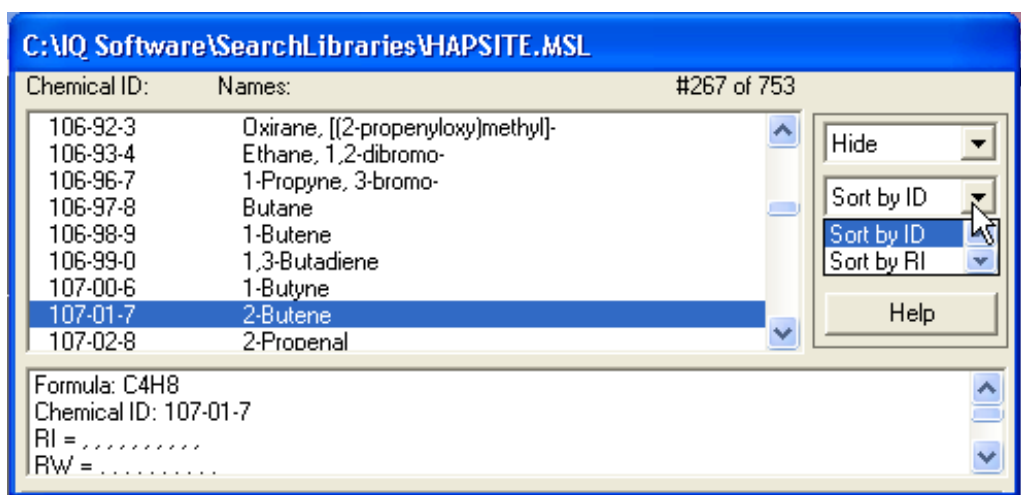


### 13.6.2 View Function in AMDIS

The **View** function can be accessed by selecting the **View** button displayed below or by following through step 3 of the previous section and selecting **View**.



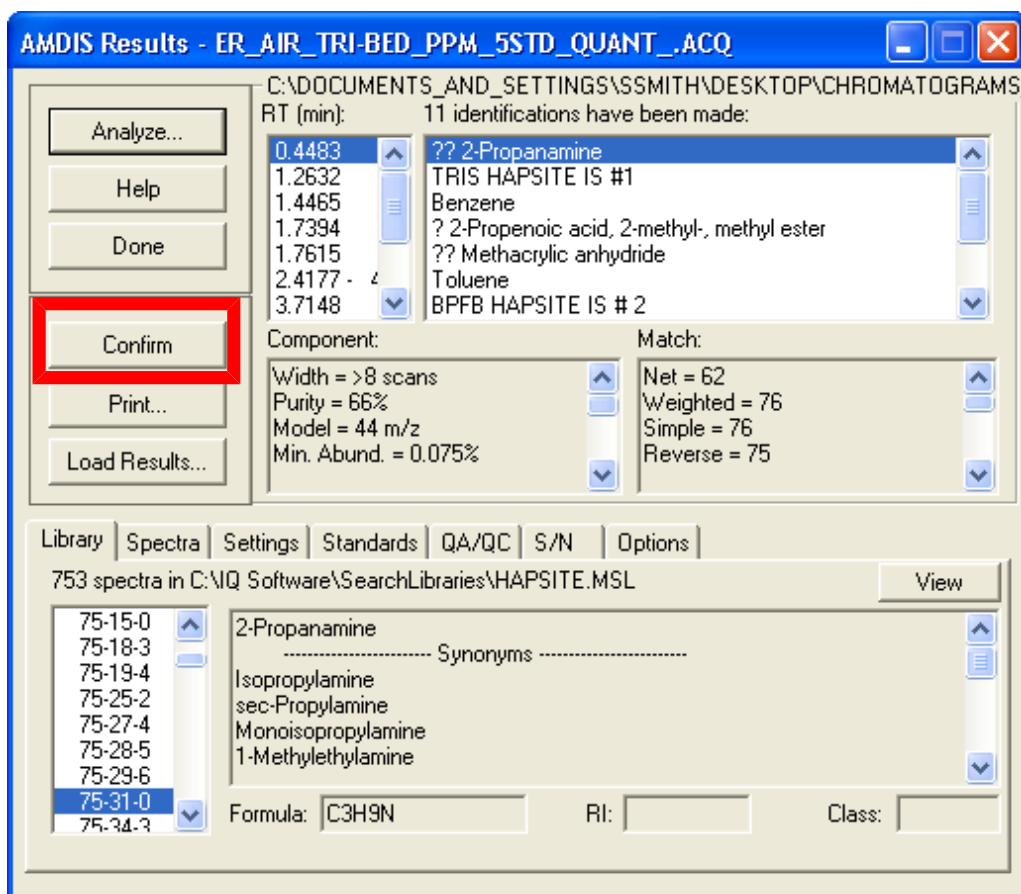
This function displays the components of the **HAPSITE.msl** library. This list can be sorted by retention index, name or CAS number.



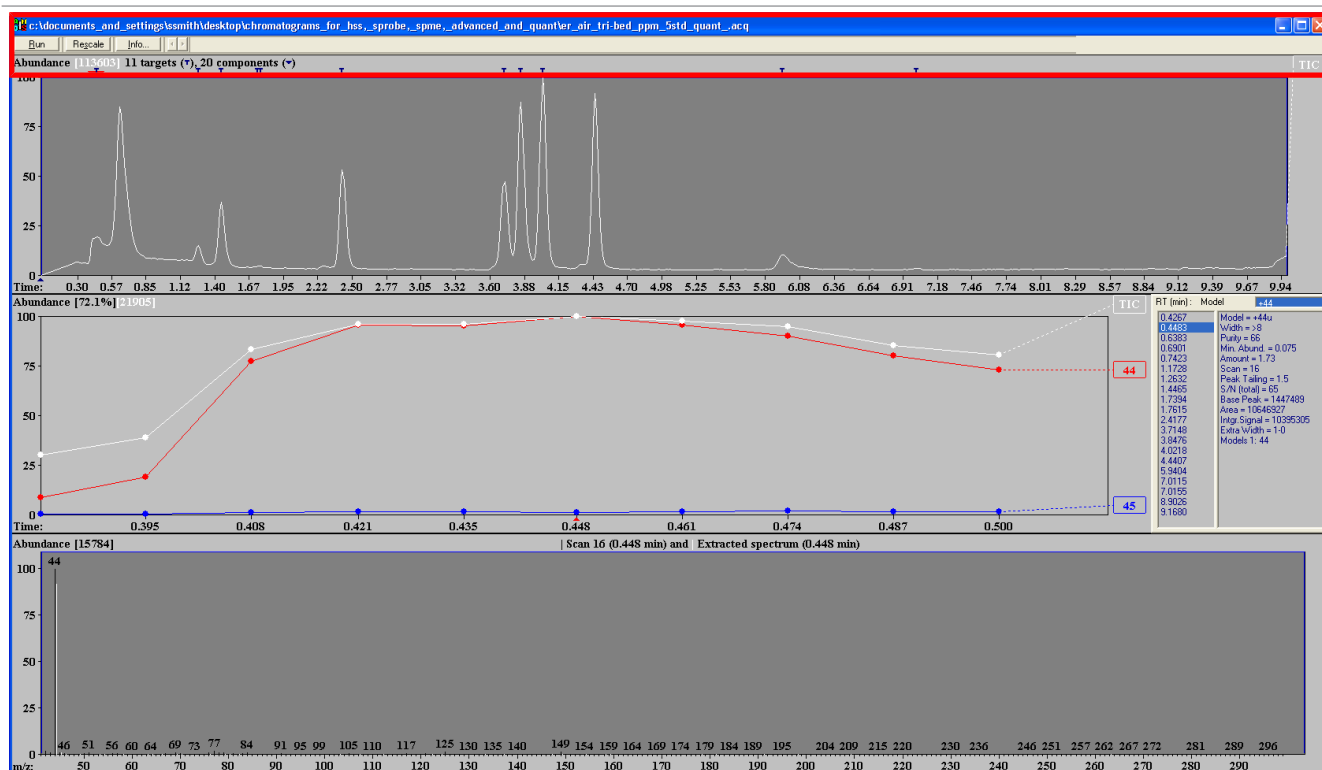
### 13.6.3 Confirm Screen in AMDIS

The **Confirm** function in AMDIS allows for unidentified peaks to be located by AMDIS and export them to NIST for identification. See below for instruction on using **Confirm**.

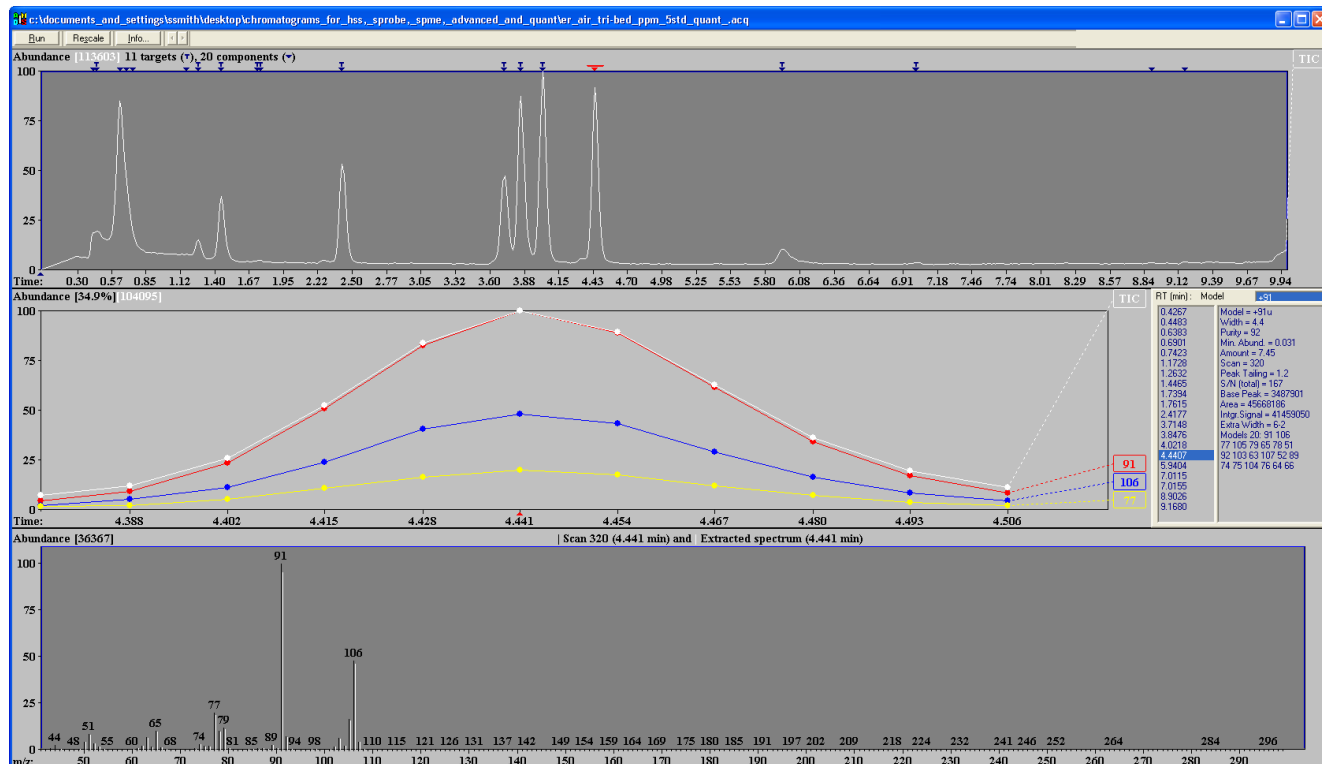
- 1 Click the **Confirm** button.



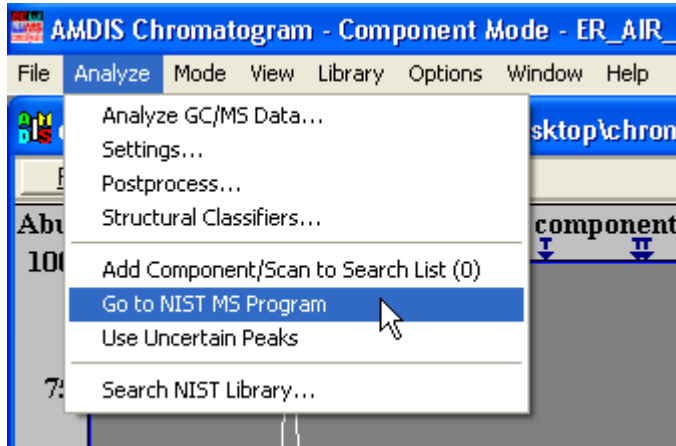
- 2 The **Confirm** page will be displayed. An arrow located about the peak indicates that a compound has been found. A **T** over the arrow indicates that the compound has been identified by AMDIS.



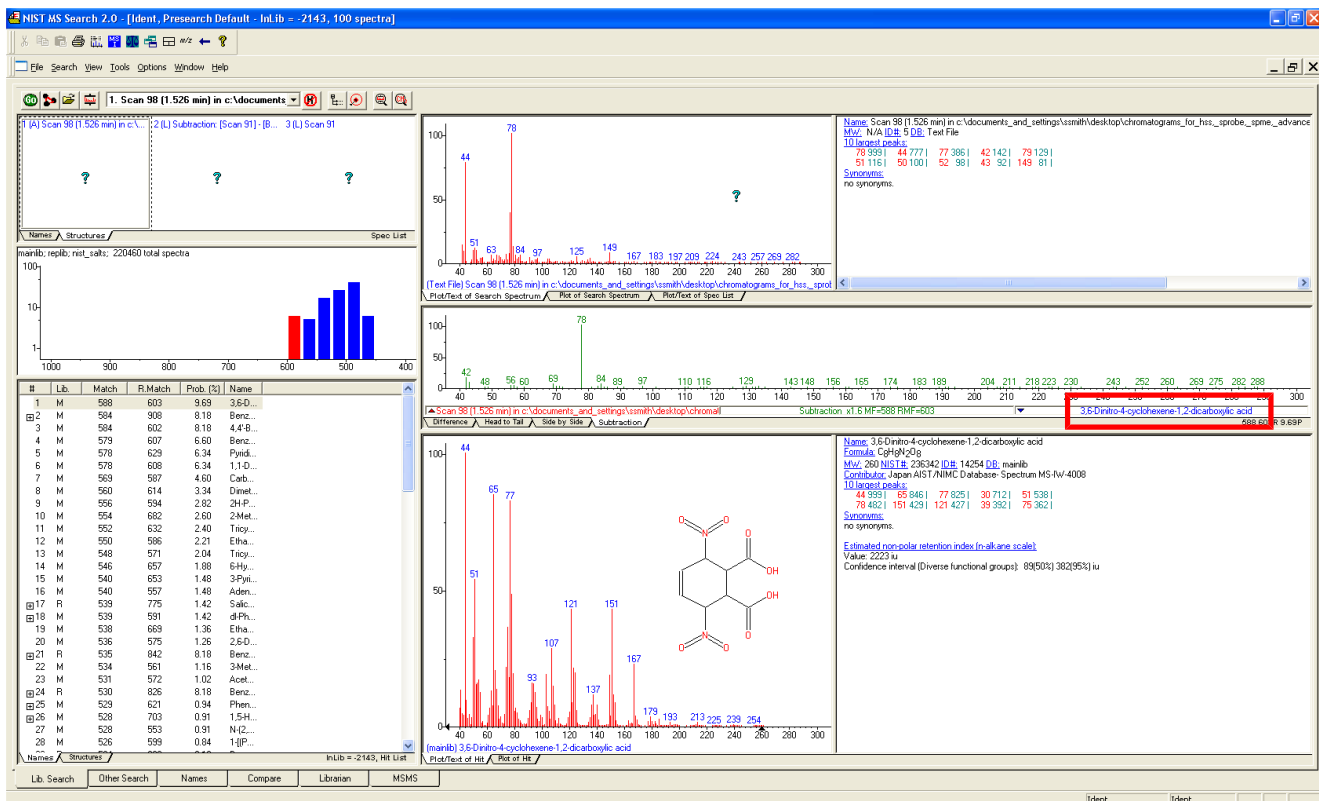
3 If a peak has not been identified, click on the arrow above it. The arrow will turn red.



4 Click Analyze then click Go to NIST MS Program.



5 The spectra is exported to NIST. NIST will identify the unknown compound.



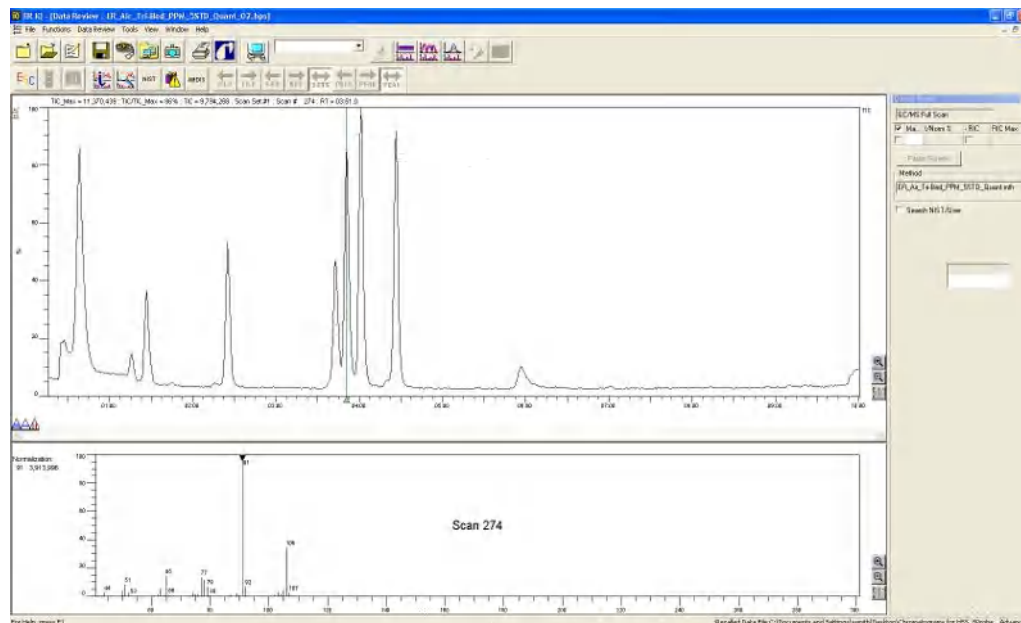
6 Alternately, if a NIST Search is not desired, select **File** followed by **Go to Results** to return to the Results page.

## 13.7 NIST Library Searches

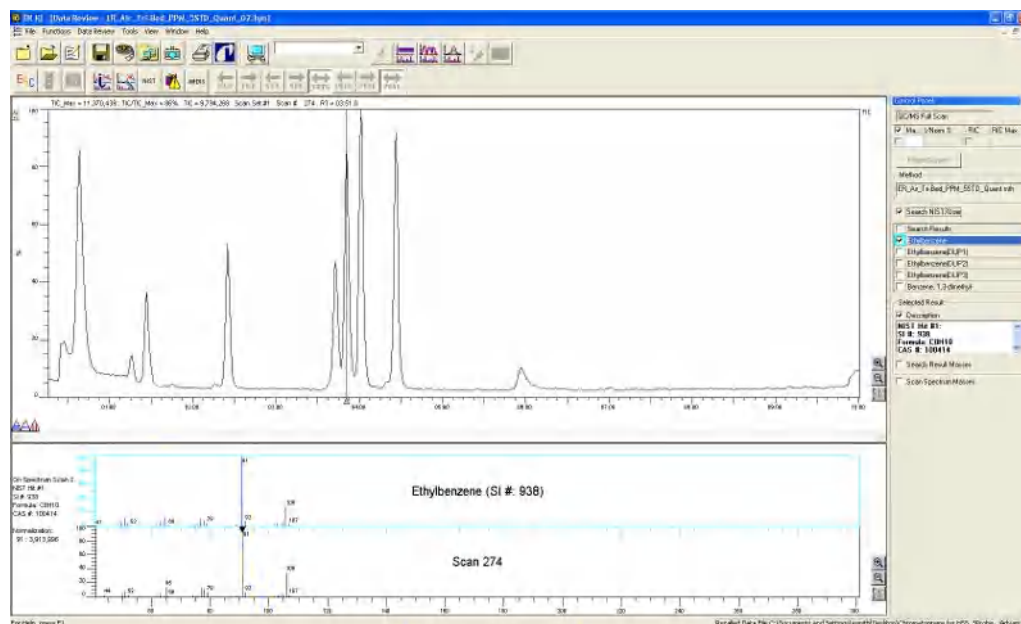
The laptop will come pre-loaded with identification software from the National Institute of Standards and Technology's (NIST) Mass Spectral Search Program, which contains approximately 192,000 spectra. This library compares the sample spectra to the library spectra in order to determine the SI number based upon purity and fit, the ratio of the intensities of the unknown spectra to the library spectra.

✓ Refer to Accessing the Data Review Feature [▶ 206] to open a data file.

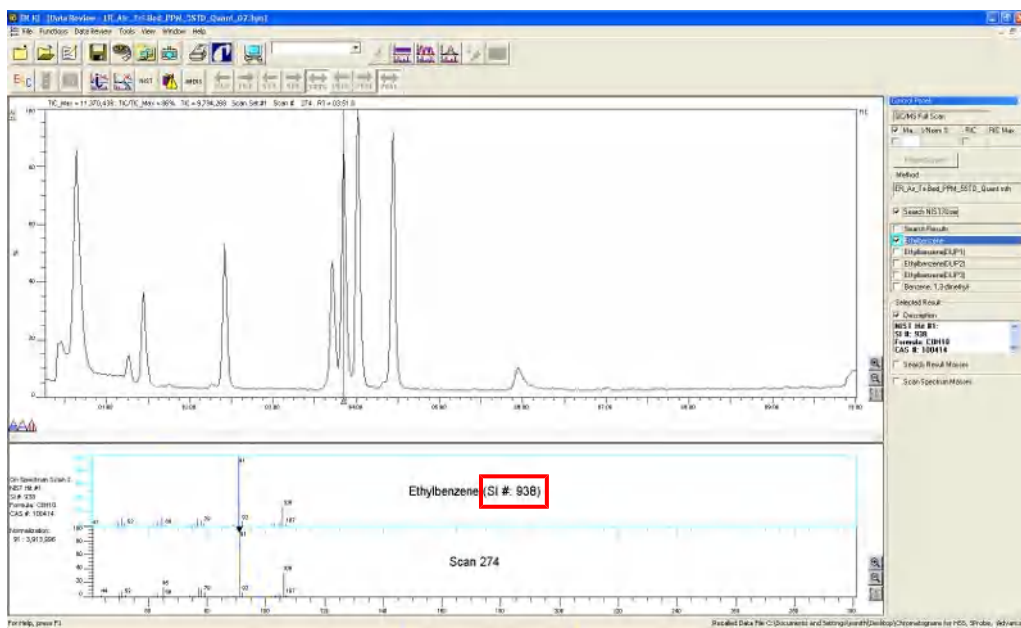
- 1 Double-click on the peak of interest. The green scan cursor will relocate to the peak. Use the arrow keys on the laptop to adjust the scan cursor. The optimal location of the scan cursor is at the apex of the peak.



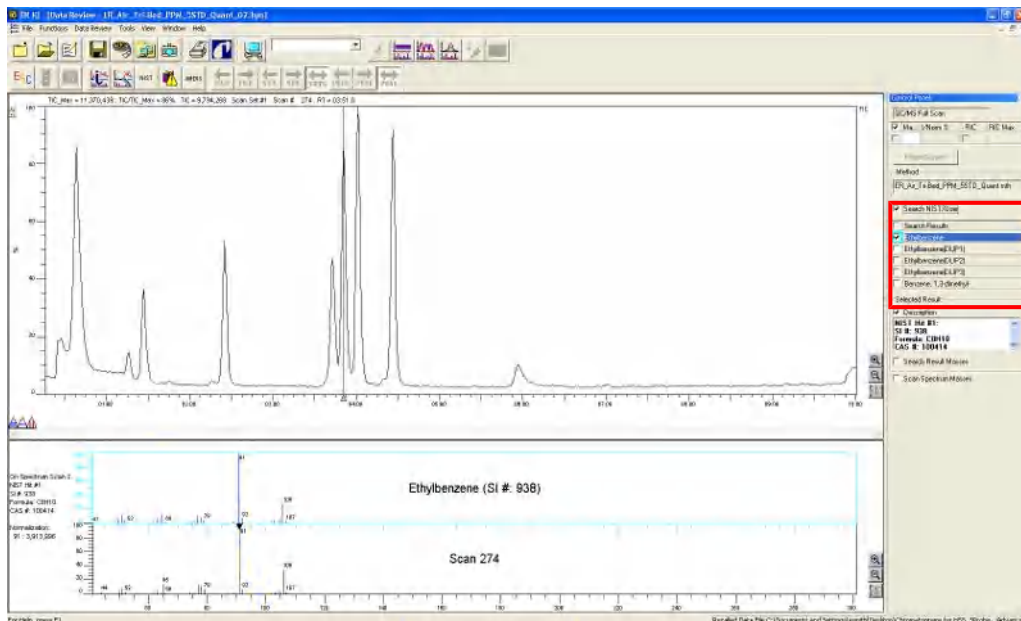
- 2 Check the **Search NIST/User** box in the **Control Panel**. The library identification and the library spectra will be displayed above the spectra of the sample.



- 3 The **Similarity Index Number (SI #)** will be located next to the library identification. A number of 700 and above indicates a good match. A number of 800 and above indicates a very good match. A number of 900 and above is an excellent match. A match of 1000 is a perfect match.

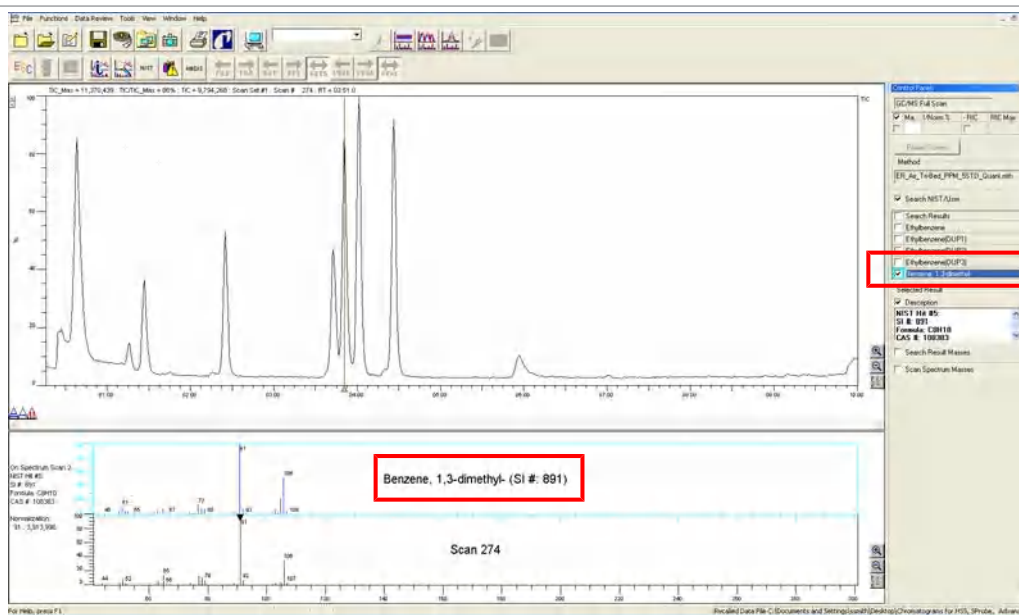


- 4 The **Search Results** box shows five identifications from the spectral search. The result with the highest SI number will be displayed first. If the program identifies the same compound more than once, it will display **DUP**, for duplicate, next to the name of the compound. Duplication increases the confidence in the identification. Therefore, if a compound has four duplicates and a high SI number, the confidence in the identification will be high.

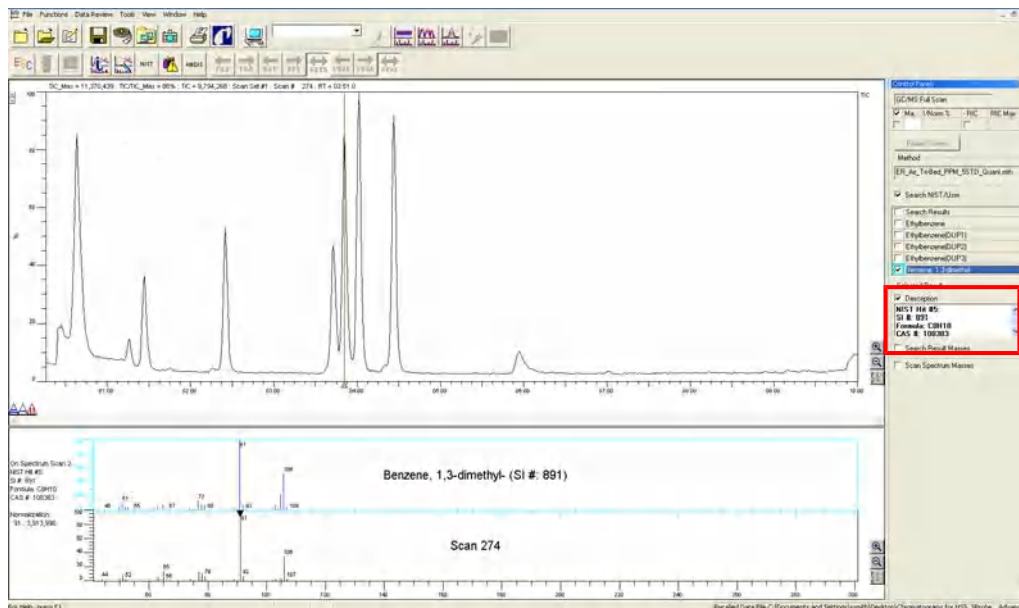


- 5 To view the spectra for a different library identification, highlight the name of the desired compound.





6 If the **Description** box is checked, the highlighted hit, the SI, the formula, and CAS number is displayed.



7 If the **Search Result Masses** box is checked, the masses and relative intensities for the current scan is displayed as a table for the NIST library spectrum.

Control Panel: x

GC/MS:Full Scan

Ma... I/Norm %     - RIC    RIC Max

Pause Screen

Method

ER\_Air\_Tri-Bed\_PPM\_5STD\_Quant.mth

Search NIST/User

Search Results

Ethylbenzene

Ethylbenzene(DUP1)

Ethylbenzene(DUP2)

Ethylbenzene(DUP3)

Benzene, 1,3-dimethyl-

Selected Result

Description

**NIST Hit #5:**    ▲  
**SI #: 891**        ▲  
**Formula: C8H10**    ▲  
**CAS #: 108383**    ▼

Search Result Masses

Mass	% Relative Intensity
<input checked="" type="checkbox"/> 91	100.00
<input checked="" type="checkbox"/> 106	52.05
<input checked="" type="checkbox"/> 105	23.22
<input checked="" type="checkbox"/> 77	13.51
<input checked="" type="checkbox"/> 51	10.61
<input checked="" type="checkbox"/> 39	8.71
<input checked="" type="checkbox"/> 92	8.01
<input checked="" type="checkbox"/> 65	7.61
<input checked="" type="checkbox"/> 78	7.51
<input checked="" type="checkbox"/> 79	7.41

Scan Spectrum Masses

- 8** If the **Scan Spectrum Masses** box is checked, the masses and relative intensities are displayed as a table for the unknown spectrum.

Method  
ER\_Air\_Tri-Bed\_PPM\_5STD\_Quant.mth

Search NIST/User

Search Results

Ethylbenzene

Ethylbenzene(DUP1)

Ethylbenzene(DUP2)

Ethylbenzene(DUP3)

Benzene, 1,3-dimethyl-

Selected Result

Description

**NIST Hit #2:**  
**SI #: 928**  
**Formula: C8H10**  
**CAS #: 100414**

Search Result Masses

Mass	% Relative Intensity
<input checked="" type="checkbox"/> 91	100.00
<input checked="" type="checkbox"/> 106	33.63
<input checked="" type="checkbox"/> 51	21.12
<input checked="" type="checkbox"/> 39	15.62
<input checked="" type="checkbox"/> 65	13.81
<input checked="" type="checkbox"/> 77	11.81
<input checked="" type="checkbox"/> 27	10.11
<input checked="" type="checkbox"/> 92	9.91
<input checked="" type="checkbox"/> 78	9.51
<input checked="" type="checkbox"/> 50	9.01

Scan Spectrum Masses

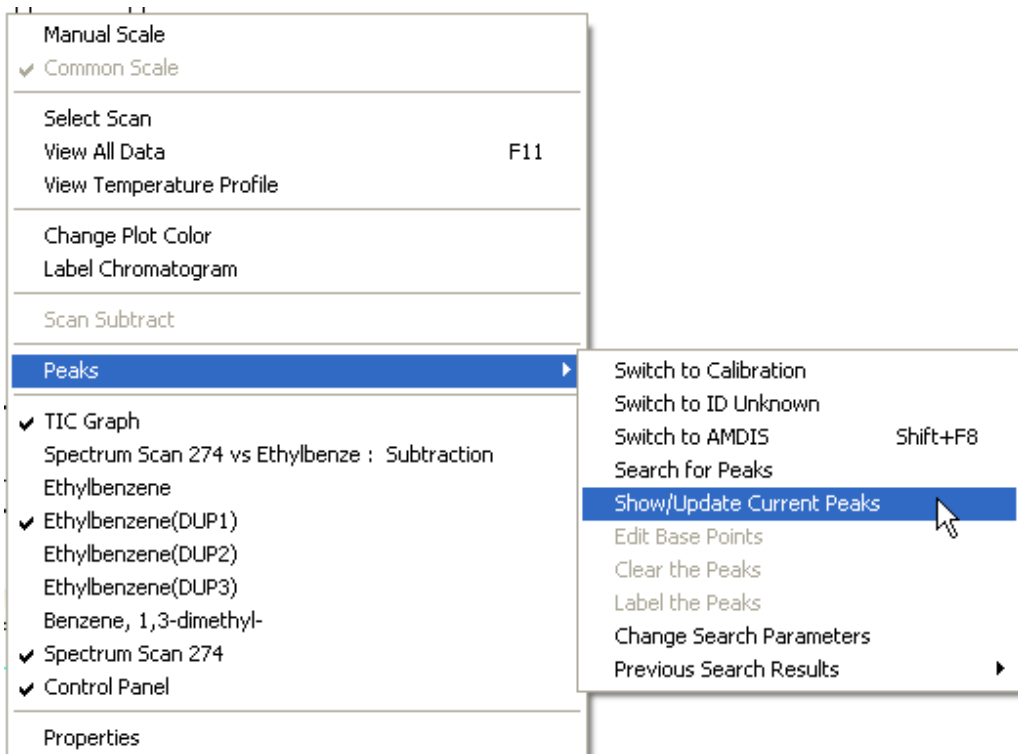
Mass	% Relative Intensity
<input checked="" type="checkbox"/> 91	100.00
<input checked="" type="checkbox"/> 106	34.56
<input checked="" type="checkbox"/> 65	14.27
<input checked="" type="checkbox"/> 77	13.74
<input checked="" type="checkbox"/> 78	11.84
<input checked="" type="checkbox"/> 51	8.47
<input checked="" type="checkbox"/> 92	7.33
<input checked="" type="checkbox"/> 79	7.12
<input checked="" type="checkbox"/> 63	5.30
<input checked="" type="checkbox"/> 105	4.70

## 13.8 Current Peaks

The **Show/Update Current Peaks** function will search the entire chromatogram to qualitatively identify each peak. The **Show/Update Current Peaks** function searches in the same manner as the **Search NIST/User** function. After performing the search, the software will list all of the compounds that were identified in the chromatogram.

## 13.8.1 Show/Update Current Peaks

- 1 The **Show/Update Current Peaks** function is accessed by right-clicking on the chromatogram. Mouse over **Peaks** and click on **Show/Update Current Peaks**.



⇒ The Show/Update Current Peaks window displays.

**Peaks Found For ER\_Air\_Tri-Bed\_PPM\_5STD\_Quant\_**

Select Mass: TIC      Add Peaks

Number of Peaks: 21

Ret. Time	Scan Range	Peak	Area	% Area	Hits Found
00:00:26	10 - 21	15	12382799	2.02	
00:00:38	21 - 48	29	67221560	10.95	
00:01:15	72 - 83	77	3995055	0.65	
00:01:26	83 - 106	91	17392822	2.83	
00:01:45	109 - 119	115	514986	0.08	
00:02:15	149 - 157	153	822028	0.13	
00:02:25	157 - 177	165	27386510	4.46	
00:03:12	219 - 233	225	298265	0.05	
00:03:43	248 - 269	264	27294950	4.45	
00:03:51	269 - 281	274	47765924	7.78	
00:04:01	281 - 297	287	53503876	8.72	
00:04:10	297 - 304	299	687652	0.11	
00:04:26	304 - 337	319	51721676	8.43	
00:05:56	422 - 452	434	8331637	1.36	

Mass

TIC

Hide Graph

Search in NIST

Search in AMDIS

Search

Description:

NIST Hit #1:  
SI #: 419  
Formula: C9H8CIN3O  
CAS #: 719482

Redo Peak Search

Peak Search Param

NIST Search Setup

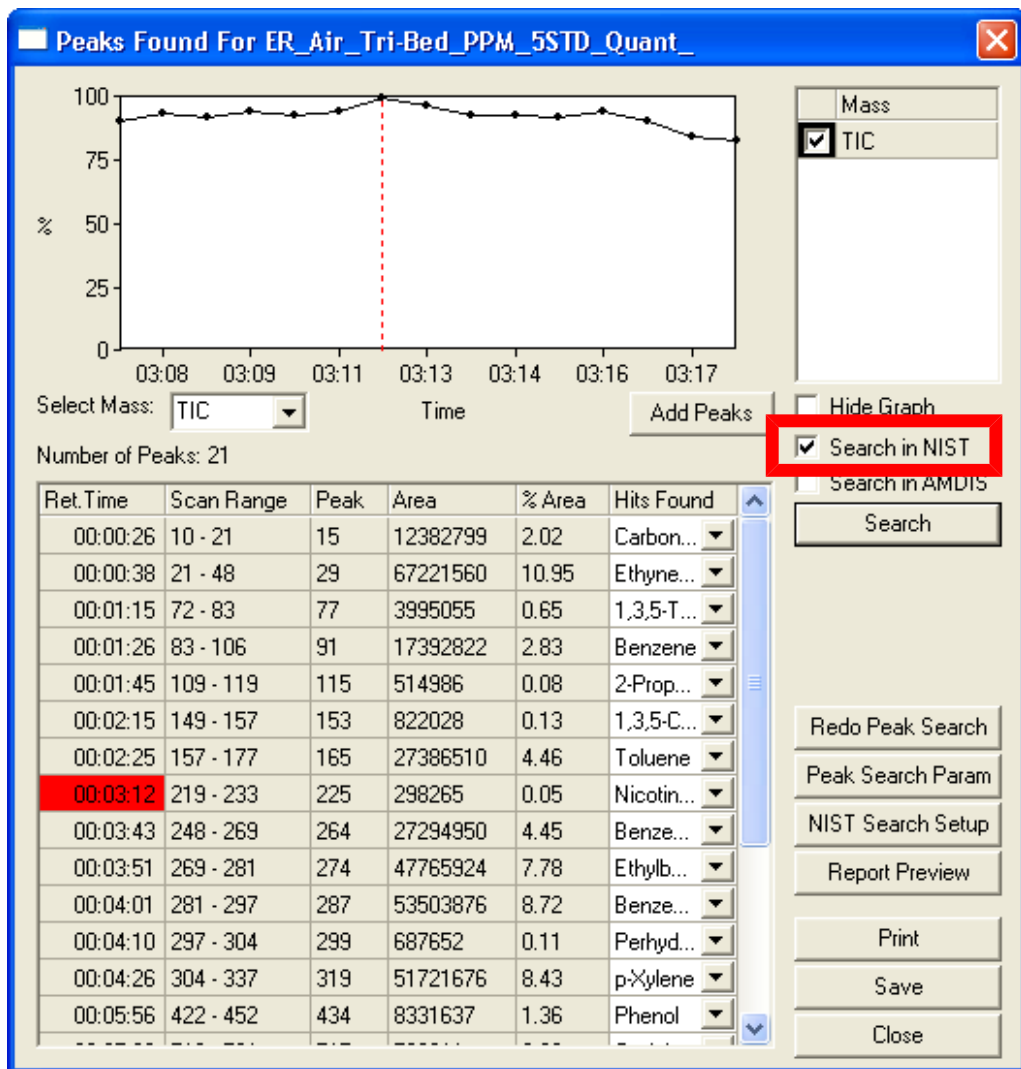
Report Preview

Print

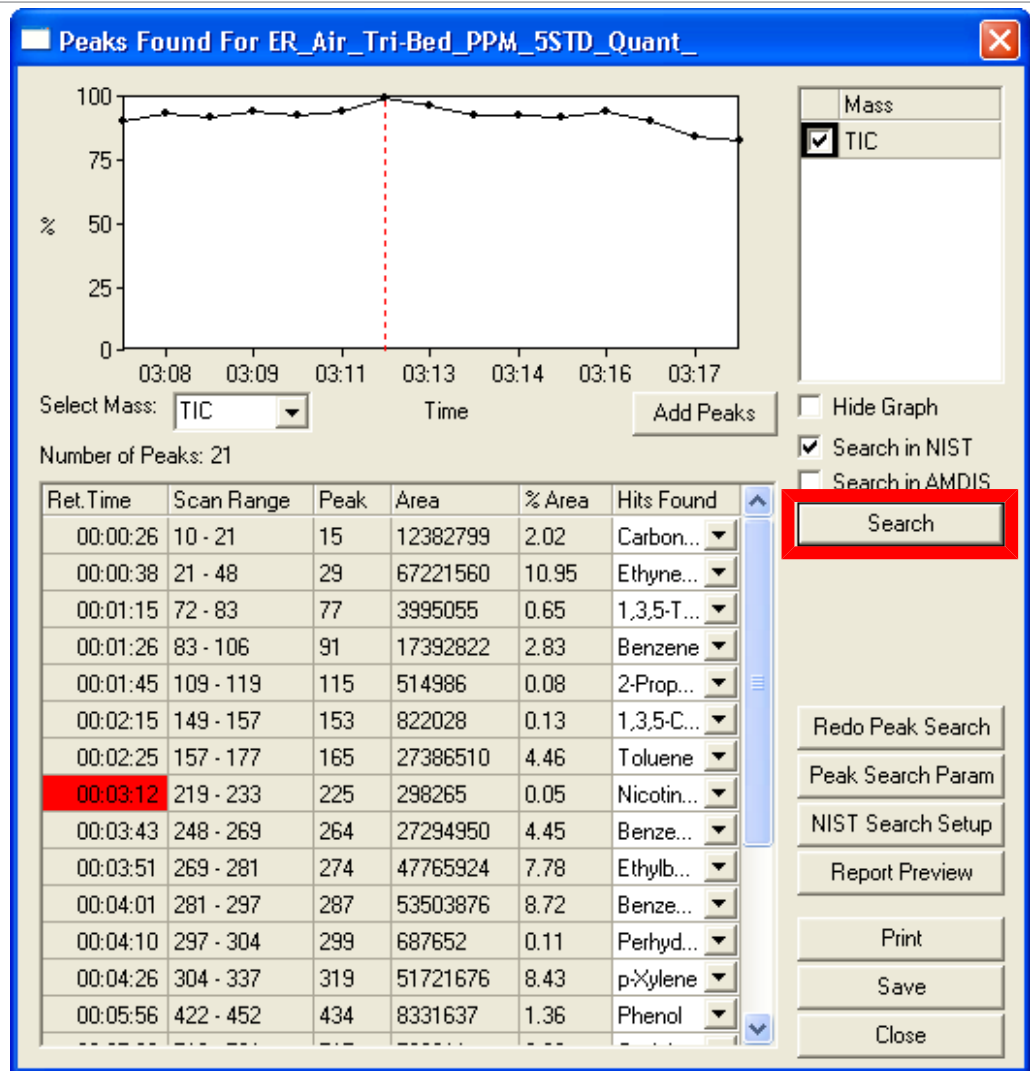
Save

Close

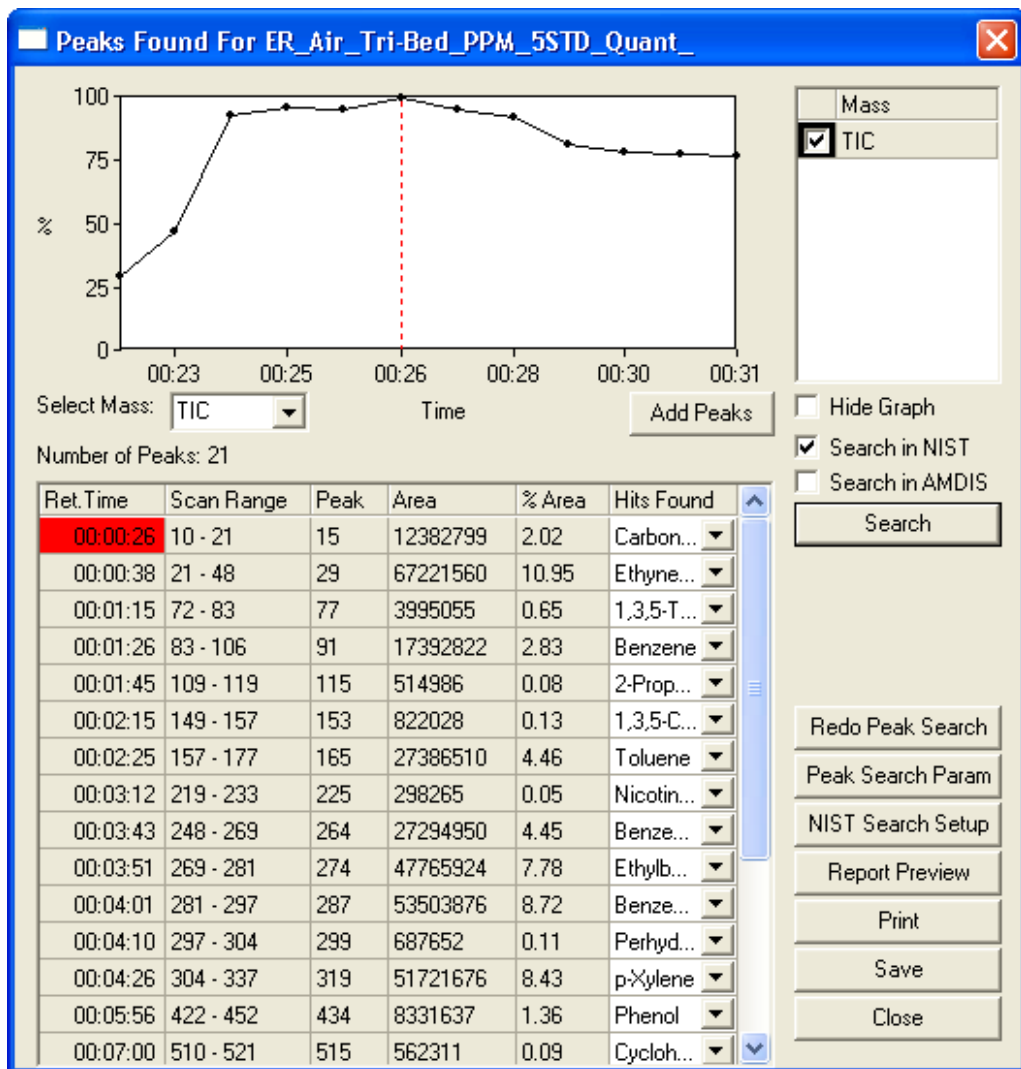
2 Check the **Search in NIST** box.



3 Click **Search**.

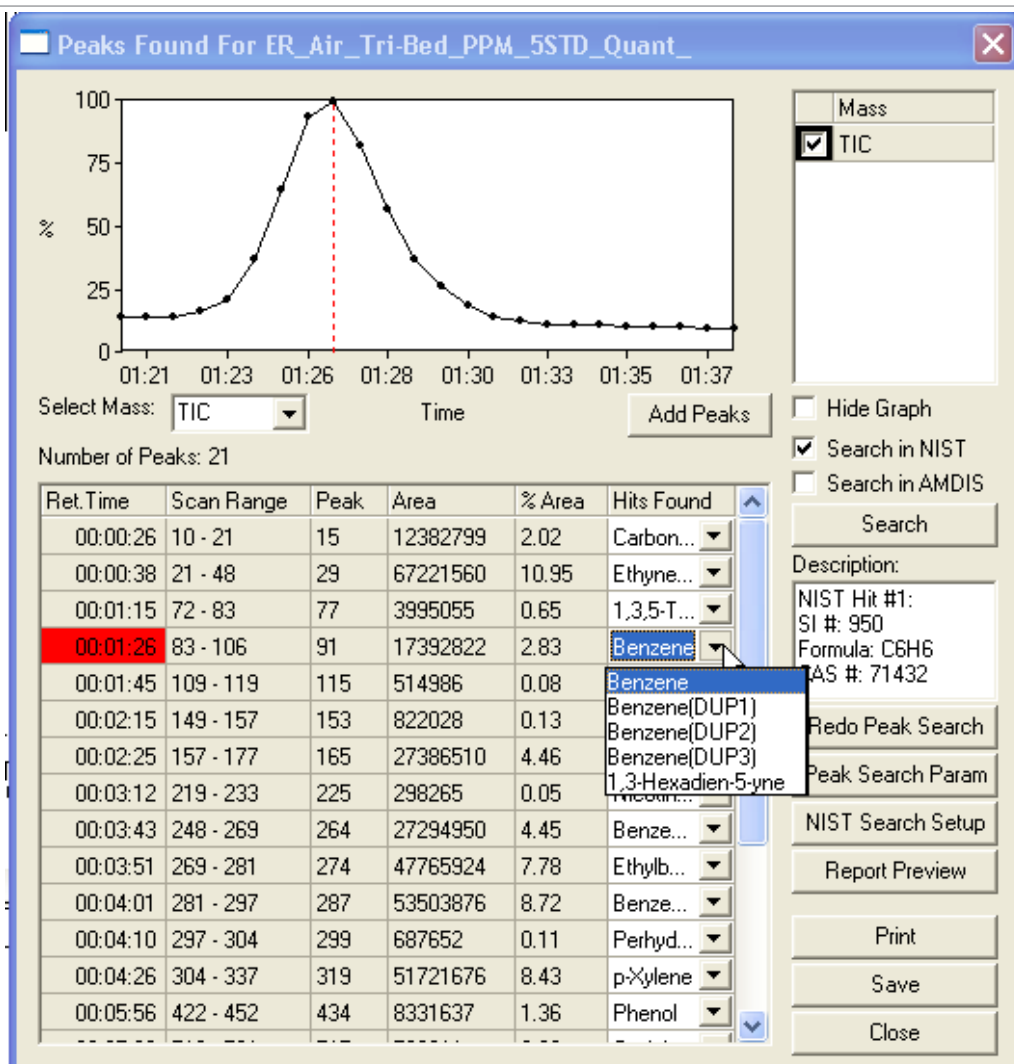


4 A NIST search is performed on the peaks that NIST has located. The **Hits Found** column is populated.



- 5 Each identification has a drop-down menu. Five hits are displayed in each menu.





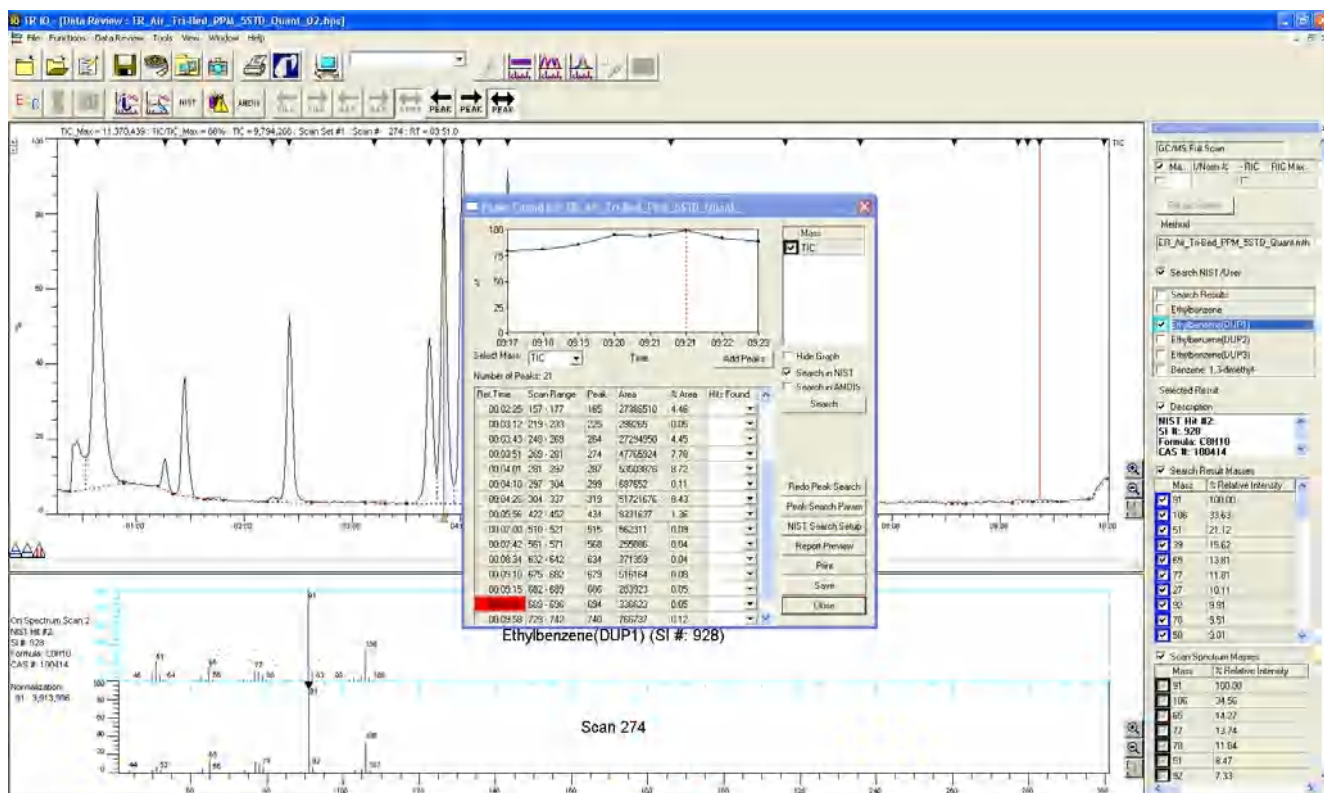
- 6 Check the **Search in AMDIS** box. The software will search the peaks using the AMDIS library. The AMDIS identification is located in the drop-down menu below the NIST hits.



This is not a true AMDIS search. AMDIS will not search the entire chromatogram. It will only search the peaks that NIST has located.

### 13.8.1.1 Show/Update Current Peaks Window Description

In the chromatogram beneath the **Show/Update Current Peaks** window, each detected peak is labeled with a black triangle. Pink dots appear at the base of each peak. These dots are used to determine the peak area.



On the **Show/Update Current Peaks** window, the highlighted peak is displayed with the dots along the peak representing each individual scan. The following is also displayed:

Number of Peaks	The number of peaks that have been identified by the Show/Update Current Peaks program.
Retention Time	The time the compound elutes from the column.
Scan Range	The range of scans that encompass the peak.
Area	The area of the peak.
Percent Area	The ratio of the TIC of the peak to the total TIC multiplied by 100.
Add Peaks	The peaks that were not automatically located by the software can be added to the <b>Show/Update Current Peaks</b> window using the <b>Range Tool</b> . See <a href="#">Range Tool [ 256]</a> .
Hide Graph	Checking the <b>Hide Graph</b> box will remove the graph from the <b>Show/Update Current Peaks</b> window.

Redo Peak Search	The software will clear the identifications from the <b>Hits Found</b> column.
Peak Search Parameters	See Setting Up a Quantitative Search [▶ 342] for more information.
NIST Search Parameters	Allows the pathway for the NIST libraries to be set. The library pathways are set at the factory, but may need reset if the software is reloaded. See NIST Search Setup [▶ 243] for instructions.
Report Preview	The information in the <b>Show/Update Current Peaks</b> is displayed in a text format. See Show/Update Current Peaks [▶ 236] for instructions.

### 13.8.1.2 Peak Search Parameters

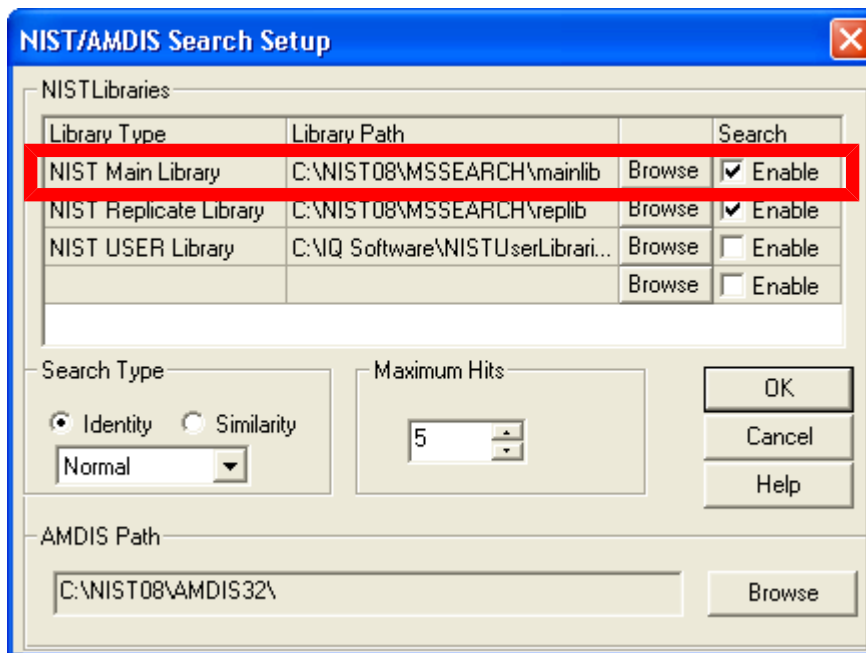
Some of the parameters for peak searching can be selected. These include the **Min RIC Area**, **Min TIC Area**, the **Min** and **Max Width**, the **Mass Range**, the **Net Fit**, the NIST library used for identification and the number of identifications that are displayed by the NIST library.

Library Name	The selected library will be used to make AMDIS identifications.
Maximum NIST Hits	NIST will display the setpoint number of identifications.

### 13.8.1.3 NIST Search Setup

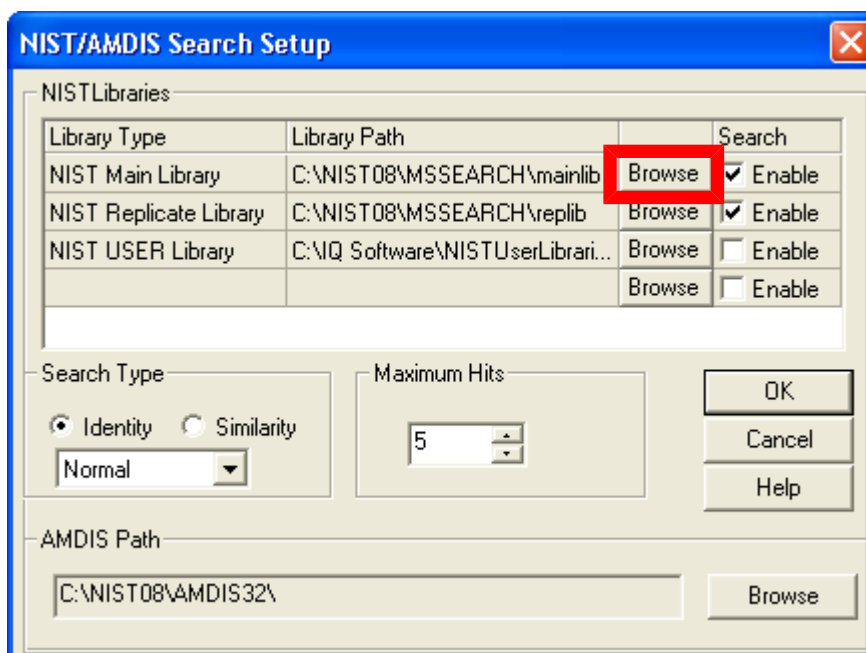
If NIST is reloaded onto the laptop, the library pathway may need to be reset.

If the libraries have properly loaded, the pathways will be set to folders displayed in the figure below.

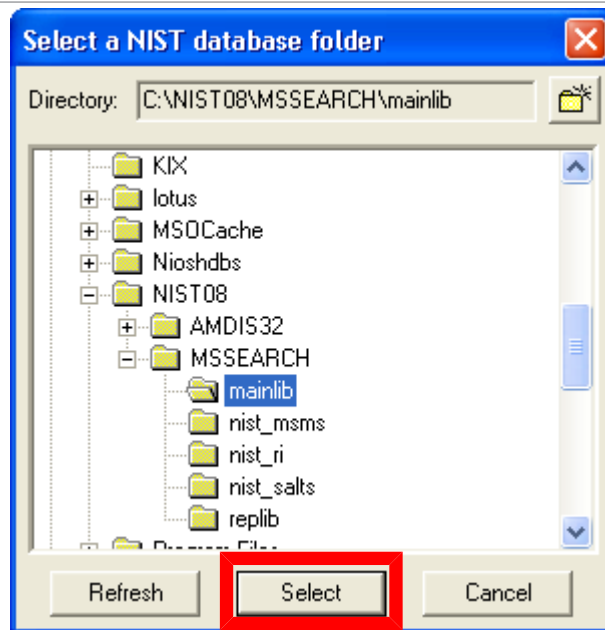


To reset the **NIST Main Library**:

- 1 Click **Browse...**

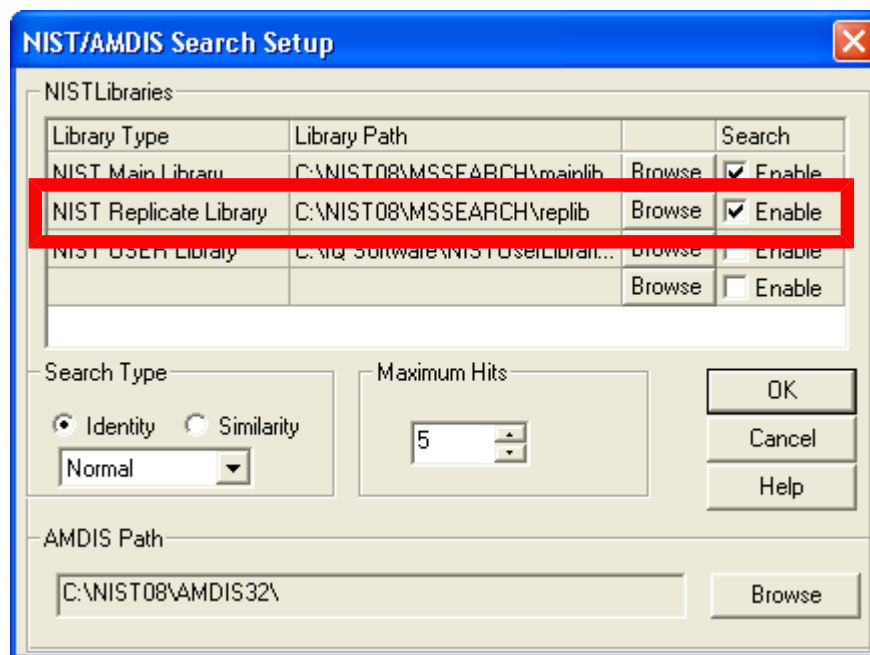


- 2 Select the **NIST Main Library** from the folder displayed. Click **Select** to set the library.

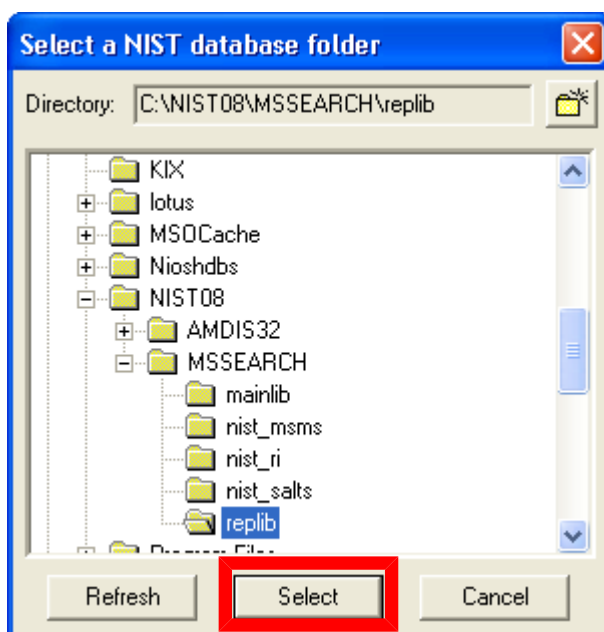


To reset the **NIST Replicate Library**:

- 1 Click **Browse...**

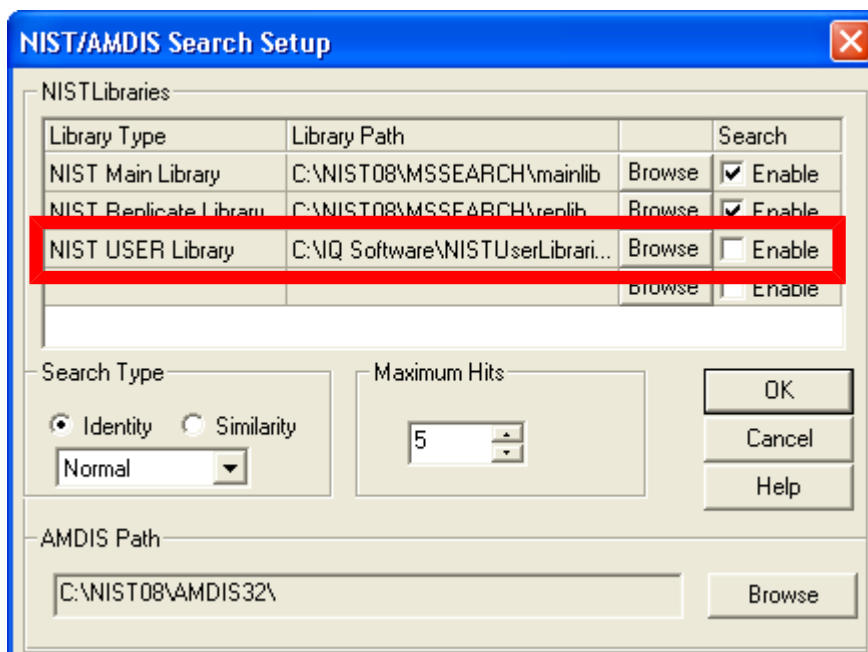


- 2 Select the **NIST Replicate Library** from the folder displayed. Click **Select** to set the library.

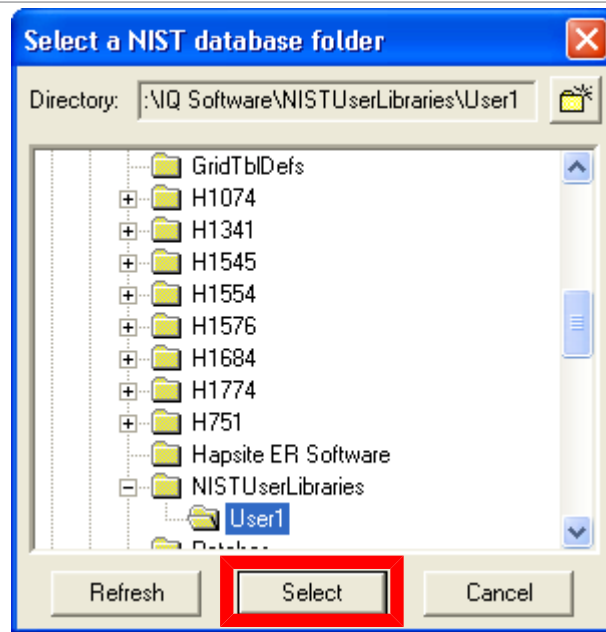


To reset the **NIST USER Library**:

- 1 Click **Browse...**



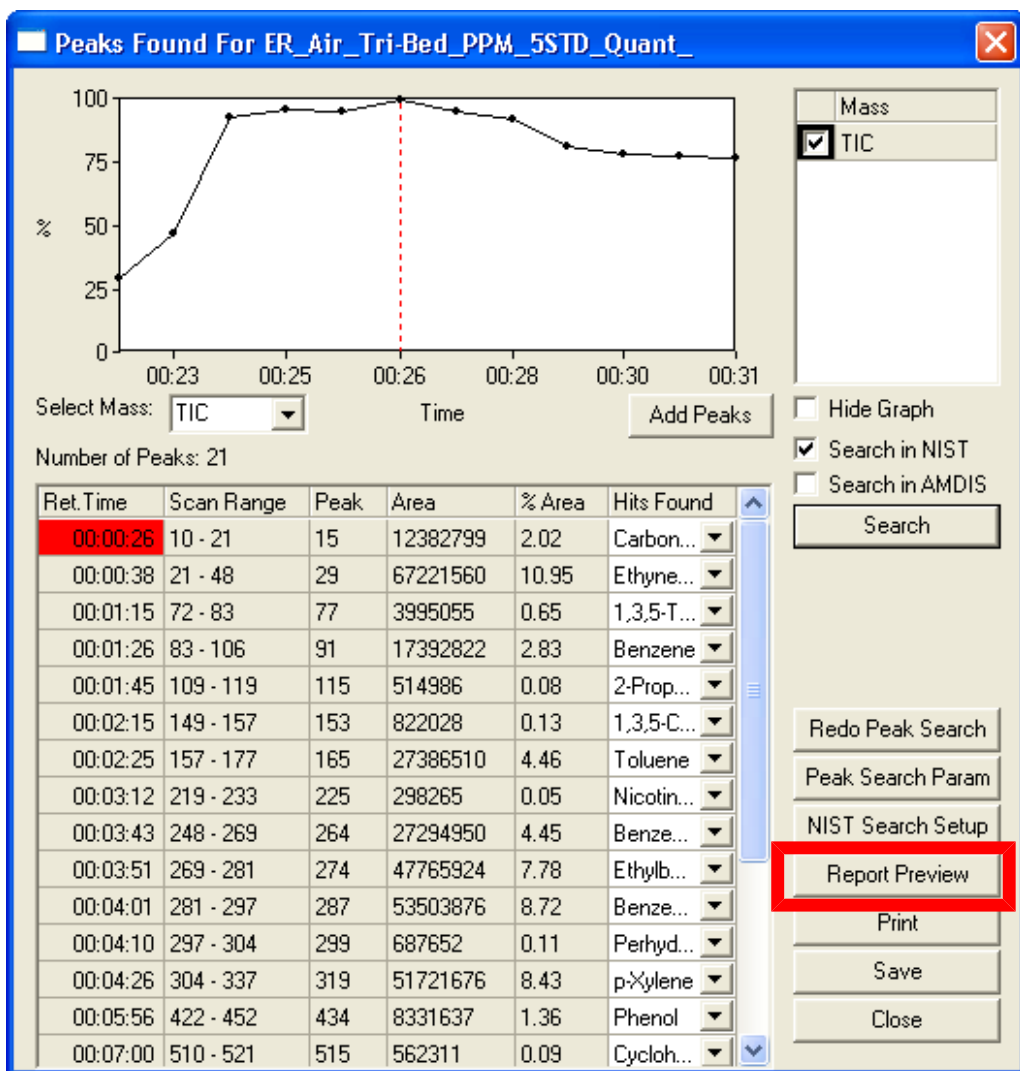
- 2 Select the **NIST USER Library** from the folder displayed. Click **Select** to set the library.



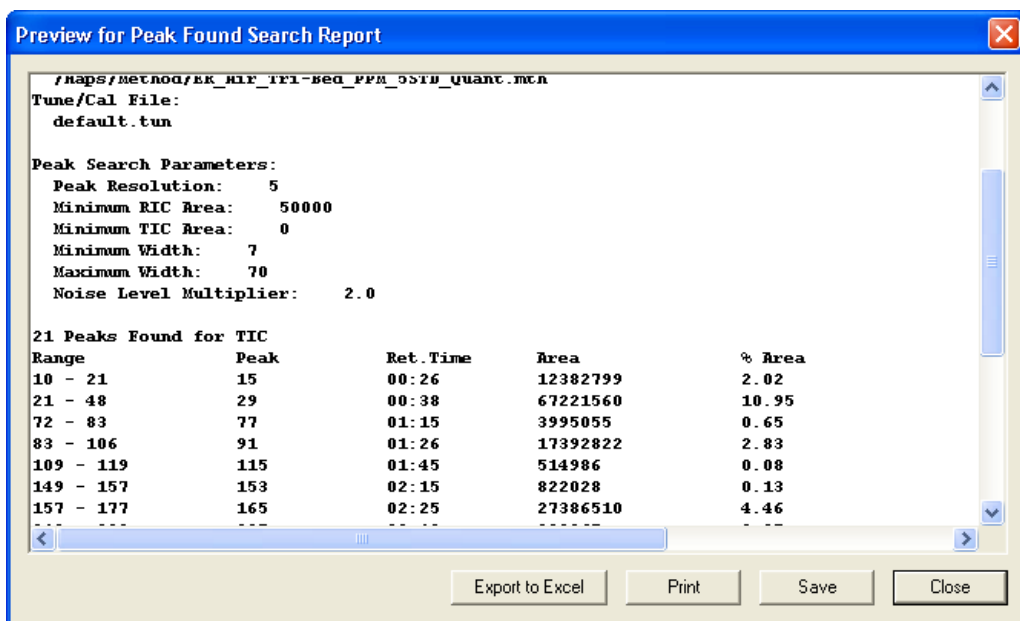
#### 13.8.1.4 Report Preview

**Report Preview** reformats the **Show/Update Current Peaks** window into a text file.

- 1 To view the report, click the **Report Preview** button.

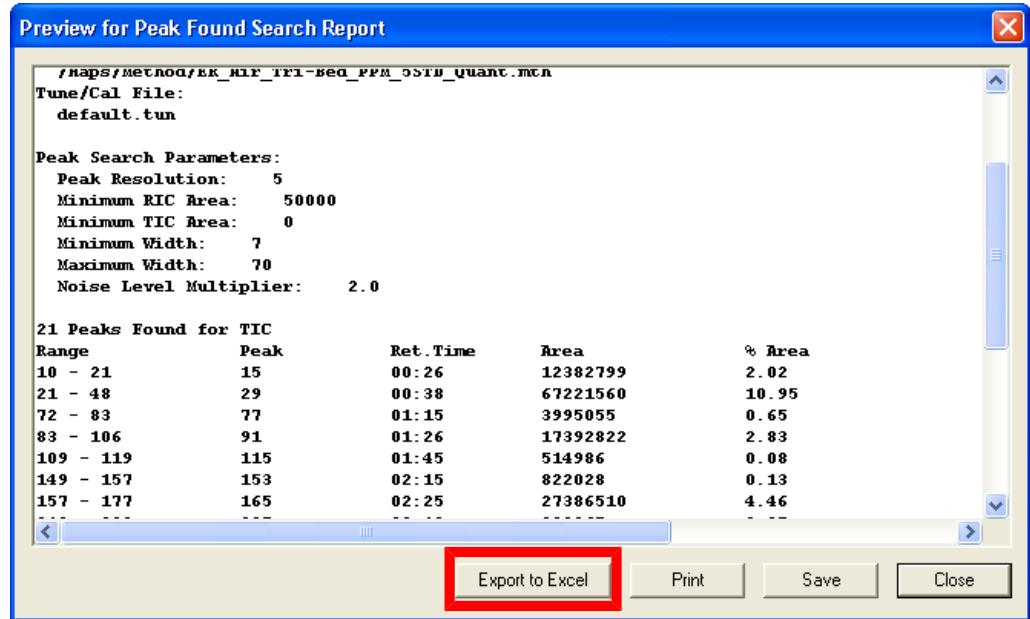


2 The report is displayed.

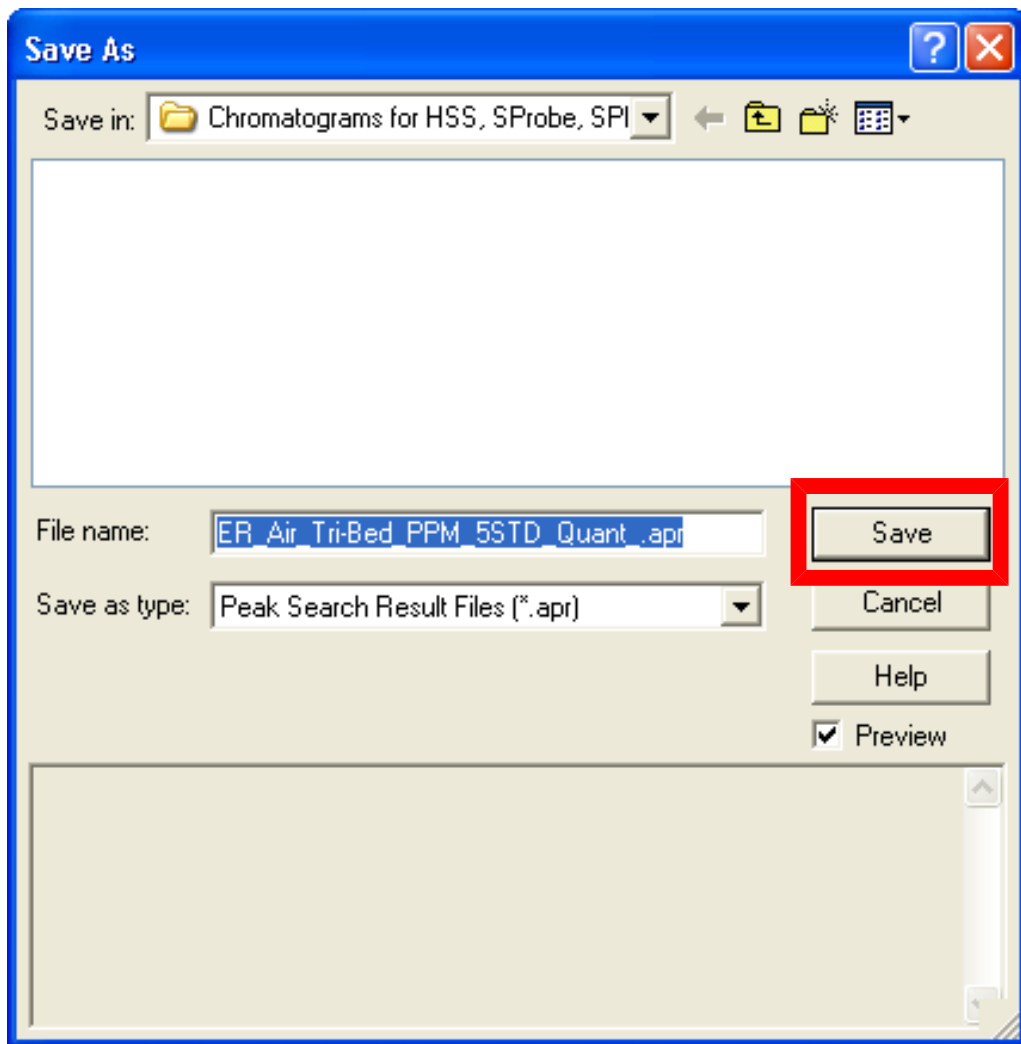




- The report can be exported to Excel for further data analysis. Click **Export to Excel**.



- The report will need to be saved before Excel will open. Click **Save**.



5 The report opens in Excel.

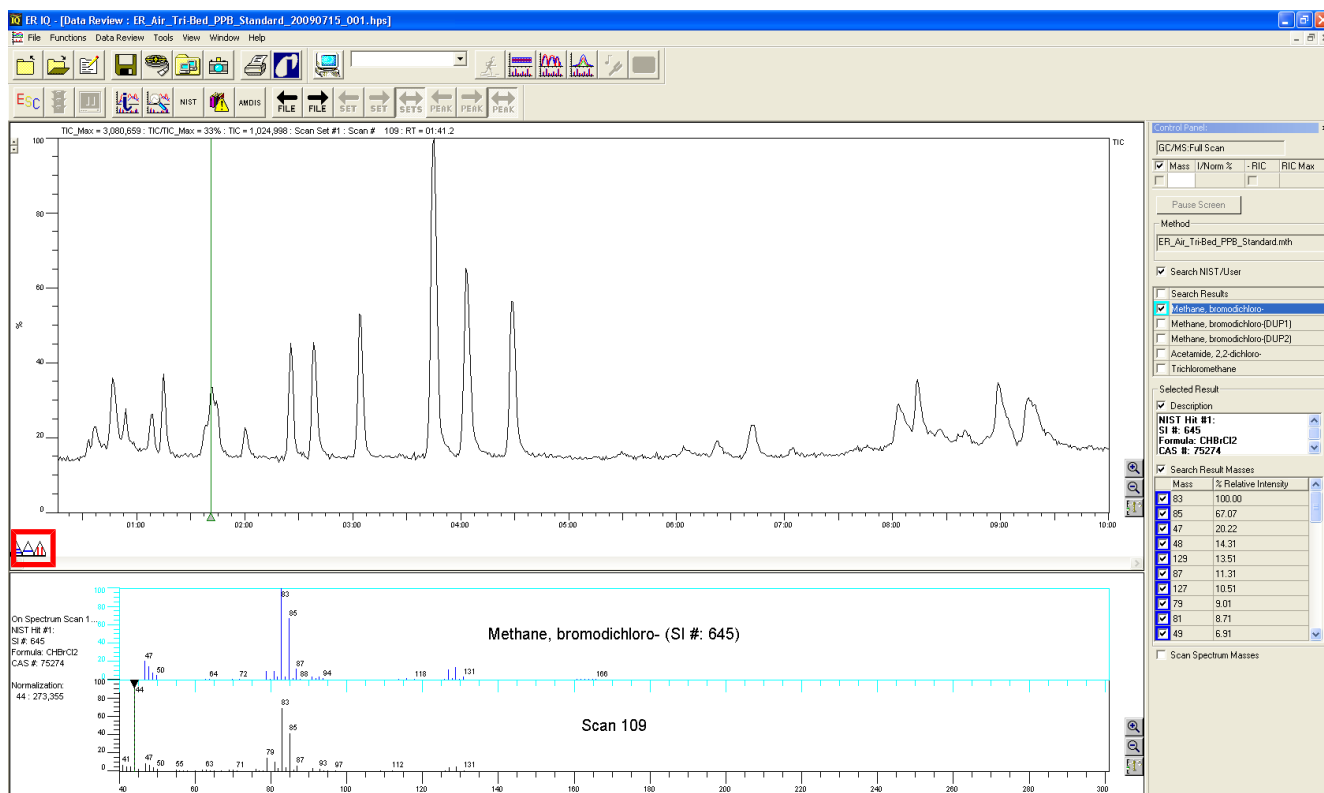
The screenshot shows a Microsoft Excel spreadsheet titled 'ER\_Air\_Tri-Bed\_PPM\_5STD\_Quant\_apr'. The active sheet is 'Peak Found Search Report'. The data is organized into sections: Full Scan Data, GPS Info, Acquisition Date and Time, Acquisition Method, Tune/Cal File, Peak Search Parameters, and a table of 21 peaks found for TIC.

Range	Peak	Ret. Time	Area	% Area	
26	21-Oct	15	0.26	12382799	2.02
27	21 - 48	29	0.38	67221560	10.95
28	72 - 83	77	1.15	3995055	0.65
29	83 - 106	91	1.26	17392822	2.83
30	109 - 119	115	1.45	514986	0.08
31	149 - 157	153	2.15	822028	0.13
32	157 - 177	165	2.25	27386510	4.46
33	219 - 233	225	3.12	298265	0.05
34	249 - 260	254	3.43	27784947	4.45

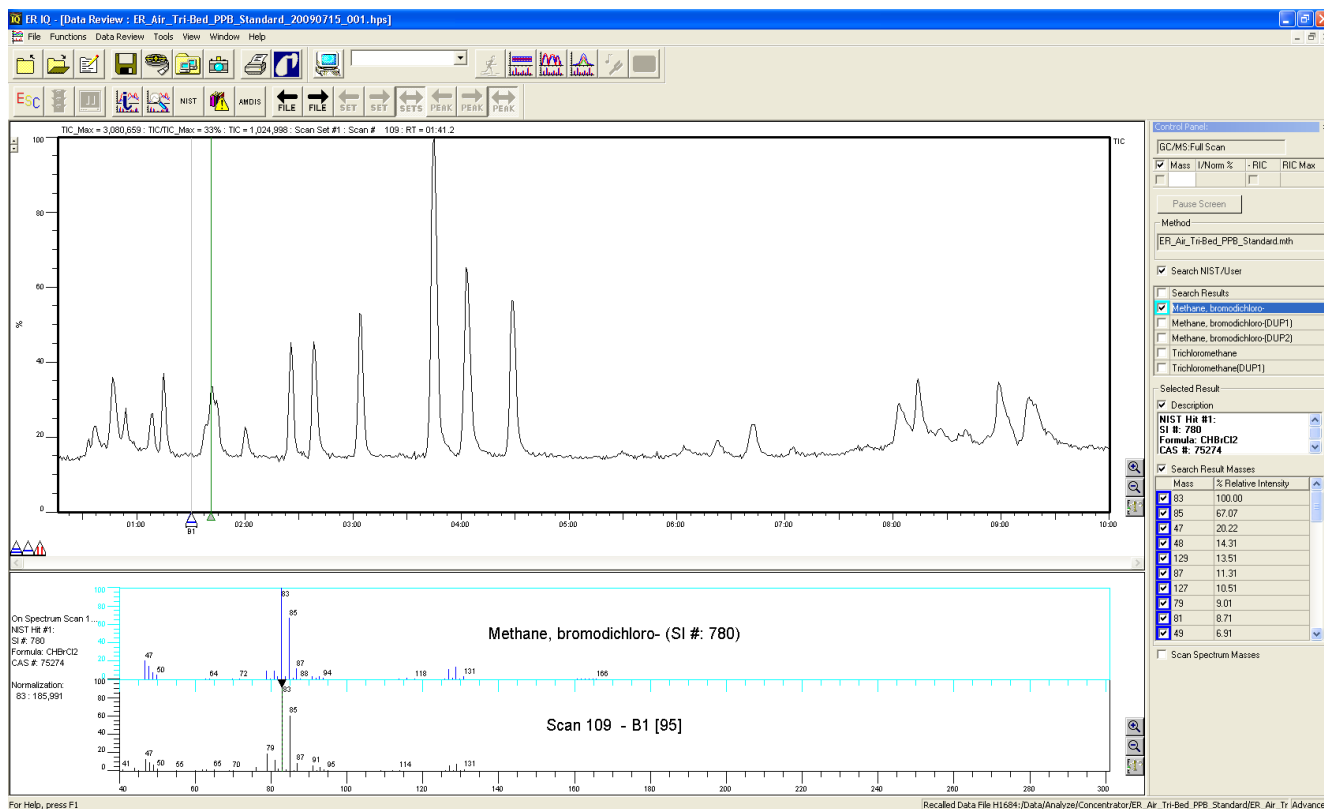
### 13.8.2 Background Subtract

**Background Subtract** will remove masses in the spectrum that are caused by background interference. Using **Background Subtract** will increase the SI number of the identification when the low SI number is a result of high background. Follow the instructions below to perform a **Background Subtract**.

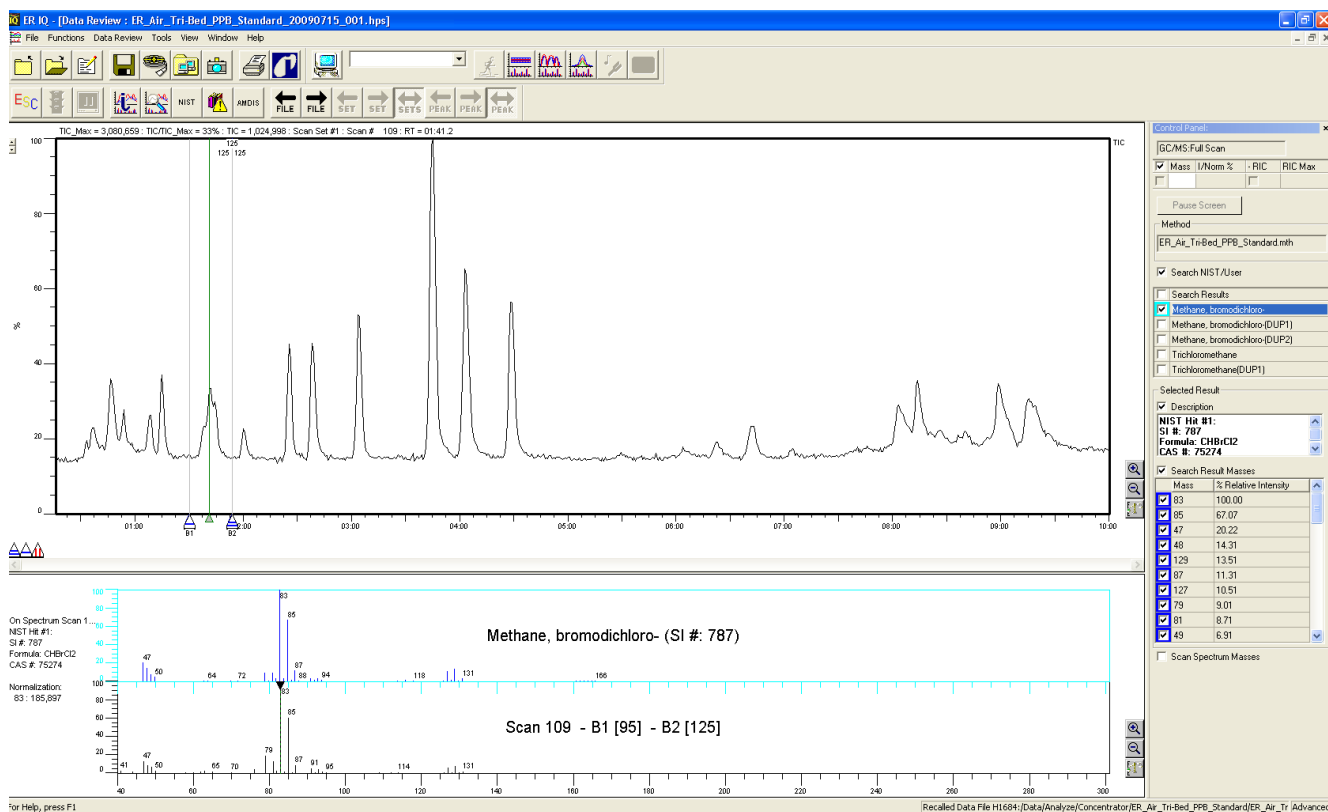
- 1 Perform a **NIST Library Search** by checking the **Search NIST/User** box in the **Control Panel**.
- 2 If the SI number is low and the background is high, select the blue **Background Subtract** triangle from the lower left side of the chromatogram.



- 3 Drag to an area that is representative of the background on either side of the selected peak. The background masses at this location are automatically subtracted from the peak.

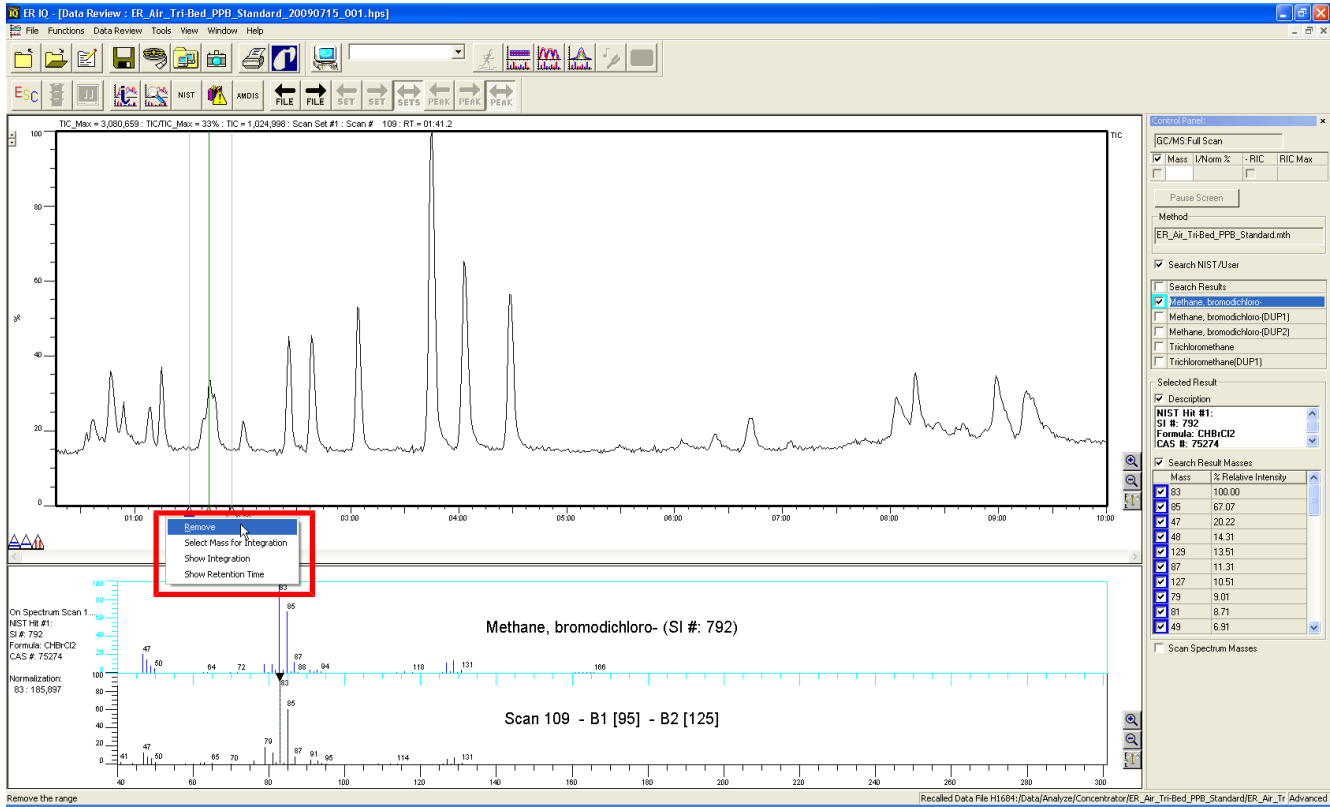


- If the background on the opposite side of the peak differs from the subtracted background, a second background subtract can be used.



All background subtractions are indicated in the **Spectrum** window by the designation **Scan Number - B1(range) - B2(range)**.

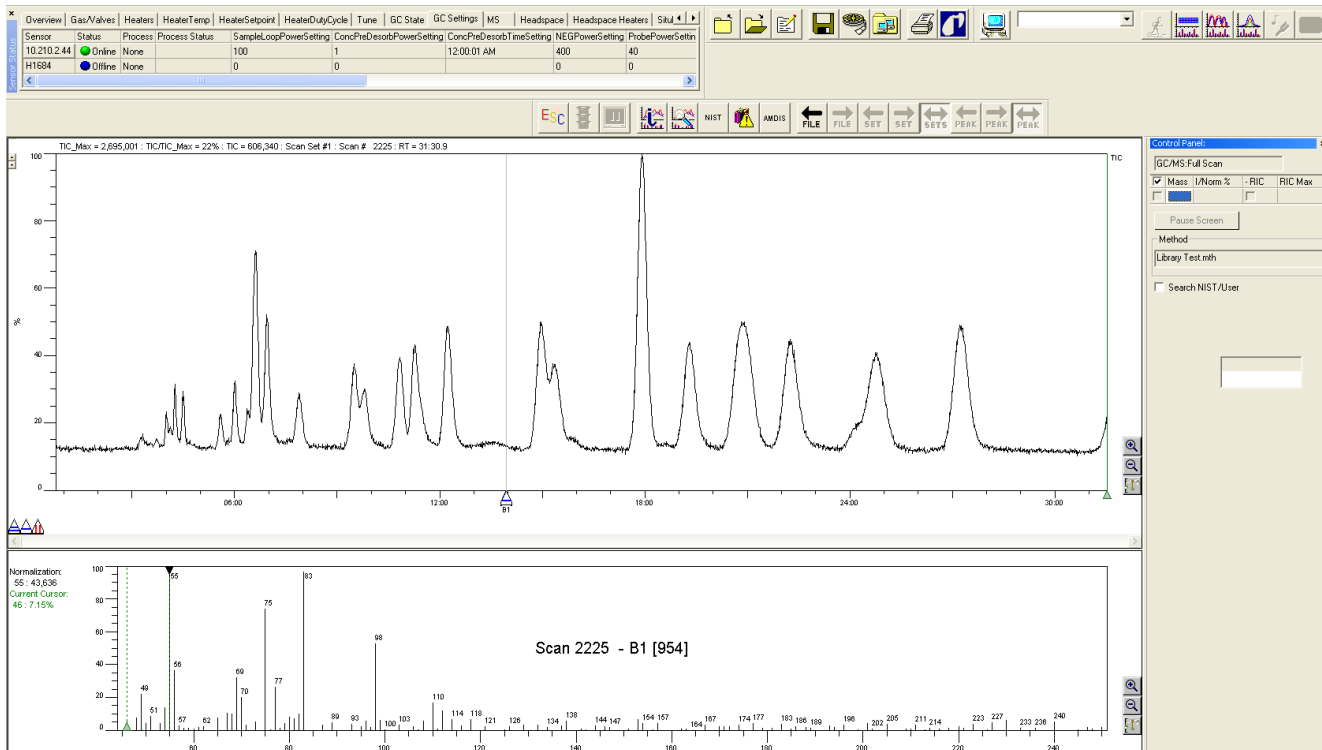
- To remove **Background Subtract** from the chromatogram, place the cursor over the **Background Subtract** triangle, right-click and select **Remove**.



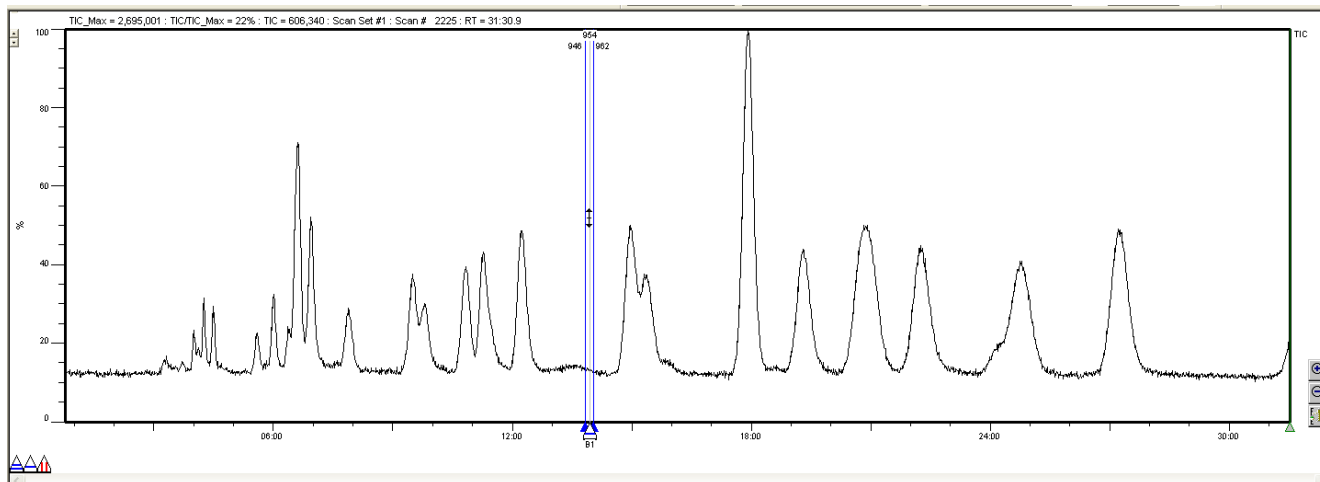
### 13.8.2.1 Background Subtraction Using a Range of Points

Background from a range of points can be subtracted, if desired.

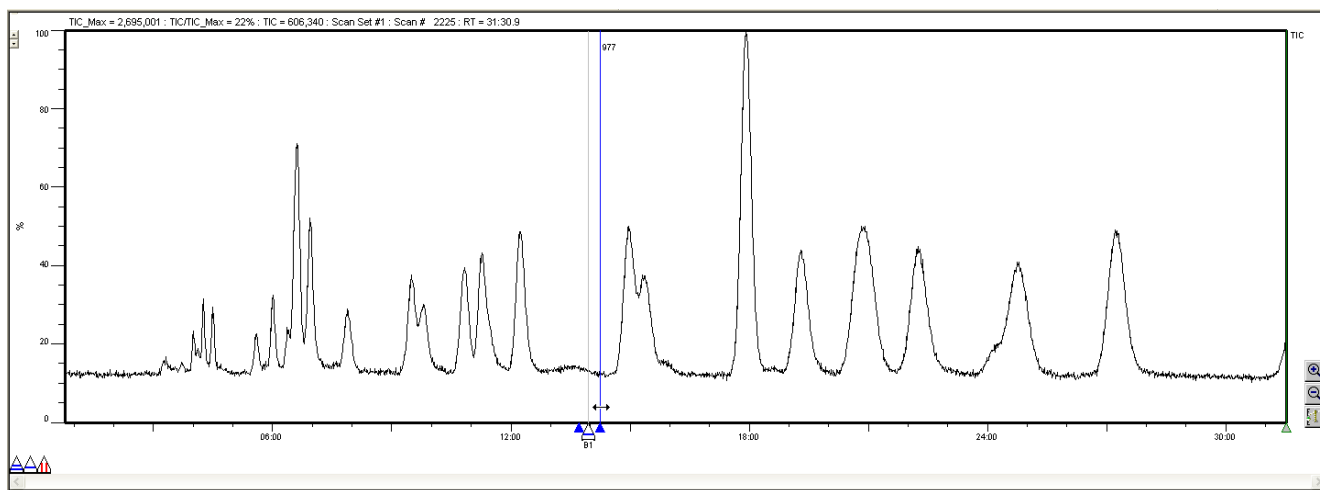
- 1 Place the **Background Subtract** triangle at the apex of the small peak.



- 2 Mouse over the gray line located above the **Background Subtract** triangle. The cursor will change to a vertical double-headed arrow. Left-clicking and holding, while moving the double headed arrow upwards, widens the background range. Moving the arrow downwards, narrows the range of the background. The width of the range is represented by two small, blue triangles.



- 3 The left and right side boundaries can be manually adjusted by clicking on the smaller blue triangle and dragging it to the desired location.



This procedure can be repeated by using the second **Background Subtract** triangle.

### 13.8.2.2 Additional Features of the Background Tool

By placing the mouse over a **Background Subtract** triangle and right-clicking, see the figure below, the following menu will be displayed:

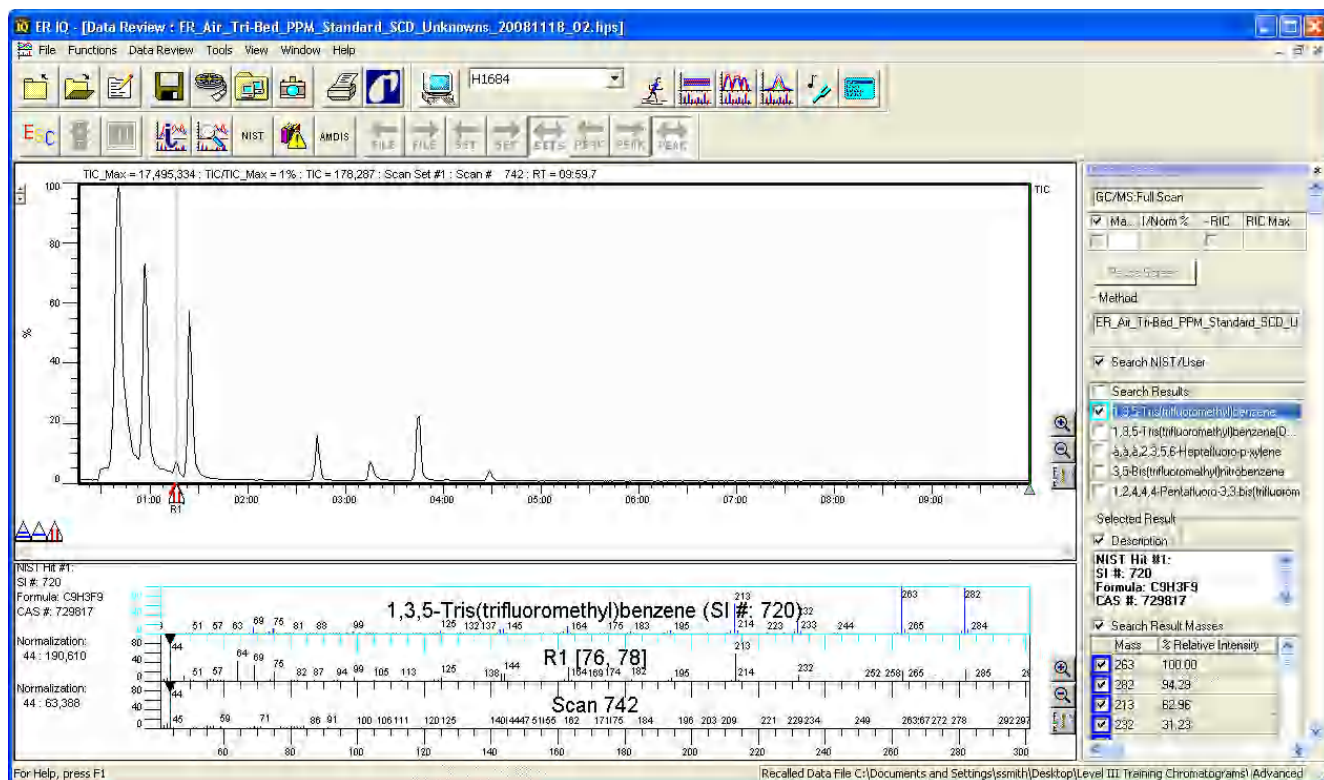
Remove
Select Mass for Integration
Show Integration
Show Retention Time

Remove	Removes the <b>Background Subtract</b> triangle.
Select Mass for Integration	Selects either the TIC or a mass fragment for integration.
Show Integration	Displays the integration on the x-axis.
Show Retention Time	Displays the retention time on the x-axis.

### 13.8.3 Range Tool

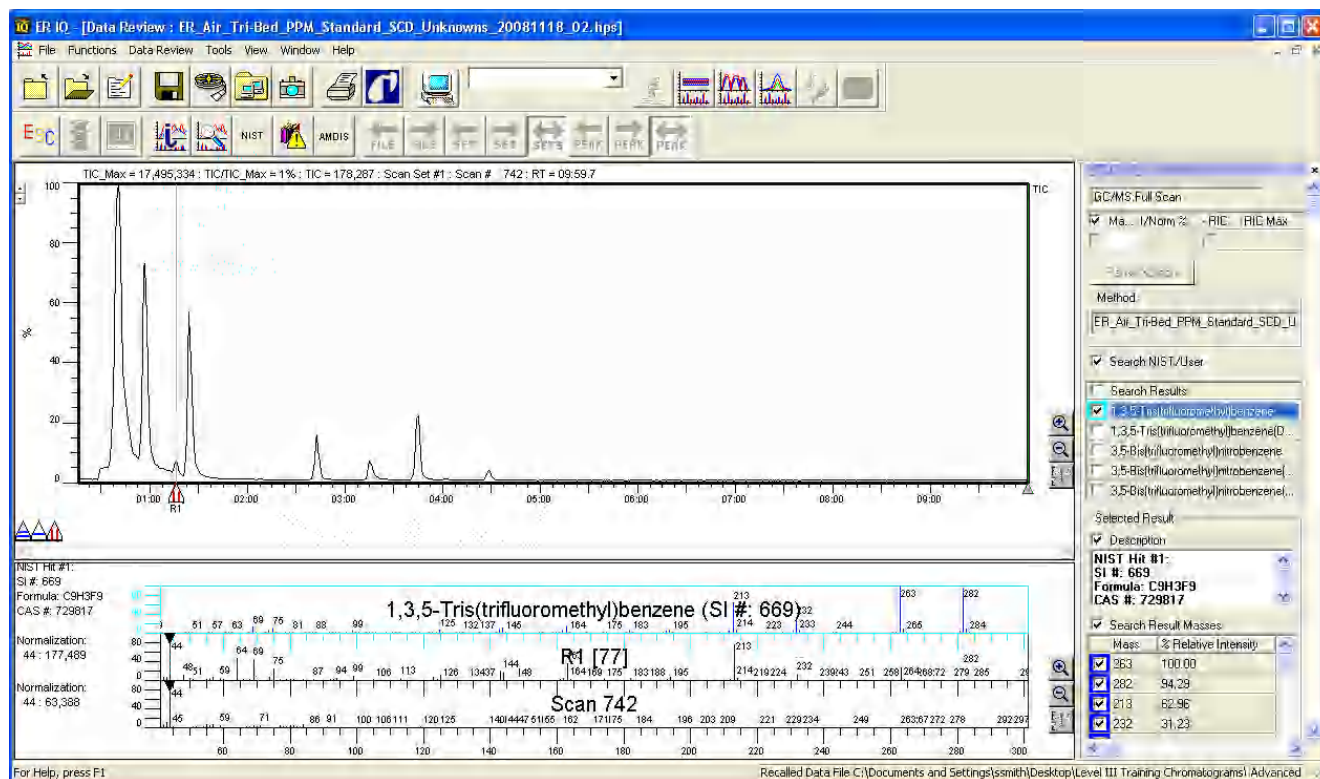
The Range Tool is a red-striped triangle located at the bottom left side of the chromatogram. It is used to average spectra over a “range” of scans across a given peak, especially when the analytes are low in concentration. It can also be used to select a section of a peak or reintegrate peaks. The SI numbers for the selected compound will increase when using the **Range Tool**. Follow the instructions below to use the **Range Tool**.

- 1 Place the cursor on the red-striped triangle, which is the **Range Tool**. Left-click, hold and drag the triangle to the location where the scans should be averaged.

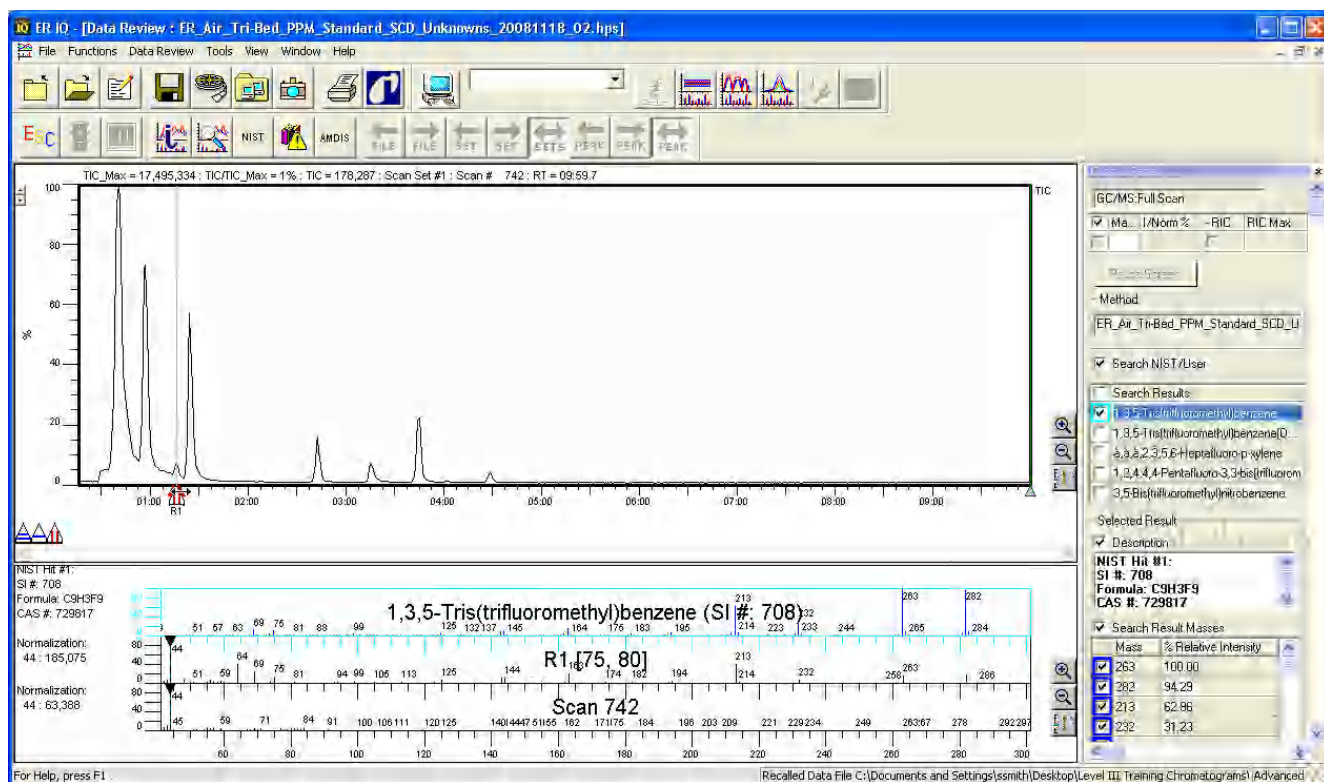




- 3 Move the cursor to the tip of the **Range Tool** triangle. The cursor will change to a vertical double-headed arrow. Left-click, hold and move the double-headed arrow upwards to widen a range. Moving the arrow downwards narrows the range. The red range lines should intersect the peak sides at 50% of their height.



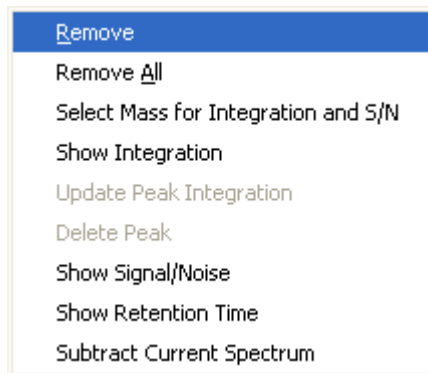
- 3 The left and right side boundaries can be manually adjusted by clicking on the smaller red triangle and dragging it to the desired location.



All ranges are indicated in the spectrum window by the designation: R1 [Range Start Scan, Range End Scan].

### 13.8.3.1 Additional Features of the Range Tool

By placing the mouse over the **Range Tool** triangle and right-clicking, the following menu is displayed.



Remove	Removes the range cursor.
Select Mass for Integration	Selects the TIC or a specific mass fragment for reintegration.
Show Integration	Displays the integration on the x-axis.
Show Retention Time	Displays the retention time on the x-axis.

Show Signal/Noise	Shows <b>Signal to Noise</b> ratio. A background must be selected using <b>Background Subtract</b> first. Refer to Background Subtract [ 251].
Subtract Current Spectrum	Subtracts the spectrum at the point where the green scan cursor is located from the range.

## 13.9 Displaying Reconstructed Ion Chromatograms (RIC)

RIC plots are used to locate specific compounds in a chromatogram. A RIC plot of the top three or more mass fragments can help locate the peak of interest. Follow the instructions below to create a RIC plot.

**The NIST program uses the term peak instead of mass fragment. However, the terms are synonymous.**

Alternately, double-clicking on a mass in the **Scan** window will automatically insert the selected mass in the **Control Panel** table and display the RIC for the selected mass.

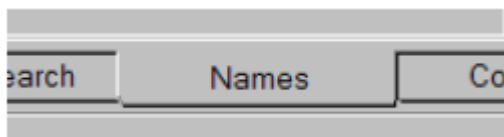
When the box in the **Control Panel** labeled **-RIC** is checked, the TIC/RIC window displays the TIC minus the RIC selected.

- 1 Either from the **System Setup** screen or the **Data Review** screen, double-click on the **NIST** icon.

NIST

NIST

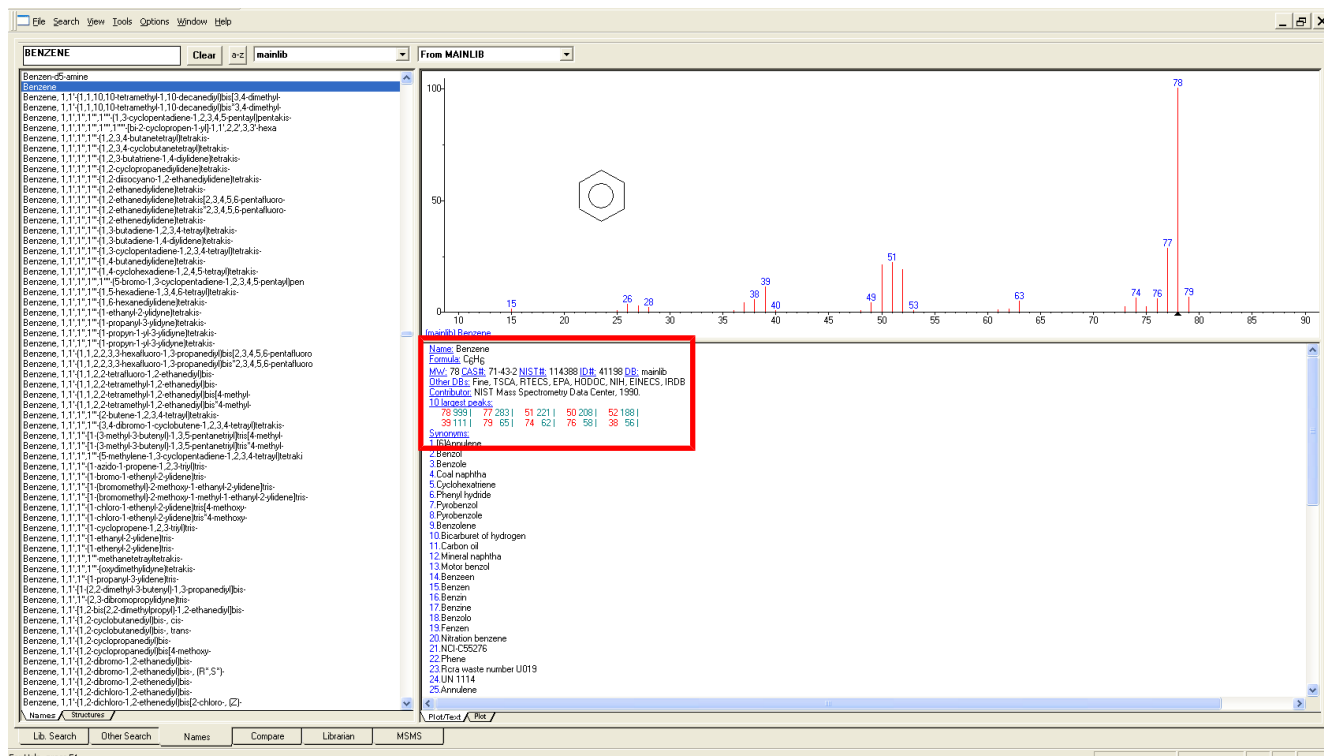
- 2 Click on the **Names** tab at the bottom of the NIST screen.



- 3 Enter the name of the compound in the box on the top left of the screen. (i.e., benzene).



- 4 In the bottom right box, the **10 Largest Peaks** is listed. Make a note of the three largest mass peaks that are between 45-300 amu.



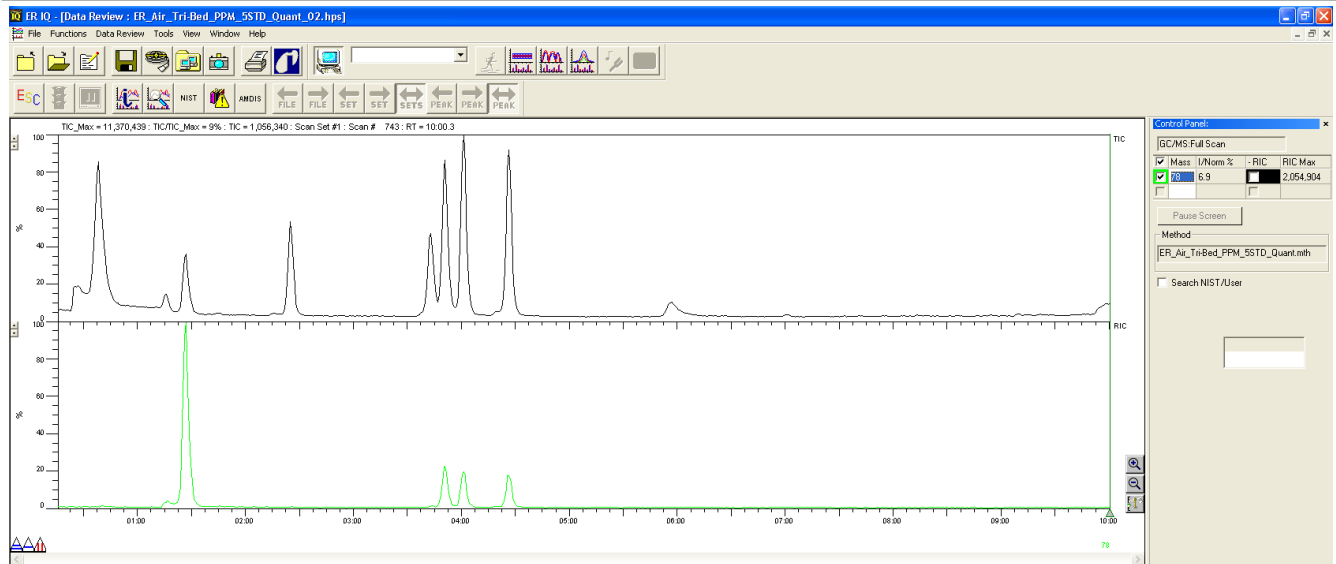
### 10 largest peaks:

78 999	77 283	51 221	50 208	52 188
39 111	79 65	74 62	76 58	38 56

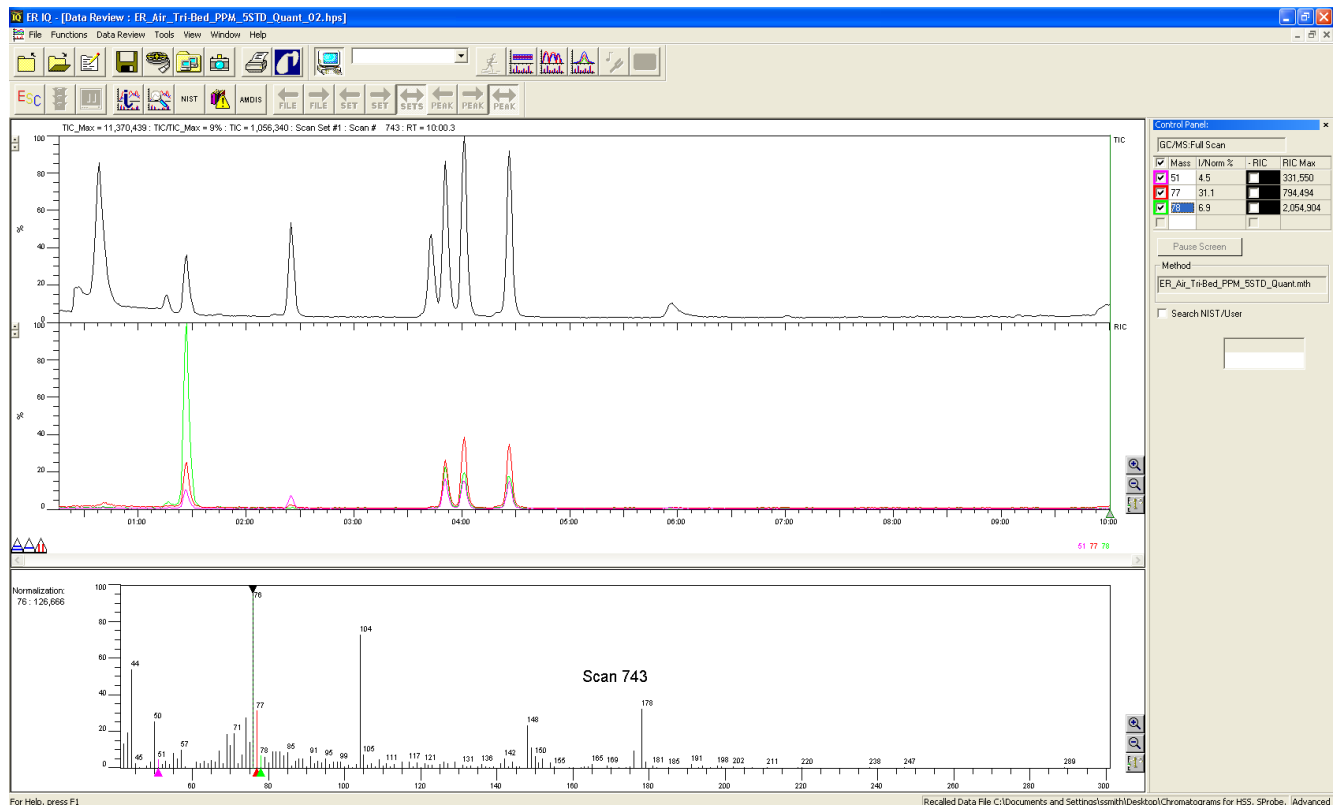
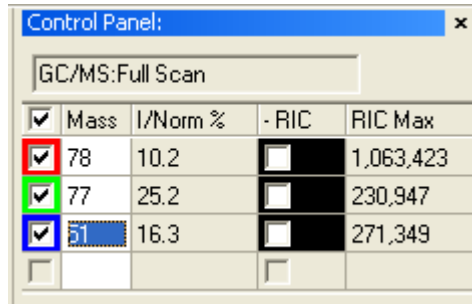


Peaks are listed in order from the largest to the smallest. For example, benzene's three largest peaks are masses 78, 77 and 51.

- Minimize the NIST window and return to the **Data Review** screen displaying the chromatogram.
- Enter the largest peak, 78 for benzene, into the **Control Panel** underneath the **Mass** column. Press **Enter**. The RIC plot is displayed underneath the TIC window. A new row will be created in the **Control Panel** for entering additional peaks.



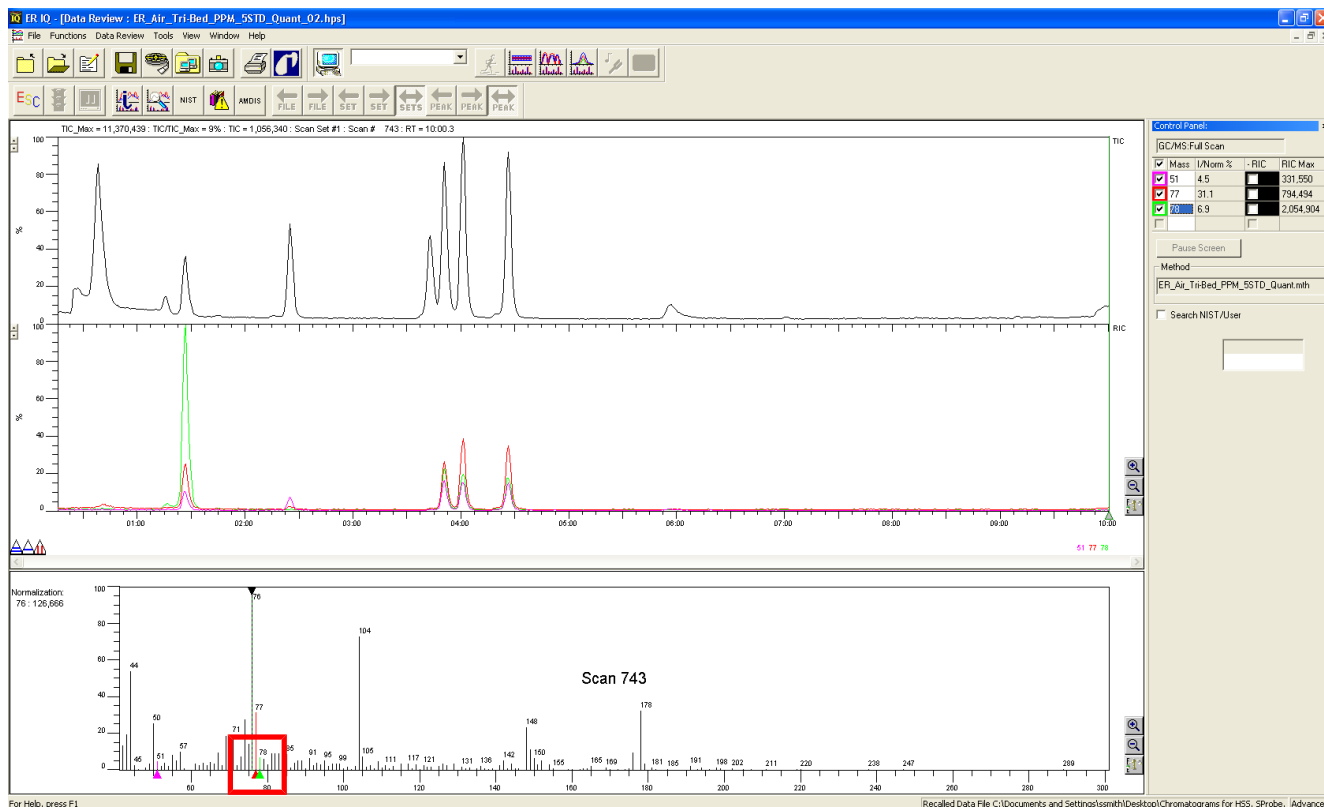
7 Enter the two or more remaining peaks into the **Control Panel**.



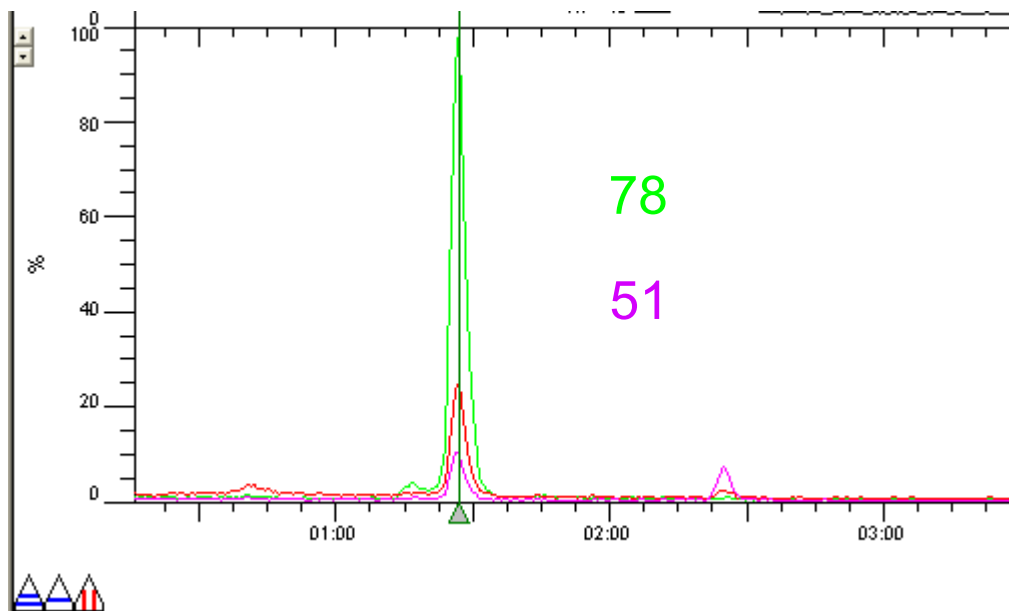


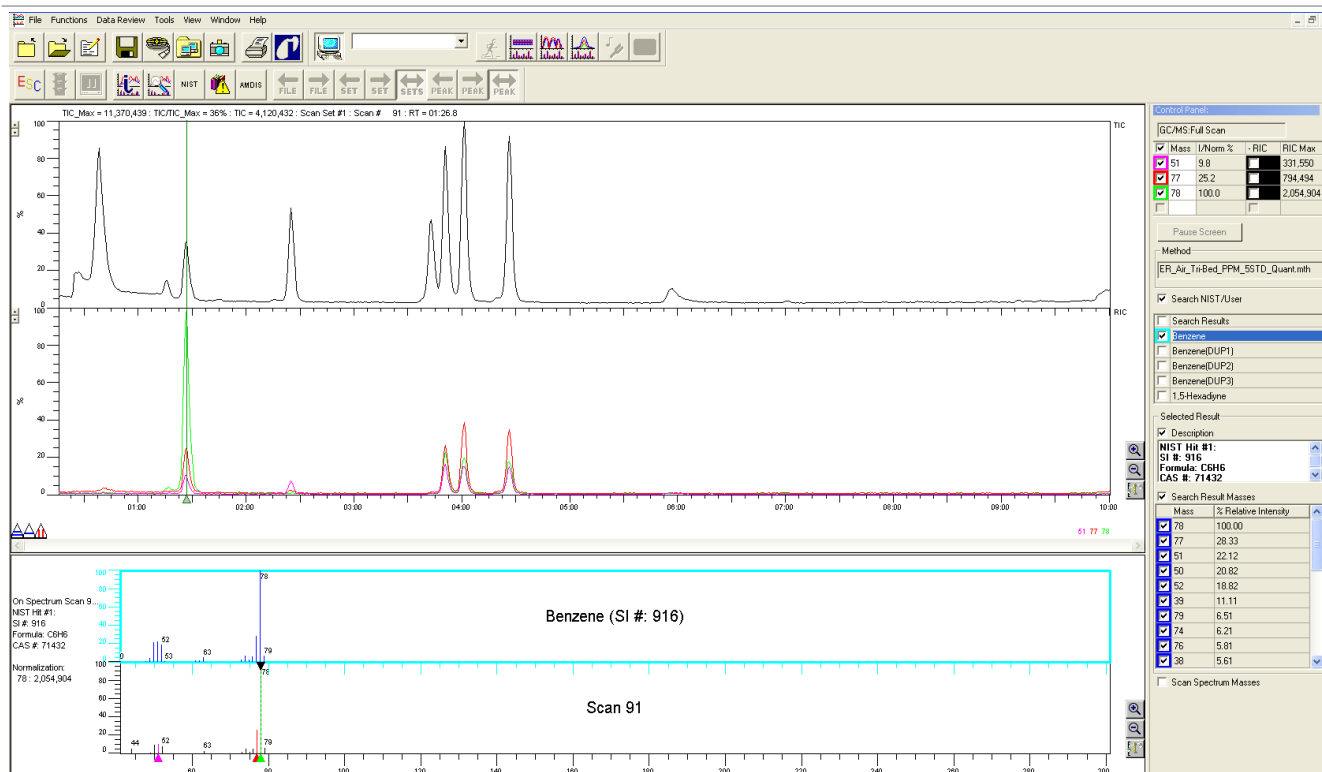
This RIC window can be closed by unchecking the masses selected in the **Control Panel**.

- 8 Alternately, click on the desired mass fragments in the **Spectrum** window to create a RIC plot.



- 9 The compound may be present in the unknown sample if all three peaks (mass fragments) align in the RIC plot. Use the **Search NIST/User** program to confirm identification of the suspected compound.





In this example, the largest peak (mass fragment) is 78, which is displayed in green. This is the highest RIC plot peak. The smallest peak was 51, which is displayed in pink. This is the lowest RIC plot peak.



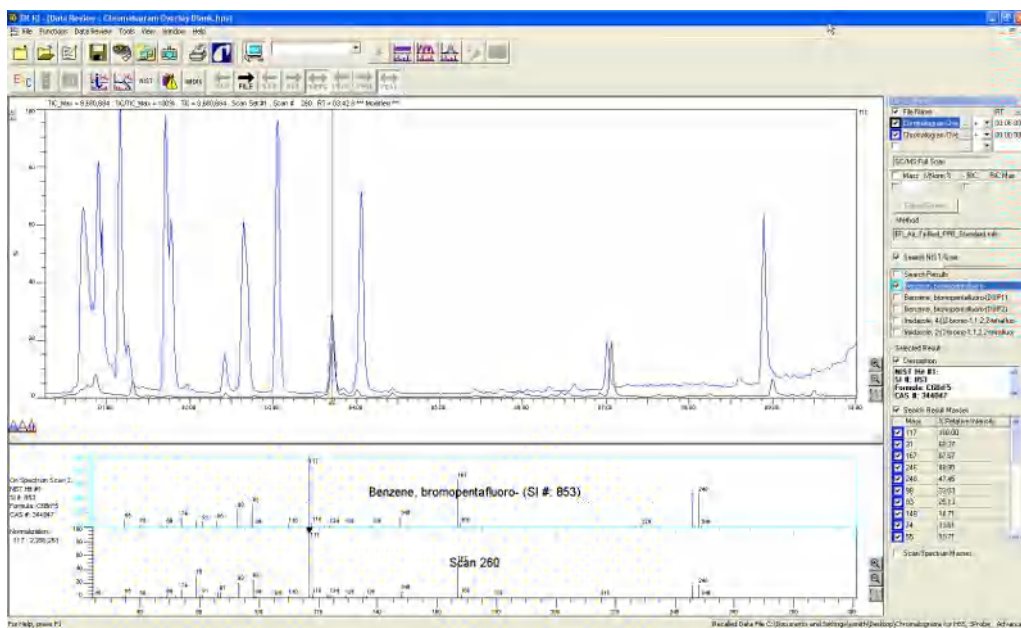
There may or may not be a peak present in the TIC window.

- 10 The compound was not detected in the sample if all three peaks (mass fragments) are not present or do not align in the RIC plot.

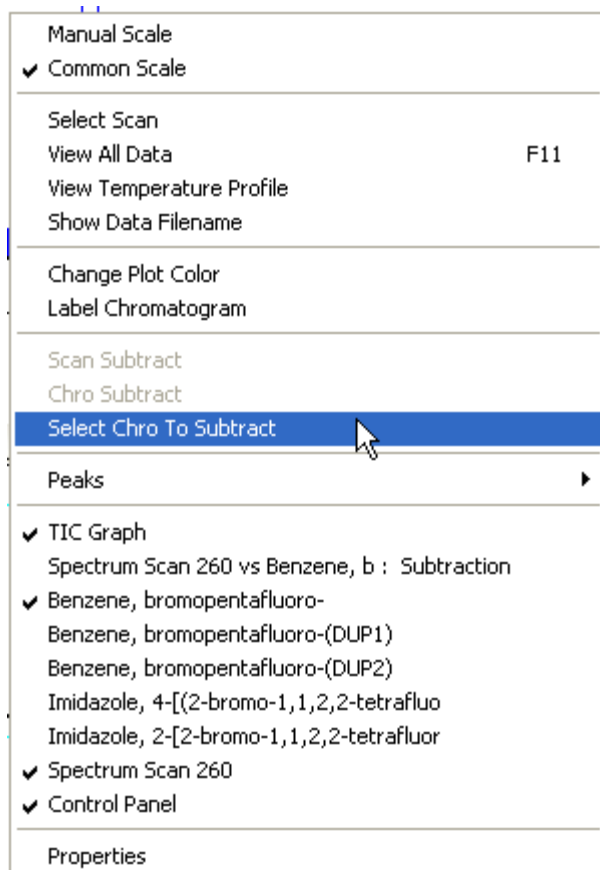
## 13.10 Chromatogram Subtract

This feature subtracts the TIC from one chromatogram from the TIC of another chromatogram. This is generally used to subtract the blank from the sample and verify the presence of a compound of concern.

- 1 Overlay the desired chromatograms by using Chromatogram Overlay. Refer to Chromatogram Overlay [▶ 203].
- 2 Select the peak for the desired compound. Record the TIC.

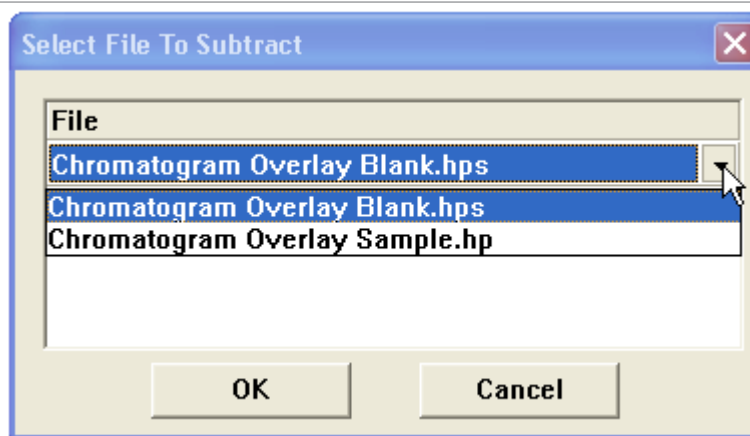


3 Right-click on the chromatogram. Click **Select Chro to Subtract**.

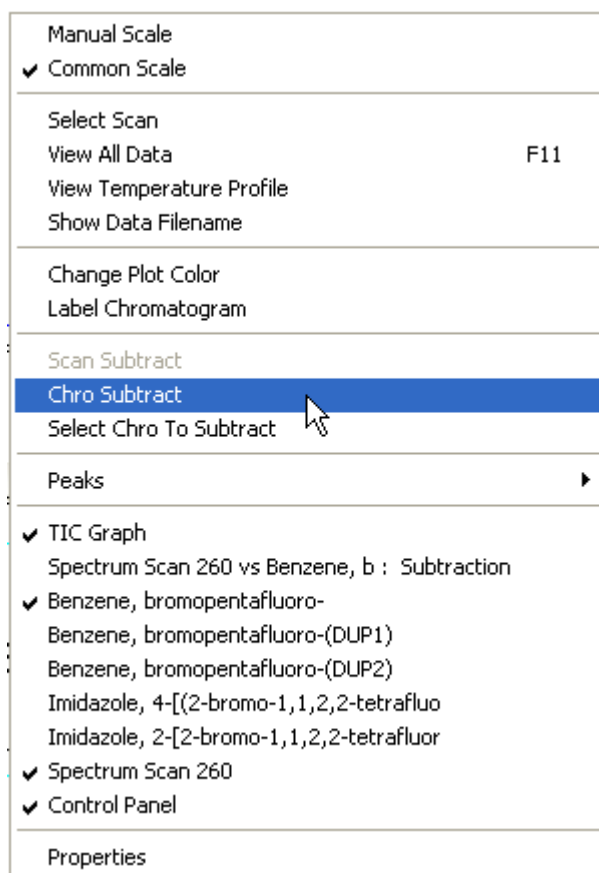


4 Select the desired file for subtraction from the drop-down menu. This will generally be the file for the blank.





- 5 Right-click on the chromatogram. Right-click on the chromatogram. Click **Select Chro to Subtract**.



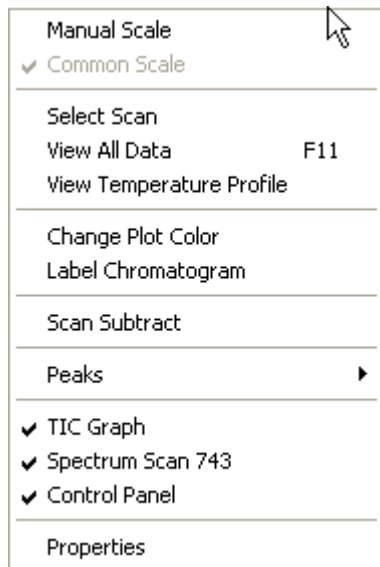
- 6 The desired chromatogram is subtracted. Note the new TIC of the selected peak.



## 13.11 Right-Click Menus Within Data Review

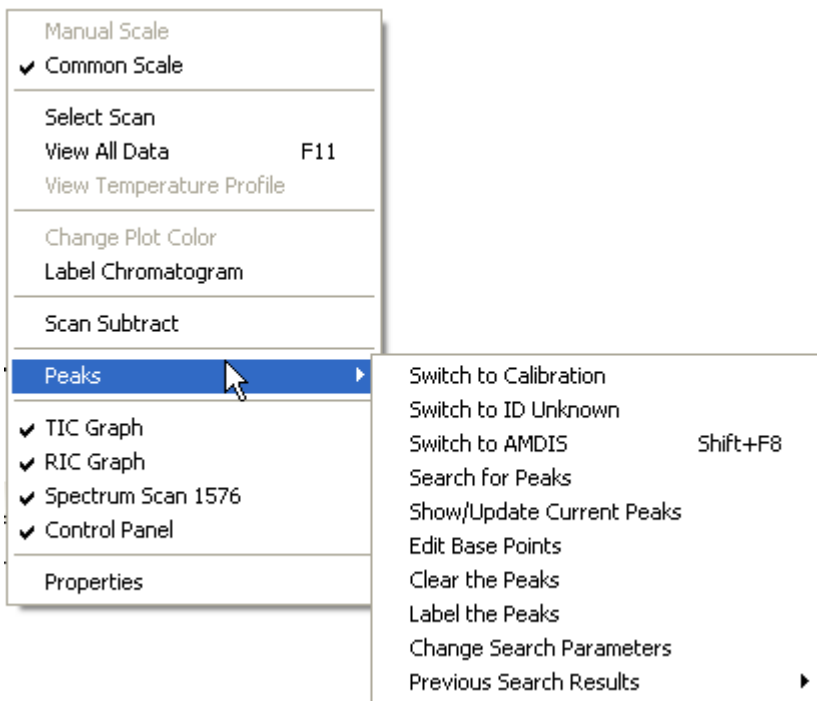
### 13.11.1 Right-Clicking in the TIC Window

The figure below shows the function available when right-clicking on the TIC window.



Common Scale	When checked, all RIC plots will be plotted to the same scale; when not checked all RIC plots will be individually scaled to 100%.
Select Scan	Allows the scan cursor to select a specific scan in order to view the desired mass spectrum.
View All Data	Rescales the plot to display the entire run. Also accessed by <b>F-11</b> .
View Temperature	Plots the GC temperature profile of the method.
Change Plot Color	Changes the color of the TIC plot.
Label Chromatogram	Displays a text box to label the chromatogram. The location of the label can be adjusted with the cursor and saved with the data file.
Scan Subtract	Subtracts the current scan from the displayed RIC plots.

## Peaks submenu

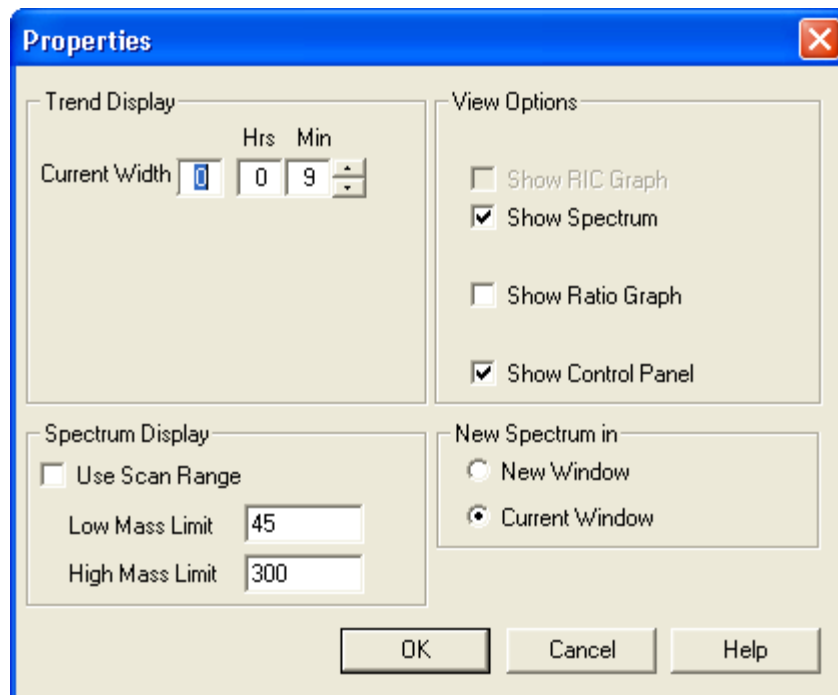


Switch to Calibration	Opens the <b>Calibrate</b> function. See Calibration [▶ 370].
Switch to ID Unknowns	Opens the <b>ID Unknowns</b> function. See ID Unknowns [▶ 395].
Switch to AMDIS	Opens the AMDIS program. Refer to Analyzing Data Using AMDIS [▶ 222].
Search for Peaks	Searches the chromatogram for peaks. Performs the same function as <b>Show/Update Current Peaks</b> . Refer to Show/Update Current Peaks [▶ 236].
Show/Update Current Peaks	Searches the chromatogram for peaks. Refer to Show/Update Current Peaks [▶ 236].
Edit Base Points	To move the base point, double-click on the desired new location for the base point. This function is used to manually reintegrate the peak.
Clear the Peaks	Clears the identification of peaks from the TIC graph after using <b>Search for Peaks</b> .
Label the Peaks	Labels identified peaks with retention time and area.
Change Search Parameters	Modifies current peak search parameters. See Setting Up a Quantitative Search [▶ 342].
Previous Search Results	View results from a previous search. (Drop-down menu of previously opened data files.)
TIC Graph	When checked, displays TIC window.
RIC Graph	When checked, displays the RIC window.

Spectrum Scan ###	When checked, displays <b>Spectrum</b> window for the current scan.
Control Panel	When checked, displays the <b>Control Panel</b> .
Properties	Allows access to the <b>Properties</b> of the display. See Properties Menu [▶ 269].

### 13.11.1.1 Properties Menu

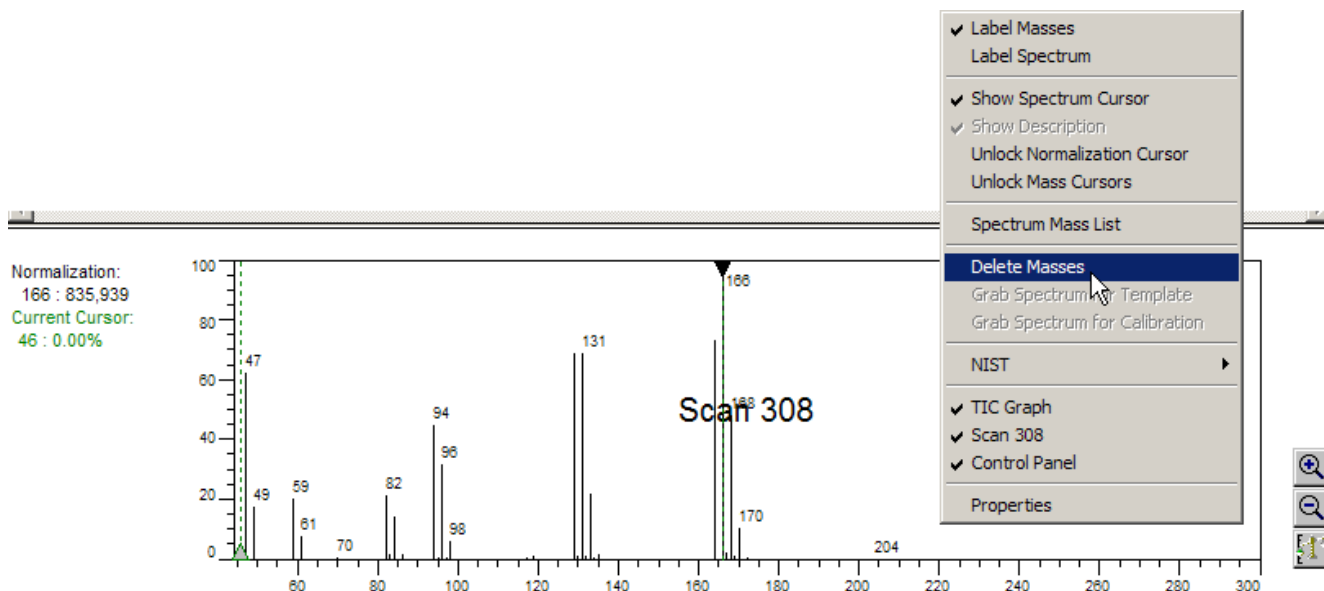
The **Properties** option displays the following options:



Current Width	The width of the graph can be set to the desired time point.
Show Spectrum	The <b>Spectrum</b> will be automatically displayed upon opening a data file when this box is checked.
Show Control Panel	The <b>Control Panel</b> will be automatically displayed upon opening a data file when this box is checked.
Use Scan Range	The masses for the scan range of the method will be displayed.
Low Mass Limit	HAPSITE ER will display masses in the spectrum above this limit.
High Mass Limit	HAPSITE ER will display masses in the spectrum below this limit.

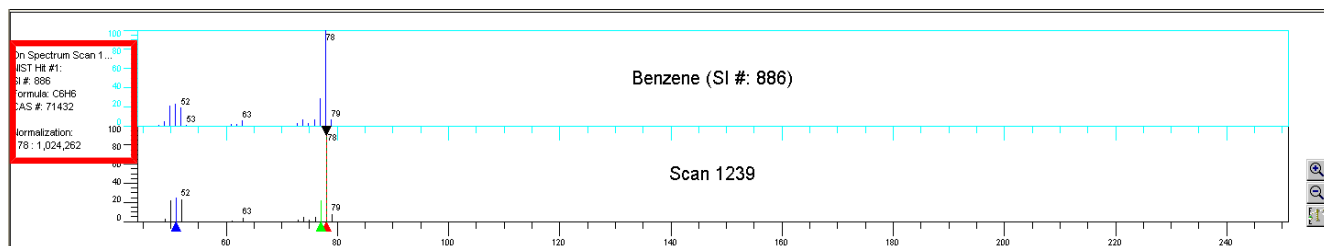
### 13.11.2 Spectrum Window

Right-clicking in the Spectrum window accesses the menu shown in the figure below.



Label Masses	When checked, it displays the atomic weight of the mass fragments in the <b>Spectrum</b> window.
Label Spectrum	Displays a text box in order to manually label the spectrum.
Show Spectrum Cursor	Displays the spectrum cursor in the spectrum window.
Show Description	This displays the SI number, the NIST hit number, the formula, CAS number and the normalization number next to the spectrum.

Show description is only active if Search NIST/User is selected.

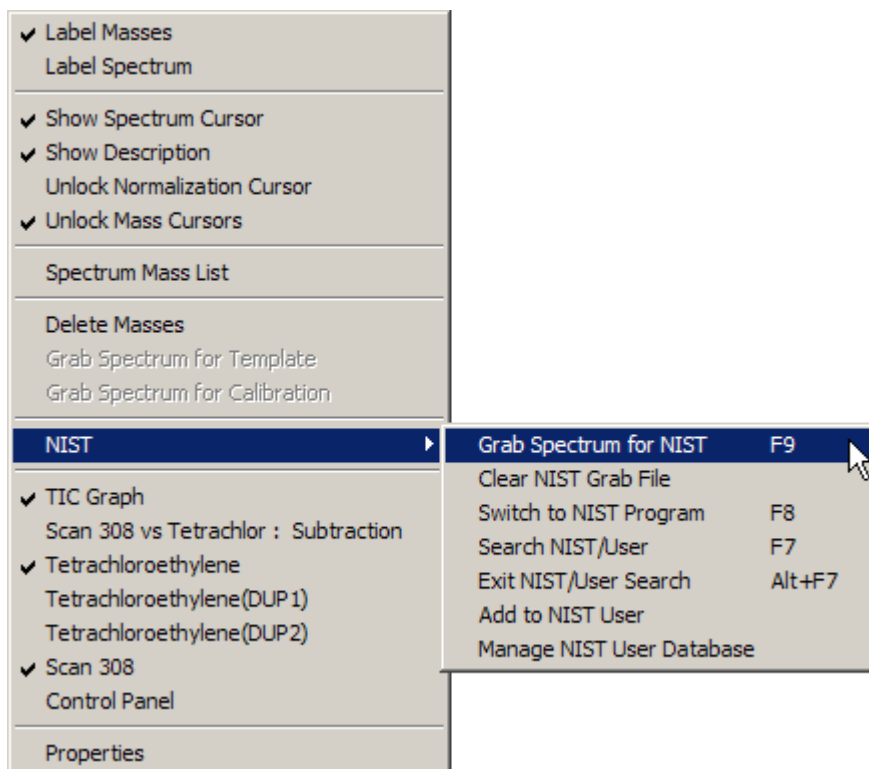


Unlock Normalization Cursor	Must be unlocked to move the normalization cursor to a mass other than the largest mass fragment.
Unlock Mass Cursors	Unlocks the mass cursors to reassign a new color to the mass fragment when using RIC plots.
Spectrum Mass List	Displays a report of all the masses in the spectrum.

Delete Masses	Deletes masses from the mass spectrum display to manually subtract the background. (Does not delete data.)
Grab Spectrum for Template	Used for Quantitative methods. See Calibration [ ▶ 370].
Grab Spectrum for Calibration	Used for Quantitative methods. See Calibration [ ▶ 370].
NIST	Allows the analyst to utilize the NIST database for qualitative identification of the displayed spectrum. Refer to Analyzing Data Using NIST [ ▶ 271].
TIC Graph	When checked, displays TIC window.
Spectrum Scan ###	When checked, displays the Spectrum window.
Control Panel	When checked, displays the Control Panel.
Properties	Accesses display properties.

### 13.11.3 Analyzing Data Using NIST

By right-clicking on the **Spectrum** window, the NIST menu is displayed.

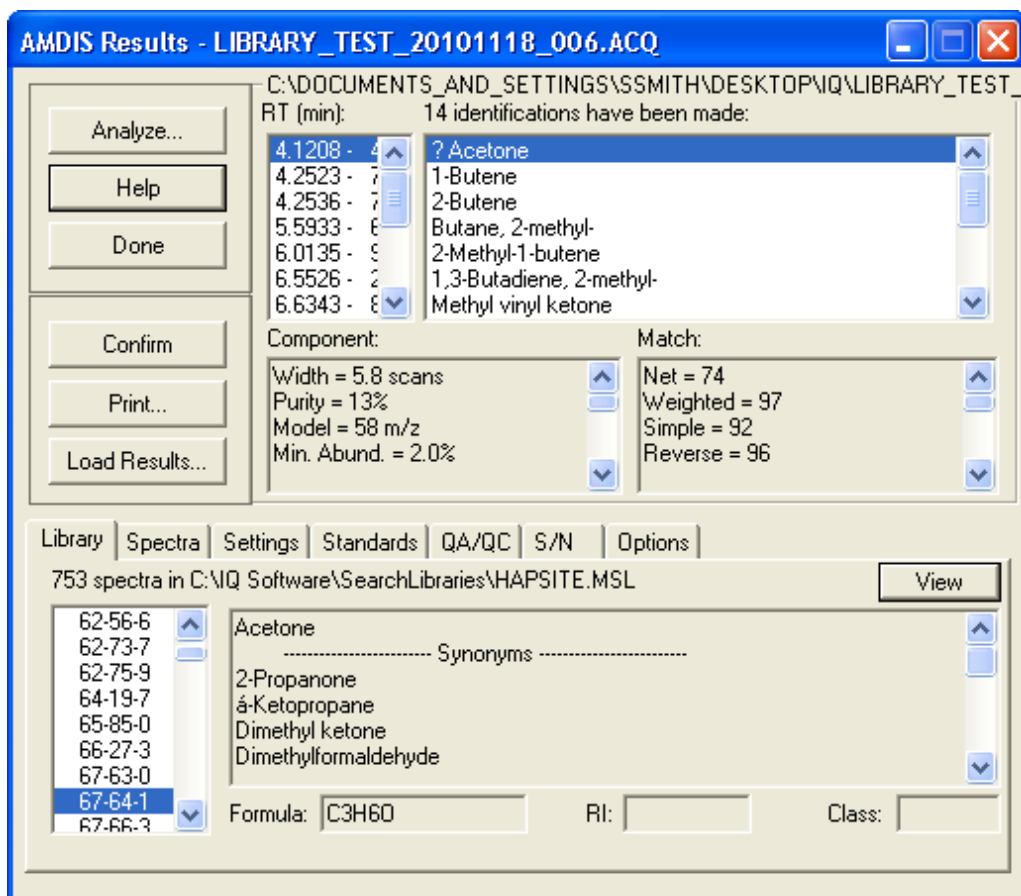


Grab Spectrum for NIST (F9)	This function will select a file to be exported into the NIST database program.
Clear NIST Grab file	Clears the list of previously selected files.
Switch to NIST Program (F8)	Starts the NIST database program and will export any selected files to NIST database program.

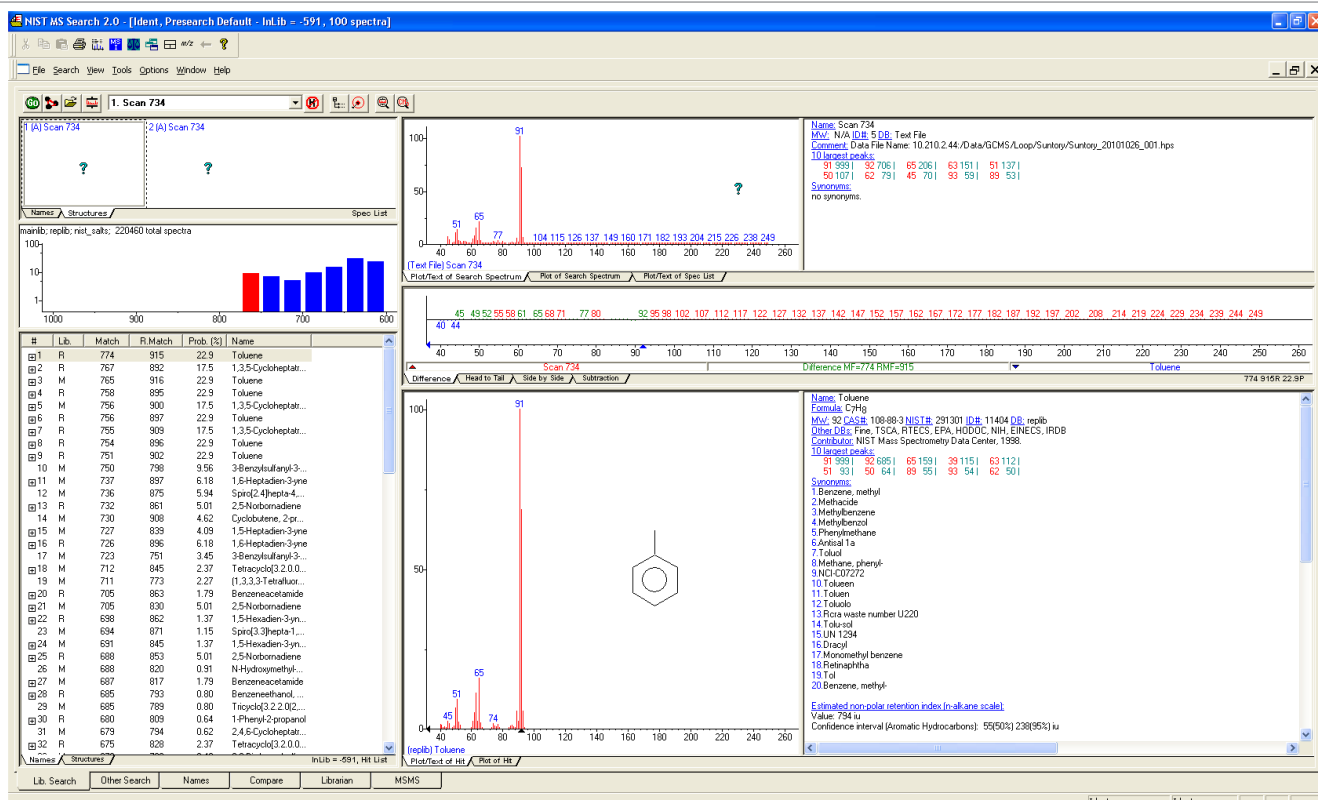
Search for NIST/Uder (F7)	Starts the NIST Library search. Refer to NIST Library Searches [ 230].
Exit Search NIST/User (Alt+F7)	Exits the <b>Search NIST/User</b> Library search function.
Add to NIST User	Adds selected spectrum to the <b>Search NIST/User</b> Library.
Manage NIST User Database	Displays, deletes or plots entries in a <b>Search NIST/User</b> Library.

### 13.11.4 NIST Database Program

The NIST database program is third-party software that is included with the HAPSITE ER. Instructions for using the software are located by selecting **HELP** from the Menu selection in either the AMDIS or NIST program.



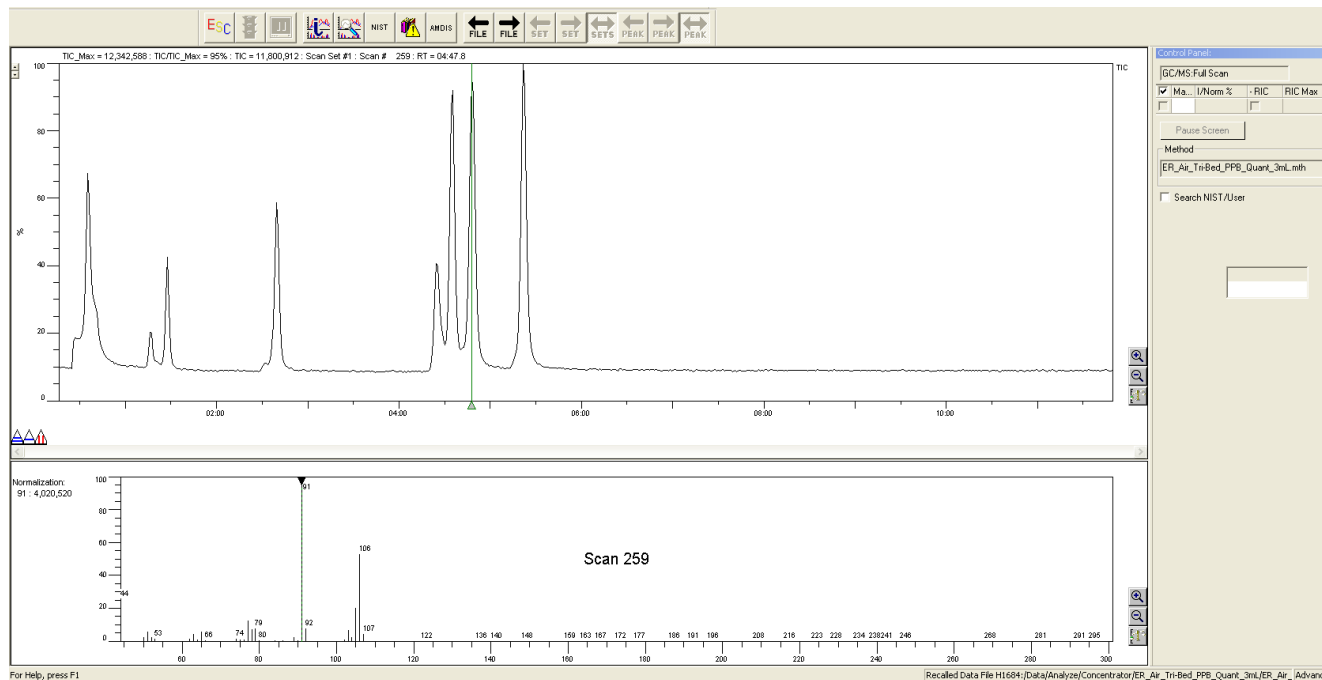




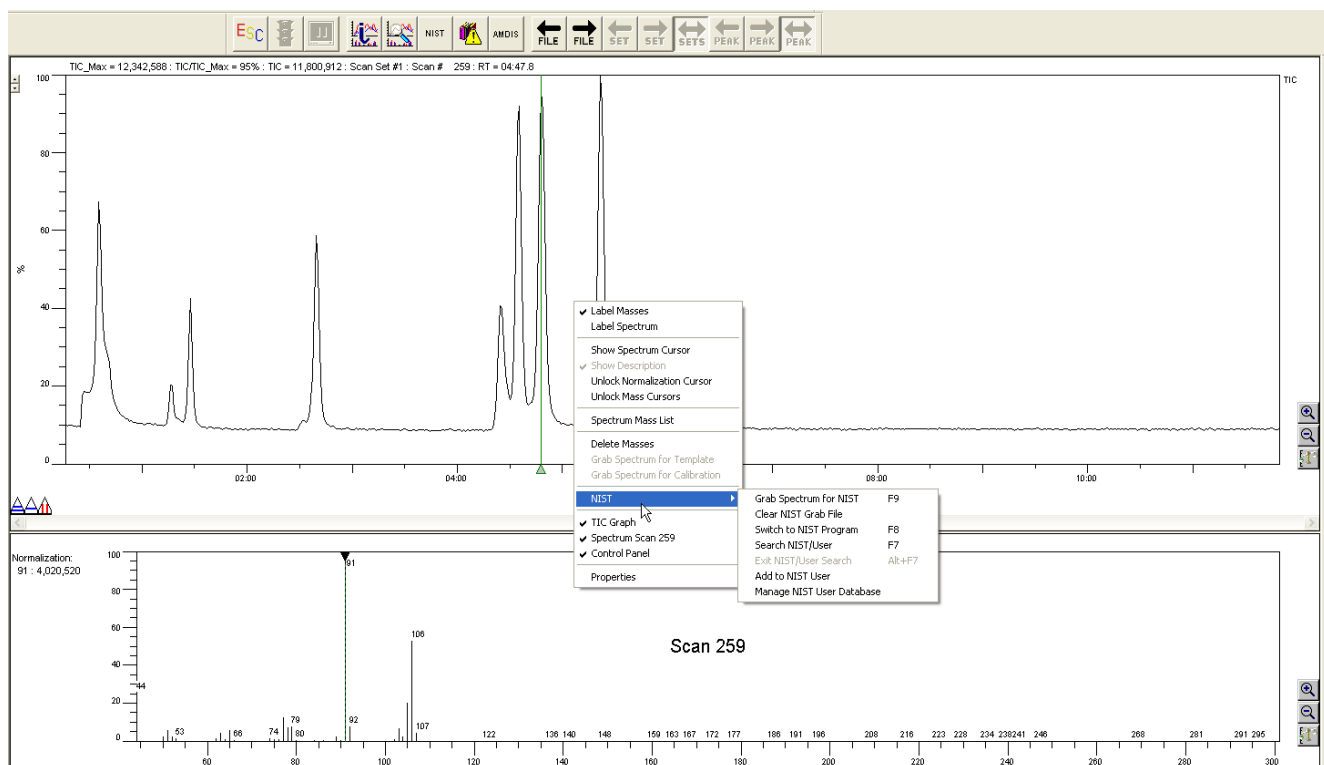
### 13.11.5 Grab Spectra for NIST

To export the spectrum to the NIST database:

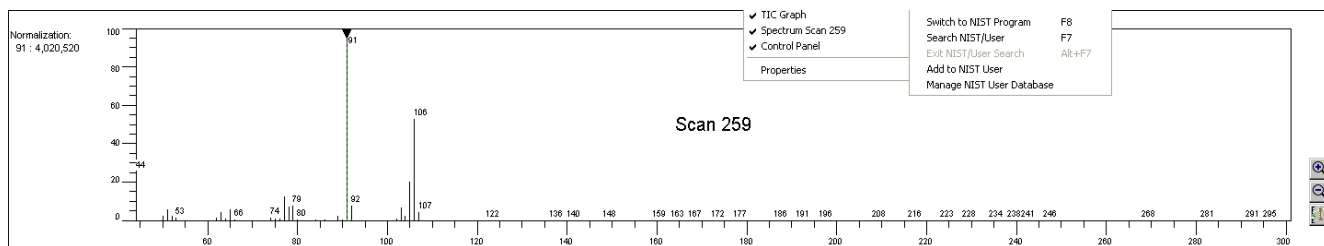
- 1 Double-click on the desired peak in the TIC/RIC window.



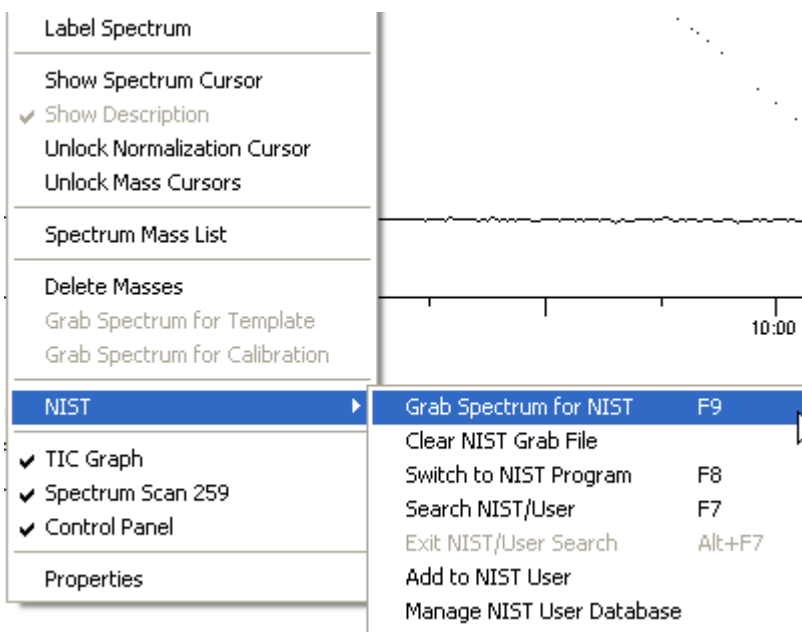
- 2 Place the cursor in the Spectrum window and right-click.



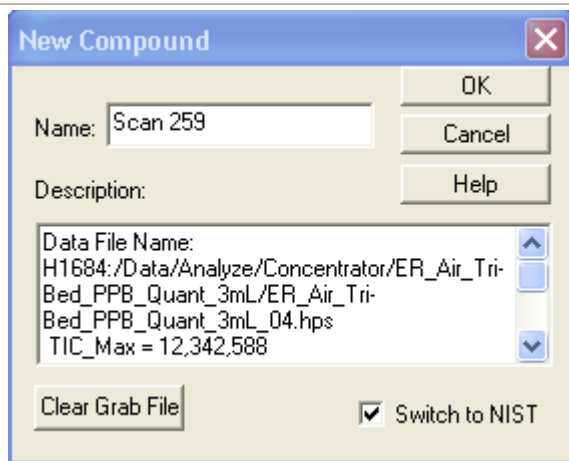
**3 Select NIST.**



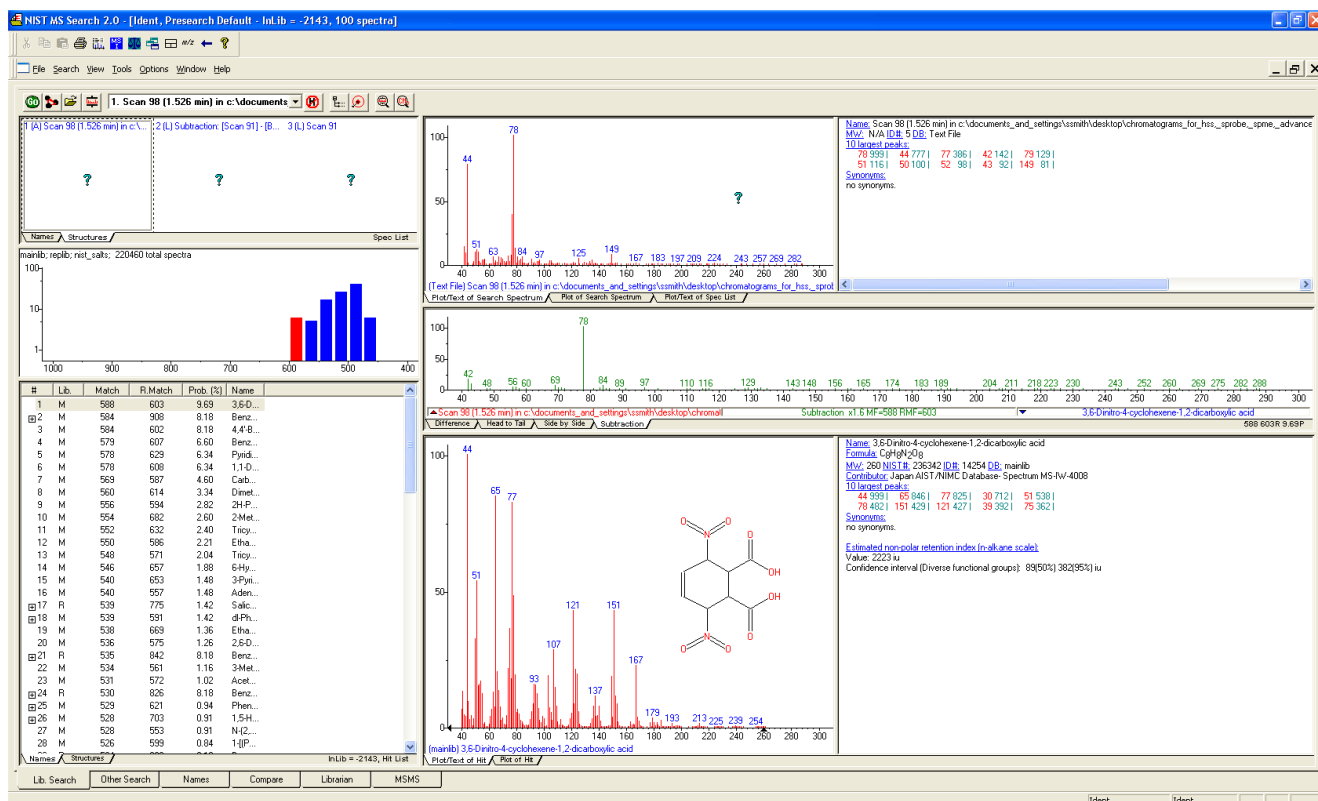
**4 Click Grab Spectrum for NIST.**



**5 Click Switch to NIST Program.**



6 The identification is displayed on the screen.



# 14 Tune

## 14.1 Introduction to AutoTune and Manual Tune

The tune of a Mass Spectrometer (MS) determines the quality of the mass spectrum produced by the system. The MS performance will run an autotune upon start-up and after 12 hours of continuous operation. Tuning is normally accomplished by the AutoTune program, which automatically sets and adjust all parameters, however, the user can set the parameters by manual tuning.

HAPSITE ER uses two gas internal standards which contain mass fragments that span the mass range of interest. The internal standards are:

- 1,3,5-Tris (trifluoromethyl) benzene
- Bromopentafluorobenzene

## 14.2 AutoTune

AutoTune can be started from the front panel or from the laptop.

### 14.2.1 Starting AutoTune from the Manual Tune Screen or Laptop Computer

- 1 Double-click on the **ER IQ** icon.



- 2 Double-click on the **Tune** icon.



Tune



**Manual Tune** is an advanced user function. Refer to Set Access Level [▶ 168] for instructions on changing access levels.

- 3 Wait until the **EM and Emission** buttons on the **Control Panel** turn green. Click the **Tune** icon.

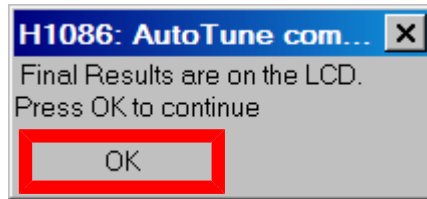




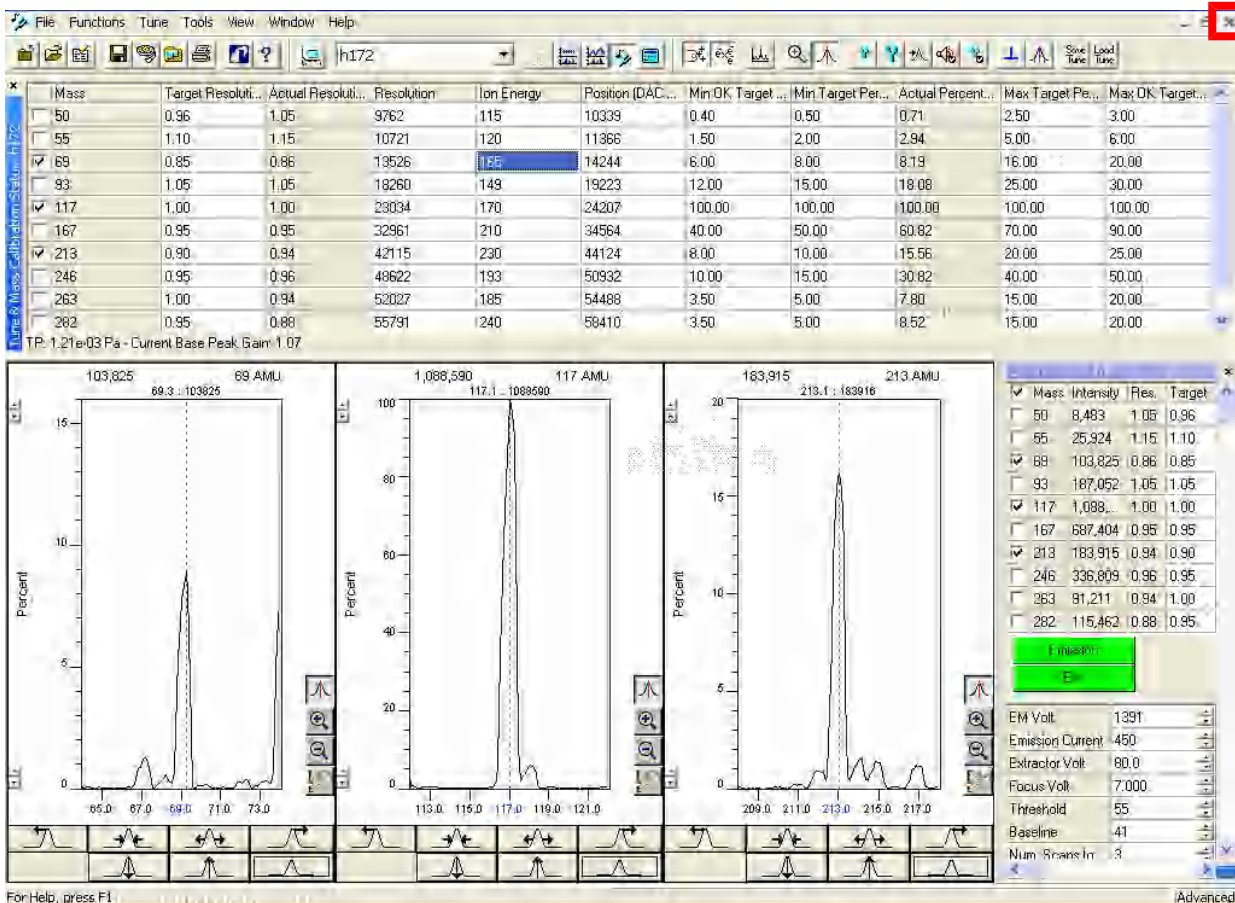
**CAUTION**

Adjusting other parameters without proper training may damage the instrument.

- 4 Allow HAPSITE ER to AutoTune. When AutoTune is finished, the message **Final Results are on the LCD** are displayed. Click **OK**.



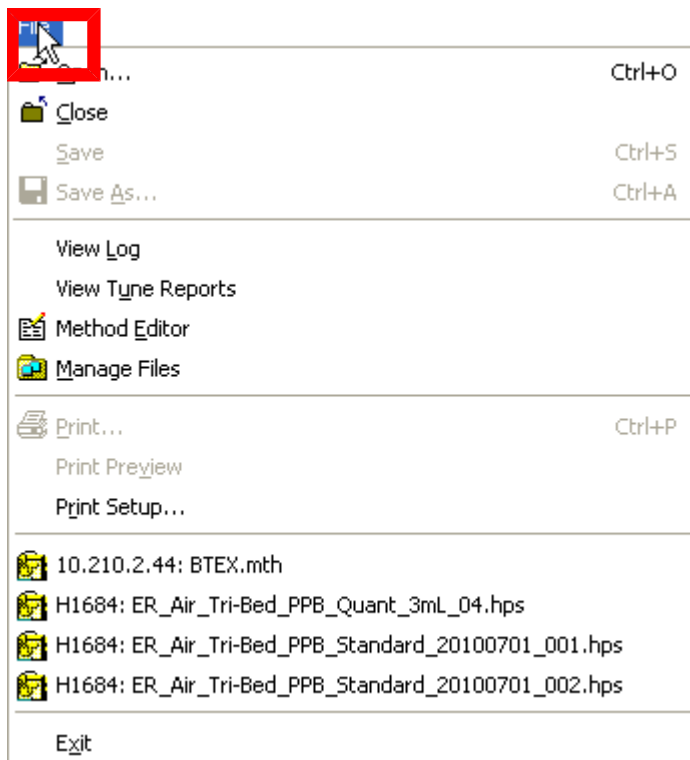
- 5 Close the manual tune screen by clicking the X on the top right corner.



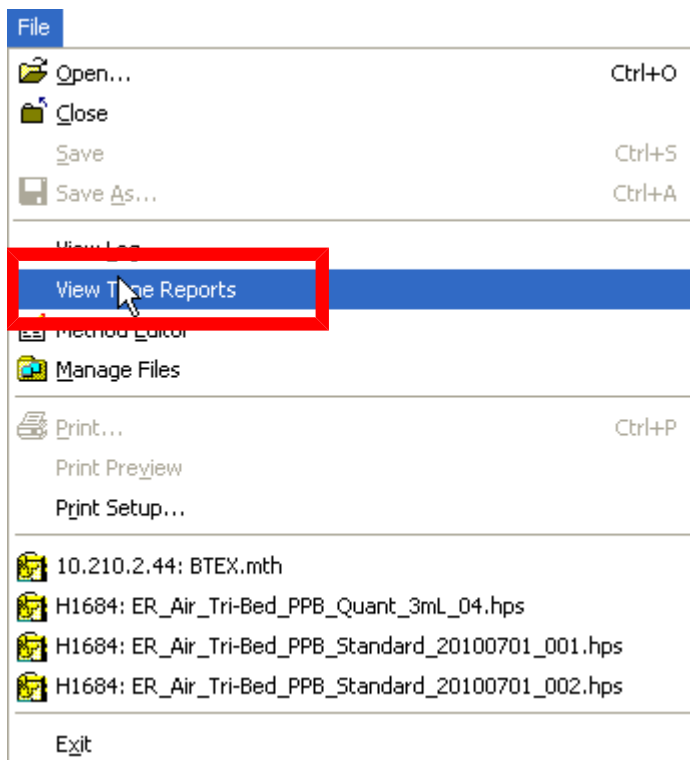
### 14.3 Viewing a Tune Report

The most current tune report can be viewed from the front panel display or from the laptop. Past tune reports can be viewed from the laptop.

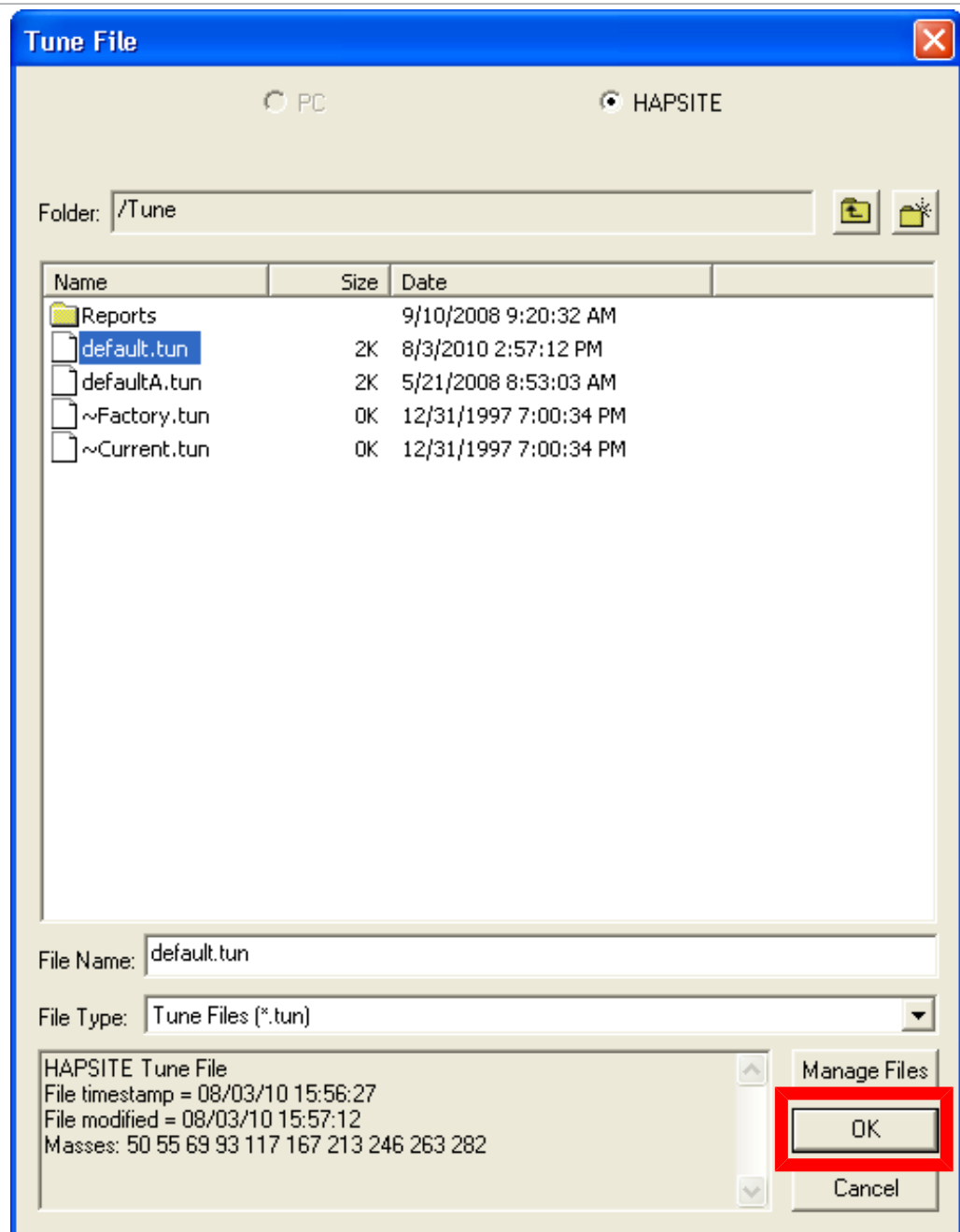
- 1 To view the report from the laptop computer, select **File**.



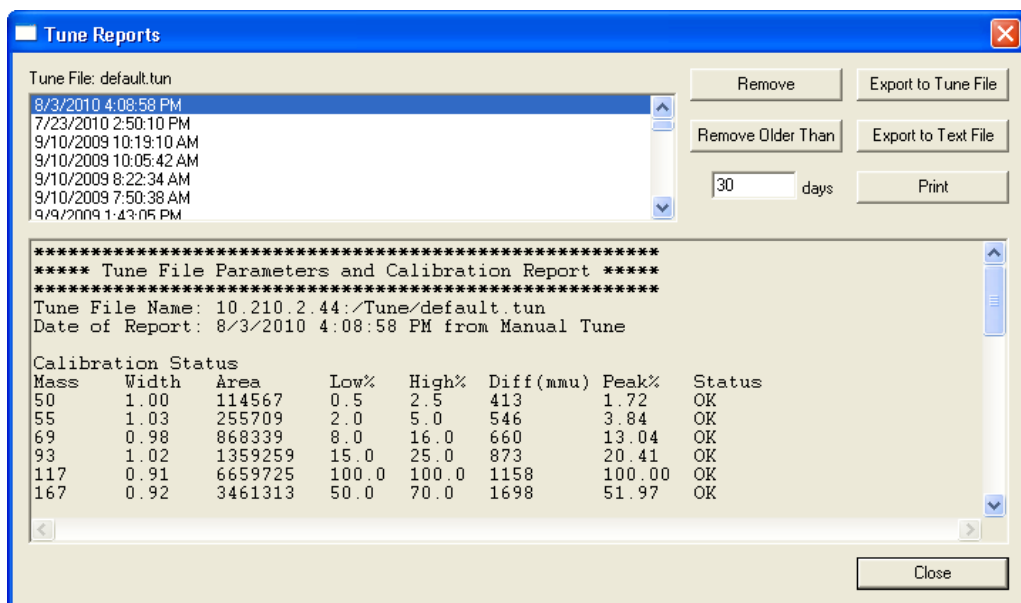
2 Select **View Tune Reports** from the drop-down menu.



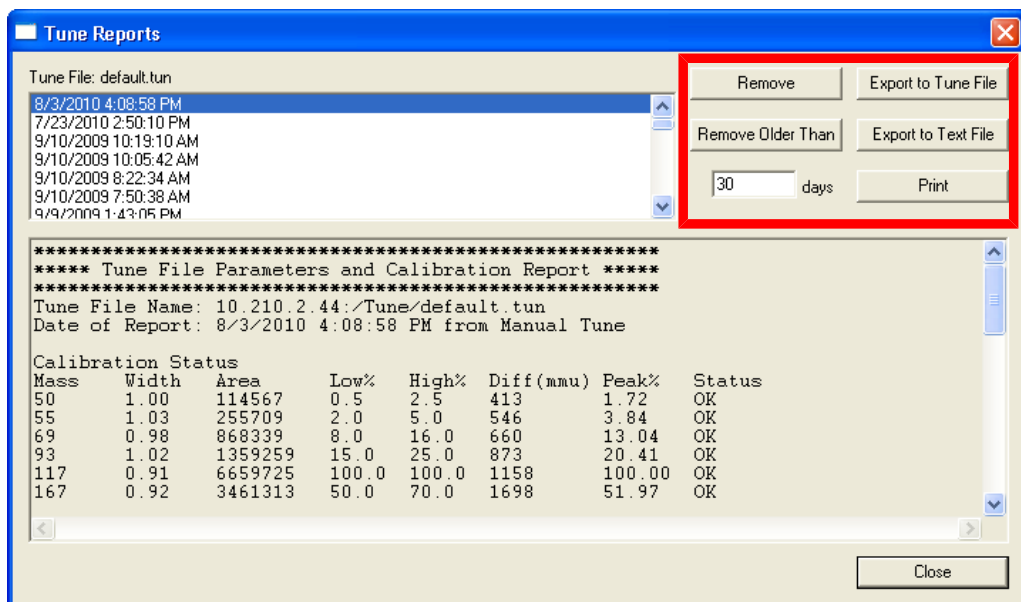
3 Highlight the `default.tun` file and press **OK**.



- 4 The **Tune Reports** are displayed. **Tune Reports** are stored, by default, for 30 days.



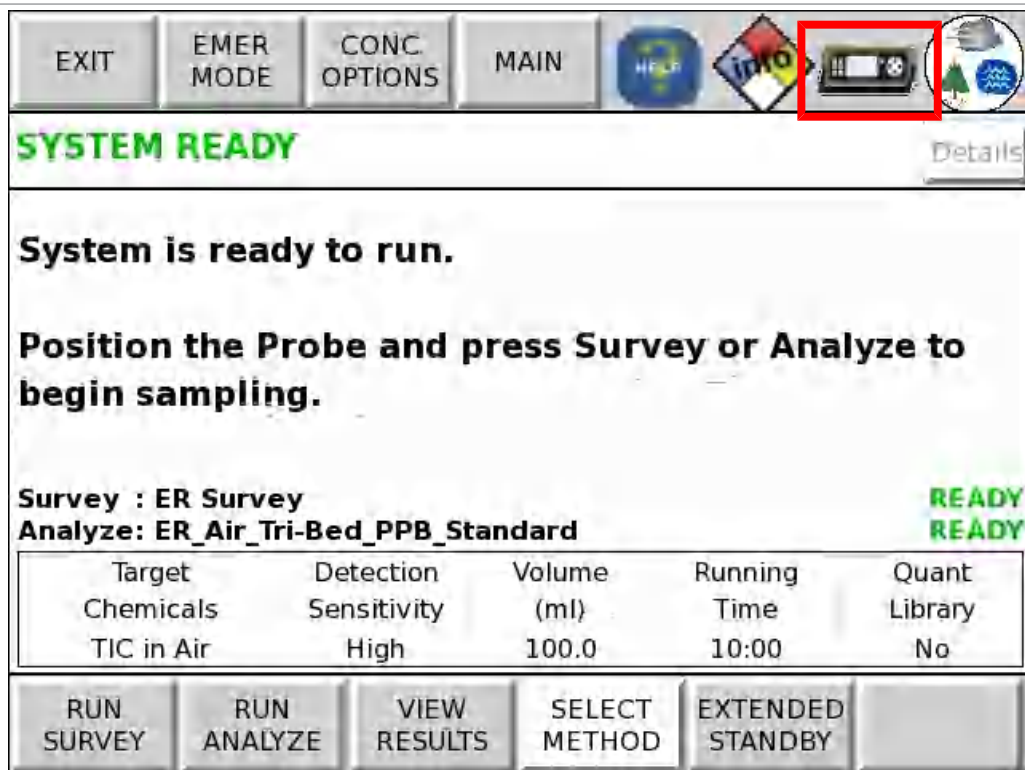
### 14.3.1 Tune Report Options



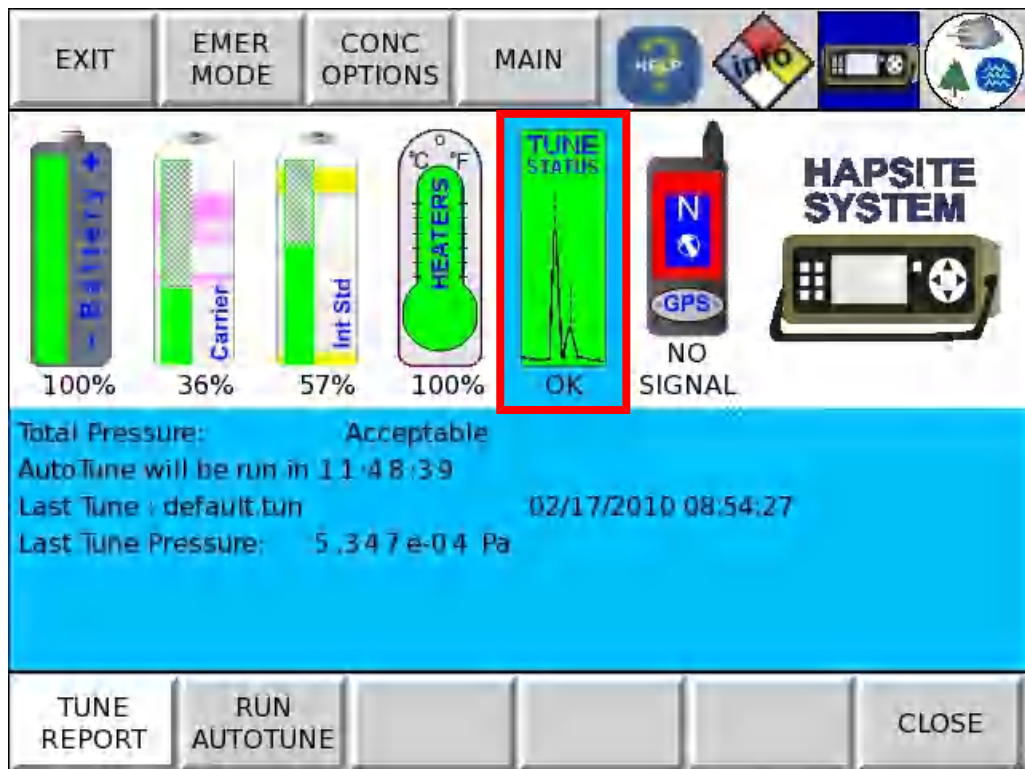
Remove	Deletes the selected report. <b>No confirmation is requested.</b>
Remove Older Than	Deletes files older than the number of days specified. Confirmation is requested before the files are deleted.
Export to Text File	Creates a text file of the tune report.
Print	Prints the selected tune report.

- 1 To view the **Tune Report** from the front panel display, touch the HAPSITE ER icon or push the **SYSTEM STAT** button until the HAPSITE ER icon is highlighted.

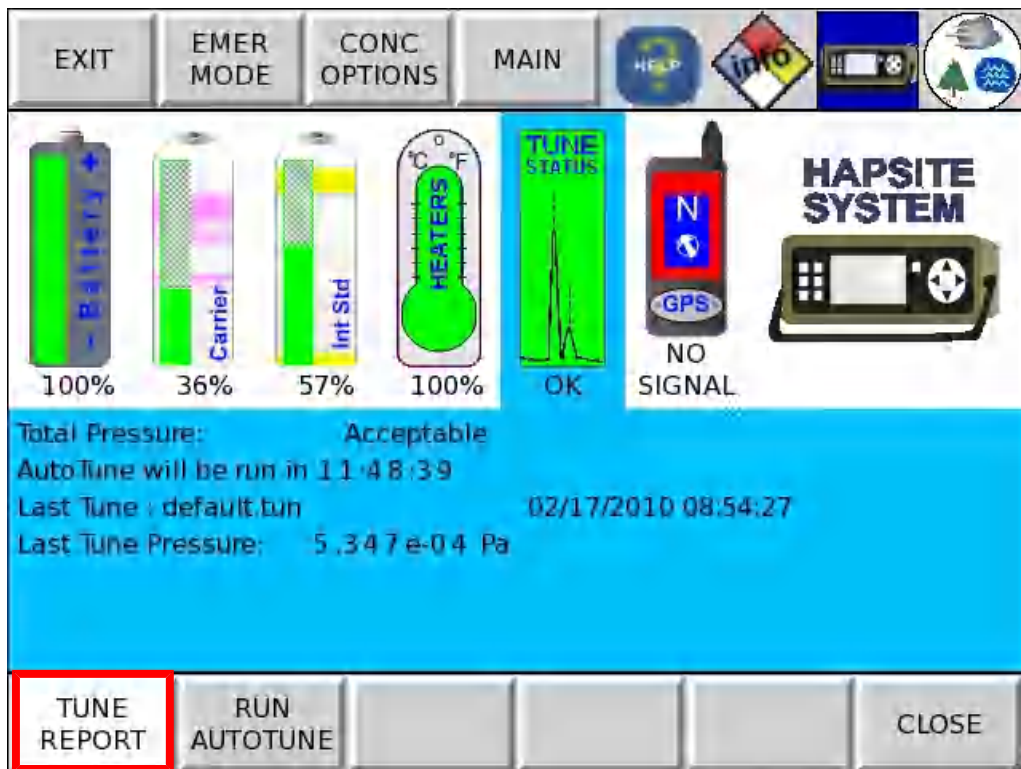




2 Touch the **TUNE** icon.



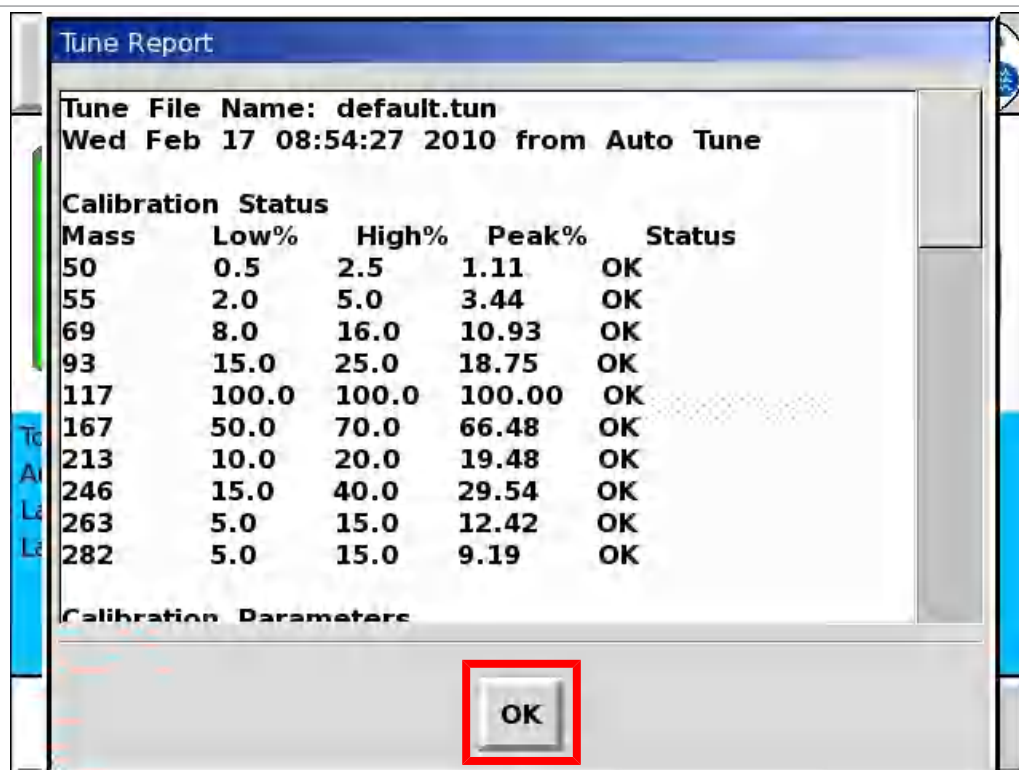
3 Touch the **TUNE REPORT** button or use the arrow keys to highlight the **TUNE REPORT** button. The last tune report is displayed.



4 To scroll through the tune report, use up or down arrows keys.



5 Touch OK or push OK SEL to exit the screen.



## 14.4 Performing Manual Tune

Manual tunes are a standard routine maintenance practice for HAPSITE ER and should be performed once every 4 to 6 months to maintain optimal performance of the unit's mass spectrometer.

Routine manual tunes will improve the accuracy of compound identifications, and provide indications of the health of the mass spectrometer.

The following procedure outlines the steps in manually tuning HAPSITE ER. If performing this task for the first time, we recommend contacting INFICON directly for support.

### 14.4.1 Manual Tune Variables

The goal of Manual Tune is to adjust the inputs, such that the outputs fall within appropriate ranges.

- Instrument Outputs:**
- Base Peak Gain(BPG)
  - Ion Percentages
  - Status Column

- Primary User Inputs/  
Editable**
- Ion Resolutions
  - Ion Energies
  - EM Voltage

- Secondary Inputs/ Editables**
- Focus Voltage
  - Emission Current
  - Baseline + Threshold

### 14.4.2 \*Outputs

**Base Peak Gain** BPG influences sensitivity.

- (BPG)**
- HAPSITE ER ideal setting is 0.5 (range is 0.4 to 0.6)

Mass	Target Re...	Actual Res...	Resolution	Ion Energy	Position (DA...	Min OK Tar...	Min Target P...	Actual Perce...	Max Target P...	Max OK Targ...
<input type="checkbox"/> 50	0.90	0.92	9678	99	10591	0.40	0.50	0.77	2.50	3.00
<input type="checkbox"/> 55	0.90	0.89	10660	100	11650	1.50	2.00	2.01	5.00	6.00
<input checked="" type="checkbox"/> 69	0.85	0.86	13419	112	14622	6.00	8.00	6.37	16.00	20.00
<input type="checkbox"/> 93	0.90	0.92	18160	118	19745	12.00	15.00	13.05	25.00	30.00
<input checked="" type="checkbox"/> 117	1.10	1.08	22868	140	24849	100.00	100.00	100.00	100.00	100.00
<input type="checkbox"/> 167	0.95	0.98	32767	177	35498	40.00	50.00	35.61	70.00	90.00
<input checked="" type="checkbox"/> 213	1.05	1.08	41851	207	45293	8.00	10.00	9.74	20.00	25.00
<input type="checkbox"/> 246	0.90	0.94	48367	220	52289	10.00	15.00	17.98	40.00	50.00
<input type="checkbox"/> 263	1.10	1.08	51740	248	55937	3.50	5.00	6.74	15.00	20.00
<input type="checkbox"/> 282	1.15	1.21	55481	255	59980	3.50	5.00	5.87	15.00	20.00

- Current Base Peak Gain: 0.32 (Low)

**Ion Percentages** Actual Percentages are listed in the Mass Calibration table, outlined in red. The range of acceptable values is presented in the 4 adjacent columns, outlined in blue in the figure below.

**Example:** The percentage of mass 50, first row, should fall within 0.5 to 2.5%, and must fall within 0.4 to 3.0%, for the mass spec to be properly calibrated.

Mass	Target Re...	Actual Res...	Resolution	Ion Energy	Position (DA...	Min OK Tar...	Min Target P	Actual Perce.	Max Target P...	Max OK Targ..
<input type="checkbox"/> 50	0.90	0.92	9678	99	10591	0.40	0.50	0.77	2.50	3.00
<input type="checkbox"/> 55	0.90	0.89	10660	100	11650	1.50	2.00	2.01	5.00	6.00
<input checked="" type="checkbox"/> 69	0.85	0.86	13419	112	14622	6.00	8.00	6.37	16.00	20.00
<input type="checkbox"/> 93	0.90	0.92	18160	118	19745	12.00	15.00	13.05	25.00	30.00
<input checked="" type="checkbox"/> 117	1.10	1.08	22868	140	24849	100.00	100.00	100.00	100.00	100.00
<input type="checkbox"/> 167	0.95	0.98	32767	177	35498	40.00	50.00	35.61	70.00	90.00
<input checked="" type="checkbox"/> 213	1.05	1.08	41851	207	45293	8.00	10.00	9.74	20.00	25.00
<input type="checkbox"/> 246	0.90	0.94	48367	220	52289	10.00	15.00	17.98	40.00	50.00
<input type="checkbox"/> 263	1.10	1.08	51740	248	55937	3.50	5.00	6.74	15.00	20.00
<input type="checkbox"/> 282	1.15	1.21	55481	255	59980	3.50	5.00	5.87	15.00	20.00

- Current Base Peak Gain: 0.32 (Low)

Boxes shaded with red, like those shown in the figure above, indicate that the actual percentage is outside that range for that fragment (row). For example, in the third row of the table above for mass 69, the actual percentage is 6.37 when it should fall above 8.00. Here, mass 69 requires adjustment of the Resolution and/or Ion Energy to correct the Actual Percentage.

**Status Column** The Status Column provides categorical view of the actual percentages. The values **OK, OK Low, OK High, Low** or **High** indicate whether the actual percentage for that ion are within best range (OK) or outside (Low or High). Values of High or Low are not acceptable. Adjust the corresponding mass fragments.

### 14.4.3 \*Inputs

**Target Resolution** Resolution refers to the width of the measured mass peak in amu. The range for the Target Resolution is 0.85 and 1.10. Adjusting Resolution influences the Actual Percentages.

Mass	Target Res.	Actual Res.	Resolution	Ion Energy	Position (DA)	Min DK Tar.	Min Target P.	Actual Perc.	Max Target P.	Max DK. Targ.
50	0.90	0.93	978	99	10591	0.40	0.50	1.21	2.50	3.00
55	0.90	0.89	10660	100	11650	1.50	2.00	3.19	5.00	6.00
69	0.95	0.98	1405	112	14622	6.00	8.00	14.17	16.00	20.00
93	0.90	0.91	1160	118	19745	12.00	15.00	20.61	25.00	30.00
117	0.90	0.93	2895	140	24849	100.00	100.00	100.00	100.00	100.00
167	0.95	0.97	3767	177	35498	40.00	50.00	57.75	70.00	90.00
213	1.05	1.13	4851	207	45293	8.00	10.00	18.49	20.00	25.00
246	0.90	0.93	4937	220	52289	10.00	15.00	30.53	40.00	50.00
263	1.10	1.06	5740	248	55937	3.50	5.00	13.34	15.00	20.00
282	1.15	1.32	5581	255	59980	3.50	5.00	11.83	15.00	20.00

Wider resolutions mean larger percentages (measuring over a wider section of the MS window). As these are adjusted, watch and observe the changes to the percentages.

**Adjusting Target Resolution** Adjustments are made in increments of 0.05. The number in the Actual Percentage column is affected by the target resolution adjustments. This should fall between the Max. Target and Min. Target. If the masses cannot be brought into range by adjusting the Target Resolution, adjust the Ion Energies.

**Ion Energies** Adjusting the Ion Energy adjusts the degree of electronic amplification applied to a mass fragment, and thus the intensity (height) of the mass. Ion energies should be adjusted **after** Target Resolutions.

**Ideal Values** Displays the ideal values for Ion energies for each of the 10 mass fragments.

Mass	IE Low	IE High
50	90	170
55	90	170
69	90	170
93	90	170
117	140	170
167	140	220
213	175	230
246	180	230
263	185	250

Mass	IE Low	IE High
282	190	255

Ion Energies should generally be in ascending order, Low for the smaller masses and High for the larger masses.

Perform a Mass Alignment (press F5) after each change until **OK** is reported in the Status column.

**Mass Alignment**

Perform a Mass Alignment by pressing F5. This will update the Status column readings. Perform a Mass Alignment prior to and after making adjustments to the tune parameters.

**Adjusting EM Voltage**

The BPG is adjusted using EM (Electron Multiplier) voltage. Adjustments are made using increments of 25 V. The normal operating range is 1000 to 1600 V, with newer units typically showing lower values and older units showing higher values. If your unit requires an EM volt of 1600 to 2000 to reach BPG of 0.5, please contact INFICON for support, as your unit may require service.

<input type="checkbox"/>	Mass	Intensity	Res.	Target
<input type="checkbox"/>	50	2,798	0.93	0.90
<input type="checkbox"/>	55	8,310	0.90	0.90
<input checked="" type="checkbox"/>	69	25,260	0.86	0.85
<input type="checkbox"/>	93	51,216	0.92	0.90
<input checked="" type="checkbox"/>	117	322,526	1.09	1.10
<input type="checkbox"/>	167	125,998	0.98	0.95
<input checked="" type="checkbox"/>	213	29,860	1.09	1.05
<input type="checkbox"/>	246	67,715	0.94	0.90
<input type="checkbox"/>	263	22,629	1.06	1.10
<input type="checkbox"/>	282	18,653	1.28	1.15

Emission

EM

EM Volt	1100
Emission Current	350
Extractor Volt	75.0
Focus Volt	9.000
Threshold	66
Baseline	24
Num. Scans to...	3

Reverse Rod Polarity

Apply Baseline and Threshold

Running Tune  
Base Peak Gain: 0.33 (Low)

Auto Resolve    Save Tune

Mass Cal.    Full Scan

**Observing Base Peak Gain (BPG)** Properly adjusted Base Peak Gain for a HAPSITE ER is between 0.4 to 0.6, ideally at 0.50.

#### 14.4.4 Other Inputs

If you are unable to attain a satisfactory tune using the Resolution, Ion Energies, and EM Volt, then further adjustments may be necessary. These should be made only after contacting INFICON.

##### Additional Adjustment Control

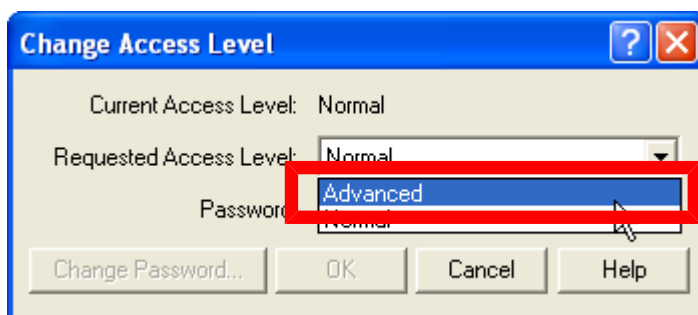
- Focus volt adjusts the relative amplification of ions larger and smaller than 117, i.e. raising amplification of larger ions and lowering smaller ions, OR raising small ions and lowering larger ions. The ideal value is between 2 to 8.
- Emission current increases the power of the ionizer. Increasing this can help raise BPG, but can also increase noise. The ideal value is 300 to 400.

Baseline and Threshold are indicative of noise, and should be less than 300 each. (Threshold will always be higher than Baseline.)

### 14.4.5 \*Set Access Level to Advanced

The **Access Level** must be set to **Advanced** to manually tune the instrument. The **Set Access Level...** is used to change ER IQ/Plus IQ user mode.

- **Normal Mode:** Allows access to default methods and data analysis
  - **Advanced Mode:** Allows access to method editing, manual tuning, file transfer, and file deletion.
- 1 On the **System Setup** window **Tools** Menu, click **Set Access Level...**
  - 2 On the Change Access Level window, select **Advanced** in the **Requested Access Level** box.



Access level is not password protected in the default settings. Advanced mode may be password protected if desired.

- 3 Click **OK**.
- 4 On the **System Setup** window, verify the Access Level is set to **Advanced**.

### 14.4.6 \*Manual Tune

- 1 Double click the icon shown in red in the figure below.
- 2 Select `default.tun` from the tuning pop-up window.
- 3 Click **OK**. It will take 10 to 20 seconds to initialize. During that time the **Emission** and **EM** boxes turn green.



The NEG (non-evaporable getters) is consumed while Manual Tune is open.

- 4 Adjust the tune parameters as discussed above until all values are within range.

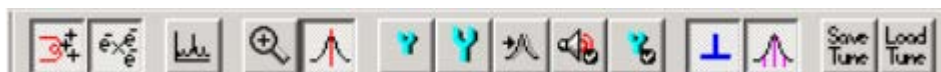















## 14.4.7 \*Save Tune

- 1 Verify that **OK** is displayed in the Status Column.
- 2 Once you are satisfied with the quality of the tune, click Save Tune at the top right of the Percentages table. Save the tune as default.tun.
- 3 Close Manual tune.

## 14.4.8 Tool Bar

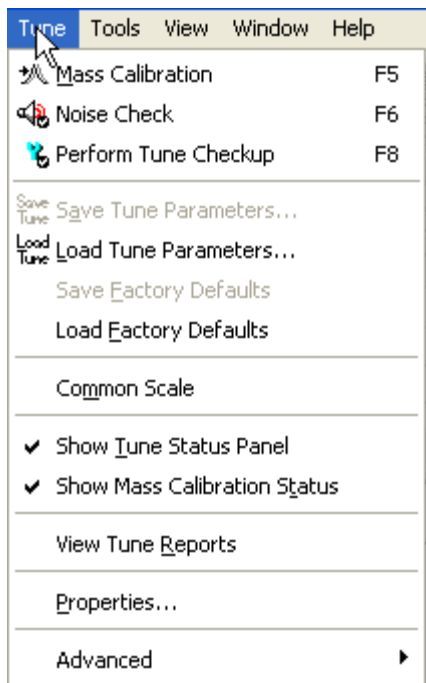
Each **Manual Tune** toolbar icon is described below.



	Filament On/Off	Turn the emission on or off.
	Multiplier On/Off	Turns the electron multiplier on or off.
	Full Scan	Switches between displaying full scan display mode and peak scan (single peak) display mode.
	Zoom	Enables the cursor to select and zoom in on a section of the screen.
	Mass Adjust	Enables the cursor to select and drag a mass peak to a different position on the mass axis.
	AutoTune	Starts the AutoTune function.
	Mass Calibration	Verifies and corrects the ten calibration masses for correct location within the mass range.
	Noise Check	Scans a “quiet” mass range (no peaks) to determine the electronic baseline and threshold noise level.
	Perform Tune Checkup	Runs a mass calibration and noise check.
	Show Target	Displays the target bar for the mass peak center and peak width at 10% peak height. Displays the target high and low percentage bars for each mass peak.
	Show Bounds	Displays the peak centroid and the target peak width at 10% peak height.
	Save Tune	Saves the tune file.
	Load Tune	Loads a new tune file and restarts tuning.

## 14.4.9 Tune Drop-Down Menu

The **Manual Tune** screen has an additional main drop-down menu, the **Tune** menu.

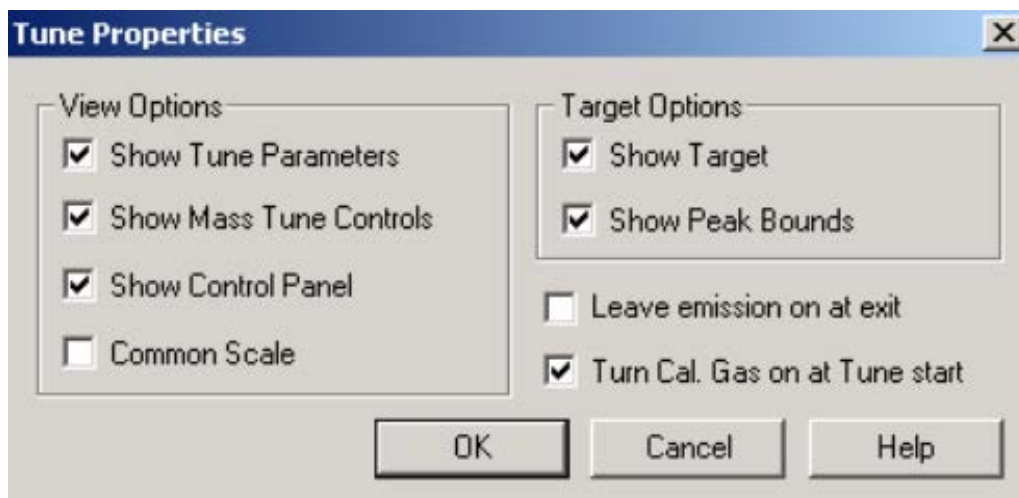


Mass Calibration	Verifies and corrects the ten calibration masses for correct location within the mass range.
Noise Check	Scans a “quiet” mass range (no peaks) to determine the electronic baseline and threshold noise level.
Perform Tune Checkup	Runs a mass calibration and noise check.
Save Tune Parameters...	Saves the tune file.
Load Tune Parameters...	Loads a new tune file and restarts tuning.
Load Factory Defaults	Loads the default tune settings from a factory tune file. This is intended to provide a starting point for tuning.
Common Scale	Sets all of the mass peak windows to the same common scale (Y-axis), based on Mass 117.
Show Tune Status Panel	Displays the <b>Tune and Mass Calibration Status</b> panel.
Show Mass Calibration Status	Displays the <b>Mass Calibration Status</b> panel.
View Tune Reports	Displays the <b>Tune Reports</b> screen.

Properties	Displays the <b>Properties</b> window, which is used to set the default screen display and startup/exit conditions for <b>Manual Tune</b> .
Advanced	Displays the <b>Advanced</b> tune functions.
Linearize DACS	Repositions the mass peaks from the internal standard gas on the mass axis by linear extrapolation of the digital to analog control settings.
AutoTune Tolerances	Sets the <b>AutoTune Tolerance</b> for mass resolution and mass axis position.



The **Advanced** tune functions should only be utilized under the direction of INFICON Support personnel.

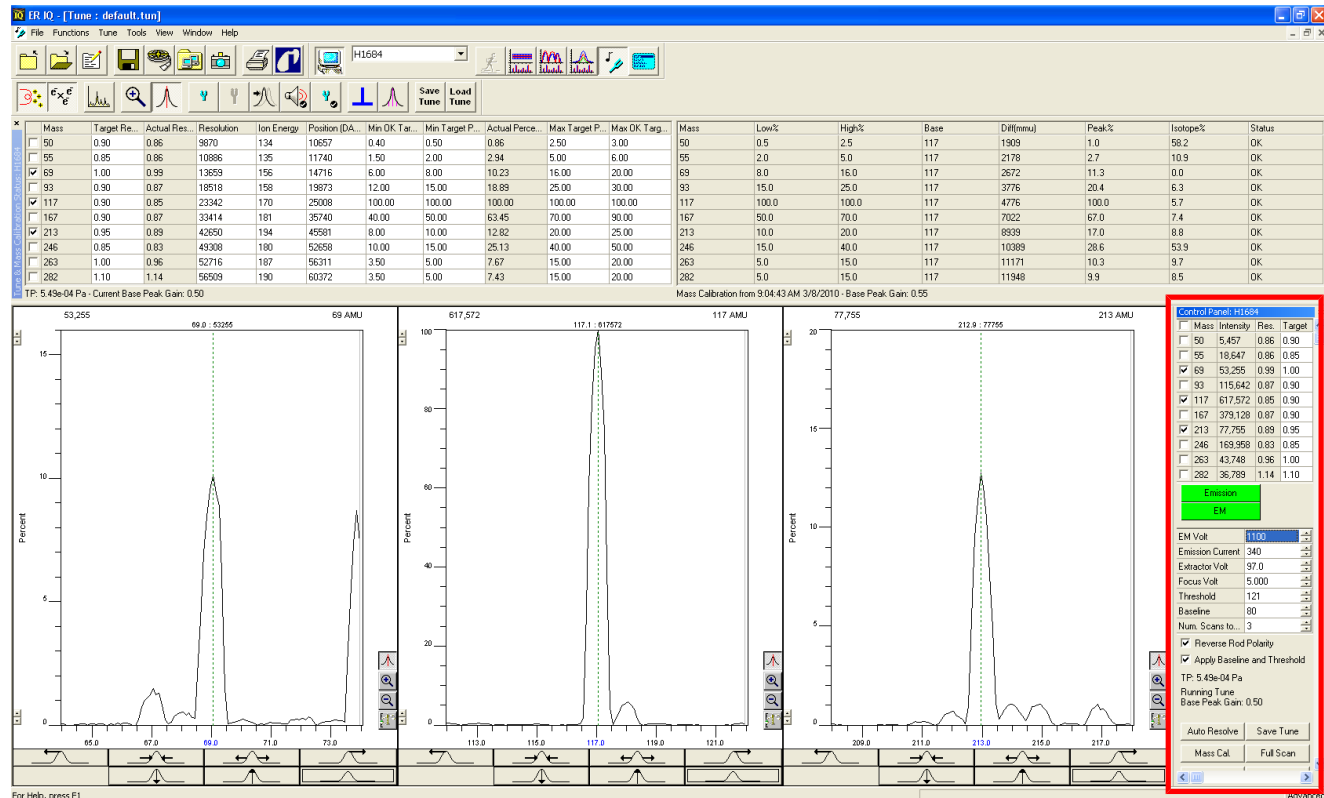


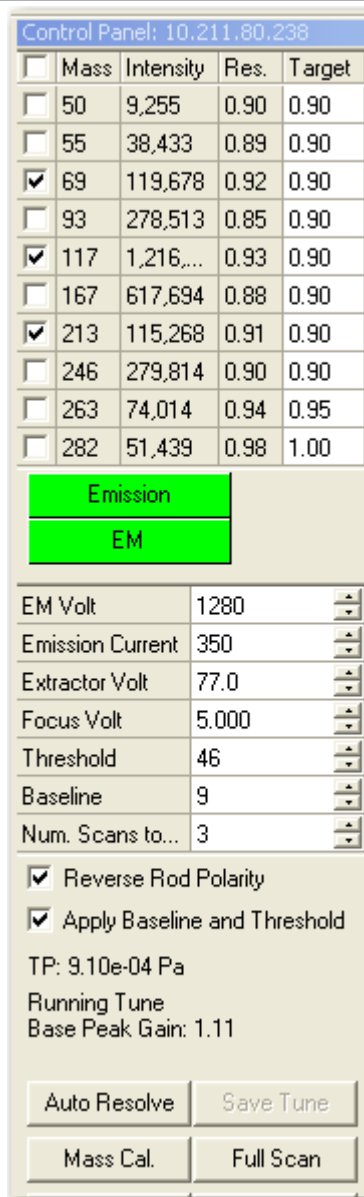
Show Tune Parameters	Displays the <b>EM Voltage, Ionizer control, Baseline, Threshold</b> and <b>Rod Polarity</b> settings on the <b>Control Panel</b> .
Show Mass Tune Controls	Displays the <b>Mass Tune Controls</b> on the <b>Mass Peak Scan</b> windows.
Show Control Panel	Displays the <b>Control Panel</b> .
Common Scale	Sets the mass peak scan windows to a common scale based on mass 117.
Show Target	Displays the target bar for the mass peak center and peak width at 10% peak height. Displays the target high and low percentage bars for each mass peak.
Show Peak Bounds	Displays the peak centroid and the target peak width at 10% peak height.
Leave emission on at exit	Leaves the filament and electron multiplier on when exiting tune. This should only be used for special service procedures.

Turn Cal. Gas on at Tune start	Turns on the calibration gas, which is the internal standard gas, when the tune program is started.
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### 14.4.10 Tune Control Panel

The **Tune Control Panel** is located on the right side of the screen and displays the individual mass peak scans, the measured intensity and the resolution.





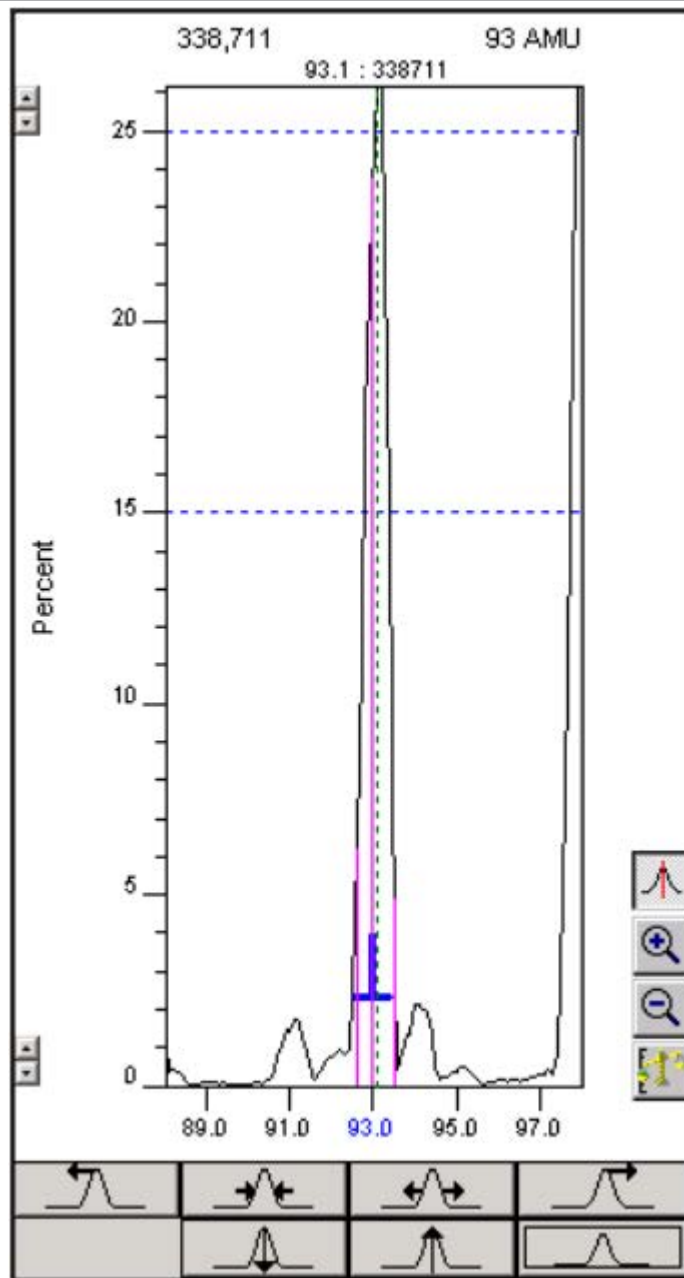
### 14.4.10.1 Tune Parameters

Target Resolution	Decreasing the <b>Target Resolution</b> narrows the peak, increases the resolution and lowers the peak percentage. Increasing the <b>Target Resolution</b> will widen the peak which decreases the resolution and increases the peak percentage.
Emission	Turns the filament on and off. Green signifies that the <b>Emission</b> is on.
EM	Turns the electron multiplier on and off. Green signifies that the electron multiplier is on. Range is 1000 to 2000.
EM voltage	Increases or decreases the gain of the system. EM voltage should be set to a value that achieves a <b>Base Peak Gain</b> between 0.4 and 0.6.

Emission Current	Optimizes the ionization efficiency of the ionizer. <b>Emission Current</b> is set to achieve maximum intensity for mass 117. Range is 300 to 400. (350 is typical.)
Extractor Volt	Optimizes the ionization efficiency of the ionizer. The <b>Extractor Volt</b> setting must be set to achieve maximum intensity for mass 117. Range is 70 to 90.
Focus Volt	Optimizes the ionization efficiency of the ionizer. The <b>Focus Volt</b> setting must be set to achieve maximum intensity for mass 117. Range is 2 to 9.
Threshold	<b>Threshold</b> determines if a measured point is used in the peak area integration. If the point is used, the baseline is subtracted before use. The threshold should be set within one standard deviation of the baseline.
Baseline	The <b>Baseline</b> is the mean value of the measured noise level.
Reverse rod polarity	Changes the rod polarity on the mass filter and select the rod polarity that provides optimal performance at mass 117.
TP	The total MS pressure. Must be below 6E-03 for instrument to operate.
Running tune base peak gain	Current measured Base Peak Gain (BPG). <b>Note:</b> The Base Peak Gain (BPG) will switch to red when BPG is outside the target range.
Auto resolve	Adjusts the resolution of all mass peaks to the target resolution.
Save tune	Save the tune file.
Mass calibration	Verifies and corrects the ten calibration masses for correct location within the mass range.
Full scan	Switches between full scan display mode and peak scan display mode
Short AutoTune	Starts the AutoTune function
Noise check	Scans a “quiet” mass range (no peaks) to determine the electronic baseline and threshold noise level.
Tune checkup	Runs a mass calibration and noise check.
Zoom	Enables the cursor to zoom into full scan or a section of the screen.
Mass adjust	Enables the cursor to select and drag a mass peak to a different position on the mass axis.



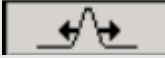




### 14.4.11 Peak Scan Window

The **Peak Scan Window**, as shown below, can be used to manually tune the mass peak.



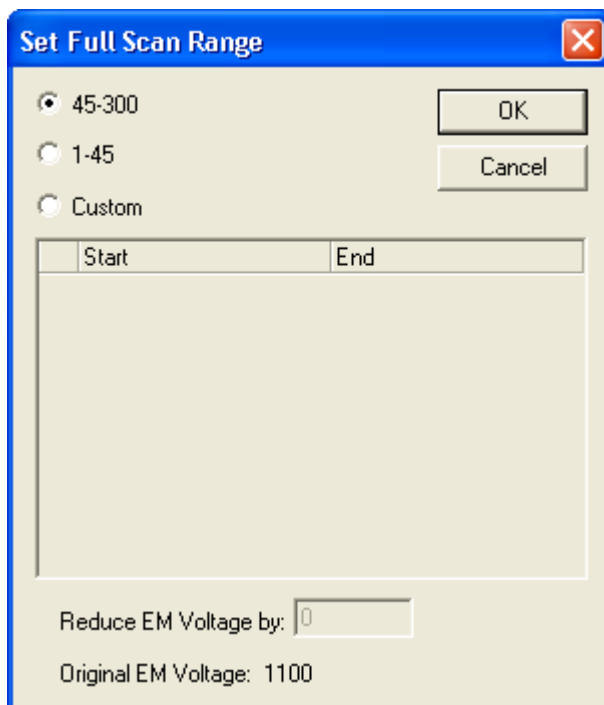
### 14.4.11.1 Peak Scan Window Control

	Mass Adjust	Enables the cursor to select a mass peak and drag the mass peak to a different position on the mass axis.
	Zoom	Enables the cursor to select and zoom into a section of the peak scan window.
	Zoom Out	Returns the window to the original X axis and Y axis scale.
	Zoom Out Y Axis	Returns the Y axis to original scale.
	Y Axis Scale	Increases or decreases the Y axis scale.

	Shifts the mass peak left
	Increases the peak resolution.
	Decreases the peak resolution.
	Shifts the mass peak right.
	Decreases the <b>Ion Energy</b> .
	Increases the <b>Ion Energy</b> .
	Zooms to a single peak scan display window.

## 14.4.12 Setting the Full Scan Range

Placing the mouse cursor on the x axis of the full scan window and right-clicking displays the **Set Full Scan Range** window. This allows a custom scan range to be entered. The scan ranges of 45 to 300 amu or 1 - 45 amu can also be selected.



The EM voltage will automatically be decreased by 500 volts (default) whenever a range below mass 45 is scanned.



### 14.4.13 Tune and Mass Calibration Status

The **Tune & Mass Calibration Status Panel** is shown below.

Mass	Target Resolution	Actual Resolution	Resolution	Ion Energy	Position (DAC Value)	Min OK Target Percen...	Min Target Percentage	Actual Percentage	Max Target Percentage	Max OK Target Percent...
<input type="checkbox"/> 50	0.90	0.84	9720	100	10301	0.40	0.50	1.68	2.50	3.00
<input type="checkbox"/> 55	0.85	0.76	10730	110	11350	1.50	2.00	4.36	5.00	6.00
<input checked="" type="checkbox"/> 69	1.00	0.89	13450	107	14223	6.00	8.00	11.24	16.00	20.00
<input type="checkbox"/> 93	0.90	0.80	18190	135	19177	12.00	15.00	20.47	25.00	30.00
<input checked="" type="checkbox"/> 117	0.95	0.82	22920	150	24133	100.00	100.00	100.00	100.00	100.00
<input type="checkbox"/> 167	0.80	0.81	32817	220	34477	40.00	50.00	52.40	70.00	90.00
<input checked="" type="checkbox"/> 213	1.10	0.96	41865	182	43974	8.00	10.00	15.26	20.00	25.00
<input type="checkbox"/> 246	0.95	0.81	48405	200	50785	10.00	15.00	21.36	40.00	50.00
<input type="checkbox"/> 263	1.10	1.00	51735	205	54297	3.50	5.00	10.33	15.00	20.00
<input type="checkbox"/> 282	1.15	1.00	55490	240	58218	3.50	5.00	8.95	15.00	20.00

TP: 1.98e-03 Pa - Current Base Peak Gain: 0.84

Show

- Mass
- Target Resolution
- Actual Resolution
- Resolution
- Ion Energy
- Position (DAC Value)
- Scan Width
- Min OK Target Percentage
- Min Target Percentage
- Actual Percentage
- Max Target Percentage
- Max OK Target Percentage
- Base Peak

Mass	The mass number of the peak.
Target Resolution	Target Resolution at 10% peak height.
Actual Resolution	Measured resolution at 10% peak height.
Resolution	Resolution value; can be used to input a change in Resolution value.
Ion Energy	Ion Energy value; can be used to input a change in Ion Energy value.
Position (DAC Value)	Current DAC setting for mass position.
Scan Width	Displays the points measured per amu.
Min OK Target Percentage	Displays the minimum target percentage required for the mass peak to meet the OK LOW criteria.
Min Target Percentage	Displays the minimum target percentage required for the mass peak to meet OK criteria. If the actual percentage is below the minimum percentage, the box will turn red.
Actual Percentage	Displays the actual measured target percentage.

Max Target Percentage	Displays the maximum target percentage required for the mass peak to meet OK criteria. If the actual percentage is above the minimum percentage, the box will turn red.
Max OK Target Percentage	Displays the maximum percentage required for the mass peak to meet the OK High criteria.
Base Peak	Displays the base peak, which is used to measure the mass peak percentage.

## 14.4.14 Mass Calibration Status

The dark gray **Mass Calibration Status** table displays the status of the last **Mass Calibration**. If the **Mass Calibration** is not displayed, select **Mass Calibration** from the **Tune** drop-down menu.

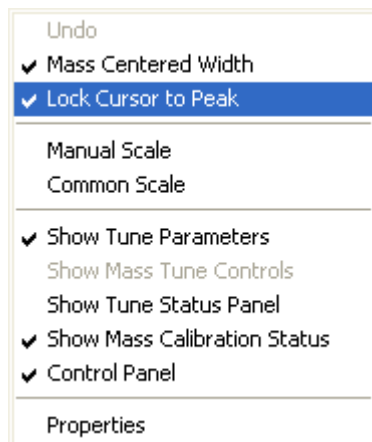
Mass	Low%	High%	Base	Diff(mmu)	Peak%	Isotope%	Status
50	0.5	2.5	117	1909	1.0	58.2	OK
55	2.0	5.0	117	2178	2.7	10.9	OK
69	8.0	16.0	117	2672	11.3	0.0	OK
93	15.0	25.0	117	3776	20.4	6.3	OK
117	100.0	100.0	117	4776	100.0	5.7	OK
167	50.0	70.0	117	7022	67.0	7.4	OK
213	10.0	20.0	117	8939	17.0	8.8	OK
246	15.0	40.0	117	10389	28.6	53.9	OK
263	5.0	15.0	117	11171	10.3	9.7	OK
282	5.0	15.0	117	11948	9.9	8.5	OK

Mass Calibration from 9:04:43 AM 3/8/2010 - Base Peak Gain: 0.55

Mass	Mass number
Low %	Minimum percentage for peak status to be displayed as OK.
High %	Maximum percentage for peak status to be displayed as OK.
Base	Reference mass for peak percentage calculations.
Diff (menu)	Provides an adjustment to DAC value for mass peak alignment when necessary. 100 mmu = 0.1 amu.
Peak %	Actual peak percentage of reference mass.
Isotope %	Percentage of the Carbon 13 isotope peak as measured against the mass fragment.
Status	Status of the mass peak
OK	Within minimum and maximum values.
OK LOW	Outside of minimum value but within acceptable tolerance.
OK HIGH	Outside of maximum value but within acceptable tolerance.
LOW	Below minimum value, needs adjustment.
HIGH	Above maximum value, needs adjustment.
FAILED	Cannot locate mass peak within window.

### 14.4.15 Scan Window Menu

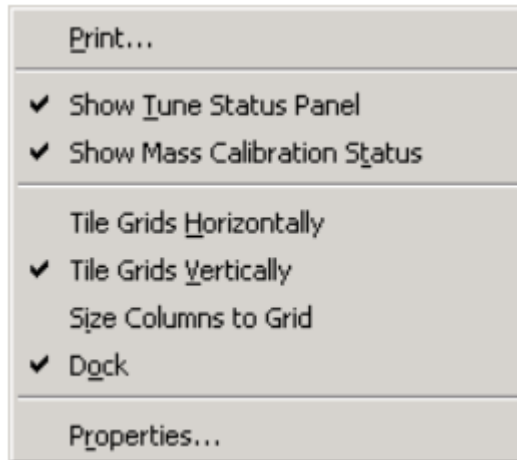
Place the mouse cursor in the **Peak Scan** or **Full Scan** window and right-click to display the menu shown in the figure below.



Undo	Returns the screen to its previous state.
Mass Centered Width	Width in amu that correctly aligns the calibration peak on the mass axis.
Lock Cursor to Peak	Locks the cursor to the mass peak to adjust the mass position
Manual Scale	Allows the mass peak windows to be set to a user defined scale.
Common Scale	Sets the mass peak scan windows to a common scaled based on mass 117.
Show Tune Parameters	Displays the <b>EM Voltage, Ionizer Control, Baseline, Threshold, and Rod Polarity</b> setting on the <b>Control Panel</b>
Show Mass Tune Controls	Displays the mass tune controls on the mass peak scan windows.
Show Tune Status Panel	Displays the <b>Tune</b> Status panel.
Show Mass Calibration Status	Displays the <b>Mass Calibration Status</b> control panel.
Control Panel	Displays the <b>Control Panel</b> .
Properties	Displays the <b>Properties</b> window.

### 14.4.16 Tune Status Window Menu

Place the mouse cursor in the **Tune Status** panel or the **Mass Calibration Status** panel and right-click to display the menu shown in the figure below.



Print...	Prints the <b>Tune Status</b> panel or the <b>Mass Calibration Status</b> panel.
Show Tune Status Panel	Displays the <b>Tune Status</b> panel.
Show Mass Calibration Status	Displays the <b>Mass Calibration Status</b> panel.
Tile Grids Horizontally	Tiles the <b>Status and Calibration Status</b> panels horizontally.
Tile Grids Vertically	Tiles the <b>Status and Calibration Status</b> panels vertically.
Size Columns to Grid	Resets the column size to the current grid.
Dock	Locks the display position to a fixed position.
Properties...	Displays the <b>Properties</b> window.

# 15 Method Editor

## 15.1 The Method Editor

The **Method Editor** function in **ER IQ** creates methods to identify and quantify volatile organic compounds. The **Method Editor** function is composed of the following pages:

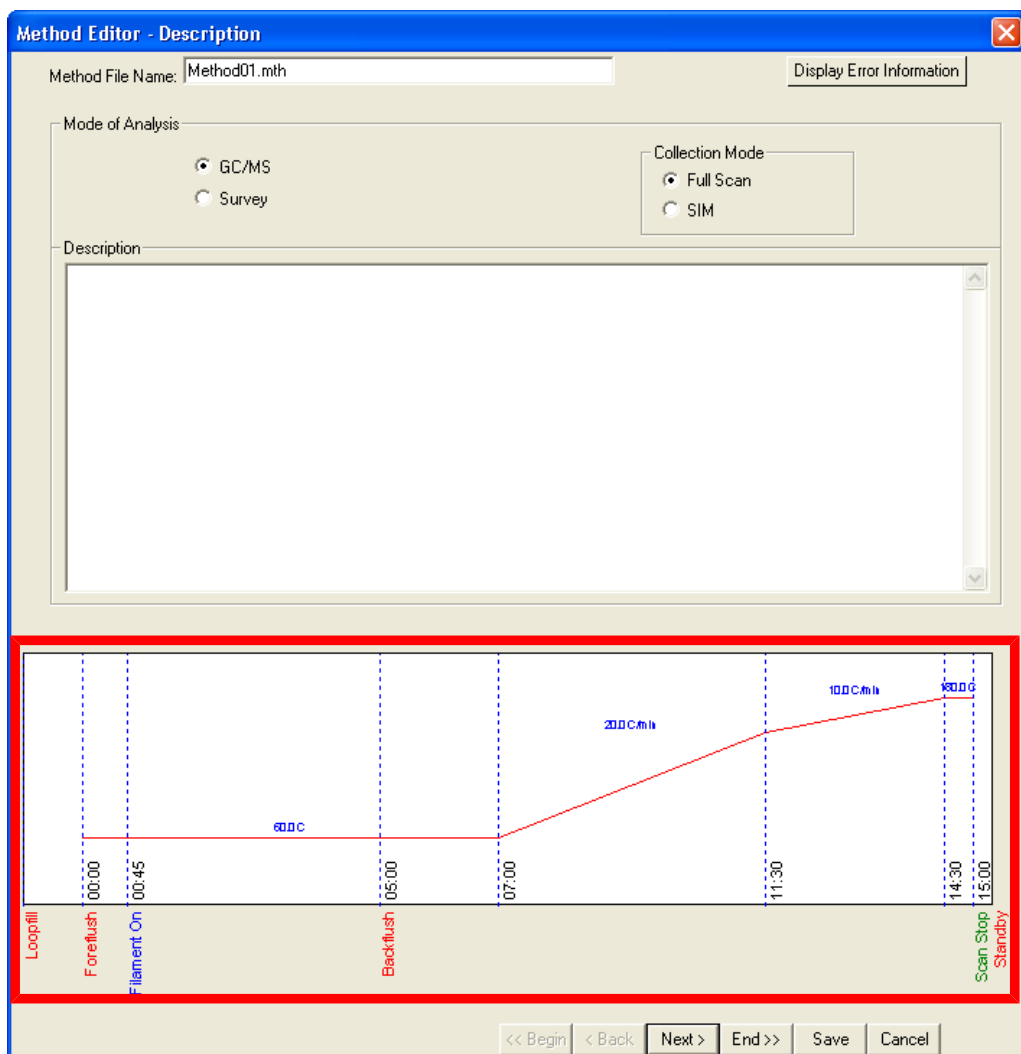
- The **Description** page for entering a description of the method.
- The **Startup** page for selecting the type of method, such as **Probe**, **Headspace**, **SituProbe** or **SPME**, to be created. Temperature settings are also selected on this page.
- The **Inlet** page defines the temperatures, timing, inlet and valve states.
- The **Search** page designates the calibration library for the method. This page also sets the **Library Search Parameters**.
- The **Data** page sets the **Data File (file extension.hps)** component and specifies where the data will be stored. By default, the data file pathway uses the pathway of IQ Software\H###\Data\method name\file name.file extension.
- A **Summary** page is provided, at the end of the **Method Editor**, to review and print the method parameters.



Methods cannot be viewed, created or changed when the access level is set to **Normal**.

---

Each page of the **Method Editor** shows a profile at the bottom of the **Inlet States** and **Temperature**. For questions relating to method development, please contact INFICON for application support.



Newly created methods start with a default set of **Inlet States** and a default **Temperature Profile**, which can be modified as required by the application.



The bottom of each page will display the inlet states, see Inlet States [▶ 313] for more information, and the temperature profile, see GC Temperature Profile [▶ 318] for more information.

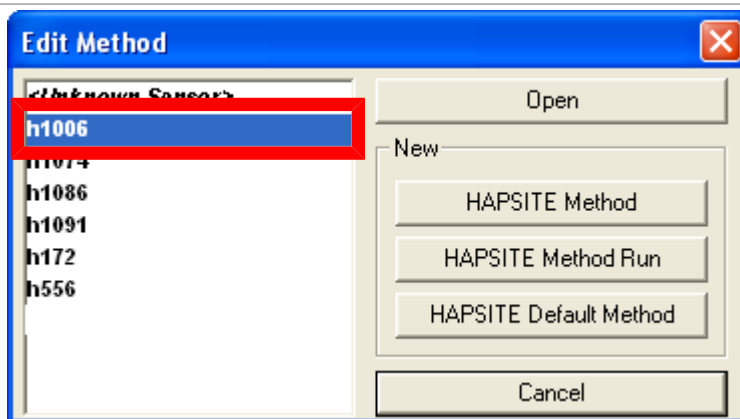
#### To access Method Editor:

- 1 On the **System Setup** screen, double-click on the **Method Editor** icon.



#### Method Editor

- 2 If more than one unit is connected to the laptop, click on the name of the desired HAPSITE ER.



There are four options for accessing a method:

Open	Opens an existing HAPSITE ER method for modification.
Method	Open a blank method template to modify as necessary.
Method Sequence	Allows a method to be automatically repeated or a series of methods to be run together. See Method Sequence [ > 365].
Default Method	Selects a default method. See Loading Default Methods [ > 303].
Cancel	Closes the <b>Edit Method</b> window.

## 15.2 Reloading Default HAPSITE Methods

Default methods can be loaded onto the laptop in case the methods have been deleted or modified.

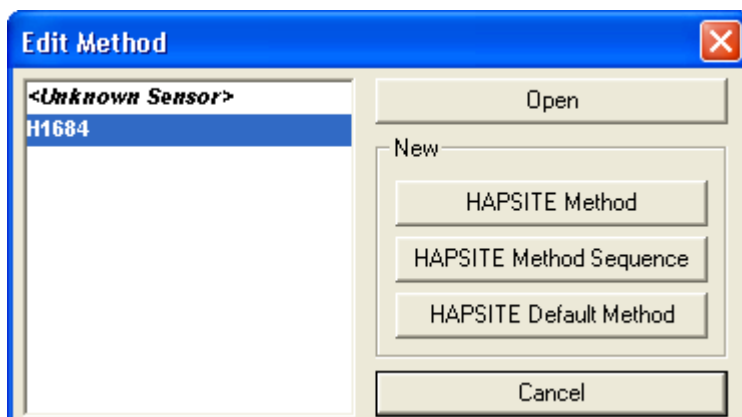
### 15.2.1 Loading Default Methods

- 1 Double-click the **Method Editor** icon.

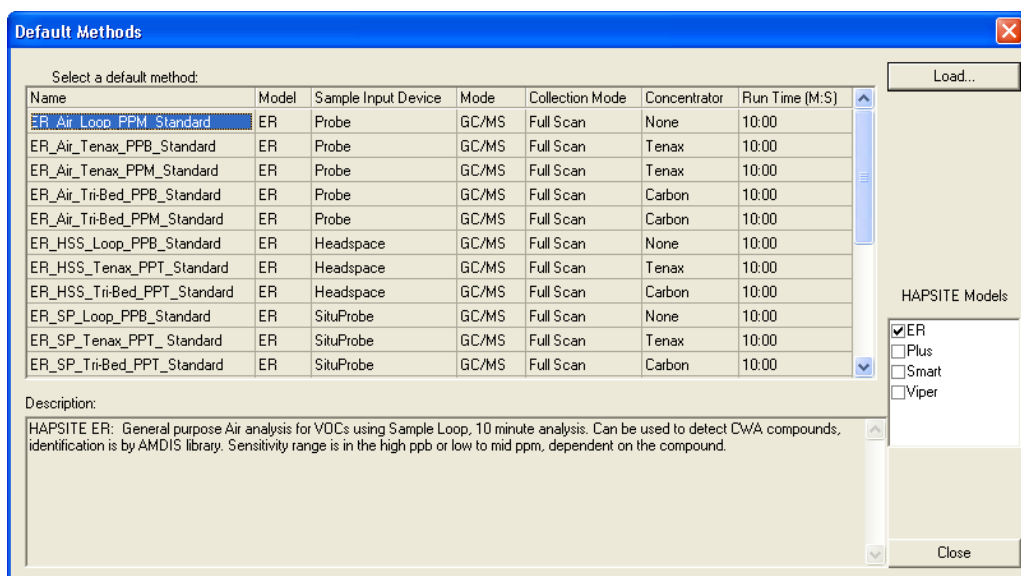


Method Editor

- 2 Select **HAPSITE Default Method** to access the default methods.



- 3 Verify that **ER** is checked on the right side of the window. Highlight the desired method and click **Load**. See Default Methods [▶ 306] for a description of the methods.



- 4 The **Description** page is displayed.



**Method Editor - Description**

Method File Name:  Display Error Information

Mode of Analysis

GC/MS Collection Mode  
 Survey  Full Scan  
 SIM

Description

HAPSITE ER: General purpose Air analysis for VOCs using Carbon concentrator, 10 minute analysis. Method will detect CWA compounds with identification by AMDIS library. Carbon concentrator covers a wide boiling point range and is usable for compounds with boiling points from -15 C up. 1 minute inlet line cleanout plus 100 mL sample collection. Sensitivity is in the low to mid ppb range, compound dependent. Method should be used only with triple bed Carbon concentrator tube when detecting CWA compounds.

Chromatogram showing temperature and flow rate changes over time. Key events are marked with vertical dashed lines: LinePurge, ConcFill, PreDesorb, Desorb Filament On, Foreflush, Backflush, and ScanStop. Temperature starts at 80°C, rises to 60°C at 02:30, then to 120°C at 04:20, and finally to 180°C at 07:40. Flow rate is 120 C/min from 04:20 to 07:40 and 250 C/min from 07:40 to 08:00.

<< Begin < Back **Next >** End >> Save Cancel

5 Click **Save** at the bottom of the **Method Editor-Description** page.

**Method Editor - Description**

Method File Name:  Display Error Information

Mode of Analysis

GC/MS  
 Survey

Collection Mode

Full Scan  
 SIM

Description

HAPSITE ER: General purpose Air analysis for VOCs using Carbon concentrator, 10 minute analysis. Method will detect CWA compounds with identification by AMDIS library. Carbon concentrator covers a wide boiling point range and is usable for compounds with boiling points from -15 C up. 1 minute inlet line cleanout plus 100 mL sample collection. Sensitivity is in the low to mid ppb range, compound dependent. Method should be used only with triple bed Carbon concentrator tube when detecting CWA compounds.

<< Begin < Back Next > End >> **Save** Cancel



Two digits are appended to the method file name (for example, 01). If the two digits are not desired, remove them before clicking **Save**.

## 15.3 Default Methods

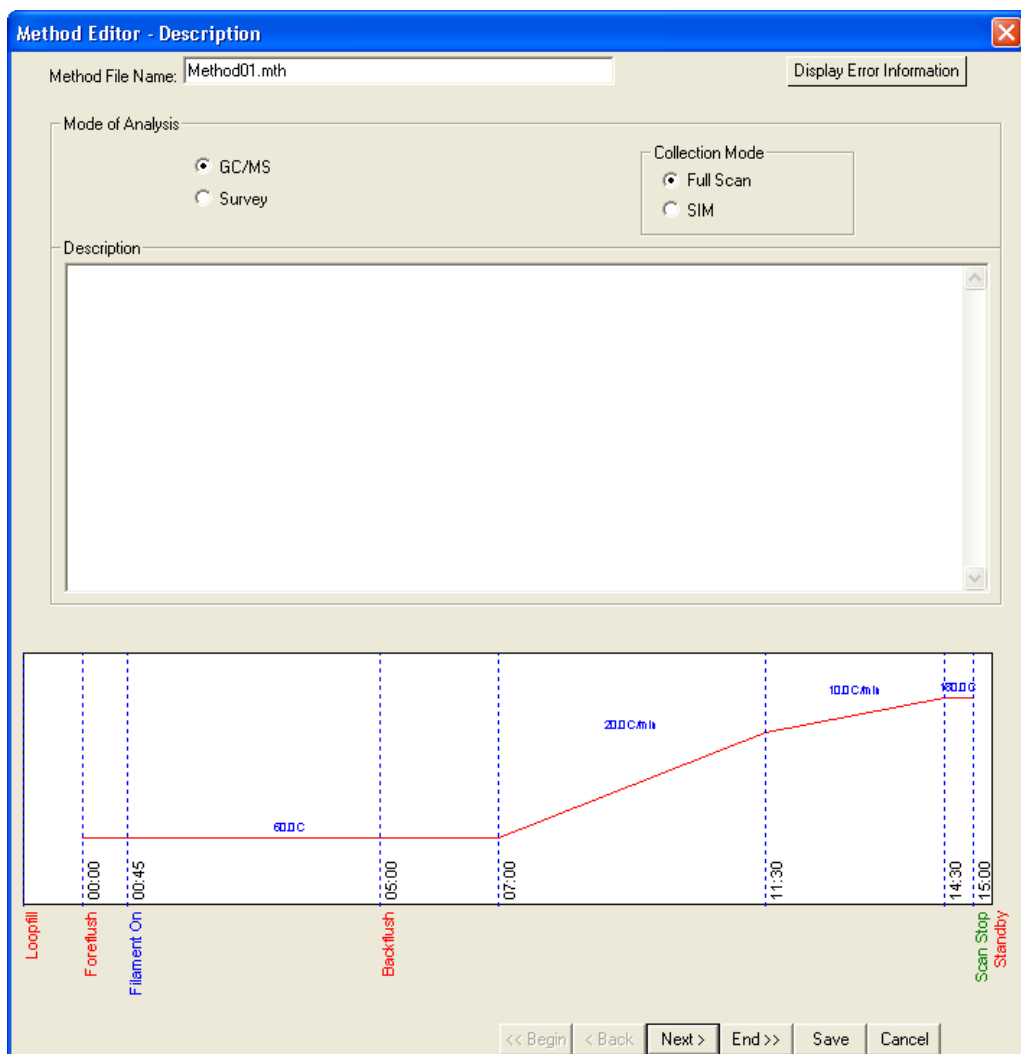
The methods found in the **Default Methods** window are general purpose methods for each of the HAPSITE ER configurations.

ER_Air_Tri-Bed_PPB_Standard	Carbon concentrator method (10 minute analysis time)
ER_Air_Tri-Bed_PPM_Standard	Carbon concentrator method to be used in lieu of ER_Air_Loop_PPM_Standard (10 minute analysis time)
ER_Air_Tenax_PPM_Standard	Tenax concentrator method to be used in lieu of ER_Air_Loop_PPM_Standard (10 minute analysis time)

ER_Air_Tenax_PPB_Standard	VOC and Chemical Warfare Agent Air Analysis using Tenax Concentrator (10 minute analysis sample time. Consists of one minute inlet purge plus one minute sample collection.)
ER_Air_Loop_PPM_Standard	VOC and Chemical Warfare Agent analysis using Sample Loop (10 minute analysis time)
ER_HSS_Tri-Bed_PPT_Standard	VOC and Chemical Warfare Agent Headspace solid/liquid analysis using the Tri-Bed concentrator (10 minute analysis time)
ER_HSS_Loop_PPB_Standard	VOC and Chemical Warfare Agent Headspace solid/liquid analysis using the Sample Loop(10 minute analysis time)
ER_HSS_Tenax_PPT_Standard	VOC and Chemical Warfare Agent Headspace solid/liquid analysis using the Tenax concentrator (10 minute analysis time)
ER_SP_Tri-Bed_PPT_Standard	VOC water analysis using the Tri-Bed concentrator (10 minute analysis time)
ER_SP_Loop_PPB_Standard	VOC water analysis using the Loop concentrator (10 minute analysis time)
ER_SP_Tenax_PPT_Standard	VOC water analysis using the Tenax concentrator (10 minute analysis time)
ER Survey	Quick screening method for VOCs. (Analysis time is determined by the user. Method will turn off after five minutes.)

## 15.4 Description Page

The first page displayed in the **Method Editor** is the **Description** page. This page will appear after clicking **Open, HAPSITE Method** and **HAPSITE Default Method**. A description of the method and the method name can be entered into this screen. A temperature profile with the inlet states is displayed at the bottom of all of the method pages.



### CAUTION

A method file ends with a file extension of .mth.

#### Mode of Analysis:

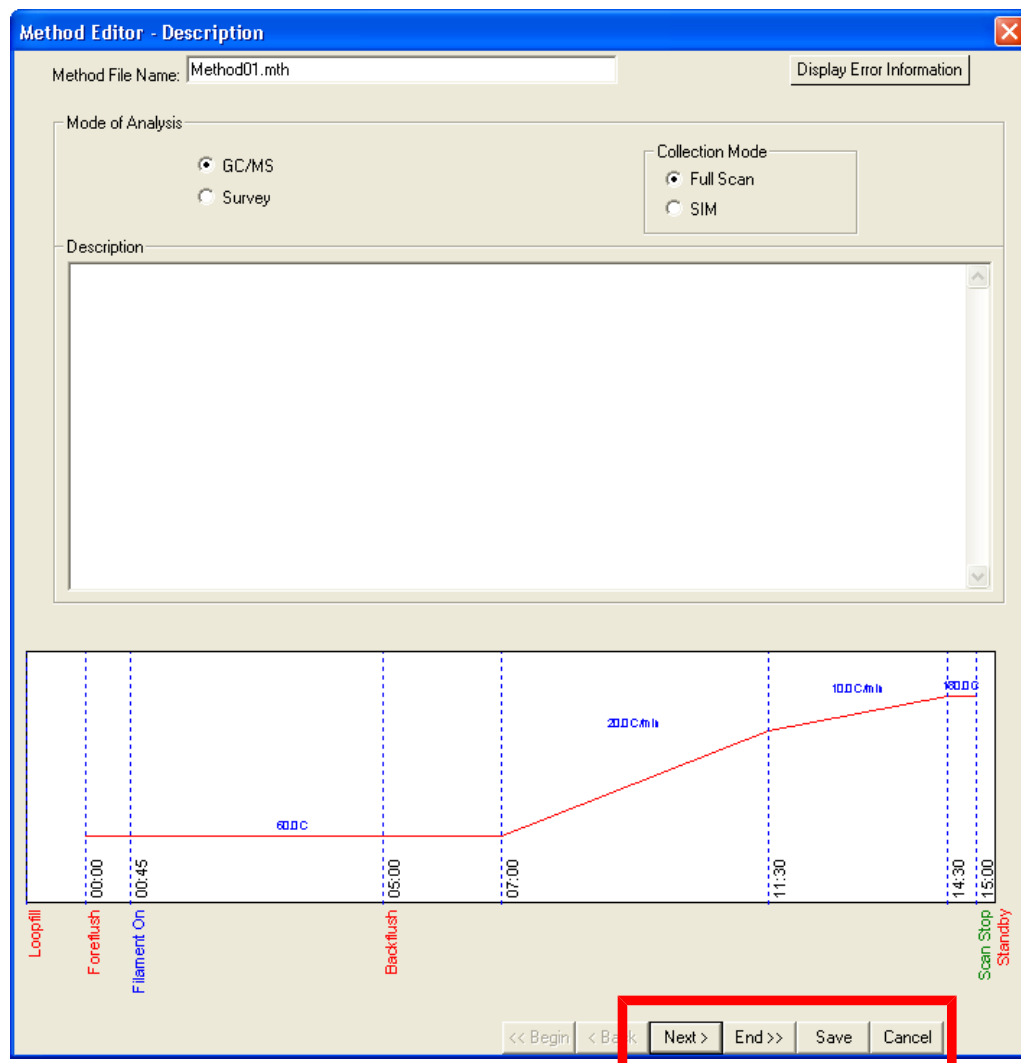
Analyze (GC/MC)	This analysis uses both the Gas Chromatograph (GC) and Mass Spectrometer (MS) to separate and analyze compounds. Compounds are identified using a library search.
Survey	This mode uses only the Mass Spectrometer to provide a near real-time response. Samples flow directly to the Mass Spectrometer and are not separated by the GC.

#### Collection Mode:

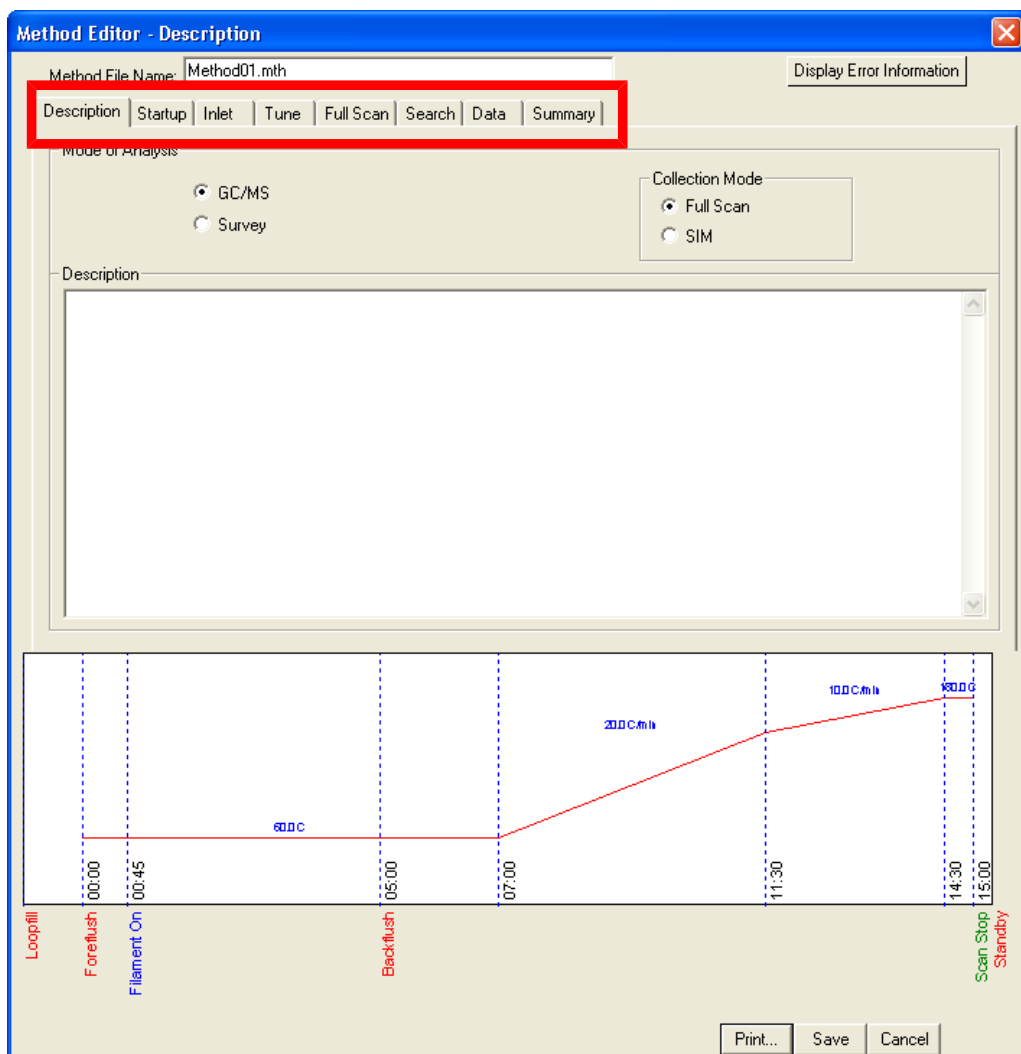
Full Scan	This mode scans all the masses across a given range, which is 42-300 for default methods. It is used to identify unknown samples. Full Scan is available for both Analyze (GC/MS) and Survey modes.
-----------	---

SIM	This stands for Selected Ion Monitoring. This collection mode is more sensitive than a full scan method, because it only scans for user selected mass fragments. Prior to creating a SIM method, the sample components must be identified and their retention times must be known. SIM mode is available in both Analyze (GC/MS) and Survey modes.
-----	--

The **Method Editor** can be run in **Wizard Mode**, which moves through the method creation in a logical sequence. Adjustments can be made using the **Back** and **Next** buttons. The figure below shows the **Wizard Mode** navigation buttons.



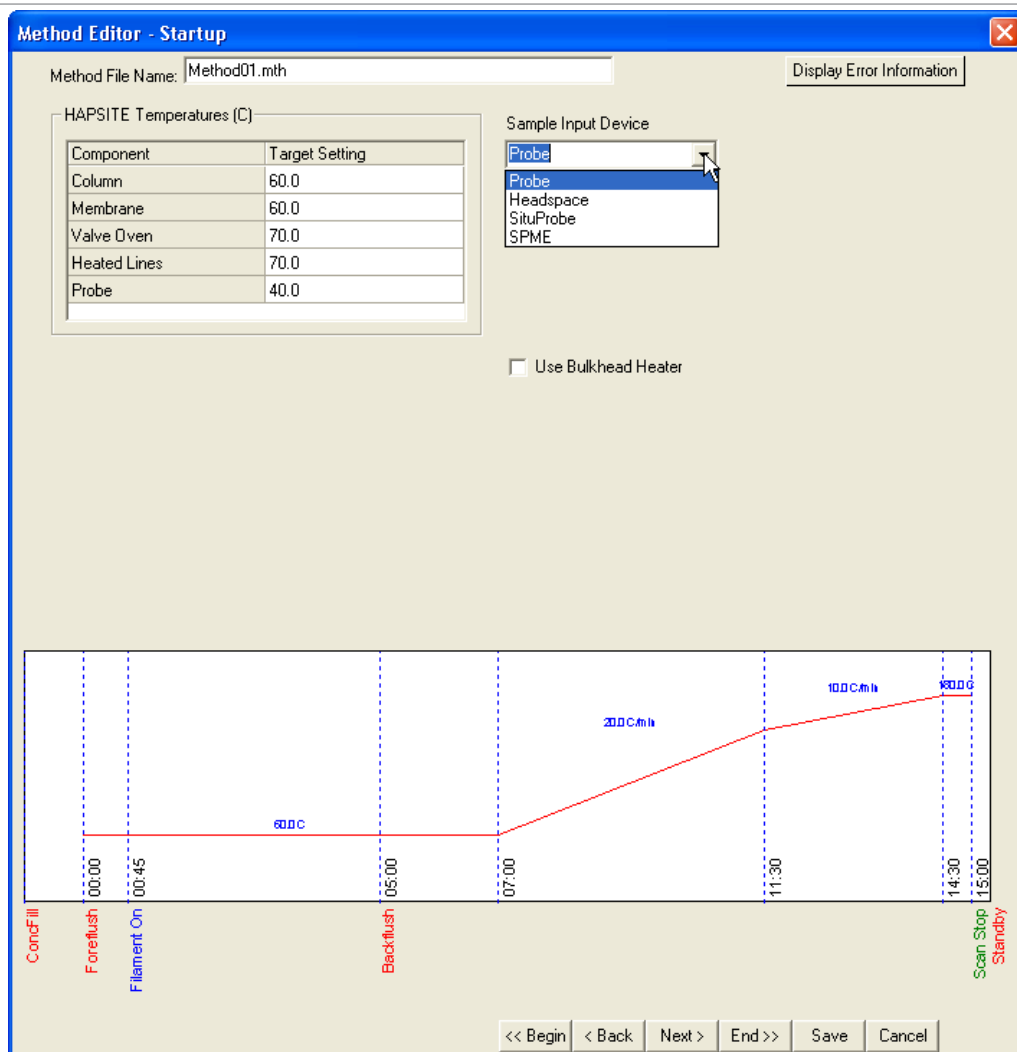
In **Non-Wizard** mode, which is recommended only for experienced users, all pages are available through a tabbed window. To change the **Wizard** mode settings, refer to Miscellaneous Tab [▶ 160] for instructions.



All method parameters on each page of the **Method Editor** are checked for synchronization and correctness. The **Method Editor** function will highlight all questionable parameters in yellow, when a discrepancy occurs. The **Method Editor** permits movement from page to page, even when errors are present.

## 15.5 Startup Page

The **Startup** page, shown in the figure below, displays the initial settings for the HAPSITE ER system heaters. The initial temperature settings for the components described in **HAPSITE Temperatures (C)** can be modified on this page. The **Sample Input Device** (that is, the **Probe**, **Headspace**, **SituProbe** or **SPME**) can be selected on this page.



The parameters on the **Startup** page are:

**HAPSITE Temperatures (°C)**

<b>Column</b>	The initial <b>Column</b> temperature setting.
<b>Membrane</b>	The target <b>Membrane</b> temperature setting.
<b>Valve Oven</b>	The target <b>Valve Oven</b> temperature setting.
<b>Probe</b>	The target <b>Probe</b> temperature setting. This setting is not available when the <b>Headspace</b> or <b>SituProbe</b> is enabled.

**Sample Input Device**

<b>Probe</b>	Select <b>Probe</b> when using the air probe to sample volatile organic compounds in the air.
<b>Headspace</b>	Select <b>Headspace</b> when using this accessory to analyze solids and liquids for volatile organic compounds.
<b>SituProbe</b>	Select <b>SituProbe</b> when using this accessory to analyze volatile organic compounds.

**Internal Standard Box**

Use Internal Standard	The <b>Use Internal Standard</b> option is available when creating <b>Survey</b> methods.
-----------------------	---

## Headspace Temperatures (°C)

Method File Name: ER\_Air\_Tri-Bed\_PPM\_Standard.mth Display Error Information

Sample Input Device: **Headspace**

HAPSITE Temperatures (C)

Component	Target Setting
Column	60.0
Membrane	80.0
Valve Oven	70.0
Heated Lines	70.0
Probe	40.0

Temperatures (C)

Component	Target Setting
Oven	80.0
Transfer Line	80.0

Use Bulkhead Heater

<b>Oven</b>	The target <b>Oven</b> temperature setting for the <b>Headspace</b> .
<b>Transfer Line</b>	The target <b>Transfer Line</b> temperature setting for the <b>Headspace</b> .

## SituProbe Temperatures (°C)

Method File Name: ER\_Air\_Tri-Bed\_PPM\_Standard.mth Display Error Information

Sample Input Device: **SituProbe**

HAPSITE Temperatures (C)

Component	Target Setting
Column	60.0
Membrane	80.0
Valve Oven	70.0
Heated Lines	70.0
Probe	40.0

Temperatures (C)

Component	Target Setting
Oven	60.0
Transfer Line	60.0
Probe	60.0

Use Bulkhead Heater

<b>Oven</b>	The target <b>Oven</b> temperature setting for the <b>SituProbe</b> .
<b>Transfer Line</b>	The target <b>Transfer Line</b> temperature setting for the <b>SituProbe</b> .
<b>Probe</b>	The target <b>Probe</b> temperature setting for the <b>SituProbe</b> sampling probe.

## SPME

Method File Name: ER\_Air\_Tri-Bed\_PPM\_Standard.mth Display Error Information

Sample Input Device: **SPME**

HAPSITE Temperatures (C)

Component	Target Setting
Column	60.0
Membrane	80.0
Valve Oven	70.0
Heated Lines	70.0
SPME	40.0

SPME Fiber:

Use Bulkhead Heater

<b>SPME Fiber</b>	Type the color of the fiber into the box.
-------------------	---



# 15.6 Inlet Page



This page is only available when creating an **Analyze** (GC/MS) method.

The **Inlet** page displays the default settings for the **Inlet States**, **GC Temperature Profiles** and **Valve States**. Adjusting settings on the **Inlet** page may affect other method parameters and/or the retention time. The **Start** time of each **Inlet State** event is displayed in combination with the temperature profile at the bottom of the **Inlet** page.

**Method Editor - Inlet**

Method File Name: ER\_Air\_Tri-Bed\_PPB\_Standard.mth Display Error Information

**Inlet States**

	Start	Volume (ml)	Duration	Inlet State
1	00:00	0.0	01:00	LinePurge
2	00:00	100.0	01:00	ConcFill
3	00:00	0.0	00:00	PreDesorb
4 Inj.	00:00	0.0	00:00	Desorb
5	00:30	0.0	02:00	Foreflush
6	02:30	0.0	07:30	Backflush
7	10:00	0.0		Standby

**Valve States for Event 1**

- SampleInjectionValve
- GCControlValve
- ISInletValve
- ISFlowValve
- InletPurgeValve
- N2DryValve
- SampleShutoffValve
- MakeUpInletValve
- SampleShrimp
- EnableV4.0
- Concentrator on
- Tubing Heat

Scan Events

Filament Delay: 15 sec

Run Time: 10 0

Concentrator:

- None
- Tenax
- Carbon

**GC Temperature Profiles**

Start	Ramp Rate	Ramp Time	Temp	Hold Time
00:00			60.0	01:00
01:00	6.0	03:20	80.0	00:00
04:20	12.0	03:20	120.0	00:00
07:40	26.0	02:18	180.0	00:02

Temp in C, Ramp Rate in C/min, Time in min:sec

Temp Profile Graph: Shows temperature (C) vs. Time (min:sec). Key points: 60.0 C (00:00), 80.0 C (01:00), 120.0 C (04:20), 180.0 C (07:40). Events: LinePurge, ConcFill, PreDesorb, Filament On, Foreflush, Backflush, Standby.

Navigation: << Begin < Back Next > End >> Save Cancel

## 15.6.1 Inlet States

Inlet States control the HAPSITE ER and accessory valve settings for sampling, analysis and purging of the HAPSITE ER. The figure below shows the grid used to program the **Inlet States**.

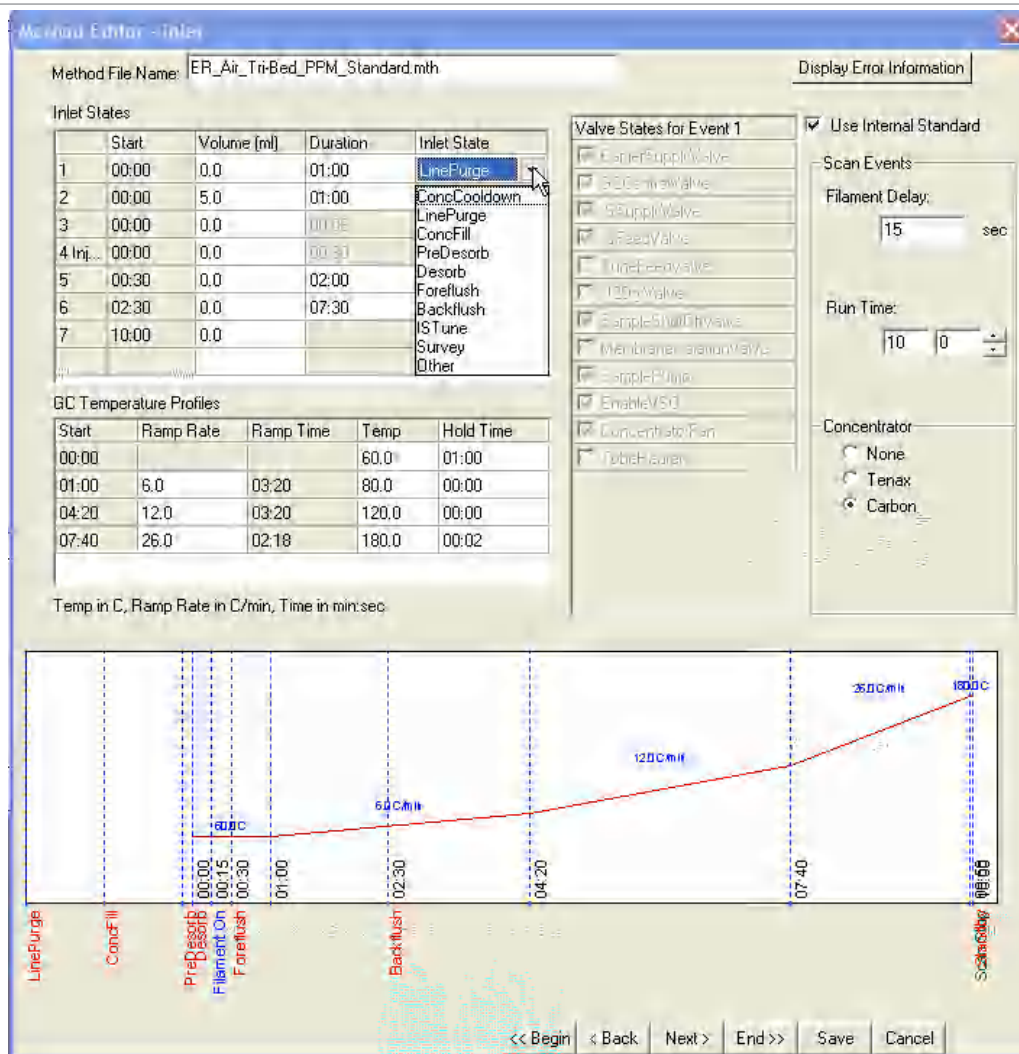
Inlet States				
	Start	Volume (ml)	Duration	Inlet State
1	00:00	0.0	01:00	LinePurge
2	00:00	100.0	01:00	ConcFill
3	00:00	0.0	00:08	PreDesorb
4 Inj..	00:00	0.0	00:30	Desorb
5	00:30	0.0	02:00	Foreflush
6	02:30	0.0	07:30	Backflush
7	10:00	0.0		Standby

GC Temperature Profiles				
Start	Ramp Rate	Ramp Time	Temp	Hold Time
00:00			60.0	01:00
01:00	6.0	03:20	80.0	00:00
04:20	12.0	03:20	120.0	00:00
07:40	26.0	02:18	180.0	00:02

Temp in C, Ramp Rate in C/min, Time in min:sec

To edit the **Inlet States** grid, select an **Inlet State** from the drop-down menu.



The following choices are available for all Analyze methods in the **Inlet States** column:

Line Purge	Directs the sample through the sample pathway and out through the exhaust vent. The sample does not pass through the concentrator.
Foreflush	Directs the carrier gas to allow the sample to flow out of the sample loop/concentrator and onto the column.
Backflush	Directs the carrier gas to the front end of the column. This state will remove non-volatile contaminants, while allowing the volatile compounds to be separated on the column.
IS Tune	Directs the internal standard to the MS for tuning.
Survey	Turns on the sampling pump and directs the sample to the inlet of the MS.
Other	Customizes each specific GC valve for a custom GC valve state. Useful for GC troubleshooting.

Standby	<b>Standby</b> is the last state of every method. <b>Standby</b> closes the <b>Membrane Isolation</b> valve and turns off the MS filament.
---------	--

The following additional **Inlet States** are available in the **Inlet States** column when a sample loop is being used:

Loopfill	Controls the sample pump and directs the sample through the sample loop.
----------	--

The following additional **Inlet States** are available in the **Inlet States** column when a concentrator is being used:

ConcFill	Controls the sample pump. This step directs the sample through the concentrator to allow the analytes to absorb to the concentrator bed.
ConcCooldown	The concentrator is cooled to a desired operating temperature.
PreDesorb	<b>PreDesorb</b> starts the desorption of analytes from the concentrator process.
Desorb	Completes the analyte desorption process. This state directs the analytes to the GC column.

The following **Inlet States** are only available in the **Inlet States** column when the **HSS** is enabled for use:

HSSample	Turns on the sample pump to direct sample through the transfer line to the HAPSITE ER. The suggested <b>HSSample</b> duration is approximately 15 seconds.
HSPurge	Directs carrier gas flow through the lines, the needle assembly and the transfer line to remove moisture and clean out the previous sample.
HSConcDry	Directs carrier gas flow through the transfer line and concentrator to remove moisture prior to sample injection. This should only be used if the <b>HSS</b> is connected to an external cylinder of carrier gas.

The following **Inlet States** are only available when the **SituProbe** is attached:

SPLinePurge	Directs carrier gas through the lines, <b>SituProbe</b> assembly and the transfer line to clear out carryover from a previous sample.
SPConcFill	Controls the sample pump and directs the sample through the concentrator
SCLoopFill	Controls the sample pump and directs the sample through the sample loop.
SPN2DryPurge	Purges the transfer line and concentrator with carrier gas before sample injection to remove moisture.

After selecting the **Inlet State**, enter the desired time period for the event in the **Duration** column.

**Method Editor - Inlet**

Method File Name:  Display Error Information

**Inlet States**

	Start	Volume (ml)	Duration	Inlet State
1	00:00	0.0	01:00	ConcFill
2 Inj...	00:00	0.0	05:00	Foreflush
3	05:00	0.0	10:00	Backflush
4	15:00	0.0		Standby

**Valve States for Event 1**

- CarrierSupplyValve
- GCControlValve
- ISSupplyValve
- ISFeedValve
- TuneFeedValve
- N2DryValve
- SampleShutOffValve
- MembraneIsolationValve
- SamplePump
- EnableVSO
- ConcentratorFan
- TubeHeater

**Scan Events**

Filament Delay:  sec

Run Time:

**Concentrator**

- None
- Tenax
- Carbon

**GC Temperature Profiles**

Start	Ramp Rate	Ramp Time	Temp	Hold Time
00:00			60.0	07:00
07:00	20.0	04:30	150.0	00:00
11:30	10.0	03:00	180.0	00:30

Temp in C, Ramp Rate in C/min, Time in min:sec

Upon entering the **Duration** settings, the **Start** time is automatically calculated for the next **Inlet State**.

Method Editor - Inlet

Method File Name: Method01.mth Display Error Information

Inlet States

	Start	Volume (ml)	Duration	Inlet State
1	00:00	0.0	01:00	ConcFill
2 Inj...	00:00	0.0	07:00	Foreflush
3	07:00	0.0	10:00	Backflush
4	17:00	0.0		Standby

Valve States for Event 1

- CarrierSupplyValve
- GCControlValve
- ISSupplyValve
- ISFeedValve
- TuneFeedValve
- N2DryValve
- SampleShutOffValve
- MembraneIsolationValve
- SamplePump
- EnableVSD
- ConcentratorFan
- TubeHeater

Scan Events

Filament Delay:  sec

Run Time:

Concentrator

- None
- Tenax
- Carbon

GC Temperature Profiles

Start	Ramp Rate	Ramp Time	Temp	Hold Time
00:00			60.0	07:00
07:00	20.0	04:30	150.0	00:00
11:30	10.0	03:00	180.0	02:30

Temp in C, Ramp Rate in C/min, Time in min:sec

<< Begin < Back Next > End >> Save Cancel

Events can be deleted from the template. Click inside the desired cell in the grid and press the **Delete** key on the laptop keyboard.

Events can be inserted into the template. Click inside the cell that will precede the desired event and press the **Insert** key on the laptop keyboard to insert a row.



Rows cannot be inserted after the **Standby** event.

## 15.6.2 GC Temperature Profile

**GC Temperature Profiles** specify the column temperature, ramp rate and hold settings for the HAPSITE ER Method. Adjusting the temperature program changes the retention times of the internal standards.

GC Temperature Profiles

Start	Ramp Rate	Ramp Time	Temp	Hold Time
00:00			60.0	07:00
07:00	20.0	04:30	150.0	00:00
11:30	10.0	03:00	180.0	00:30

Temp in C, Ramp Rate in C/min, Time in min:sec

Adjustments to the **Hold Time**, **Ramp Rate** and **Temp** columns automatically updates dependent parameters. For example, increasing the **Temp** increases the **Ramp Time** and increasing the **Hold Time** adjusts the **Start** time of the next parameter.

GC Temperature Profiles

Start	Ramp Rate	Ramp Time	Temp	Hold Time
00:00			60.0	08:00
08:00	20.0	05:00	160.0	00:00
13:00	10.0	02:00	180.0	00:30

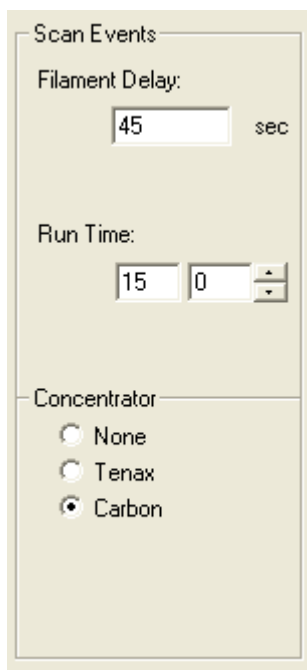
Temp in C, Ramp Rate in C/min, Time in min:sec



A maximum of four lines is permitted in this section.

### 15.6.3 Scan Events

The items displayed in the **Scan Events** field is dependent upon the type of method.



Scan Events

Filament Delay:

45 sec

Run Time:

15 0

Concentrator

None

Tenax

Carbon

The **Filament Delay** delays the turning on of the filament. This protects the filament by allowing the components of the air peak or solvents to pass through the Mass Spectrometer.



#### CAUTION

**If the Filament delay is too short, the high pressure burst caused by a solvent peak may shut down HAPSITE ER and stop the analysis.**

The **Run Time** is the amount of time that the method will run.

The type of concentrator being used is selected in the Concentrator box. The options are None, Tenax or Carbon. See Tenax Concentrator [▶ 86] and Tri-Bed Concentrator [▶ 86] for more information on differences between concentrators.

### 15.6.4 Headspace Flow Parameter

The **Scan Events** field for Headspace has an additional parameter, **Headspace Flow Pressure**. **Headspace Flow Pressure** controls the flow rate of carrier gas through the **HSS** during the **Sample** and **Purge** states. This parameter is only available when the creating **HSS** methods.



Scan Events

Filament Delay:

sec

Run Time:

Concentrator

None

Tenax

Carbon

Headspace Flow Pres.

kPa

### 15.6.5 SituProbe Flow Parameter

The **Scan Events** field for the **SituProbe** has an additional parameter, **SituProbe Flow Pressure**. **SituProbe Flow Pressure** controls the flow rate of carrier gas through the **SituProbe** during the **Sample** and **Purge** states. This parameter is only available when creating **SituProbe** methods.

Scan Events

Filament Delay:

sec

Run Time:

Concentrator

None

Tenax

Carbon

SituProbe Flow Pres.

kPa

## 15.6.6 Scan Events for SIM Methods

When creating SIM methods, the beginning and end time for each scan set will be displayed. Adjustments to these times can be made on the SIM page. See SIM Page [▶ 327] for more details.

Scan Events

Filament Delay:

45 sec

Set	Begin Time	End Time
-----	------------	----------

Concentrator

None

Tenax

Carbon

## 15.7 Tune Page

The **Tune** page contains two tabs, **Report** and **Param**. Each provide information about the **Tune** file.

### 15.7.1 Param Page

The **Param** tab displays the tune filename, which sets the MS tune parameters for the method. The default filename is `default.tun`. If a different tune file is desired, the **Browse** button can be used to locate and specify the desired tune for the method.

This page also has a **Show Details** checkbox, which will produce a grid of tune parameters contained in the file. These parameters cannot be edited. If editing is desired, refer to Tune [▶ 276].

**Method Editor - Tune** [Close]

Method File Name:  Display Error Information

Param | Report

Tune File:  PC HAPSITE Browse

Show Details

Time	Temperature (C)	Event
00:00	60.0	LinePurge
00:00	60.0	ConcFill
00:30	60.0	PreBlast
00:45	60.0	ForcFlush, Filament On
05:30	60.0	Backflush
07:00	60.0	
11:30	100.0	
14:30	180.0	Scan Stop
15:00	180.0	Standby

<< Begin < Back Next > End >> Save Cancel

Method Editor - Param

Method File Name: Method01.mth Display Error Information

Param Report

Tune File: default.tun Browse

Show Details

Mass Tune Settings

Mass	Position	Resolution	Ion Energy
50	10424	9737	120
55	11450	10683	60
69	14377	13460	135
93	19414	18215	120
117	24414	22927	148
167	34888	32811	170
213	44507	41896	190

Basic Tune Settings

EM Voltage (Volts):	1400	Threshold:	65	Points Per Amu:	10	Rod Polarity:	
Focus Voltage (Volts):	5	Baseline:	23	No. Scans/Avg:	3	<input type="checkbox"/> Tune	<input type="checkbox"/> Reverse
Extractor Voltage (Volts):	71	Base Peak:	117	Dwell (us):	400		
Emission Current (uA):	370	Base Peak Gain:	1.75825	Pressure (Pa):	0.0004191		

<< Begin < Back Next > End >> Save Cancel

## 15.7.2 Report Page

The **Report** page displays the AutoTune report in a printable format.

**Method Editor - Report**

Method File Name: ER\_Air\_Tri-Bed\_PPM\_Standard.mth Display Error Information

Param Report

Date of Report: 1/21/2011  
Time of Report: 3:00:35 PM

Calibration Status

Mass	Width	Area	Low%	High%	Diff(mmu)	Peak%	Status
50	0.86	81987	0.5	2.5	1914	1.80	OK
55	0.96	126654	2.0	5.0	2133	2.79	OK
69	0.94	408425	8.0	16.0	2744	8.98	OK
93	0.90	870025	15.0	25.0	3803	19.13	OK
117	0.91	4547472	100.0	100.0	4861	100.00	OK
167	0.92	2387806	50.0	70.0	6969	52.51	OK
213	0.98	714169	10.0	20.0	8988	15.70	OK
246	0.91	1391542	15.0	40.0	10345	30.60	OK

Auto Tune Configuration

Gain: 0.649639      Adjust Lens/Emission Ion: 117  
Base Peak Gain: 0.64      Base Peak: 117

<< Begin < Back Next > End >> Save Cancel

## 15.8 Full Scan Page

The **Full Scan** page sets the mass ranges for the method. The set can be assigned a **Scan Set Name** for easy identification, if desired. The **Filament Delay**, from the **Inlet Page** (refer to Scan Events [▶ 319]), is also shown on the **Full Scan** page. Changing the **Filament Delay** on this page may require changes to the **Inlet Page**.

**Method Editor - Full Scan**

Method File Name:  Display Error Information

Scan Set Name:  Filament Delay:  sec

Start Mass:  Skip Mass Range:

End Mass:

Dwell Time (us):  Enter skip masses and/or mass ranges separated by commas. For example: 18,28,32-44

Run Time:  min  sec

Scan Time (sec):

The following mass spectrometer parameters can be programmed:

Start Mass	The mass at which the mass spectrometer will start to scan. The starting mass can be set from 1 to 300 amu, however values between 40-50 are recommended to avoid detection of high-volatility interferences
End Mass	The mass at which the mass spectrometer will end a scan. The end mass can be set from 1-300 amu. This value must be larger than the start mass.



End the scan at least 2 amu above any mass used for compound identification. However, do not increase the end mass higher than necessary, as this will increase the scan time and a lower number of scans will be collected.

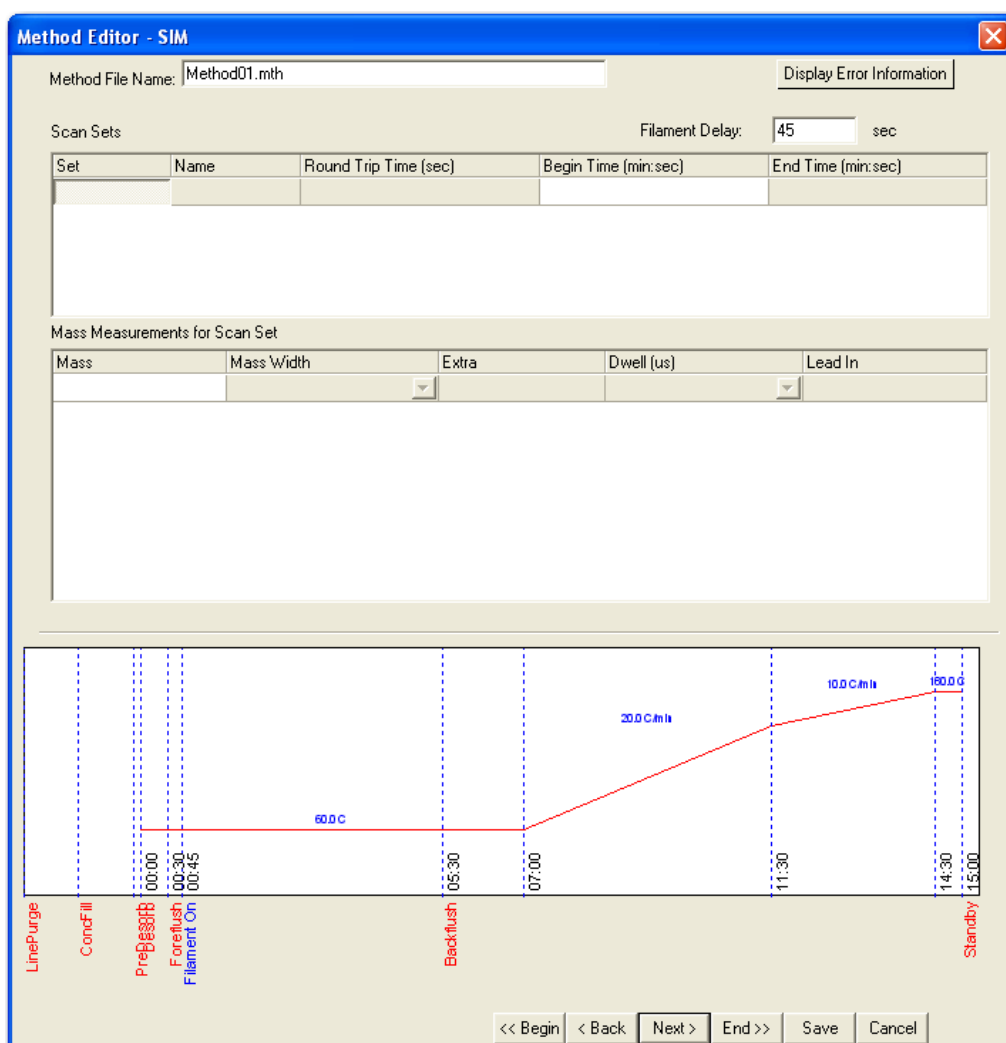
Dwell Time	The <b>Dwell Time</b> is the length of time the mass spectrometer will sample data at each sampling point. The longer the <b>Dwell Time</b> , the better the signal to noise ratio of the analyte.
Run Time	The time span of the method from start to finish.

## 15.9 SIM Page

**Selected Ion Monitoring (SIM)** scans a set of specific masses to increase the sensitivity for know compounds. The figure in the following section displays the **SIM** page.

### 15.9.1 SIM for Analyze

Each set has a **Begin Time** and an **End Time** which must be entered when programming the **Set**. An optional **Name** can also be entered at this point. After entering the times, the mass fragments for the compound can be entered into the **Mass** column. As the mass fragments are entered, the **Round Trip Time** is automatically calculated and entered in the **Scan Sets** grid.



The **Scan Sets** fields, in the order recommended for editing, are as follows:

Begin Time	The start time for mass collection.
End Time	The stop time for mass collection.

Name	Each scan set can be assigned a name for identification purposes. This entry is optional.
------	---



One of the column entries listed above must be highlighted to enable editing of the **Mass** list for that specific **Scan Set**.

Mass	The mass fragments of each column are entered in this column.
Mass Width	The width, in tenths of an amu, around the mass which the mass spectrometer will scan. For example, a <b>Mass Width</b> of 0.6 will scan 0.3 amu on each side of the peak.
Extra	This sets the number of extra scans, from 0 - 10, for each mass. Extra scans lower the detection limits by increasing the intensity within the mass spectrometer. Extra scans should be used when scanning for compounds with concentrations of ppb or lower.
Dwell	<b>Dwell</b> is the amount of time the software will search each for the selected mass. The dwell can be set from 100 $\mu$ s - 5,000 $\mu$ s. 400 $\mu$ s is recommended. Increasing the <b>Dwell</b> decreases the detection limit.
Lead In	<b>Lead In</b> determines the number of points the mass spectrometer will skip prior to scanning the desired mass peak. Best practice is to set the <b>Lead In</b> to at least a 1000 $\mu$ s delay prior to collecting data. The delay is based on <b>Lead In</b> multiplied by the <b>Dwell</b> .



The **Mass Width**, **Extra**, **Dwell** and **Lead In** values for a new entry are automatically populated based upon the entry listed above.

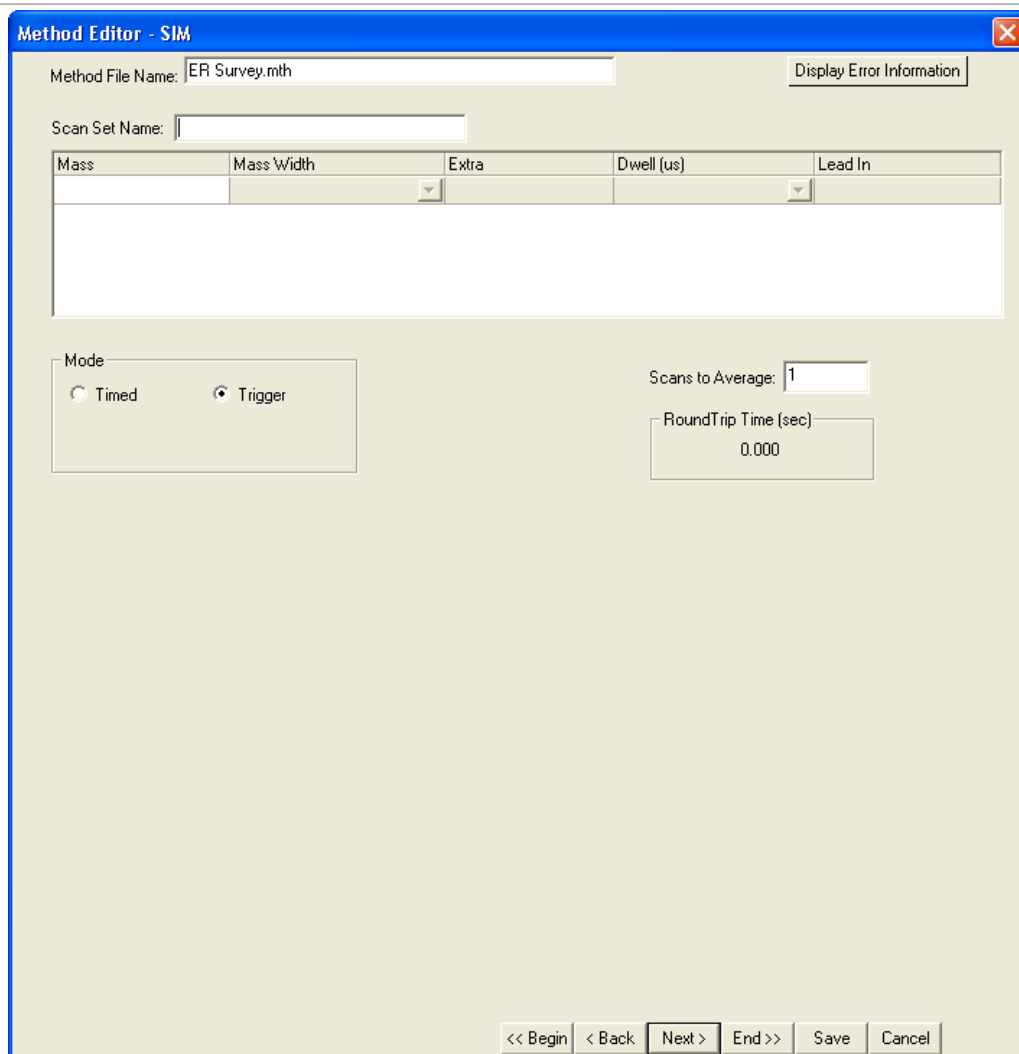


To fill any column with the entry listed above, click in the desired cell and press Ctrl+D.

## 15.9.2 SIM for Survey

The SIM page for Survey mode provides the ability to create only one scan set.





Scan Set Name	References the specific set of ions being defeated.
Timed Mode	The Survey method will run for a programmed amount of time.
Trigger Mode	The method will stop when the <b>STOP</b> button or <b>SURVEY RUN</b> button is selected.
Scans to Average	Determines the number of scans that will be collected and averaged before the results are displayed on the chromatogram.

### 15.9.3 Creating a SIM Method

✓ Follow Step 1 through Step 4 of Reloading Default HAPSITE Methods [▶ 303].

- 1 Change the **Collection Mode** to **SIM**.

The screenshot shows the 'Method Editor - Description' window. At the top, the 'Method File Name' is 'ER\_Air\_Tri-Bed\_PPB\_StandardSIM.mth'. Below this, the 'Mode of Analysis' section has 'GC/MS' selected. The 'Collection Mode' section has 'SIM' selected, which is highlighted with a red box. The 'Description' text area contains the following text: 'HAPSITE ER: General purpose Air analysis for VOCs using Carbon concentrator, 10 minute analysis. Method will detect CWA compounds with identification by AMDIS library. Carbon concentrator covers a wide boiling point range and is usable for compounds with boiling points from -15 C up. 1 minute inlet line cleanout plus 100 mL sample collection. Sensitivity is in the low to mid ppb range, compound dependent. Method should be used only with triple bed Carbon concentrator tube when detecting CWA compounds.'

Below the description is a chromatogram plot showing temperature (C) and flow rate (ml/min) over time. The plot is divided into several stages by vertical dashed lines:

- LinePurge
- ConcFill
- PrePurge
- Filament On
- Foreflush
- Backflush
- Standby

The temperature profile is as follows:

- 00:00: 60°C
- 01:00: 60°C
- 02:30: 60°C
- 04:20: 120°C
- 07:40: 260°C
- 08:00: 180°C

At the bottom of the window are navigation buttons: '<< Begin', '< Back', 'Next >', 'End >>', 'Save', and 'Cancel'.

2 Select **Next** until the **SIM** page is displayed.

Method Editor - Description

Method File Name: ER\_Air\_Tri-Bed\_PPB\_StandardSIM.mth

Display Error Information

Mode of Analysis

- GC/MS
- Survey

Collection Mode

- Full Scan
- SIM

Description

HAPSITE ER: General purpose Air analysis for VOCs using Carbon concentrator, 10 minute analysis. Method will detect CWA compounds with identification by AMDIS library. Carbon concentrator covers a wide boiling point range and is usable for compounds with boiling points from -15 C up. 1 minute inlet line cleanout plus 100 mL sample collection. Sensitivity is in the low to mid ppb range, compound dependent. Method should be used only with triple bed Carbon concentrator tube when detecting CWA compounds.

LinePurge  
ConcFill  
PreDesorb  
Filament On  
Foreflush  
Backflush  
Standby

100C  
60C/min  
120C/min  
250C/min  
180C

00:00  
00:15  
00:30  
01:00  
02:30  
04:20  
07:40  
08:00

<< Begin < Back **Next >** End >> Save Cancel

- 3 For the **Begin Time**, enter in the number displayed in the **Filament Delay**. For default ER methods, this is 15 seconds.

Method Editor - SIM

Method File Name: ER\_Air\_Tri-Bed\_PPB\_StandardSIM.mth Display Error Information

Scan Sets Filament Delay: 15 sec

Set	Name	Round Trip Time (sec)	Begin Time (min:sec)	End Time (min:sec)
1		0.000	00:15	00:00

Mass Measurements for Scan Set 1

Mass	Mass Width	Extra	Dwell (us)	Lead In

<< Begin < Back Next > End >> Save Cancel

- 4 Enter the desired **End Time** so that the **Begin Time** and the **End Time** surround the expected retention time of the compound.

**Method Editor - SIM**

Method File Name:  Display Error Information

Scan Sets Filament Delay:  sec

Set	Name	Round Trip Time (sec)	Begin Time (min:sec)	End Time (min:sec)
1		0.000	00:15	02:00

Mass Measurements for Scan Set 1

Mass	Mass Width	Extra	Dwell (us)	Lead In

5 Enter the name of the chemical of interest.

Method Editor - SIM

Method File Name: ER\_Air\_Tri-Bed\_PPB\_StandardSIM.mth Display Error Information

Scan Sets Filament Delay: 15 sec

Set	Name	Round Trip Time (sec)	Begin Time (min:sec)	End Time (min:sec)
1	Benzene	0.000	00:15	02:00

Mass Measurements for Scan Set 1

Mass	Mass Width	Extra	Dwell (us)	Lead In

<< Begin < Back Next > End >> Save Cancel

6 Enter at least three mass fragments for the selected chemical of interest.

Method Editor - SIM

Method File Name: ER\_Air\_Tri-Bed\_PPM\_StandardSIM.mth Display Error Information

Scan Sets Filament Delay: 15 sec

Set	Name	Round Trip Time (sec)	Begin Time (min:sec)	End Time (min:sec)
1		0.240	00:15	02:00

Mass Measurements for Scan Set 1

Mass	Mass Width	Extra	Dwell (us)	Lead In
51.0	0.6	10	1000	3
77.0	0.6	10	1000	3
78.0	0.6	10	1000	3

7 It is recommended that the **Dwell Time** is adjusted until the **Round Trip** is approximately one second.

Method Editor - SIM

Method File Name: ER\_Air\_Tri-Bed\_PPM\_StandardSIM.mth Display Error Information

Scan Sets Filament Delay: 15 sec

Set	Name	Round Trip Time (sec)	Begin Time (min:sec)	End Time (min:sec)
1	Benzene	1.000	00:15	02:00

Mass Measurements for Scan Set 1

Mass	Mass Width	Extra	Dwell (us)	Lead In
51.0	0.6	10	4165	3
77.0	0.6	10	4165	3
78.0	0.6	10	4165	3

<< Begin < Back Next > End >> Save Cancel

8 Repeat Step 4 through Step 7 if successive chemicals are desired.



The **End Time** for the final SIM compound must be the same as the end run time for the method.

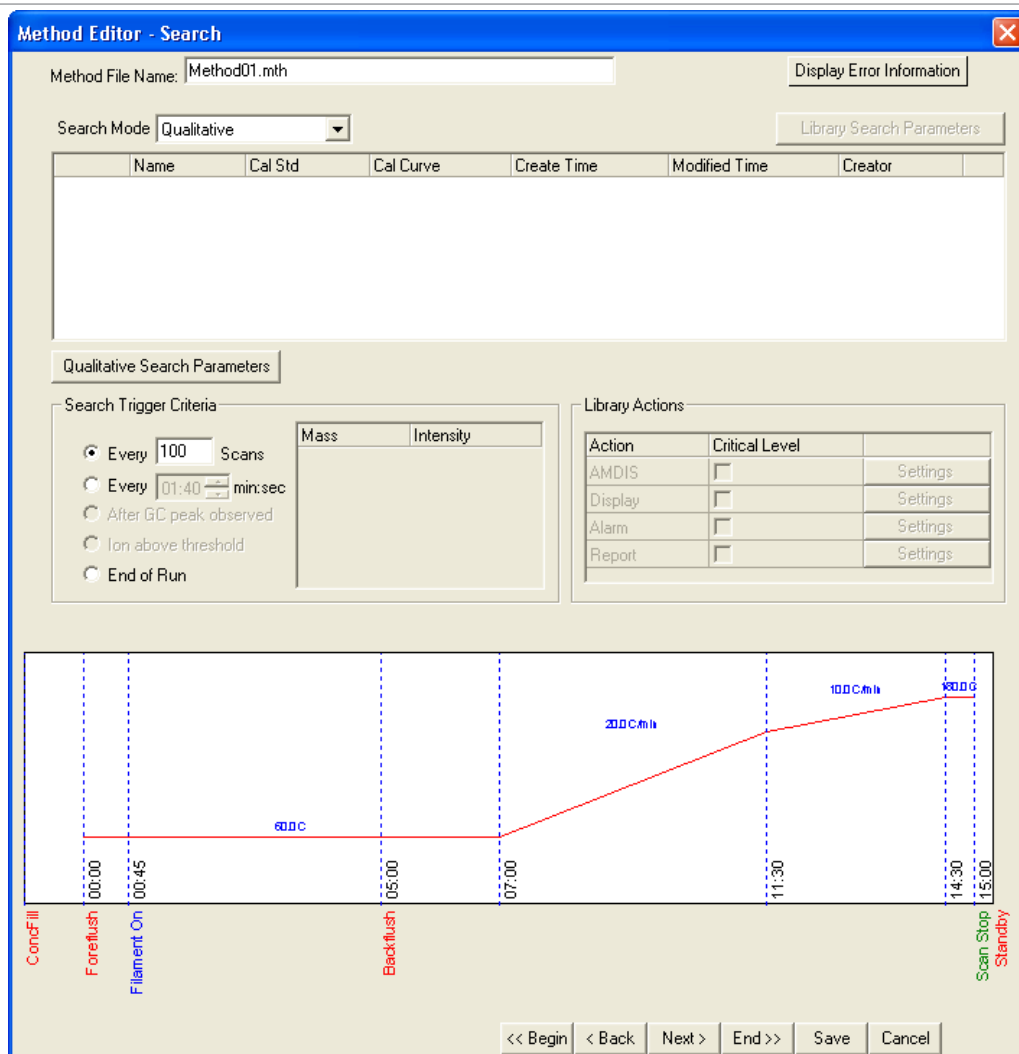


**AMDIS** and the **Search NIST/User** libraries are not available when using a SIM method.

## 15.10 Search Page

The **Search Page** sets the necessary parameters to qualify and quantify data. To quantify data, a calibration library must be created. See Calibration [▶ 370], for instructions on creating a calibration library.





There are four choices in the **Search Mode** drop down menu.

**SIM Methods only allow No Search as the search option.**

No Search	If this option is selected, a library search will not be conducted and a report will not be displayed on the front panel at the end of the run.
Qualitative	Searches AMDIS during a run to provide near real-time identifications. A report will be generated at the end of the run and can be viewed on the front panel display.
Quantitative	Generates a <b>Quantitative (Quant)</b> report at the end of the run by referencing the designated library.
Qualitative/ Quantitative	Searches AMDIS to provide identifications during a run and generates a <b>Quantitative</b> report.

## 15.10.1 Setting Up a Qualitative Search



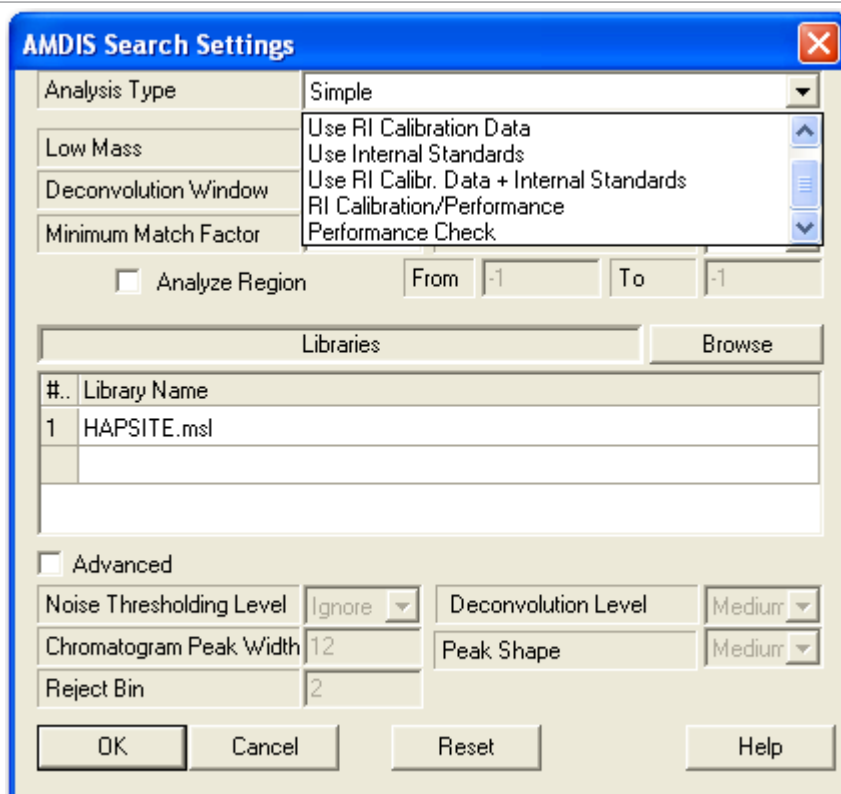
### ⚠ CAUTION

**Only trained users should modify methods. Changing parameters may result in incorrect data.**

To set up a qualitative search, the drop-down menu for the Search Mode must be set to **Qualitative**. AMDIS will be used to identify the sample components. The search parameters can be modified using the **Qualitative Search Settings** button.

AMDIS Search Settings				
Analysis Type	Simple			
Low Mass	45	High Mass	250	
Deconvolution Window	8	Sensitivity	14	
Minimum Match Factor	70	Resolution	Medium	
<input type="checkbox"/> Analyze Region	From	-1	To	-1
Libraries		Browse		
#.	Library Name			
1	HAPSITE.msl			
<input type="checkbox"/> Advanced				
Noise Thresholding Level	Ignore	Deconvolution Level	Medium	
Chromatogram Peak Width	12	Peak Shape	Medium	
Reject Bin	2			
OK		Cancel	Reset	Help

The figure below lists the different analysis types available for the search.



Low Mass	45	High Mass	300
Deconvolution Window	8	Sensitivity	30
Minimum Match Factor	60	Resolution	Medium

Simple	The mass spectral data is used to identify the compounds. The calculated match factor is only based upon the quality of the match between the deconvoluted component spectra and the target library spectra.
RI Calibration Data	This type of analysis uses an external calibration file. If the identified compound is not within a specified retention window, the program will penalize the match factor by a specified amount.
RI Calibration Data + Internal Standard	In this mode, the retention indices are calculated from the external calibration file. The internal standards are used to ensure that the instrument is functioning properly and that the samples were prepared properly. The internal standards are not used to calculate retention indices.
RI Calibration/ Performance	This analysis establishes the correlation between the retention time of a component and the retention index using the set of standards specified in the calibration library.

Performance Check	This analysis verifies that the HAPSITE ER is properly identifying performance standards. The analysis does not perform a calibration.
Low Mass	The lowest mass in the range of masses being considered.
Deconvolution Window	The number of adjacent peaks subtracted from the deconvoluted peak.
Minimum Match Factor	The threshold net match factor value for an identification to be reported. Values at or above 80 are good matches, 70-79 are fair and less than 70 is poor. For most cases, a match factor of 70 is the minimum that should be used if identification rather than detection is desired.
High Mass	The highest mass in the range being considered.
Sensitivity	Sets the sensitivity for the method. If the sensitivity is set too low, an increase in noise and broad peaks may result. If the sensitivity is set too high, it increases the risk of false positives.
Resolution	The resolution can be set to high, medium or low. The default setting is medium. This setting affects peak shape. Higher resolution results in sharper peaks, while lower resolution results in broader ones.

If **Analyze Region** is selected, AMDIS only searches in the selected scan range. When **Analyze Region** is off (i.e., unchecked), the software searches the entire range specified by **Low Mass** and **High Mass**.

The HAPSITE.MSL is the default AMDIS library for the system.

Libraries		Browse
##	Library Name	
1	HAPSITE.msl	

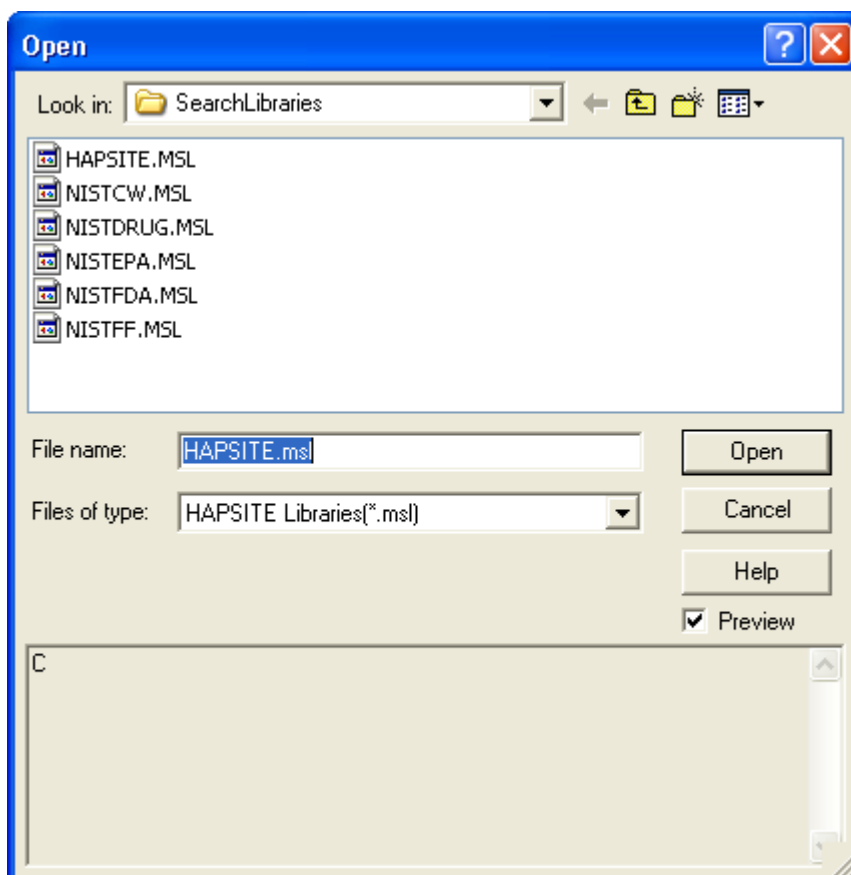
### INFICON recommends using HAPSITE.MSL

To view other library choices, select the **Browse** button. There are several small and specific libraries in addition to the HAPSITE.MSL. Many of the compounds found in these small libraries, that can be detected by the HAPSITE ER, are incorporated in the HAPSITE.MSL file.

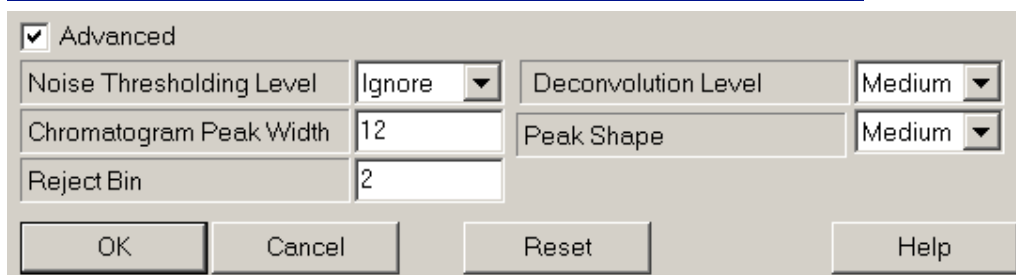
#### AMDIS Libraries:

- HAPSITE.MSL
- NISTEPA.MSL
- NISTCW.MSL
- NISTFDA.MSL

- NISTFF.MSL
- NISTDRUG.MSL



**Advanced Settings:**



**INFICON does not recommend changing the Advanced Settings.**

Noise Thresholding Level	Refers to the minimum signal recorded. Will filter out noise along the baseline.
Chromatogram Peak Width	Deconvoluted peaks will maintain same shape, because the width, in amus, has been specified.
Reject Bin	Rejects peaks that have less than a set number of scans.
Deconvolution Level	As the level of deconvolution increases, the software increases the separation between peaks. The default setting is medium, but low and high options are available.
Peak Shape	The shape requirement allows all of the deconvoluted peaks to maintain the same shape. As the shape requirement increases, the shape of the individual ions will be more uniform.

The **Search Trigger Criteria** section of the **Search** page determines when an **AMDIS** search will be run. There are three choices.

The screenshot shows a dialog box titled "Search Trigger Criteria". On the left, there are five radio button options:
 

- Every 100 Scans
- Every 00:00 min:sec
- After GC peak observed
- Ion above threshold
- End of Run

 To the right of these options is a table with two columns: "Mass" and "Intensity". The table is currently empty.

Every ___ Scans	Determines the scan interval for running an AMDIS search. The default value for this is 100 scans.
Every ___ min:sec	Determines the time intervals for running an AMDIS search.
End of Run	An AMDIS search will only be conducted at the end of a run.

## 15.10.2 Setting Up a Quantitative Search

Once a calibration library has been created, the **Library Search Parameters** button is activated. The **Library Search Parameters** functions set the peak identification criteria of the library compounds, as well as the unknown analytes.

Method Editor - Search

Method File Name: ER\_Air\_Tri-Bed\_PPM\_Quant.mth Display Error Information

Search Mode: Quantitative Library Search Parameters

Name	Cal Std	Cal Curve	Create Time	Modified Time	Creator	
ER Air PPM Quant Lib...	<input checked="" type="checkbox"/> Interna	Linear, forced through or...	6/24/2009 7:57:52 ...	4/21/2010 12:54:33 ...	INFICON, I...	Edit

Qualitative Search Parameters

Search Trigger Criteria

- Every 100 Scans
- Every 00:00 min:sec
- After GC peak observed
- Ion above threshold
- End of Run

Mass	Intensity
------	-----------

Library Actions

Action	Critical Level	
AMDIS	<input type="checkbox"/>	Settings
Display	<input type="checkbox"/>	Settings
Alarm	<input type="checkbox"/>	Settings
Report	<input type="checkbox"/>	Settings

Temperature Profile Graph:

- Line Purge
- Conc Fill
- Pre-Burn
- Filament On
- Foreflush
- Backflush
- 11:00
- Scan Stop
- Standby

Temperature: 20C/min, 300C/min, 180C

Navigation: << Begin < Back Next > End >> Save Cancel

Clicking the **Library Search Parameters** button on the **Method Editor Search** page displays the following window.

### 15.10.3 Peak Search

The peak search section is comprised of the parameters that are used in distinguishing a peak from the baseline.

Search Window	This value defines the acceptable retention time range for a peak. The default value is 20 seconds. When using the default value, the window is 10 seconds on either side of the expected retention time in order for the software to make an identification.
Min RIC Area	The area of the intensity of the largest mass fragment of the peak must be above this setpoint.
Min TIC	The area of the intensity of the total ion count for the peak must be above this setpoint.



Window Expand Factor	This option multiplies the retention time of the peak by the <b>Window Expand Factor</b> to give a period of time by which the search window will be expanded. For example, if the peak retention time is 10 minutes and the <b>Window Expand Factor</b> is set to its default setting of 0.05, the 10 minute retention time will be multiplied by the 0.05 <b>Window Expand Factor</b> to equal 30 seconds. Then, 30 seconds is added to the <b>Search Window</b> . If the default value of the <b>Search Window</b> is 20 seconds, adding 30 seconds from the <b>Window Expand Factor</b> to the <b>Search Window</b> would increase the search range to 50 seconds.
Min. Width	This value is the minimum number of scans per peak, which designates the area measurement for peak integration. Any peaks with fewer scans than this value will be disregarded by the software. Decreasing this number will result in the software accepting broader peaks.
Min. Fit	This compares the mass intensities of the compound to those saved in the library. Reasonable values depend on the selectivity of the calibration, but typically 0.5 to 0.9 is used. A higher <b>Min. Fit</b> number is more discriminative.
Peak Resolution (dx)	This number indicates the minimum number of scans between two peaks. It is used to determine whether a peak should be considered a single peak or if the peak should be split into two separate peaks.
Max Width	This value is the maximum number of scans per peak, which designates the area measurement for peak integration. Any peaks with more scans than this value will be disregarded by the software. Increasing this number will result in the software accepting broader peaks.
Min. Purity	This compares the purity level of the detected peak to the mass peak in the library. Reasonable values depend on the selectivity of the calibration, but typically 0.5 to 0.9 is used. A higher <b>Min. Purity</b> number is more discriminative.
Noise Level Mult	The peak intensity must be greater than the product of the <b>Noise Level Mult</b> number multiplied by the baseline noise in order to be identified as an analyte.
Precedence Level	Determines if the search uses the global parameters or compound-specific parameters. Leaving this set to zero allows the use of specific search parameters for individual compounds as discussed in Calibration [▶ 370].
Min. Area	This number discriminates against low responses which are usually attributed to noise rather than analyte detection. Increase this number to 10,000 or more if false positives are encountered.
Max Width	The peak must contain less scans than the setpoint number.
Low Mass	NIST will only use masses above this setpoint to make an identification.
High Mass	NIST will only use masses below this setpoint to make an identification.
Minimum Match Factor	The net fit in AMDIS must be above this number.

The **Reset** button resets the entered values to the default settings in the **Peak Search** window.

Reset

The **Elimination Rules** section gives you parameters for peaks to be reported. There are three options.

Elimination Rules

Keep no more than 10 peaks  Keep peaks above 15 %

Maximum NIST Hits 10

Keep no more than	This check box determines the number of peaks that will be displayed. If ten is selected, the ten peaks with the largest areas will be displayed.
Keep peaks above	When this box is checked, only peaks above the desired percent intensity will be displayed. Fifteen is generally used as the low end for intensity.
Maximum NIST Hits	This value is the number of matches that will be reported by NIST.



This section has a **Reset** button which will reset the entered values to the default settings.

## 15.10.4 Alarm

On the main **Method Editor Search** page, the **Alarm** option in the **Library Actions** box activates when a calibrated library has been saved to the method. To enable the **Alarm** option:

- 1 Check the **Alarm** box.

**Method Editor - Search**

Method File Name: ER\_Air\_Tri-Bed\_PPM\_Quant.mth Display Error Information

Search Mode: Quantitative Library Search Parameters

Name	Cal Std	Cal Curve	Create Time	Modified Time	Creator	
ER Air PPM Quant Lib...	<input checked="" type="checkbox"/> Interna	Linear, forced through or...	6/24/2009 7:57:52 ...	4/21/2010 12:54:33 ...	INFICON, I...	Edit

**Qualitative Search Parameters**

Search Trigger Criteria

Every 100 Scans  
 Every 00:00 min:sec  
 After GC peak observed  
 Ion above threshold  
 End of Run

Mass	Intensity
------	-----------

**Library Actions**

Action	Critical Level	
AMDIS	<input type="checkbox"/>	Settings
Display	<input type="checkbox"/>	Settings
<b>Alarm</b>	<input checked="" type="checkbox"/> Per Analyte	Settings
Report	<input type="checkbox"/>	Settings

Chromatogram showing temperature profile over time. The temperature starts at 80°C, remains constant until 11:00, then rises to 300°C by 14:30. Key events are marked: Line Purge, Cone Fill, Pre-Burn, Filament On, Foreflush, Backflush, and Scan Stop Standby.

<< Begin < Back Next > End >> Save Cancel

- 2 Enter the desired alarm level into the box with the units. The alarm is displayed when any analyte is detected at a concentration above the alarm level. To enter in alarm levels for individual analytes, see the figure below.

Method Editor - Search

Method File Name: ER\_Air\_Tri-Bed\_PPM\_Quant.mth Display Error Information

Search Mode: Quantitative Library Search Parameters

Name	Cal Std	Cal Curve	Create Time	Modified Time	Creator	
ER Air PPM Quant Lib...	<input checked="" type="checkbox"/> Interna	Linear, forced through or...	6/24/2009 7:57:52 ...	4/21/2010 12:54:33 ...	INFICON, I...	Edit

Qualitative Search Parameters

Search Trigger Criteria

Every 100 Scans  
 Every 00:00 min:sec  
 After GC peak observed  
 Ion above threshold  
 End of Run

Mass	Intensity
------	-----------

Library Actions

Action	Critical Level	
AMDIS	<input type="checkbox"/>	Settings
Display	<input type="checkbox"/>	Settings
Alarm	<input checked="" type="checkbox"/> 10 ppm	Settings
Report	<input type="checkbox"/>	Settings

<< Begin < Back Next > End >> Save Cancel

3 Click **Yes** to confirm that the alarm level is correct as entered.

ER IQ

Set Critical Level for all analytes in Library "ER Air PPM Quant Library" to 10 ppm?

**Yes** No

### 15.10.5 Edit Options

Clicking the **Edit** box displays the following information about the calibration library.

Method Editor - Search

Method File Name: ER\_Air\_Tri-Bed\_PPM\_Quant.mth Display Error Information

Search Mode: Quantitative Library Search Parameters

Name	Cal Std	Cal Curve	Create Time	Modified Time	Creator	
ER Air PPM Quant Lib...	<input checked="" type="checkbox"/> Interna	Linear, forced through or...	6/24/2009 7:57:52 ...	4/21/2010 12:54:33 ...	INFICON,	<b>Edit</b>

Qualitative Search Parameters

Search Trigger Criteria

- Every 100 Scans
- Every 00:00 min:sec
- After GC peak observed
- Ion above threshold
- End of Run

Mass	Intensity
------	-----------

Library Actions

Action	Critical Level	Settings
AMDIS	<input type="checkbox"/>	Settings
Display	<input type="checkbox"/>	Settings
Alarm	<input type="checkbox"/>	Settings
Report	<input type="checkbox"/>	Settings

<< Begin < Back **Next >** End >> Save Cancel

The **Analyte List** is displayed.

Library Analyte List - ER Air PPM Quant Library

Name	CAS#	Target Ion	RT Time	Standard	Conc.	IS Ref.
TRIS_42	729-81-7	42.0	01:16 680	Internal	10.52	1
TRIS_213	729-81-7	213.0	01:16 680	Internal	10.52	2
BPFB_79	344-04-7	74.0	04:09 660	Internal	5.36	3
BPFB_98	344-04-7	98.0	04:09 660	Internal	5.36	4
BPFB_117	344-04-7	117.0	04:09 660	Internal	5.36	5

TRIS\_42

Mass Peaks | Calibration | Search Parameters | Actions

Mass	Intensity	Tolerance
72.0	100	-1
71.0	94	-1
42.0	55	-1
213.0	44	-1
69.0	34	-1
41.0	26	-1
263.0	22	-1
163.0	21	-1
282.0	20	-1
75.0	19	-1
143.0	13	-1
144.0	12	-1

Template/Calibration Files

File Name	Temp	File Saved Time	Conc.	Unit
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 3:55:06...	0.1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:01:22...	1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:44:18...	0.75	ppm

Calibration Original

View Report

OK Cancel

The name of the compound is displayed in the name column, followed by the CAS number, the target ion and the predicted retention time. In the **Standard** column, either **Internal** or **Analyte** is selected. If **Internal** is selected, the compound is an internal standard. If **Analyte** is selected, the compound is an analyte of interest.

Library Analyte List - ER Air PPM Quant Library

Name	CAS#	Target Ion	RT Time	Standard	Conc.	IS Ref.
TRIS_42	729-81-7	42.0	01:16 680	Internal	10.52	1
TRIS_213	729-81-7	213.0	01:16 680	Internal	10.52	2
BPFB_79	344-04-7	74.0	04:09 660	Internal	5.36	3
BPFB_98	344-04-7	98.0	04:09 660	Internal	5.36	4
BPFB_117	344-04-7	117.0	04:09 660	Internal	5.36	5

TRIS\_42

Mass Peaks | Calibration | Search Parameters | Actions

Mass	Intensity	Tolerance
72.0	100	-1
71.0	94	-1
42.0	55	-1
213.0	44	-1
69.0	34	-1
41.0	26	-1
263.0	22	-1
163.0	21	-1
282.0	20	-1
75.0	19	-1
143.0	13	-1
144.0	12	-1

Template/Calibration Files

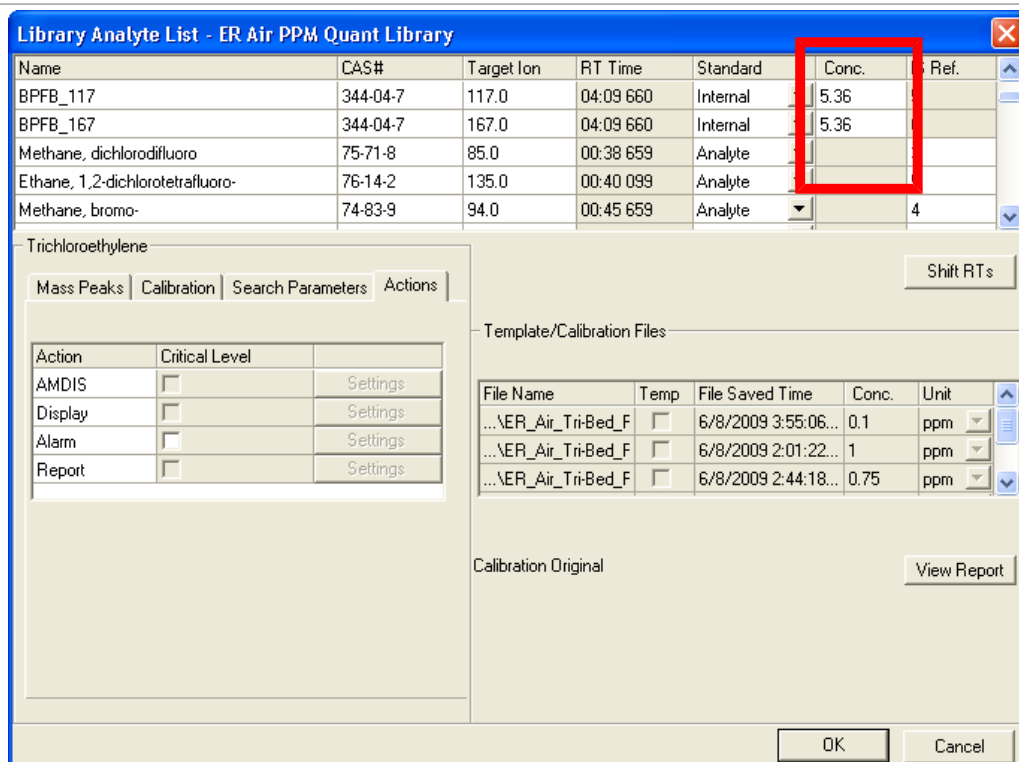
File Name	Temp	File Saved Time	Conc.	Unit
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 3:55:06...	0.1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:01:22...	1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:44:18...	0.75	ppm

Calibration Original

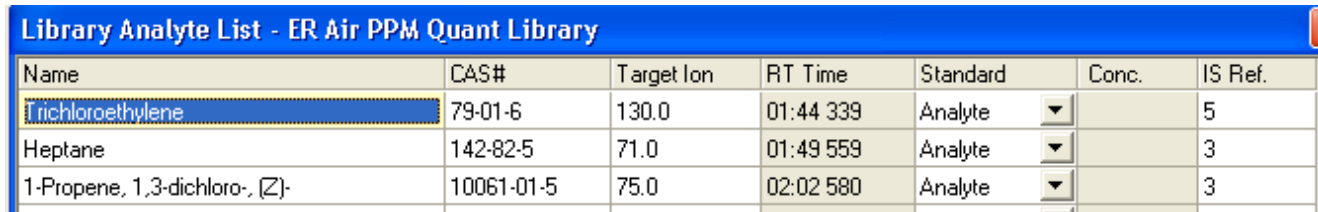
View Report

OK Cancel

The **Conc.** (concentration) column is populated for internal standards. It is blank if the compound is an analyte.



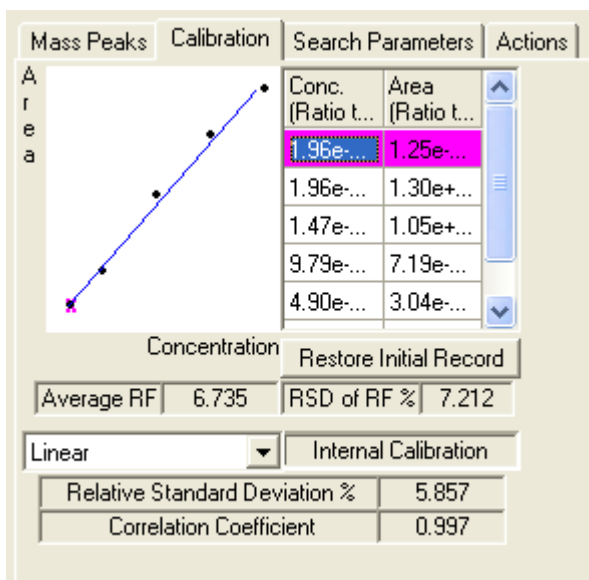
In the **IS Ref** column, all internal standards are given a number. For the air internal standards, this is 1-6. The analyst, when creating a method, will assign a number, (1-6 for the air internal standard) to each analyte. The assigned number is based upon the closeness of the target ion of the analyte to the closeness of the target ion of the internal standard. For instance, trichloroethylene has a target ion of 130. The internal standard, BPFB\_117, has a target ion of 117 and was assigned the number 5. Therefore, the analyst would enter 5 into the **IS Ref** column for trichloroethylene, because BPFB\_117 is the closest internal standard.



On the **Mass Peaks** tab, the mass fragments for the highlighted compound are displayed with their intensity.

Mass	Intensity	Tolerance
130.0	100	-1
132.0	89	-1
95.0	86	-1
97.0	52	-1
60.0	46	-1
88.0	36	-1
134.0	28	-1
58.0	24	-1
94.0	10	-1
59.0	9	-1
99.0	8	-1
96.0	7	-1

On the **Calibration** tab, the calibration curve for the analyte is displayed. See Calibration [▶ 370].



For information on the **Search Parameters** tab, refer to Peak Search [▶ 344].



Mass Peaks | Calibration | Search Parameters | Actions

Search Window Size: 00:30

Window Expand Factor: 0.05

Peak Resolution (dx): 5      Minimum Area: 50000

Noise Level Mult: 2      Minimum Fit: 0.75

Minimum Width: 7      Minimum Purity: 0.75

Maximum Width: 70      Precedence Level: 0

The **Alarm** tab allows an alarm level to be entered for each individual compound. To enter an alarm:

- 1 Highlight the desired compound.

Library Analyte List - ER Air PPM Quant Library

Name	CAS#	Target Ion	RT Time	Standard	Conc.	IS Ref.
Trichloroethylene	79-01-6	130.0	01:44 339	Analyte		5
Heptane	142-82-5	71.0	01:49 559	Analyte		3
1-Propene, 1,3-dichloro-, (Z)-	10061-01-5	75.0	02:02 580	Analyte		3
Methyl Isobutyl Ketone	108-10-1	43.0	02:03 300	Analyte		1
1-Propene, 1,3-dichloro-, (E)-	10061-02-6	75.0	02:16 679	Analyte		3

Trichloroethylene

Mass Peaks | Calibration | Search Parameters | Actions

Action	Critical Level	
AMDIS	<input type="checkbox"/>	Settings
Display	<input type="checkbox"/>	Settings
Alarm	<input checked="" type="checkbox"/>	Settings
Report	<input type="checkbox"/>	Settings

Template/Calibration Files

File Name	Temp	File Saved Time	Conc.	Unit
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 3:55:06...	0.1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:01:22...	1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:44:18...	0.75	ppm

Calibration Original      View Report

OK      Cancel

- 2 Check the **Alarm** box.

Library Analyte List - ER Air PPM Quant Library

Name	CAS#	Target Ion	RT Time	Standard	Conc.	IS Ref.
Trichloroethylene	79-01-6	130.0	01:44 339	Analyte		5
Heptane	142-82-5	71.0	01:49 559	Analyte		3
1-Propene, 1,3-dichloro-, (Z)-	10061-01-5	75.0	02:02 580	Analyte		3
Methyl Isobutyl Ketone	108-10-1	43.0	02:03 300	Analyte		1
1-Propene, 1,3-dichloro-, (E)-	10061-02-6	75.0	02:16 679	Analyte		3

Trichloroethylene

Mass Peaks | Calibration | Search Parameters | Actions

Action	Critical Level	
AMDIS	<input type="checkbox"/>	Settings
Display	<input type="checkbox"/>	Settings
Alarm	<input checked="" type="checkbox"/> 1	Settings
Report	<input type="checkbox"/>	Settings

Template/Calibration Files

File Name	Temp	File Saved Time	Conc.	Unit
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 3:55:06...	0.1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:01:22...	1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:44:18...	0.75	ppm

Calibration Original

View Report

Shift RTs

OK Cancel

3 Enter the desired concentration followed by the desired units.

Library Analyte List - ER Air PPM Quant Library

Name	CAS#	Target Ion	RT Time	Standard	Conc.	IS Ref.
Trichloroethylene	79-01-6	130.0	01:44 339	Analyte		5
Heptane	142-82-5	71.0	01:49 559	Analyte		3
1-Propene, 1,3-dichloro-, (Z)-	10061-01-5	75.0	02:02 580	Analyte		3
Methyl Isobutyl Ketone	108-10-1	43.0	02:03 300	Analyte		1
1-Propene, 1,3-dichloro-, (E)-	10061-02-6	75.0	02:16 679	Analyte		3

Trichloroethylene

Mass Peaks | Calibration | Search Parameters | Actions

Action	Critical Level	
AMDIS	<input type="checkbox"/>	Settings
Display	<input type="checkbox"/>	Settings
Alarm	<input checked="" type="checkbox"/> 1 ppm	Settings
Report	<input type="checkbox"/>	Settings

Template/Calibration Files

File Name	Temp	File Saved Time	Conc.	Unit
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 3:55:06...	0.1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:01:22...	1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:44:18...	0.75	ppm

Calibration Original

View Report

Shift RTs

OK Cancel

The **Shift RTs** option allows the predicted retention time for the highlighted analyte to be shifted by a desired amount of time. To shift the retention time:

1 Click **Shift RTs**.

Name	CAS#	Target Ion	RT Time	Standard	Conc.	IS Ref.
Trichloroethylene	79-01-6	130.0	01:44 339	Analyte		5
Heptane	142-82-5	71.0	01:49 559	Analyte		3
1-Propene, 1,3-dichloro-, (Z)-	10061-01-5	75.0	02:02 580	Analyte		3
Methyl Isobutyl Ketone	108-10-1	43.0	02:03 300	Analyte		1
1-Propene, 1,3-dichloro-, (E)-	10061-02-6	75.0	02:16 679	Analyte		3

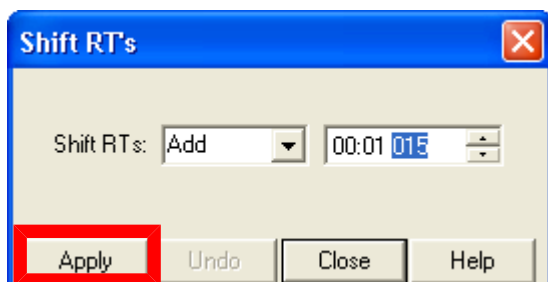
Mass	Intensity	Tolerance
130.0	100	-1
132.0	89	-1
95.0	86	-1
97.0	52	-1
60.0	46	-1
88.0	36	-1
134.0	28	-1
58.0	24	-1
94.0	10	-1
59.0	9	-1
99.0	8	-1
96.0	7	-1

2 The **Shift RTs** window is displayed.

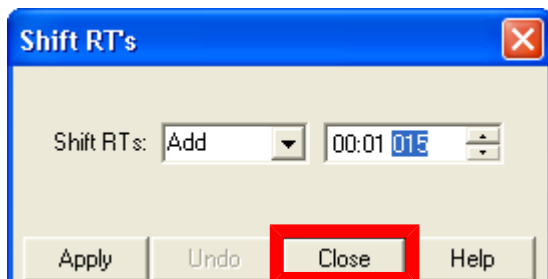
3 Select **Add** or **Subtract** from the menu.

4 Type in the desired amount of time.

5 Click **Apply**.



6 Click **Close**.



## 15.10.6 Template/Calibration Files

The first column will display the names of the files that were used to create the calibration curve, time that the file was saved, the concentration of the file and the units.

Template/Calibration Files				
File Name	Temp	File Saved Time	Conc.	Unit
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:01:22...	1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:44:18...	0.75	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 3:02:41...	0.5	ppm

## 15.10.7 View Reports

Clicking the **View Reports** button will display the **Calibration Response Report**.

**Library Analyte List - ER Air PPM Quant Library**

Name	CAS#	Target Ion	RT Time	Standard	Conc.	IS Ref.
TRIS_42	729-81-7	42.0	01:16 680	Internal	10.52	1
TRIS_213	729-81-7	213.0	01:16 680	Internal	10.52	2
BPFB_79	344-04-7	74.0	04:09 660	Internal	5.36	3
BPFB_98	344-04-7	98.0	04:09 660	Internal	5.36	4
BPFB_117	344-04-7	117.0	04:09 660	Internal	5.36	5

TRIS\_42

Mass Peaks | Calibration | Search Parameters | Actions

Mass	Intensity	Tolerance
72.0	100	-1
71.0	94	-1
42.0	55	-1
213.0	44	-1
69.0	34	-1
41.0	26	-1
263.0	22	-1
163.0	21	-1
282.0	20	-1
75.0	19	-1
143.0	13	-1
144.0	12	-1

Template/Calibration Files

File Name	Temp	File Saved Time	Conc.	Unit
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 3:55:06...	0.1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:01:22...	1	ppm
... \ER_Air_Tri-Bed_F	<input type="checkbox"/>	6/8/2009 2:44:18...	0.75	ppm

Calibration Original View Report

OK Cancel

The default window that will be displayed is the **Internal Standard Calibration Response Table**. This table will display the file names, the area of the peak and the response factor (the ratio between the signal produced by the analyte and the quantity of the analyte which produces a signal).

Calibration Response Report

Internal Standard:  
Analytes:  
All

Reports: Calibration Response Table

FULL SCAN Calibration Response Table  
HAPSITE method: /Haps/Method/Analyze/Concentrator  
Method Description:  
HAPSITE ER: General purpose Air analysis for VOC  
Tune File: default.tun  
Target Library: ER Air PPM Quant Library  
Last Modified: 4/21/2010 12:54:33 PM

$Q = RT + (0.30.00 / 2 + RT * 0.050)$   
Min Fit = 0.400; Min Pur = 0.100; Min Area = 500

Internal Standards

I.S. #1 -- TRIS\_42  
Concentration = 10.52 4 Calibration Points

pt.	File	Area	Resp. Factor
1	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_001	1247023	110614.3485
2	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_002	397478	94817.3370
3	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_003	659647	62704.1204
4	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_004	309908	29458.9519

Average RF = 7.639869e+004; RSD of RF = 50.76354%

I.S. #2 -- TRIS\_213  
Concentration = 10.52 5 Calibration Points

pt.	File	Area	Resp. Factor
1	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_005	610712	50952.4690
2	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_001	650456	61830.4156
3	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_002	679866	64626.0420
4	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_003	644804	61223.1532
5	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_004	652115	61908.1152

Average RF = 6.155804e+004; RSD of RF = 3.81243%

I.S. #3 -- BPEH\_79  
Concentration = 5.36 5 Calibration Points

pt.	File	Area	Resp. Factor
1	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_005	530193	100409.9693
2	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_001	541454	101017.5581
3	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_002	616170	114957.1567
4	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_003	545279	101731.1192
5	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_004	574317	106962.1475

Average RF = 1.050154e+005; RSD of RF = 5.84322%

I.S. #4 -- BPEH\_98  
Concentration = 5.36 5 Calibration Points

Export to Excel Save to File Print Close

By selecting analyte from the drop-down menu, the **Analyte Standard Calibration Response Table** will be displayed. The **Analyte Standard Calibration Response Table** contains the same information as the **Internal Standard Calibration Table**, but pertains to the calibrated analytes.

**Calibration Response Report**

Internal Standards  
 Analyte: All  
 Reports: Calibration Response Table

FULL SCAN Calibration Response Table  
 HAPSITE method: /Maps/Method/Analyze/Concentrator  
 Method Description:  
 HAPSITE ER: General purpose Air analysis for VOC  
 Tune File: default.tun  
 Target Library: ER Air PPM Quant Library  
 Last Modified: 4/21/2010 12:54:33 PM

$\sigma = RT \pm (0.30.00 / 2 * RT * 0.050)$   
 Min Fit = 0.400; Min Pur = 0.100; Min Area = 500

**Analytes**

Analyte #1 -- Methane, dichlorodifluoro  
 5 Calibration Points  
 Linear calibration curve  
 Concentration =  $(8.8080e+000)(AREA^{*2}) + (7.8005e-002)(AREA) + 6.9299e-004$

pt.	File	Conc.	Cratio	Area	Aratio	Resp. Factor
1	ER_Air_Tri-Med_PPM_QuantTes	1.050e-001	1.959e-002	147161	2.734e-001	1.39582e+001
2	ER_Air_Tri-Med_PPM_QuantTes	1.050e+000	1.959e-001	1378345	2.546e+000	1.29949e+001
3	ER_Air_Tri-Med_PPM_QuantTes	7.075e-001	1.462e-001	1056061	1.704e+000	1.15992e+001
4	ER_Air_Tri-Med_PPM_QuantTes	5.250e-001	2.795e-002	753215	1.301e+000	1.41020e+001
5	ER_Air_Tri-Med_PPM_QuantTes	2.625e-001	4.097e-002	328966	5.738e-001	1.17163e+001

Average RF = 1.207420e+001; RSD of Average RF = 9.24407%  
 RSD of Curve Fit = 8.73272%

Analyte #2 -- Ethane, 1,2-dichlorotetrafluoro-  
 4 Calibration Points  
 Linear calibration curve  
 Concentration =  $(8.8090e+000)(AREA^{*2}) + (3.0732e+000)(AREA) + -6.3191e-003$

pt.	File	Conc.	Cratio	Area	Aratio	Resp. Factor
1	ER_Air_Tri-Med_PPM_QuantTes	3.000e-001	1.020e-001	270489	4.531e-002	2.47041e-001
2	ER_Air_Tri-Med_PPM_QuantTes	7.350e-001	1.371e-001	238505	4.040e-002	2.94652e-001
3	ER_Air_Tri-Med_PPM_QuantTes	4.900e-001	2.442e-002	155081	2.672e-002	2.92245e-001
4	ER_Air_Tri-Med_PPM_QuantTes	2.450e-001	4.571e-002	72170	1.210e-002	2.64025e-001

Average RF = 2.748900e-001; RSD of Average RF = 0.20094%  
 RSD of Curve Fit = 10.30364%

Analyte #3 -- Methane, bromo-  
 5 Calibration Points  
 Linear calibration curve  
 Concentration =  $(8.8000e+000)(AREA^{*2}) + (1.6545e-001)(AREA) + 4.3087e-003$

pt.	File	Conc.	Cratio	Area	Aratio	Resp. Factor
1	ER_Air_Tri-Med_PPM_QuantTes	1.050e-001	1.959e-002	164285	1.079e-001	5.50023e+000

Export to Excel Save to File Print Close

Selecting **All** will display the information contained in the **Internal Standard Calibration Report** and the **Analyte Standard Calibration Report**.

**Calibration Response Report**

Internal Standards  
Analytes  
All

Reports: Calibration Response Table

FULL SCAN Calibration Response Table  
HAPSITE method: /Haps/Method/Analyze/Concentrator  
Method Description:  
HAPSITE ER: General purpose Air analysis for VOC  
Tune File: default.tun  
Target Library: ER Air PPM Quant Library  
Last Modified: 4/21/2010 12:54:33 PM

$Q = RT + (-0.30.00 / 2 + RT * 0.050)$   
Min Fit = 0.400; Min Pur = 0.100; Min Area = 500

Internal Standards

I.S. #1 -- TRIS\_42  
Concentration = 10.52 4 Calibration Points

pt.	File	Area	Resp. Factor
1	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_001	1247023	110614.3485
2	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_002	397478	94817.3370
3	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_003	659647	62704.1204
4	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_004	309908	29458.9519

Average RE = 7.639869e+004; RSD of RE = 50.76354%

I.S. #2 -- TRIS\_213  
Concentration = 10.52 5 Calibration Points

pt.	File	Area	Resp. Factor
1	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_005	610712	50952.4690
2	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_001	650456	61830.4156
3	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_002	679866	64626.0420
4	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_003	644804	61293.1532
5	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_004	652115	61908.1152

Average RE = 6.155804e+004; RSD of RE = 3.81243%

I.S. #3 -- BPEH\_79  
Concentration = 5.36 5 Calibration Points

pt.	File	Area	Resp. Factor
1	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_005	530193	100409.9693
2	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_001	541454	101017.5581
3	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_002	616170	114957.1567
4	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_003	545279	101731.1192
5	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_004	574317	106962.1475

Average RE = 1.050154e+005; RSD of RE = 5.84322%

I.S. #4 -- BPEH\_98  
Concentration = 5.36 5 Calibration Points

Export to Excel Save to File Print Close

The **Cal/Quant Report** can be viewed by selecting **Calibration Report** from the drop-down menu. The **Cal/Quant Report** will display the same information as a **Quantitative Report**. Refer to Reports [▶ 210] for more details. In the top right corner, the peak search parameters are also displayed. Refer to Peak Search [▶ 344].



**Calibration Response Report**

Internal Standards  
 Analytes  
 All

Tune File: default.tun  
 Target Library: ER Air PPM Quant Library  
 Last Modified: 4/21/2010 12:54:33 PM

$W = RT \pm (0.30.00 / 2 + RT + 0.050)$   
 Min Fit = 0.480; Min Pur = 0.100; Min Area = 5000  
 Width = 1 - 70 scans; Res = 5 scans; NLM = 2.000

Linear, forced through origin calibration curve

---

**Internal Standards**

**I.5. #1 -- TRIS\_42**  
 Concentration = 10.52 4 Calibration Points

pt.	File	Area	Resp. Factor
1	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_001	1247023	110614.3485
2	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_002	397478	94817.3370
3	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_003	659647	62704.1204
4	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_004	309908	29458.9519

Average RF = 7.639869e+004; RSD of RF = 50.76354%

**I.5. #2 -- TRIS\_213**  
 Concentration = 10.52 5 Calibration Points

pt.	File	Area	Resp. Factor
1	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_005	610712	50952.4690
2	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_001	650456	61830.4156
3	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_002	679866	64626.0420
4	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_003	644804	61293.1532
5	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_004	652115	61908.1152

Average RF = 6.155804e+004; RSD of RF = 3.31243%

**I.5. #3 -- BPEH\_79**  
 Concentration = 5.36 5 Calibration Points

pt.	File	Area	Resp. Factor
1	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_005	530193	100409.0693
2	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_001	541454	101017.5581
3	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_002	616170	114957.1567
4	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_003	545279	101731.1192
5	ER_Air_Tri-Bed_PPM_QuantTest2_20090608_004	574317	106962.1475

Average RF = 1.050154e+005; RSD of RF = 5.34322%

**I.5. #4 -- BPEH\_98**  
 Concentration = 5.36 5 Calibration Points

Export to Excel Save to File Print Close

## 15.11 Data Page

The **Data Page** customizes the names and the storage location of the data files for the method.

**Method Editor - Data**

Method File Name:  Display Error Information

---

**Data File Information**

Use Default Filename

Enter Filename Format:  File Increment Digits:

**Date and Time Appendix**

None  
  Date Only  
  Date and Time  
  As Suffix  
 As Prefix

Auto increment filenames

Use Default Directory

Browse...

Save Data

Save Data to Removable Drive (HAPSITE Only)

**Data Display**

Manual TIC Y Scale Max

Counts

e.g. 5000000 Counts

Note: A value of 0 disables default manual scale

---

<< Begin   < Back   Next >   End >>   Save   Cancel

### 15.11.1 Data File Information

**Data File Information**

Use Default Filename

Enter Filename Format:  File Increment Digits:

**Date and Time Appendix**

None  
  Date Only  
  Date and Time  
  As Suffix  
 As Prefix

Auto increment filenames

Use default filename

When checked, the method will use a default format for the data filename. The default filename is a combination of the method filename, the date and the sample run number.

File increment digits	Sets the number of digits appended to the data file name. By default, File Increment Digits is set to three digits.
-----------------------	---

### 15.11.2 Date and Time Appendix

If desired, the data and time can be added to the data file name using the following options:

**None:**

A date and time will not be added to the file name.

The screenshot shows the 'Method Editor' interface. At the top, there are two input fields: 'Enter Filename Format:' containing 'Method01' and 'File Increment Digits:' with a dropdown set to '3'. Below these is a preview box showing 'Method01\_000.hps'. The 'Date and Time Appendix' section has three radio buttons: 'None' (selected), 'Date Only', and 'Date and Time'. To the right are two more radio buttons: 'As Suffix' and 'As Prefix'. A checked checkbox labeled 'Auto increment filenames' is at the bottom.

**Date Only:**

The date will be added to the filename.

- yyyy is the year the data was collected
- mm is the month the data was collected
- dd is the day the data was collected

The screenshot shows the 'Method Editor' interface. The 'Enter Filename Format:' field contains 'Method01' and 'File Increment Digits:' is set to '3'. The preview box shows 'Method01\_yyyymmdd\_000.hps'. In the 'Date and Time Appendix' section, the 'Date Only' radio button is selected. 'As Suffix' and 'As Prefix' are also visible. The 'Auto increment filenames' checkbox is checked.

**Date and Time:**

Both the date and time will be added to the data file name. **hh** is the hour data collection was started. **mm** is the minute data collection was started. **ss** is the second data collection was started

The screenshot shows the 'Method Editor' interface. The 'Enter Filename Format:' field contains 'Method01' and 'File Increment Digits:' is set to '3'. The preview box shows 'Method01\_yyyymmdd\_hhmmss\_000.hps'. In the 'Date and Time Appendix' section, the 'Date and Time' radio button is selected. 'As Suffix' and 'As Prefix' are also visible. The 'Auto increment filenames' checkbox is checked.

**As Suffix:**

When **Date and Time** is selected, the date and time are added to the end of the filename.

Enter Filename Format:  File Increment Digits:

Date and Time Appendix:

None  Date Only  Date and Time  As Suffix

Auto increment filenames  As Prefix

**As Prefix:**

When **Date and Time** is selected, the date and time are added to the beginning of the filename.

Data File Information

Use Default Filename

Enter Filename Format:  File Increment Digits:

Date and Time Appendix:

None  Date Only  Date and Time  As Suffix

As Prefix

**Save Data to****Removable Drive:**

Data is saved to the USB on the HAPSITE ER as well as to the HAPSITE ER hard drive in the folder (directory) shown immediately above this check box.

### 15.11.3 Data Display

A **Manual Response Y** number can be entered, which will scale the Y-axis of the chromatogram to the desired counts. If there is not a number in this section, the TIC will automatically scale to the largest number.

Data Display

Manual TIC Y Scale Max

Counts

e.g. 5000000 Counts

Note: A value of 0 disables default manual scale

## 15.12 Summary Page

The **Summary** page provides selections to display the selected components of the method in a text report. The method settings can be reviewed in this report before the method is saved.

## 15.13 Method Sequence

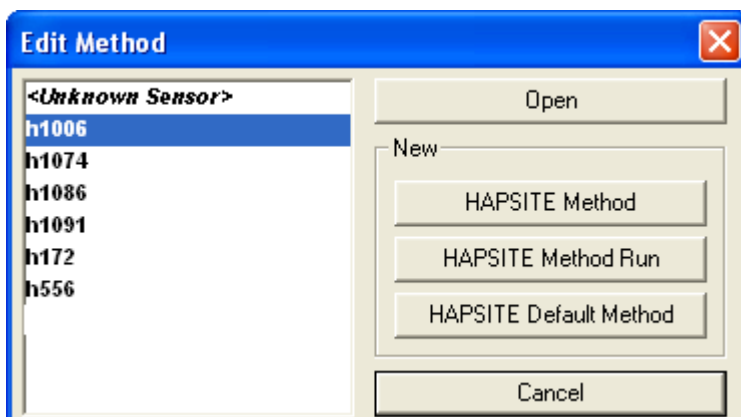
A series of methods can be configured to run back to back or at timed intervals. Follow the instructions below to sequence a method.

- 1 Double-click the **Method Editor** icon.

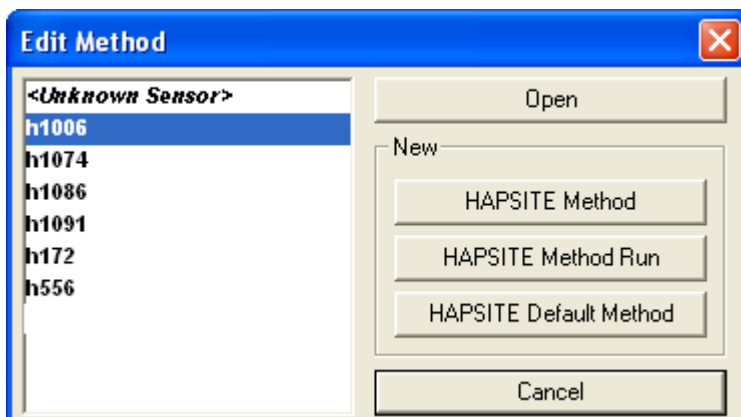


Method Editor

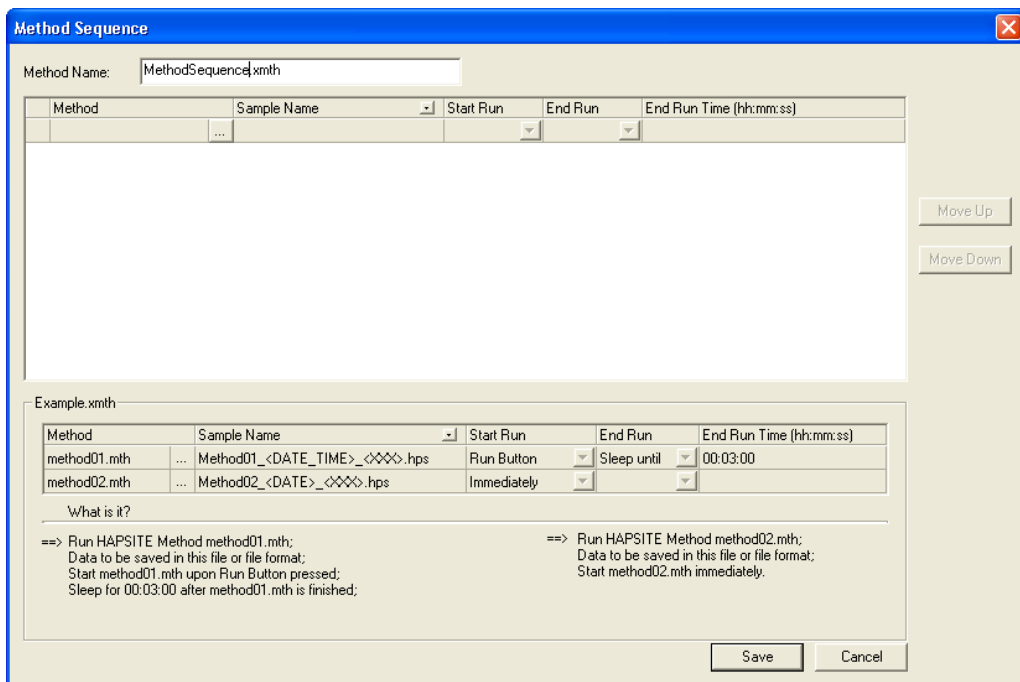
- 2 If more than one unit is connected to the laptop, click on the name of the desired HAPSITE ER.



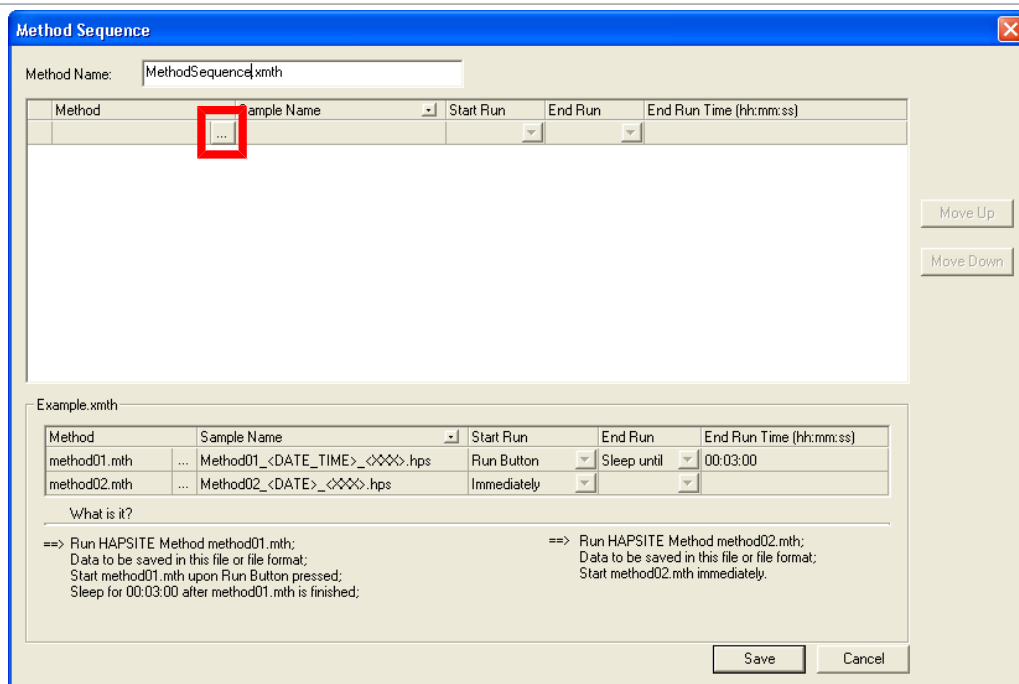
- 3 Click the **HAPSITE Method Sequence** option.



- 4 If desired, type in a new name for the method. Ensure that the file extension ends in **.xmth**.

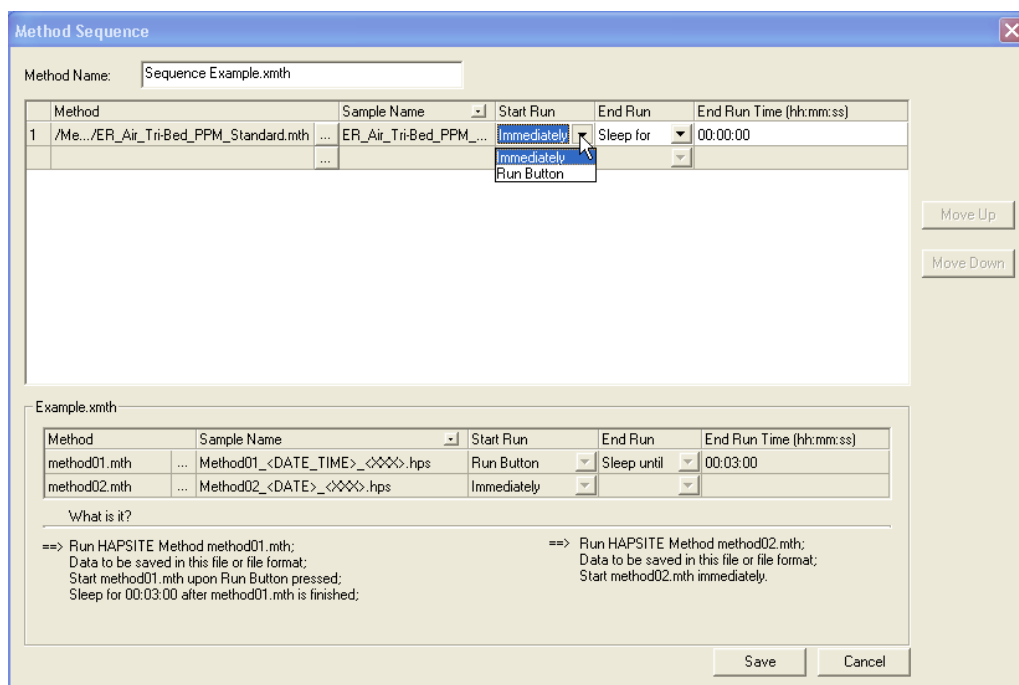


- 5 Click the button that is highlighted in the figure below.



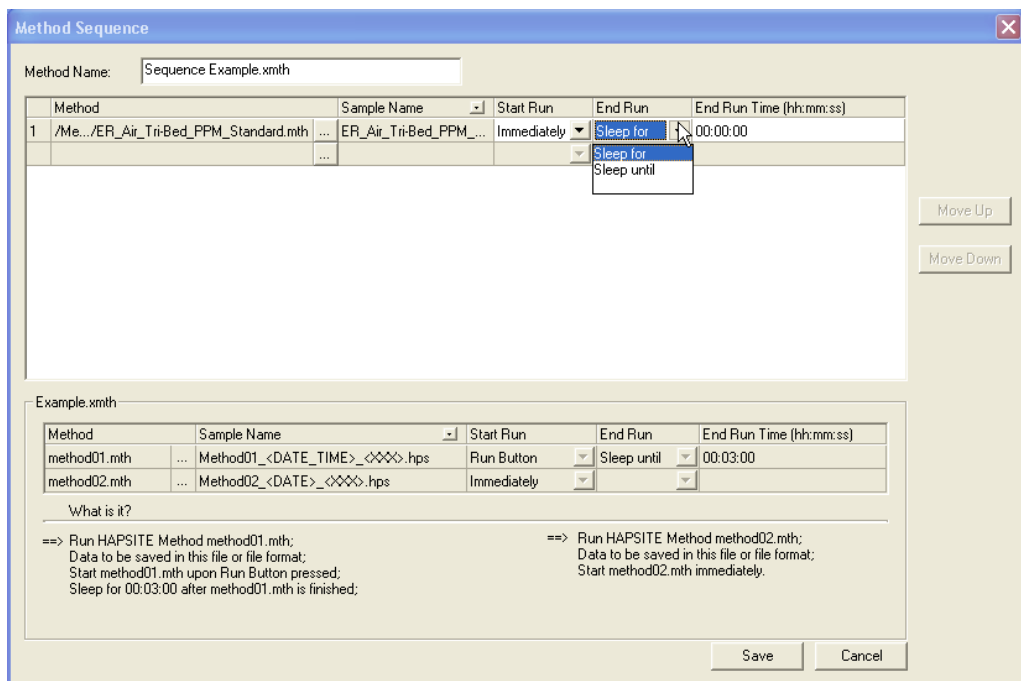
6 Double-click on the desired folder to access the desired method. For instructions on selecting folders, refer to Accessing the Data Review Feature [▶ 206].

7 Select **Immediately** or **Run Button** from the drop-down menu to start the analysis. The **Immediately** option runs the method as soon as the previous method has finished. The **Run Button** option requires the user to select **Run** to start the next method.



8 Select the timing between sample runs.

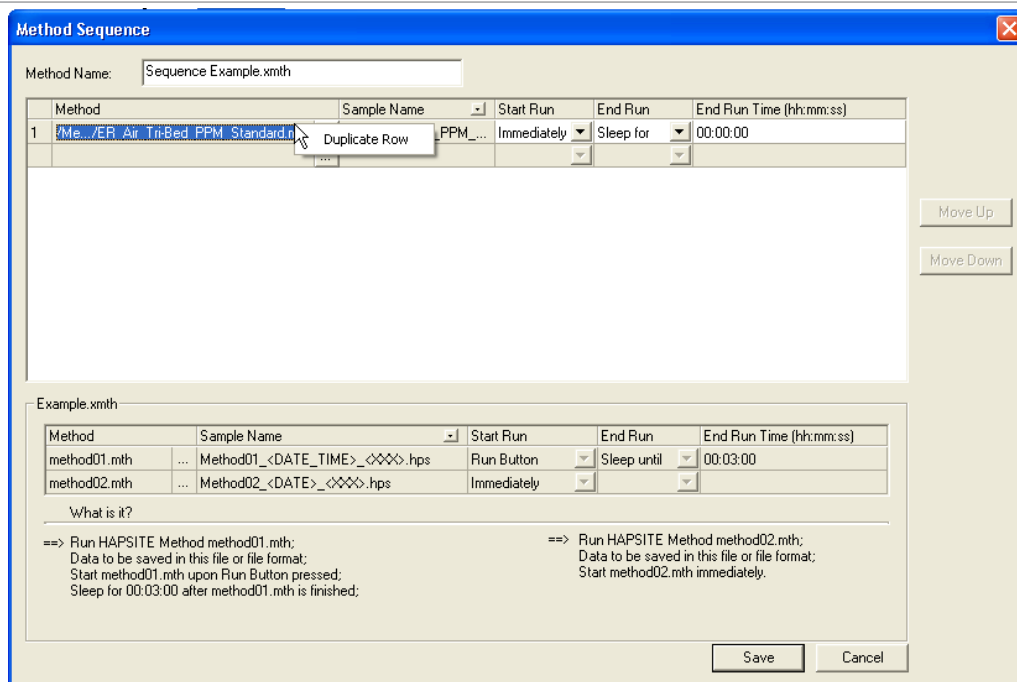
- 9 Select **Sleep for** if a lapse in time is desired. For example, if 1:30 is entered, the second method will run an hour and a half after the first method finishes.
- 10 Select **Sleep until** to enter a specific time. For example, if 1:30 is entered, the second method will start at 1:30 a.m.



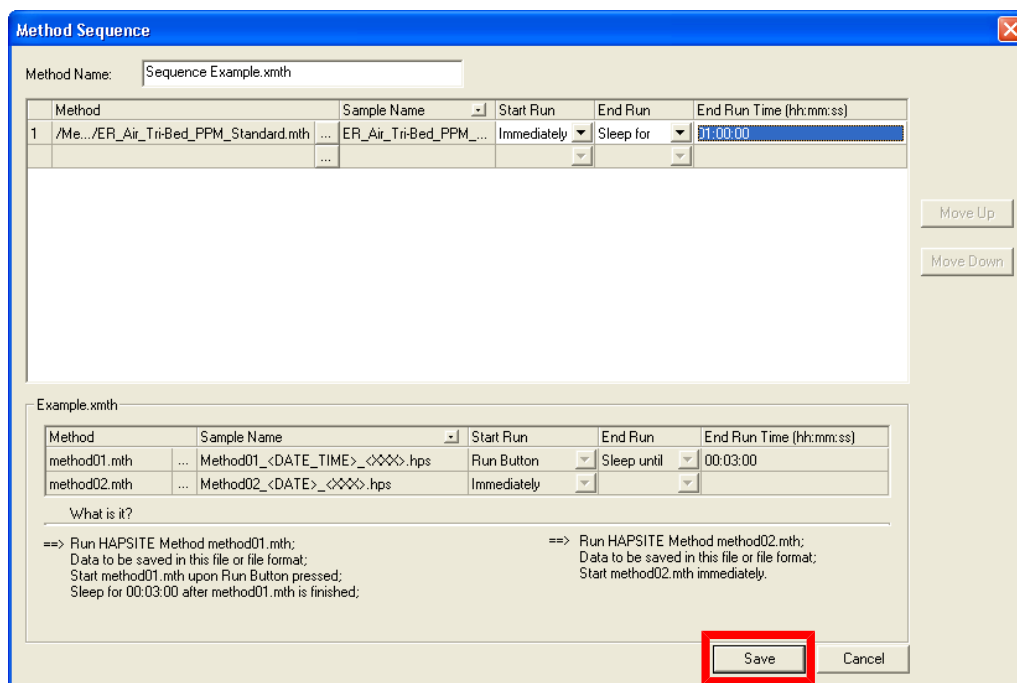
**Sleep until** uses 24 hour notation.

- 11 Add multiple runs by repeating steps 5-10. Alternately, right-click and select **Duplicate Row**.





12 Select **Save** to save the method.



13 Select the desired location for saving the method. The method can be saved to the laptop or the HAPSITE ER by clicking the desired option at the top of the window.

## 16 Calibration

### 16.1 Introduction to Quantitative Analysis

A HAPSITE ER method can be developed to collect and quantify sample data. Quantitative analysis involves creating a calibration library of target compounds, and associating target compound responses with concentration results. This library contains the analyte name, analyte area, the retention time and the response factor used to calculate the concentration of the analyte.

### 16.2 Calibrating a Method



#### **WARNING**

**Wear appropriate Personal Protective Equipment (PPE) as advised in the MSDS of the standard(s) being used.**

✓ Prepare the standards as necessary to achieve the desired concentrations.

- 1 Run each standard separately on HAPSITE ER using the desired method. Each standard has its own separate run. The method used for HAPSITE ER can be a default method or a custom method created with the **Method Editor**.



All other components of method development described in Method Editor [▶ 301] must be made prior to running the standards.

- 2 Enter the concentration of the standard and a description in the **Data File Information** window during each sample run.

⇒ Click the **Data File Information** window.



⇒ Enter in the concentration and the units into the fields highlighted.

**Data File Information**

File Name  
Data: C:\Documents and Settings\ssmith\Desktop\Chromat\ER\_Air\_Tri-Bed\_PPM\_5ST

Sample  
Method: \Haps\MethodER\_Air\_Tri-Bed\_PPM\_5STD\_Quant.mth  
Start Time: 1/28/2009 1:58:36 PM  
GPS Info: Valid GPS Information Not Available

Conc.  
Level: 5  
Unit: ppm

Internal Standard

Name	Conc. (PPM)	Fill Date	Expiration Date
TRIS	10.60	10/2/2007	10/24/2008
BPFB	5.49	10/2/2007	10/24/2008

Description  
5 uL of BTEX standard

OK Cancel

⇒ Click **OK**.

**Data File Information**

File Name  
Data: C:\Documents and Settings\ssmith\Desktop\Chromat\ER\_Air\_Tri-Bed\_PPM\_5ST

Sample  
Method: \\Haps\MethodER\_Air\_Tri-Bed\_PPM\_5STD\_Quant.mth

Start Time: 1/28/2009 1:58:36 PM

GPS Info: Valid GPS Information Not Available

Conc.  
Level: 5  
Unit: ppm

Name	Conc. (PPM)	Fill Date	Expiration Date
TRIS	10.60	10/2/2007	10/24/2008
BPFB	5.49	10/2/2007	10/24/2008

Description  
5 uL of BTEX standard

OK Cancel



If desired, a description can be entered into the **Description** field.

- When every standard has finished running, double-click the **Calibrate** icon.



- Selecting the **Calibrate** function displays a dialog box used to select either an **Analyze (GC/MS)** method or a **Survey** method. The **Select Method First** box should remain checked. Click **OK**.

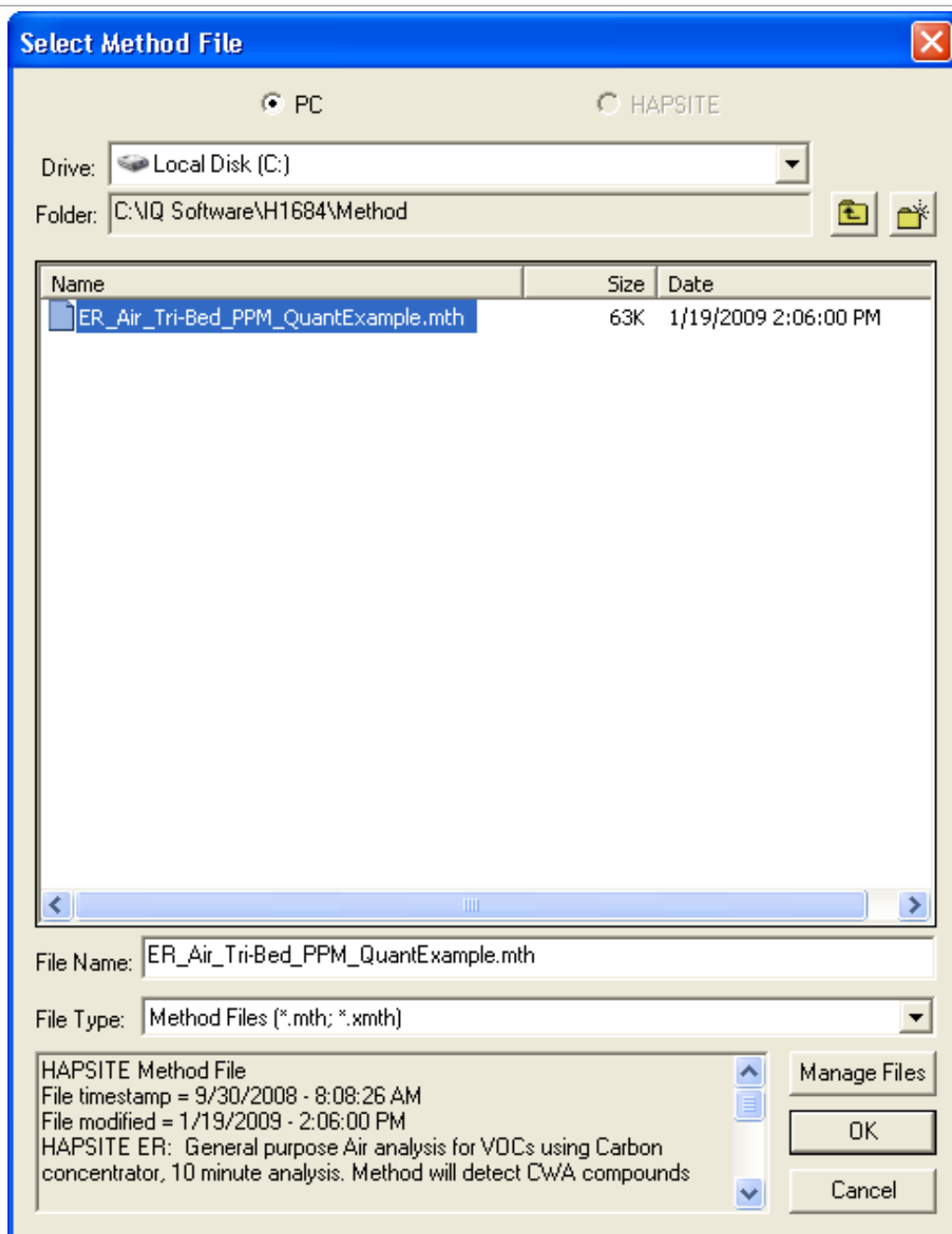
**Select File Type**

GC/MS  Survey

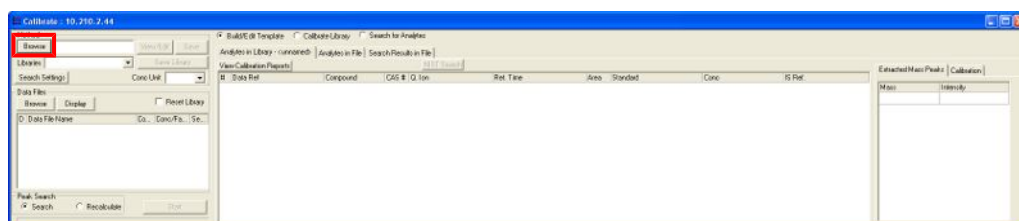
Select Method First

OK Cancel

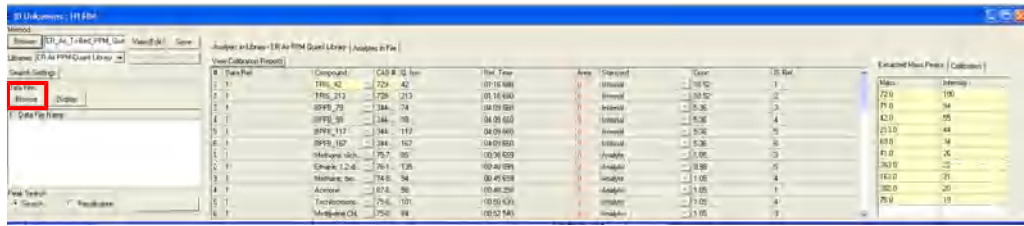
- The **Method File** window is displayed if the **Select Method First** box remained checked.



6 If the **Select Method First** box was unchecked, select **Browse** to select a method file.

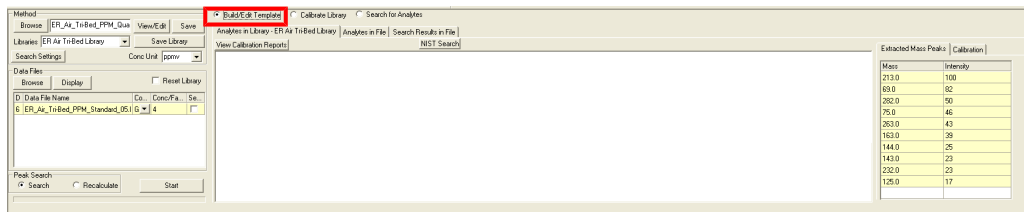


7 Click **Browse** under **Data Files**. Select the data file for library template creation.

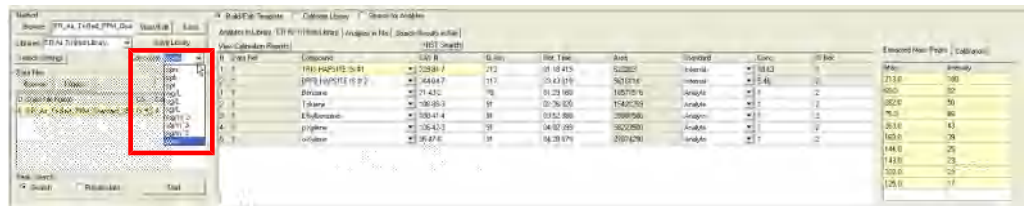


It is recommended to use a high or mid-range standard for calibration library development. Standards with low concentrations may have peaks too small to be detected with default **Search Settings**.

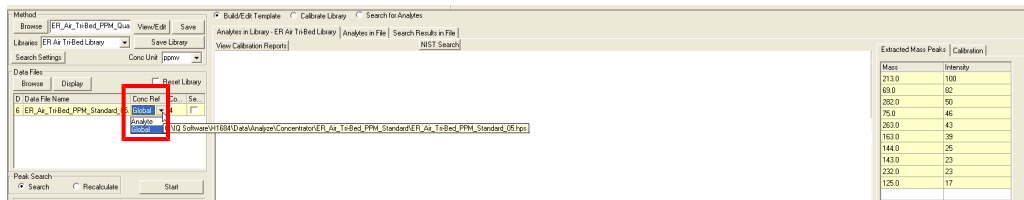
**8 Select Build/Edit Template.**



**9 Select the units.**

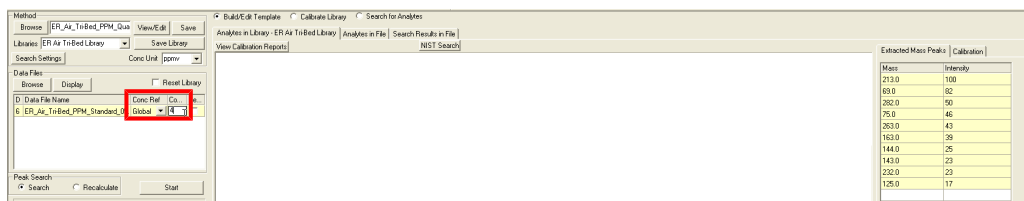


**10 Set the Concentration Reference to Global or Analyte.**

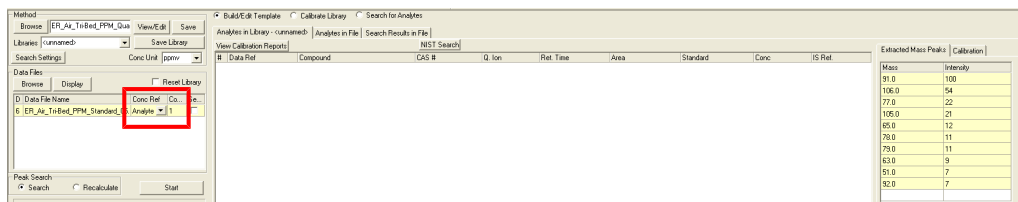


- ⇒ Select **Global** for standards that contain analytes that have the same concentration. This is most common with liquid standards diluted into a liquid.
- ⇒ Select **Analyte** for standards that contain analytes with different concentrations. This is most common with liquid standards that are diluted into a gas.

**11 If Global is selected, enter in the concentration of the standard. Step 12 is automatically completed if the information was entered in the **Data File Information** window when the sample was run. Refer to Steps 2–5.**



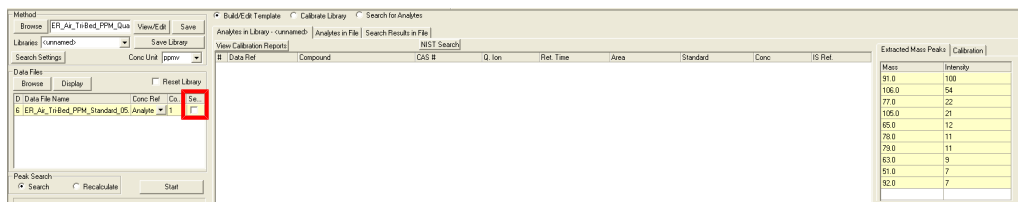
**12** If **Analyte** is selected, enter the volume of standard used for the selected data file into the field highlighted below. For example, if an analyte was run at the concentrations of 5 ppb, 10 ppb and 20 ppb, the factor for the 5 ppb data file would be 1. For the 10 ppb, 2 would be the factor, and for the 20 ppb file, 4 would be the factor. The concentration of the standard is entered into the concentration column in Step 32.



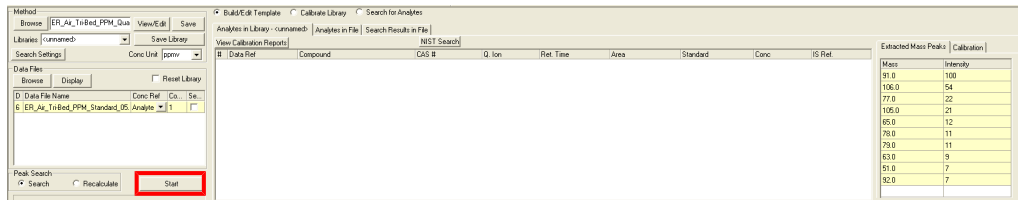
**13** Set Peak Search to Search.



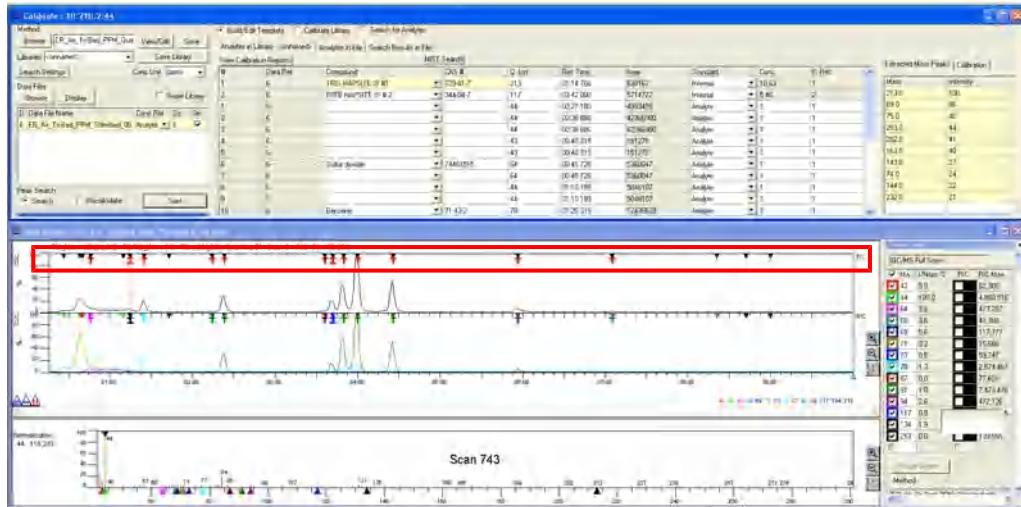
**14** Check Select.



**15** Click Start.



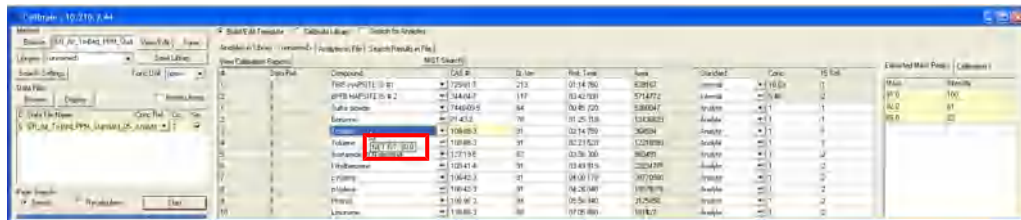
**16** All compounds that have been identified by AMDIS will be labeled with a red "T" over the apex of the peak.



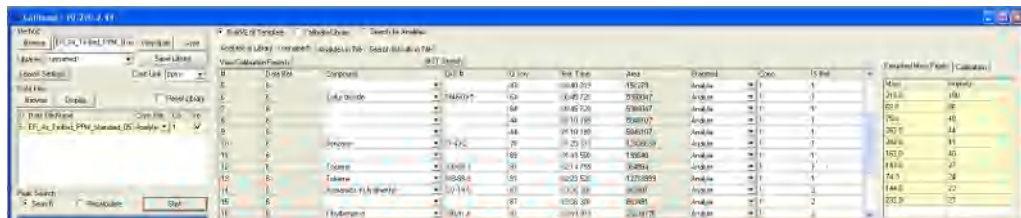
17 The highlighted compound in the library template corresponds to the peak with the red dotted line.



18 Verify that all analytes have a Net Fit greater than 70 by hovering the mouse over the analyte name.

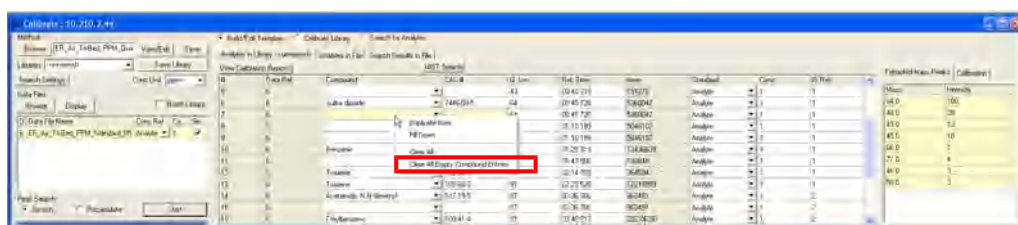


19 Verify that the retention times are correct.

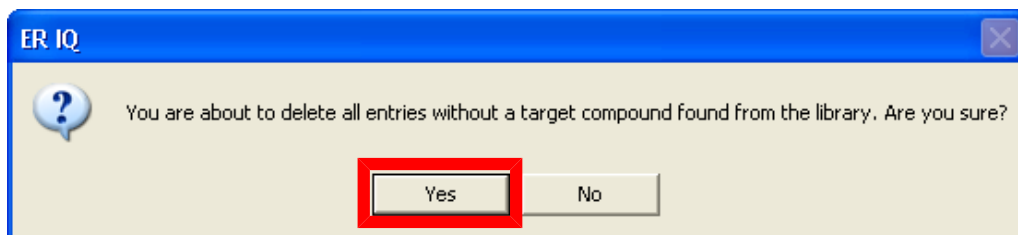




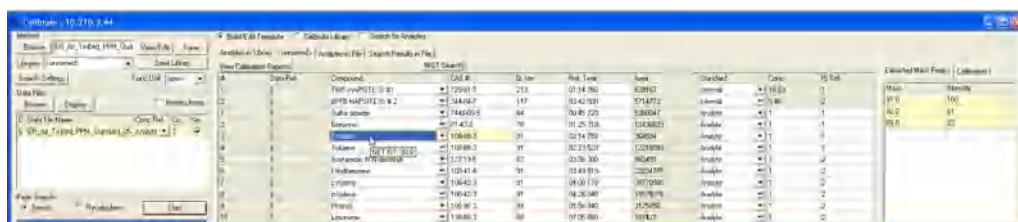
- 20 If unidentified compounds are present, which are indicated by a blank row, right-click on a compound and select **Clear All Empty Compound Entries**.



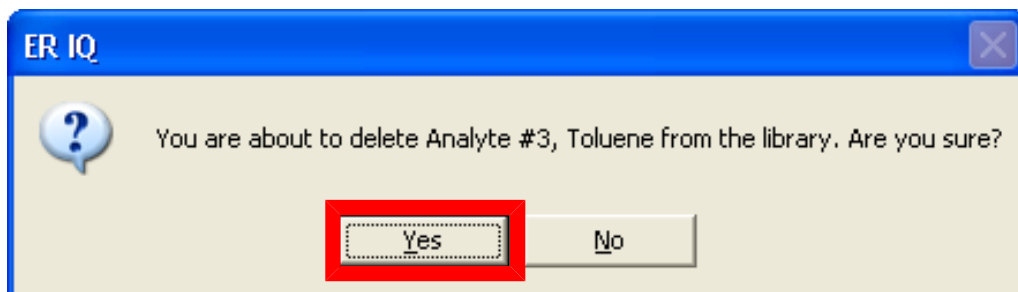
- 21 Click **Yes** to confirm the deletion of the unidentified compounds.



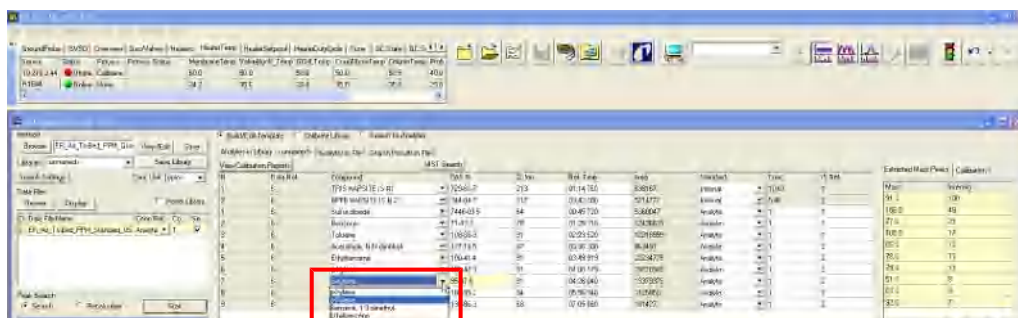
- 22 Delete any duplicate analytes, duplicate internal standards or undesired analytes from the template by highlighting the undesired compound and clicking **Delete** on the laptop keyboard.



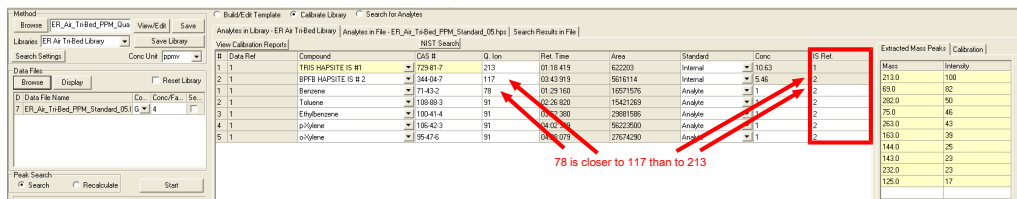
- 23 Click **Yes** to confirm the deletion of the undesired compounds.



- 24 If a compound was not correctly identified, type in the correct name. Alternately, the down arrow next to the compound name can be used to select a different name if AMDIS has identified more than one possible match.

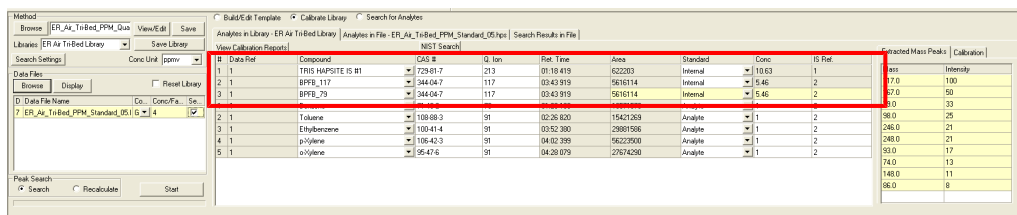


**25** Set the **IS Ref. (IS Reference)**. When using internal standards, the best practice is to use a quant ion from the internal standard that is closest in mass to the quant ion of the compound to be quantified. The software always selects the largest mass fragment in the spectrum as the quant ion. To change the quant ion, highlight the field and type in the new number.

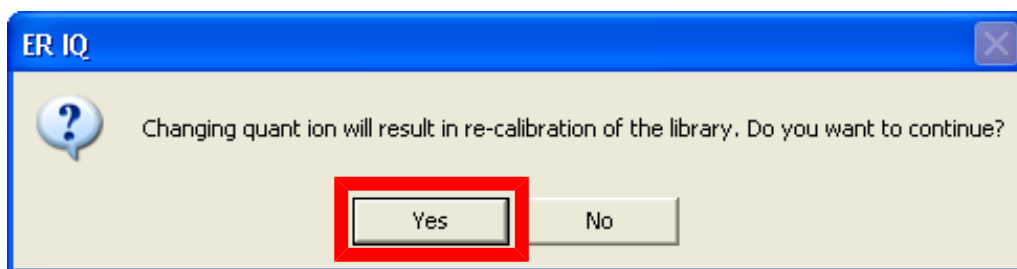


The software automatically recognizes TRIS and BPFB. It automatically enters the concentration from the IS canister into the method for calibration and quantization.

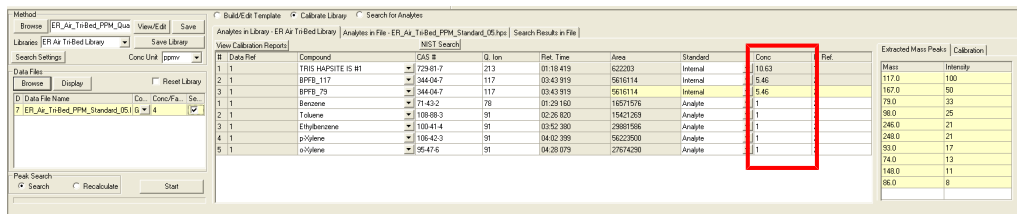
**26** More than one quant ion can be used from a single internal standard peak. For example, highlight the second internal standard and right-click. Select **Duplicate Row**. Then, change the name of the internal standard peaks to **BPFB\_79** and **BPFB\_117**. The quant ion is changed to **79** and **117**.



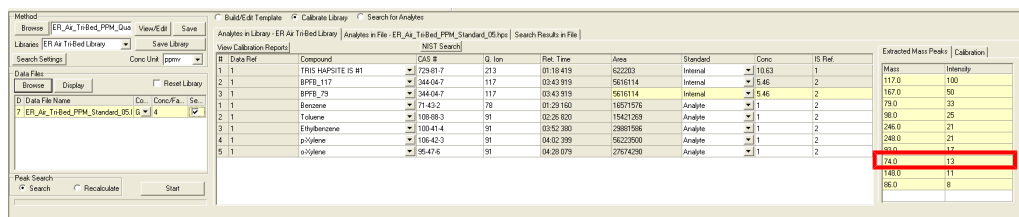
When adding more than one quant ion, the message shown below is displayed. Click **Yes** to allow the recalibration to continue.



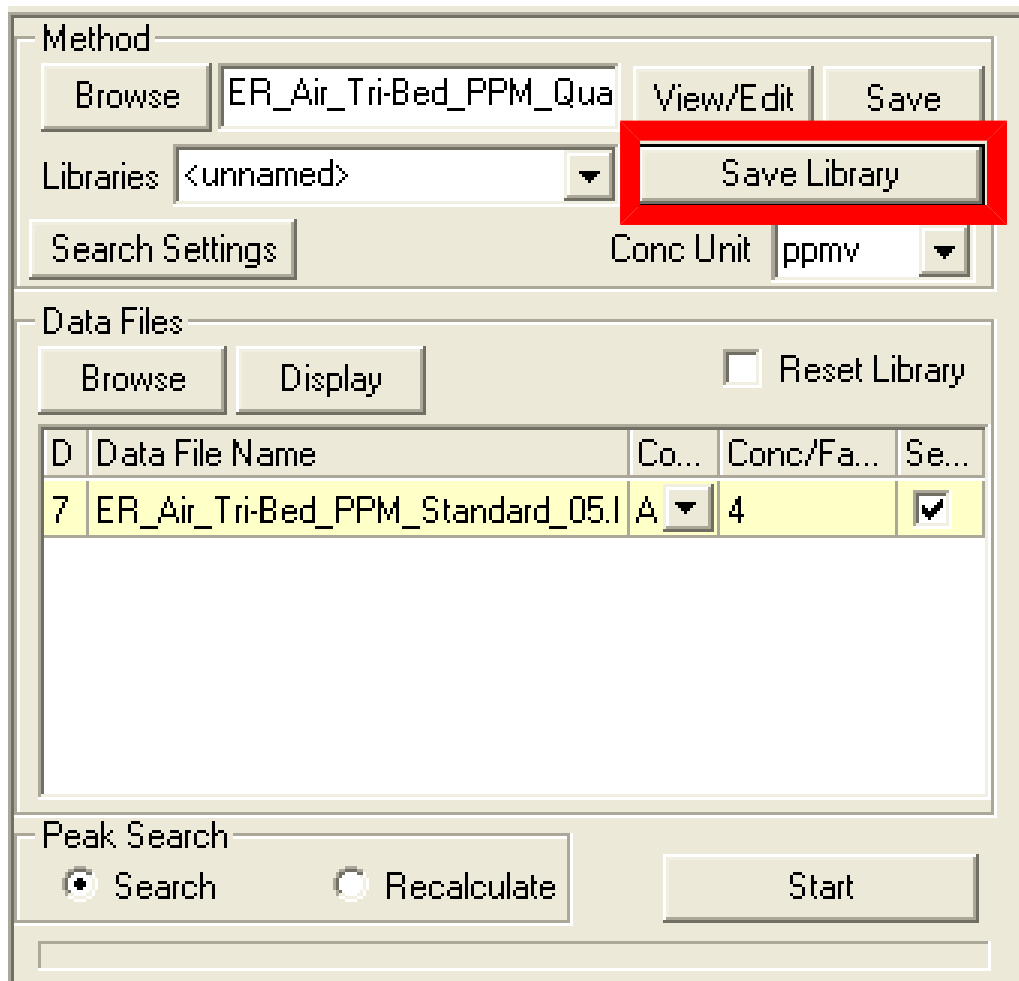
**27** Enter the lowest concentration of each analyte to the **Conc** column if **Analyte** has been selected. If **Global** is selected, this step can be skipped.



**28** The **Extracted Mass Peaks** can also be edited to delete mass fragments. To delete unwanted mass fragments, highlight the field and press the delete key, Unwanted mass fragments would be those with intensities below 15%, unless the fragmentation pattern is not very distinct.



**29** Save the template by clicking **Save Library**.



**30** Enter a library name and a user name.

Save Library ×

Enter Library Name

Enter Creator Name

To select a library doubleclick on the row

Name	Create Time	Modified Time	Creator
ER Air PPM Quant Libr...	6/24/2009 7:57:52 ...	3/18/2010 11:53:04 ...	INFICON, I...

OK Cancel

**31** Click **OK**.

Save Library ×

Enter Library Name

Enter Creator Name

To select a library doubleclick on the row

Name	Create Time	Modified Time	Creator
ER Air PPM Quant Libr...	6/24/2009 7:57:52 ...	3/18/2010 11:53:04 ...	INFICON, I...

OK Cancel

**32** To calibrate the library, click **Browse** and select the desired data files.

Method

Browse ER\_Air\_Tri-Bed\_PPM\_Qua View/Edit Save

Libraries <unnamed> Save Library

Search Settings Conc Unit ppmv

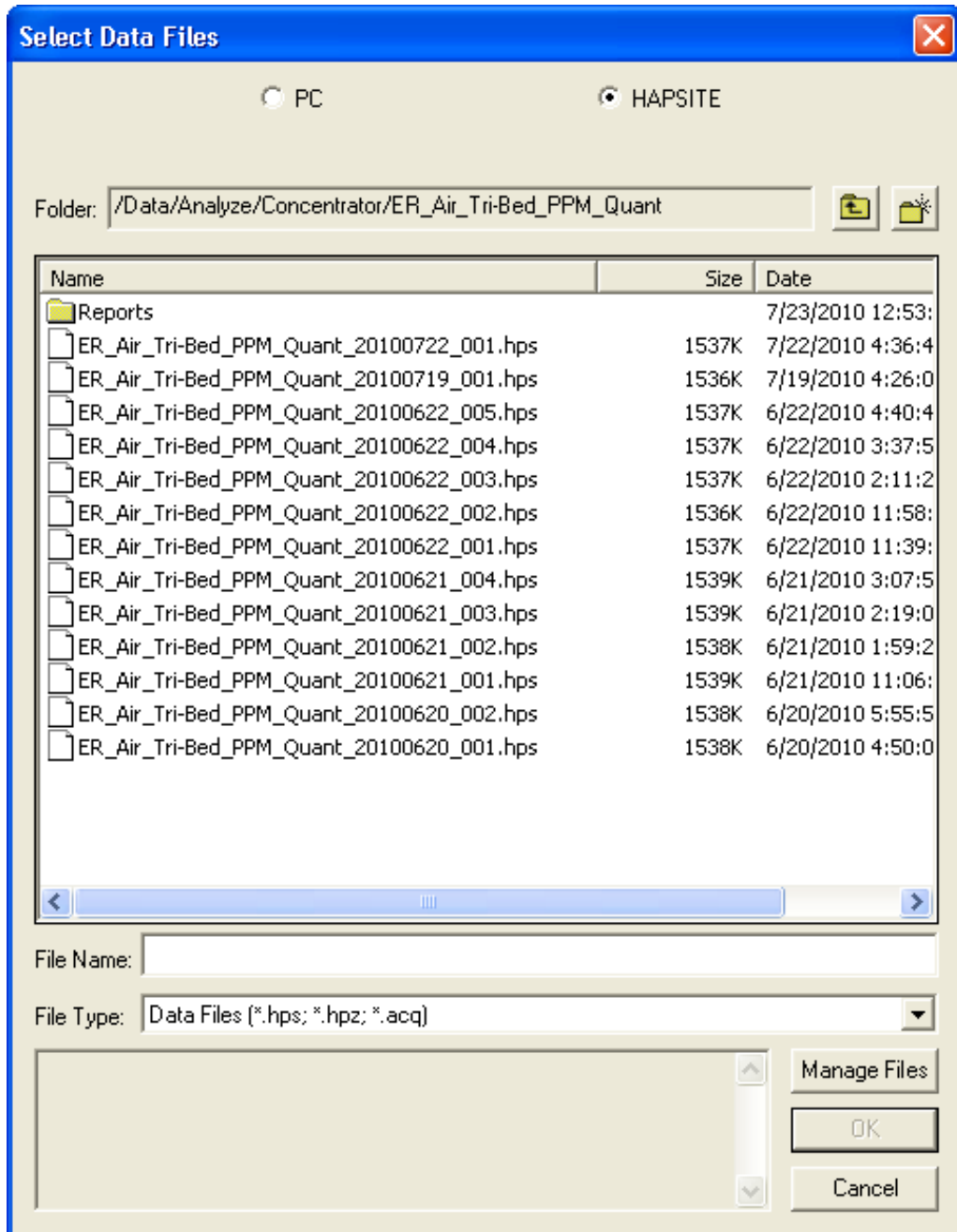
Data Files

Browse Display  Reset Library

ID	Data File Name	Co...	Conc/Fa...	Se...
7	ER_Air_Tri-Bed_PPM_Standard_05.l	A	4	<input checked="" type="checkbox"/>

Peak Search

Search  Recalculate Start



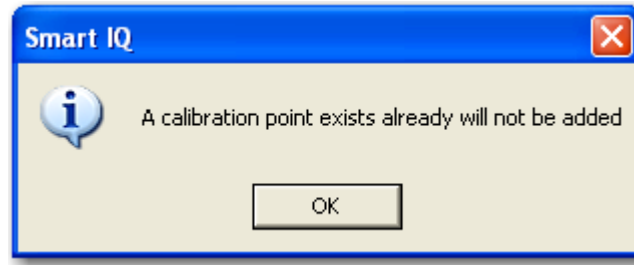
**33 Select Calibrate Library.**



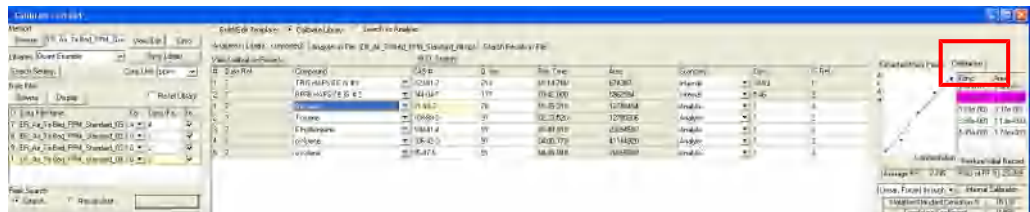
**34 Check all of the data files and click Start under Peak Search.**



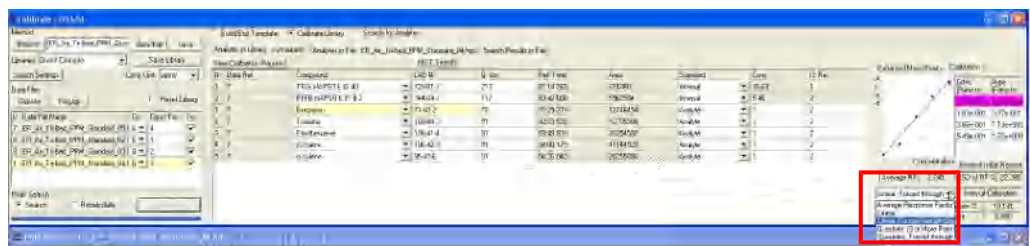
Additional calibration points can be added to the curve by following Step 10 through Step 39. Click **OK** when the **A calibration point exists already will not be added** message is displayed.



**35** Review the curves for each analyte by clicking the **Calibration** tab.

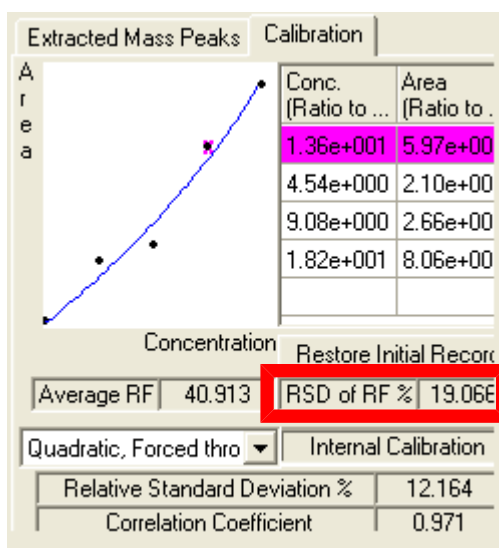


**36** Click each analyte to display the corresponding calibration curve. The curve should fit the data points. The menu provides four curve fit options: **Linear**, **Linear, Forced through the Origin**, **Quadratic** and **Quadratic, Forced through the Origin**.



The RSD of the curve varies depending upon the curve fit selected.

**37** Verify that the **RSD of RF%** is acceptable. It is recommended that the **RSD of RF%** is 30% or lower.

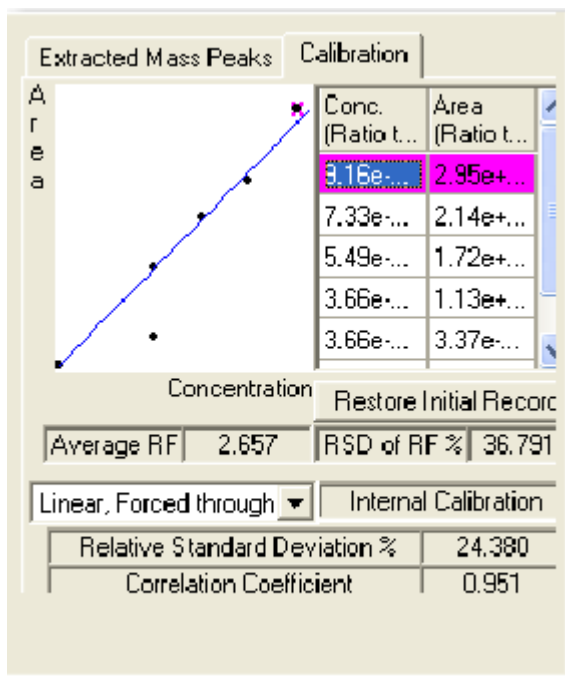


38 It is possible to delete points from the calibration curve.



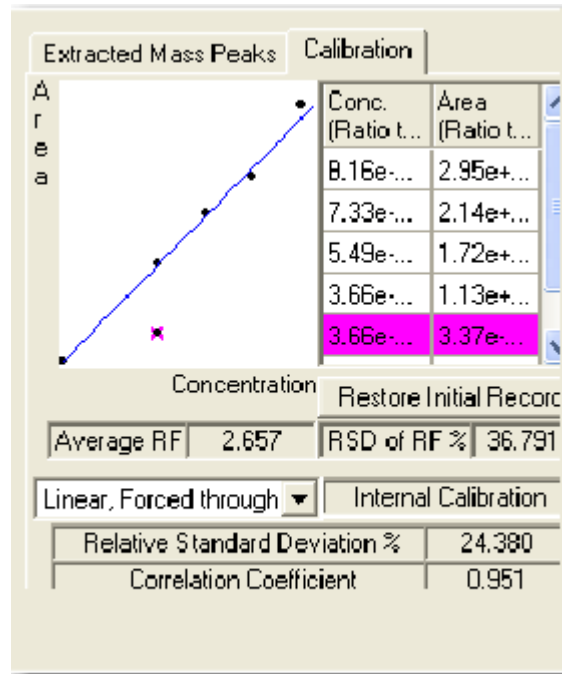
Removal of points in the middle of a calibration curve is contrary to established analytical standards. Points can be removed from the highest and lowest level of the curve, but this will affect the calibration range.

39 Click any number in the **Conc. (Ratio to IS)** column. The corresponding point is overlaid with a pink "X."

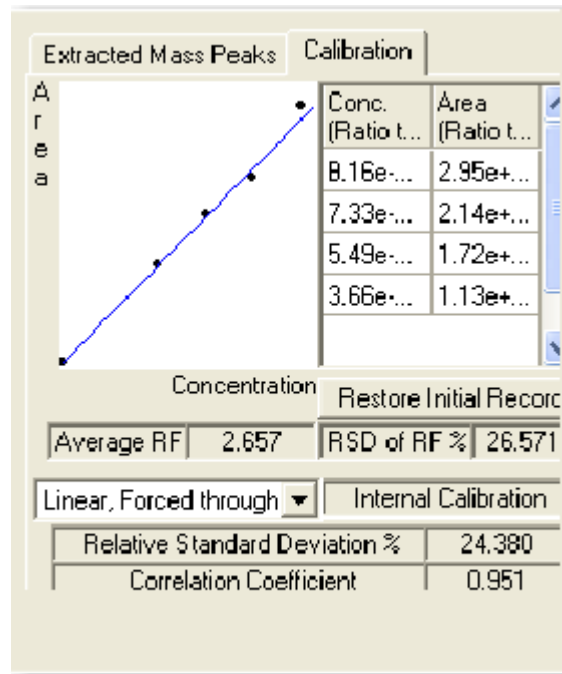


40 Use the up and down arrows to select the outlying point.

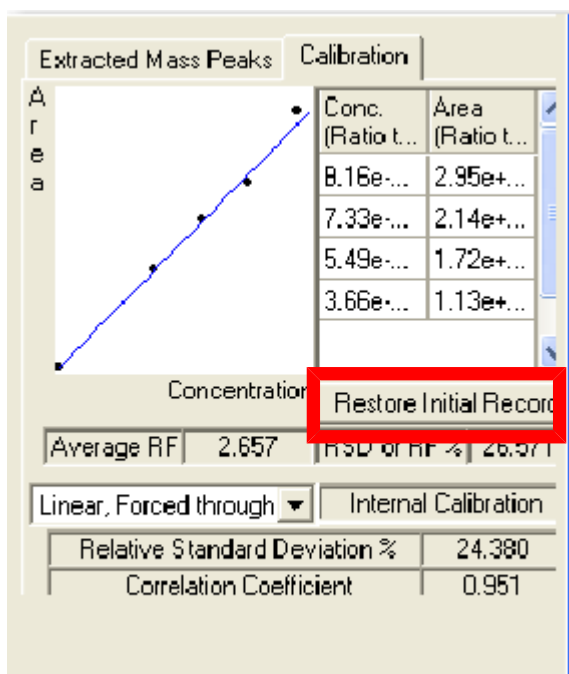




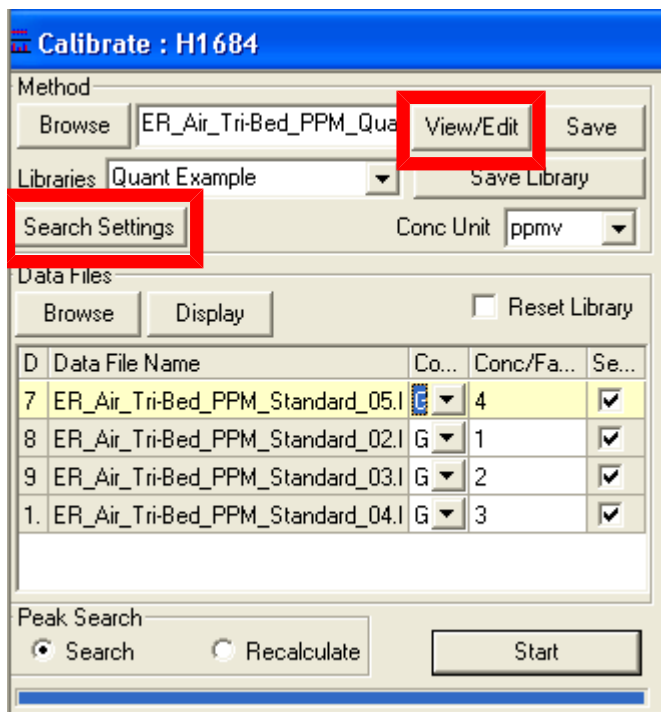
41 Click **Delete**.



If a point was inadvertently deleted, the original calibration points can be restored by clicking **Restore Initial Record**.



- 42 If a point is missing because it does not meet the peak search criteria, the peak search parameters can be adjusted. Click **Search Settings** to adjust all of the compounds at once. To adjust individual analytes, click **View/Edit**.



- 43 To recalibrate the library with new parameters, check the **Reset Library** box.

**Calibrate : H1684**

Method  
 Browse ER\_Air\_Tri-Bed\_PPM\_Qua View/Edit Save

Libraries Quant Example Save Library

Search Settings Conc Unit ppmv

Data Files  
 Browse Display  Reset Library

D	Data File Name	Co...	Conc/Fa...	Se...
7	ER_Air_Tri-Bed_PPM_Standard_05.1	G	4	<input checked="" type="checkbox"/>
8	ER_Air_Tri-Bed_PPM_Standard_02.1	G	1	<input checked="" type="checkbox"/>
9	ER_Air_Tri-Bed_PPM_Standard_03.1	G	2	<input checked="" type="checkbox"/>
1.	ER_Air_Tri-Bed_PPM_Standard_04.1	G	3	<input checked="" type="checkbox"/>

Peak Search  
 Search  Recalculate Start

**44** Verify that the **Peak Search** is set to **Search**.

**Calibrate : H1684**

Method  
 Browse ER\_Air\_Tri-Bed\_PPM\_Qua View/Edit Save

Libraries Quant Example Save Library

Search Settings Conc Unit ppmv

Data Files  
 Browse Display  Reset Library

D	Data File Name	Co...	Conc/Fa...	Se...
7	ER_Air_Tri-Bed_PPM_Standard_05.1	G	4	<input checked="" type="checkbox"/>
8	ER_Air_Tri-Bed_PPM_Standard_02.1	G	1	<input checked="" type="checkbox"/>
9	ER_Air_Tri-Bed_PPM_Standard_03.1	G	2	<input checked="" type="checkbox"/>
1.	ER_Air_Tri-Bed_PPM_Standard_04.1	G	3	<input checked="" type="checkbox"/>

Peak Search  
 Search  Recalculate Start

**45** Repeat Step 16 through Step 41.

**46** When the method is satisfactory, click **Save Library**.

Method

Browse ER\_Air\_Tri-Bed\_PPM\_Qua View/Edit Save

Libraries <unnamed> Save Library

Search Settings Conc Unit ppmv

Data Files

Browse Display  Reset Library

D	Data File Name	Co...	Conc/Fa...	Se...
7	ER_Air_Tri-Bed_PPM_Standard_05.l	A	4	<input checked="" type="checkbox"/>

Peak Search

Search  Recalculate Start

47 Click **OK**.

Save Library

Enter Library Name ER Air PPM Quant Library

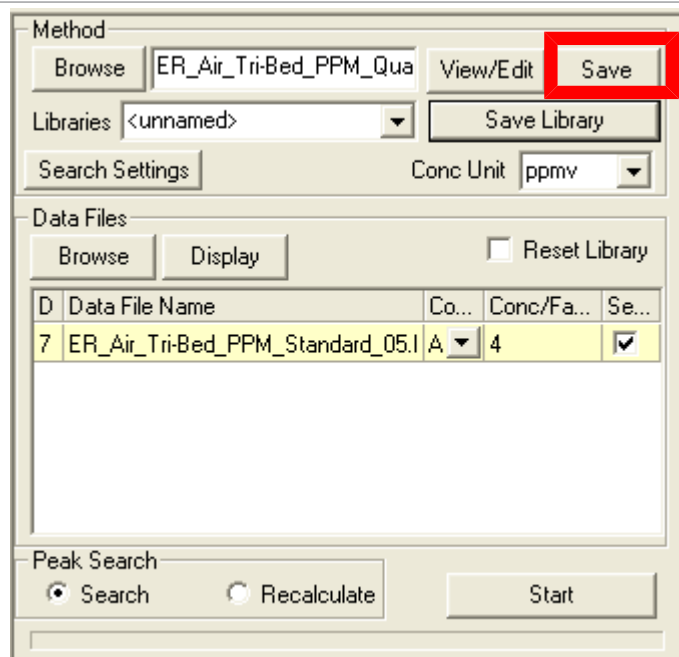
Enter Creator Name INFICON, Inc.

To select a library doubleclick on the row

Name	Create Time	Modified Time	Creator
ER Air PPM Quant Libr...	6/24/2009 7:57:52 ...	3/18/2010 11:53:04 ...	INFICON, I...

OK Cancel

48 Save the library to the method by clicking **Save**.

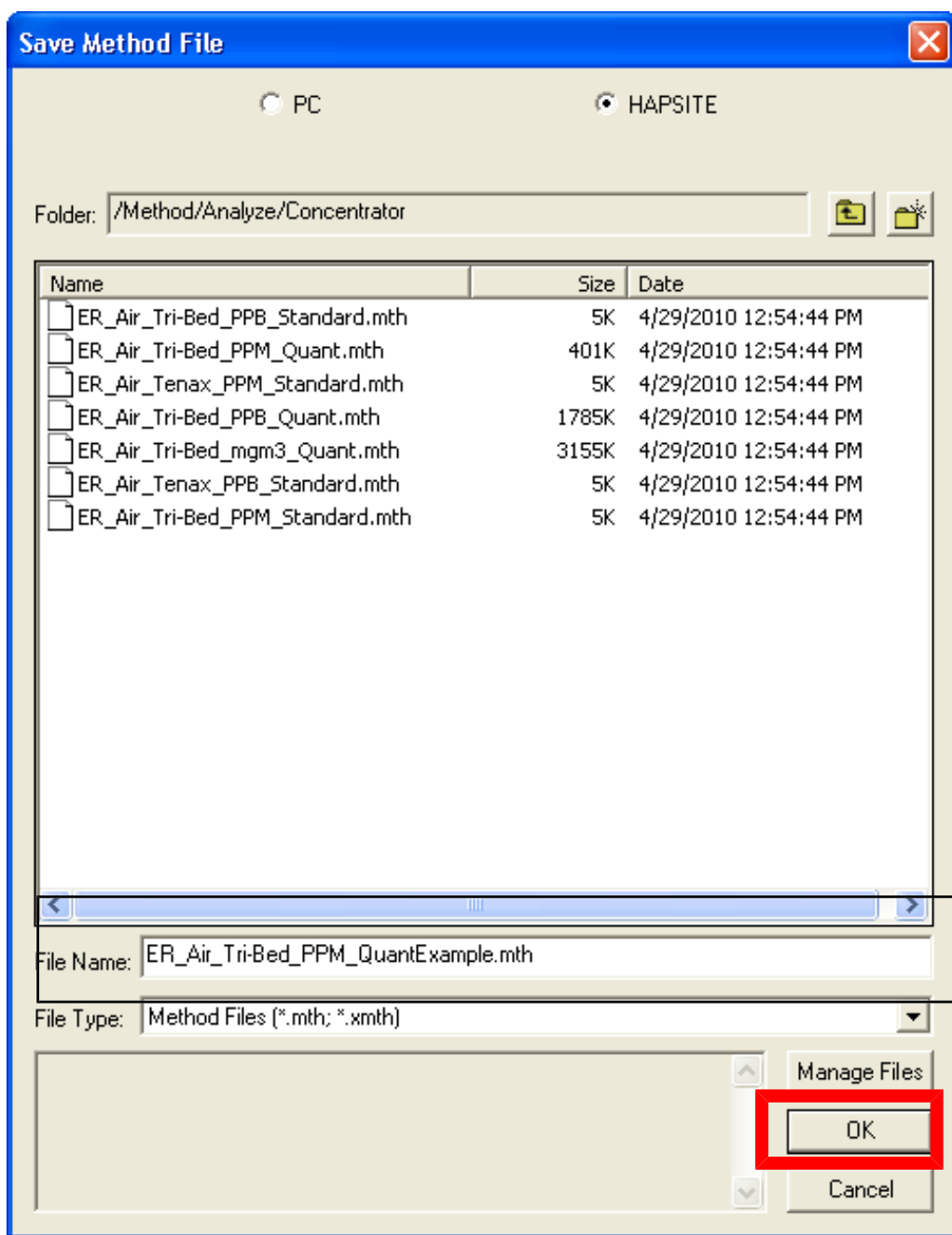


The screenshot shows a software window with the following sections:

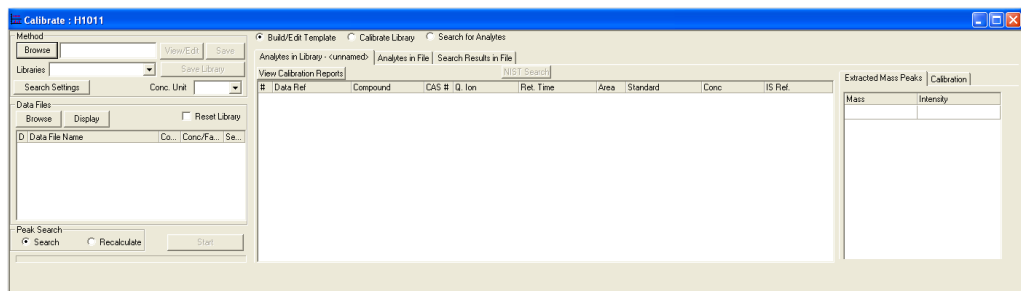
- Method:** Includes a 'Browse' button, a text field containing 'ER\_Air\_Tri-Bed\_PPM\_Qua', a 'View/Edit' button, and a 'Save' button (highlighted with a red box).
- Libraries:** A dropdown menu showing '<unnamed>' and a 'Save Library' button.
- Search Settings:** A 'Search Settings' button and a 'Conc Unit' dropdown menu set to 'ppmv'.
- Data Files:** Includes 'Browse' and 'Display' buttons, and a 'Reset Library' checkbox.
- Table:** A table with columns 'D', 'Data File Name', 'Co...', 'Conc/Fa...', and 'Se...'. The first row is highlighted in yellow and contains the following data:

D	Data File Name	Co...	Conc/Fa...	Se...
7	ER_Air_Tri-Bed_PPM_Standard_05.l	A	4	<input checked="" type="checkbox"/>
- Peak Search:** Includes radio buttons for 'Search' (selected) and 'Recalculate', and a 'Start' button.

**49** Click **OK**.



## 16.3 Definition of Terms in the Calibrate Window



### 16.3.1 Method

Browse	Allows the user to select a method for calibration.
View/Edit	Opens the Method Editor for the method that is currently being calibrated. Refer to Method Editor [▶ 301].
Save	Saves the current method.
Libraries	A drop-down menu that allows the user to select a previously saved library.
Save Library	Brings up the dialog box to save the library.
Search Settings	Displays the search parameter settings. Refer to Peak Search Parameters [▶ 243].
Conc. Unit	Used to select the concentration units.

### 16.3.2 Data Files

Browse	Used to select the data files for building and calibrating the library; when a data file is selected the data is listed as follows:
D	Shows the data file reference number.
Data File Name	Displays the data file name and storage pathway.
Conc Ref	Basis for calculating the concentration. Global (all analytes are at the same concentration) or Analyte (analytes are in file at specific concentrations).
Conc/Factor	Data file concentration of analytes if Global is selected, or concentration multiplier if Analyte is selected.
Selection	If checked, file will be processed upon clicking Start.
Display	Displays the chromatogram for the selected data file.
Reset Library	If checked, the calibration curve will be reset. All points currently contained in the library will be deleted.

### 16.3.3 Peak Search

Search	When <b>Build/Edit</b> is selected, <b>Search</b> performs a peak detection and integration on the selected files. When <b>Calibrate</b> is selected, <b>Search</b> calibrates the library and calculates the response factors.
Recalculate	Recalculates the peak areas and response factors without performing a peak search. This is most useful after manually editing the baseline points of the peak.
Start	Initiates the <b>Search</b> or <b>Recalculation</b> .

Build/Edit Template	<b>Build/Edit</b> must be selected if an analyte search, deletion of analytes or changing template parameters is desired.
Calibrate Library	Calibrate Library must be selected in order a calibration curve to be created with the desired data files.
Search for Analytes	Enables a search to be performed on the selected data file(s) without adding the detected analytes automatically to the library. This allows the data to be previewed before adding it to the library template.



When adding compounds to an existing library or Template, use **Search for Analytes**. If using **Build/Edit Template**, the original template will be overwritten by the new search.

### 16.3.4 Analytes

Analytes in Library	Displays the analytes in the library.
Analytes in File	Displays the analytes in the current display or in the selected file.
Search Results in File	If a search has been performed with <b>Search for Analytes</b> selected, a review of the analytes detected in the file is enabled. Individual analytes can then be added to the template by right clicking on the compound name and selecting <b>Add To Template</b> . To add all compounds detected in the file, select <b>Add All</b> .

#	Data Ref	Compound	CAS #	Q. Ion	Ret. Time	Area	Standard	Conc	IS Ref.
1	8			44	00:34.680	2958029	Analyte	1	0
2	8			44	00:44.040	219795136	Analyte	1	0
3	8	oxide	7446-09-5	64	00:47.159	54121992	Analyte	1	0
4	8			43	00:52.619	203193	Analyte	1	0
5	8			44	00:56.519	12652160	Analyte	1	0
6	8			44	00:56.519	12652160	Analyte	1	0
7	8			44	01:11.639	9639657	Analyte	1	0
8	8	TRIS HAPSITE IS #1	729-81-7	213	01:18.720	671357	Internal	10.63	0
8	8			69	01:17.940	533764	Analyte	1	0
10	8	TRIS HAPSITE IS #1	729-81-7	213	01:18.720	668801	Internal	10.63	0
9	8			213	01:18.720	668801	Analyte	1	0
10	8	Benzene	71-43-2	78	01:29.040	1879086	Analyte	1	0

### 16.3.5 Reports

To view **Calibration Reports**, refer to View Reports [▶ 356].

Calibration Response Table	Report that displays the response factor and curve statistics based on the selected curve type.
Calibration Report	Report that displays the area fit and purity for the calibration standards.



**NIST Search** The initial search when building a template/library is performed using the AMDIS library. If peaks are detected and loaded into the template without an identification, the **NIST Search** can be used to identify these compounds.

1 Click on an empty row without an identification.

#	Data Ref	Compound	CAS #	Q. Ion	Ret. Time	Area	Standard	Conc	IS Ref.
1	7	TRIS HAPSITE IS #1	729-81-7	213	01:14 760	674360	Internal	10.63	1
2	7	BPFB HAPSITE IS # 2	344-04-7	117	03:42 000	5962984	Internal	5.46	2
1	7	Toluene	108883	44	00:27 180	3554868	Analyte	1	1
2	7			44	00:38 880	39305556	Analyte	1	1
3	7			44	00:38 880	39305556	Analyte	1	1
4	7			43	00:40 319	283580	Analyte	1	1
5	7			43	00:40 319	283580	Analyte	1	1
6	7	Sulfur dioxide	7446-09-5	64	00:45 720	2910422	Analyte	1	1
7	7			64	00:45 720	2910422	Analyte	1	1
8	7			44	01:10 199	232294	Analyte	1	1
9	7			44	01:10 199	232294	Analyte	1	1
10	7	Benzene	71-43-2	78	01:25 319	12746454	Analyte	1	1

2 Click the **NIST Search** button.

#	Data Ref	Compound	CAS #	Q. Ion	Ret. Time	Area	Standard	Conc	IS Ref.
1	7	TRIS HAPSITE IS #1	729-81-7	213	01:14 760	674360	Internal	10.63	1
2	7	BPFB HAPSITE IS # 2	344-04-7	117	03:42 000	5962984	Internal	5.46	2
1	7	Toluene	108883	44	00:27 180	3554868	Analyte	1	1
2	7			44	00:38 880	39305556	Analyte	1	1
3	7			44	00:38 880	39305556	Analyte	1	1
4	7			43	00:40 319	283580	Analyte	1	1
5	7			43	00:40 319	283580	Analyte	1	1
6	7	Sulfur dioxide	7446-09-5	64	00:45 720	2910422	Analyte	1	1
7	7			64	00:45 720	2910422	Analyte	1	1
8	7			44	01:10 199	232294	Analyte	1	1
9	7			44	01:10 199	232294	Analyte	1	1
10	7	Benzene	71-43-2	78	01:25 319	12746454	Analyte	1	1

3 The identification from the NIST library will be displayed.

#	Data Ref	Compound	CAS #	Q. Ion	Ret. Time	Area	Standard	Conc	IS Ref.
1	7	TRIS HAPSITE IS #1	729-81-7	213	01:14 760	674360	Internal	10.63	1
2	7	BPFB HAPSITE IS # 2	344-04-7	117	03:42 000	5962984	Internal	5.46	2
1	7	Toluene	108883	44	00:27 180	3554868	Analyte	1	1
2	7			44	00:38 880	39305556	Analyte	1	1
3	7	Toluene	108883	44	00:38 880	39305556	Analyte	1	1
4	7			43	00:40 319	283580	Analyte	1	1
5	7			43	00:40 319	283580	Analyte	1	1
6	7	Sulfur dioxide	7446-09-5	64	00:45 720	2910422	Analyte	1	1
7	7			64	00:45 720	2910422	Analyte	1	1
8	7			44	01:10 199	232294	Analyte	1	1
9	7			44	01:10 199	232294	Analyte	1	1
10	7	Benzene	71-43-2	78	01:25 319	12746454	Analyte	1	1

#	Shows the analyte number in the library.
Data Ref	Displays the reference to the Data File in which the analyte was found.
Compound	Shows the compound name that is either found in AMDIS, found in NIST, or assigned by the user for the analyte.
CAS #	Shows the Chemical Abstracts Service number for the analyte from the AMDIS or NIST library.
Q Ion	Shows the <b>Quantitation Ion</b> for the analyte.
Ret. Time	Shows the <b>Retention Time</b> for the analyte.
Area	Displays the integrated area of the quant ion.

Standard	Designates the compound as an analyte or an internal standard.
Conc.	Shows the concentration of the analyte or internal standard in the displayed file.
IS Ref.	Displays the internal standard reference number for analyte quantization.



### ⚠ CAUTION

This field is not used if the concentration flag is set to Global.

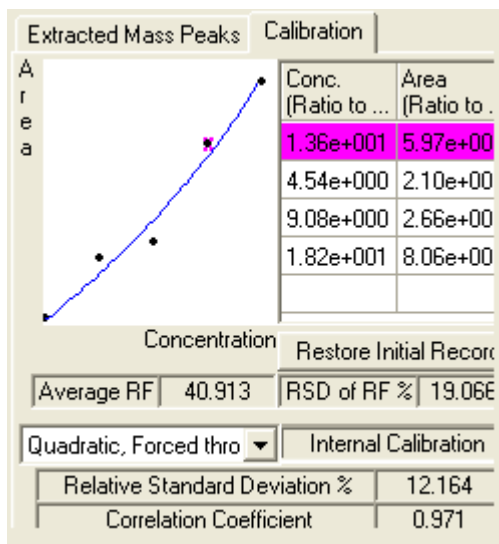
## 16.3.6 Extracted Mass Peaks

Displays the mass peaks and relative percentages for the selected analyte.

Extracted Mass Peaks		Calibration
Mass	Intensity	
213.0	100	
69.0	84	
163.0	69	
75.0	47	
144.0	40	
143.0	40	
232.0	28	
125.0	22	
99.0	16	
194.0	16	

## 16.3.7 Calibration

Displays the calibration curve statistics for the selected analyte.



## 16.4 Build/Edit Template Menu

When **Build/Edit** template is selected, right-clicking on the template will display the following options:

Duplicate Row	Creates a duplicate entry for the highlighted row.
Fill Down	Replaces the contents of all rows below the highlighted row with the name of the selected compound.
Clear All	Erases all entries in the template.
Clear All Empty Compound Entries	Deletes all entries that do not have a compound name associated with them.

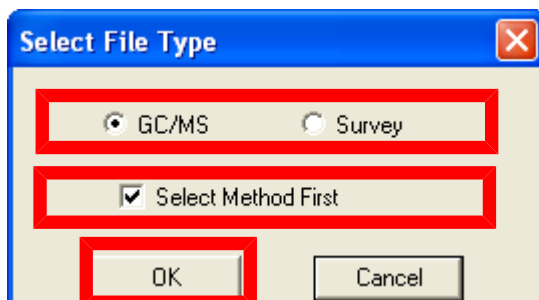
## 16.5 ID Unknowns

The **ID Unknowns** function allows the user to determine if all of the peaks in the chromatogram have been identified.

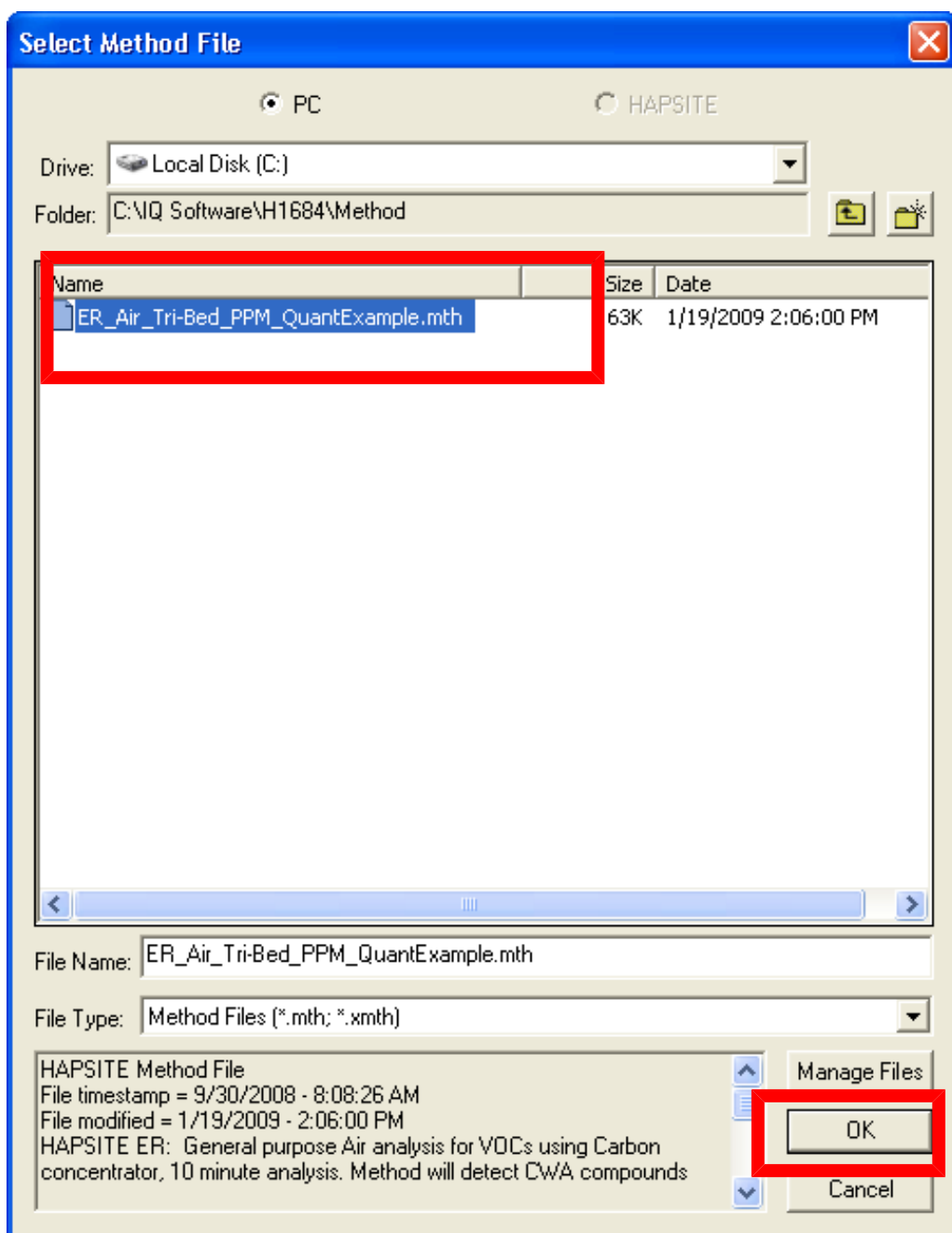
- 1 Double-click on the **ID Unknowns** function.



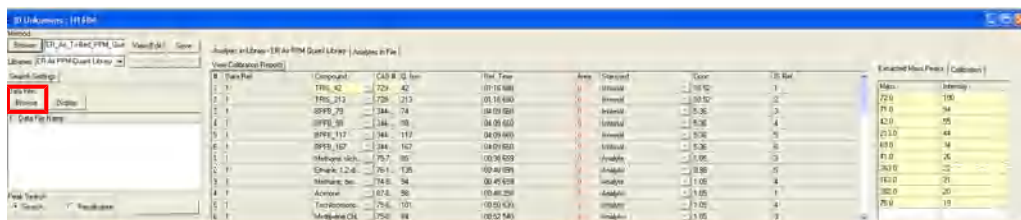
- 2 Select the type of file.



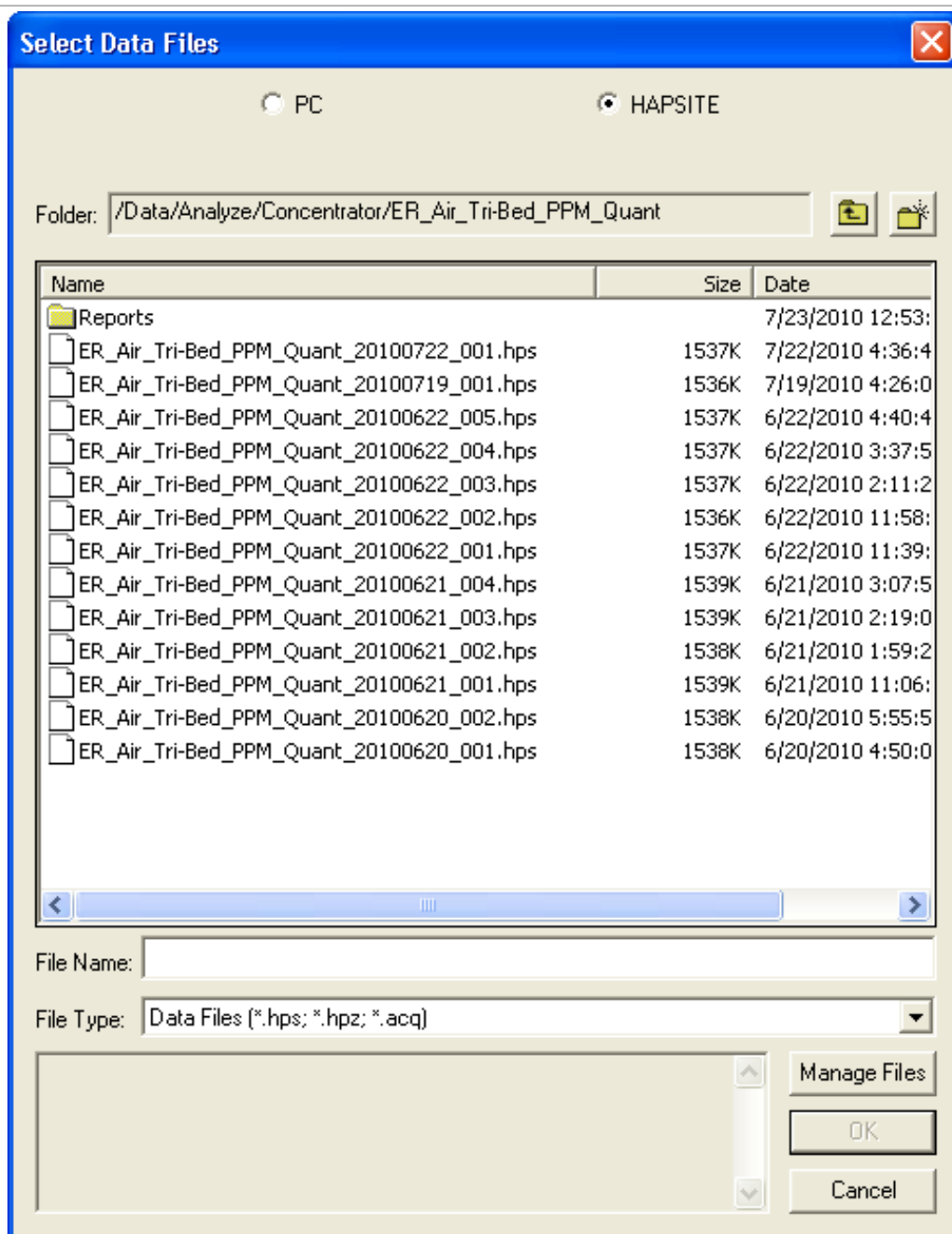
- 3 Verify that the **Select Method First** box is unchecked.
- 4 Click **OK**.
- 5 Select the desired method file. The data file that will be analyzed by **ID Unknowns** should have been generated from this file. Click **OK**.



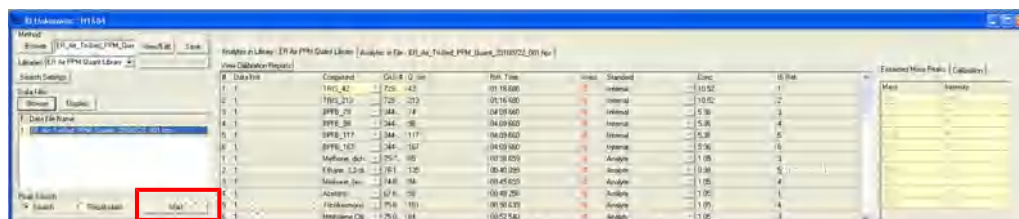
6 Click **Browse** in the **Data Files** section for the desired data file.



7 Select the desired data file.



8 Click **Start** to open the **Quant Report** and the chromatogram.



⇒ For information on reading the **Quant Report**, refer to View Reports [▶ 356].

**Unknown Report**

identification is by AMDIS library.  
Sensitivity range is in the high ppb  
or low to mid ppm, dependent on the  
compound.

Data File :  
/Data/GCMS/Loop/QuantExample/QuantExample\_20060301\_006.hps on h1091  
Acquisition Date and Time :  
3/1/2006 4:40:55 PM

Target Library: QuantExample  
Last Calibrated: 3/3/2006 9:07:57 AM

Peak Search Parameters:  
Search Window: 0:30.00  
Window Expand Factor: 0.050  
Peak Resolution: 5  
Noise Level Multiplier: 2.000  
Minimum Area: 50000  
Minimum Width: 7  
Maximum Width: 70  
Minimum Fit: 0.750  
Minimum Purity: 0.750

REC NO.	Target	Pred. RT	Internal Standard Name
1	75	2:32.34	TRIS_75
2	117	7:57.60	BPEB_79

REC NO.	Target	RT	Fit	Purity	Area	ppm	REC	Flag
1	75	2:32.97	0.992	0.915	381223	11.01	-4.40	
2	117	7:58.80	1.000	0.721	5391136	N/A	?????	Purity too low

REC NO.	Target	Pred. RT	Analyte Name
1	83	2:21.66	Trichloromethane

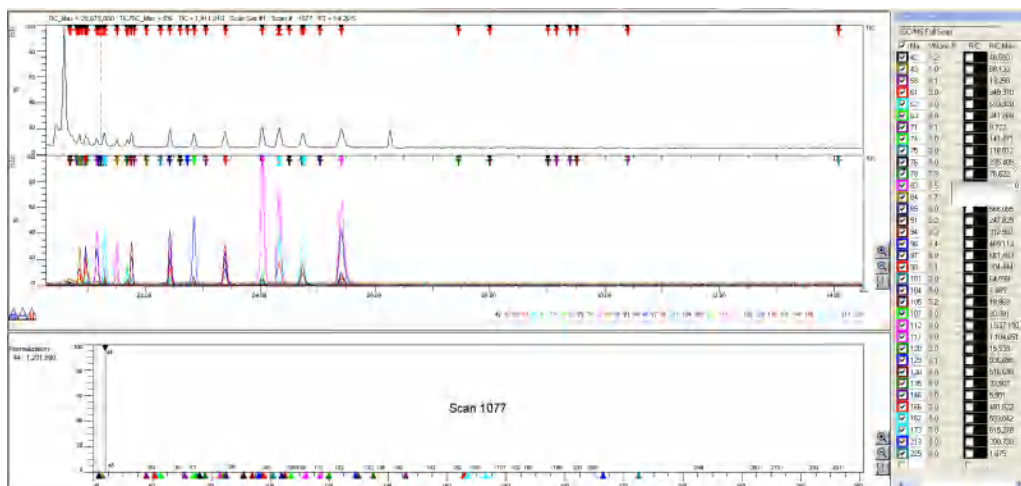
REC NO.	Target	RT	Fit	Purity	Area	ppm	Flag
1	83	2:23.78	0.993	0.807	107139744	84.05	

Include analytes not found (\*)

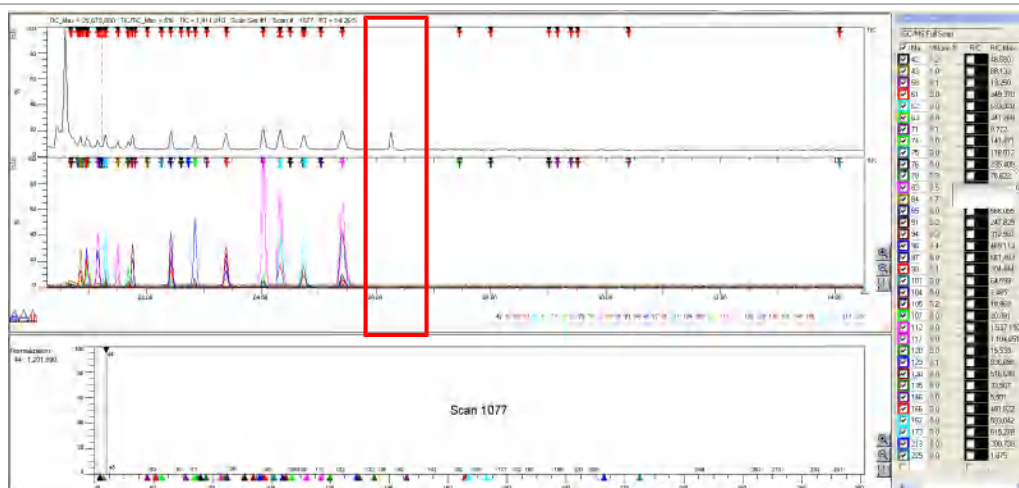
Export to Excel Save to File Print Close

9 Click **Close** to exit the **Quant Report**.

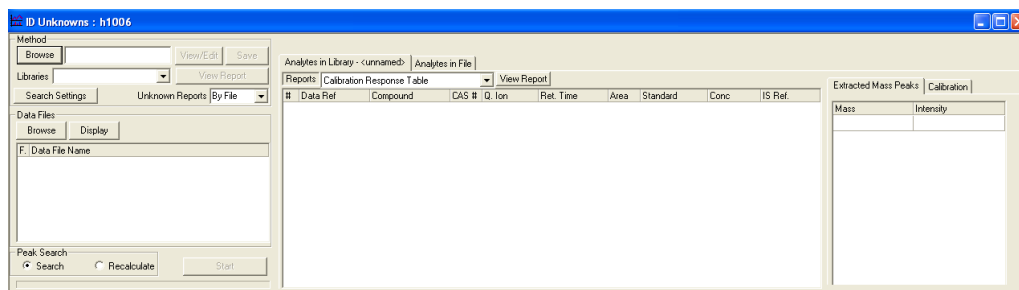
10 If the compound is part of the calibration library, **ID Unknowns** will label the peak with a "T."



11 If the compound is not part of the calibration library, it is necessary to use AMDIS (refer to Analyzing Data Using AMDIS [▶ 222]) or NIST (NIST Library Searches [▶ 230]) to make an identification.



## 16.6 Definition of Terms in the ID Unknowns Window



### 16.6.1 Method

Browse	Allows the user to select a method for calibration.
View/Edit	Opens the <b>Method Editor</b> for the method that is currently being calibrated. Refer to Method Editor [ > 301].
Save	Saves the current method
Libraries	A menu that allows the user to select a previously saved library
Save Library	Brings up the dialog box to save the library
Search Settings	Displays the search parameter settings. Refer to Peak Search Parameters [ > 243].

#### Unknown Reports:

By File	Displays report by file.
By Analyte	Displays report by analyte

### 16.6.2 Data Files

Browse	Used to select the data file for analysis.
--------	--

Display	Will display a chromatogram with a T over the compounds found in the calibration. See Display Function [ 401].
File Entry	Lists the reference number for the file.
Data File Name	Displays the data file name and pathway.

### 16.6.3 Peak Search

Search	Performs a peak detection and integration on the selected files. It produces the quantitative report.
Recalculate	Recalculates the peak areas and response factors without performing a peak search. This is most useful after manually editing the baseline points of a peak.
Start	Initiates the search for peaks or recalculates the peak search.

### 16.6.4 Analytes

Analytes in Library	Displays the analytes in the library.
Analytes in File	Displays the analytes in the currently displayed or selected file.

### 16.6.5 Reports

Calibration Response Table	Report that displays the response factor and curve statistics based on the selected curve type.
Calibration Report	Report that displays the area fit and purity for the calibration standards.
View Report	Displays the selected calibration report.
#	Shows the analyte number in the library.
D	Data Reference: lists the reference to the Data File in which the analyte was found.
Compound	Shows the compound name found in AMDIS, NIST library or assigned by the user for the analyte.
CAS #	Shows the Chemical Abstracts Services number for the analyte from the AMDIS or NIST library.
Q Ion	Shows the quantization ion for the analyte.
Ret. Time	Shows the retention time for the analyte.
Area	Displays the integrated area of the quant ion.
Standard	Designates the compound as an analyte or an internal standard.

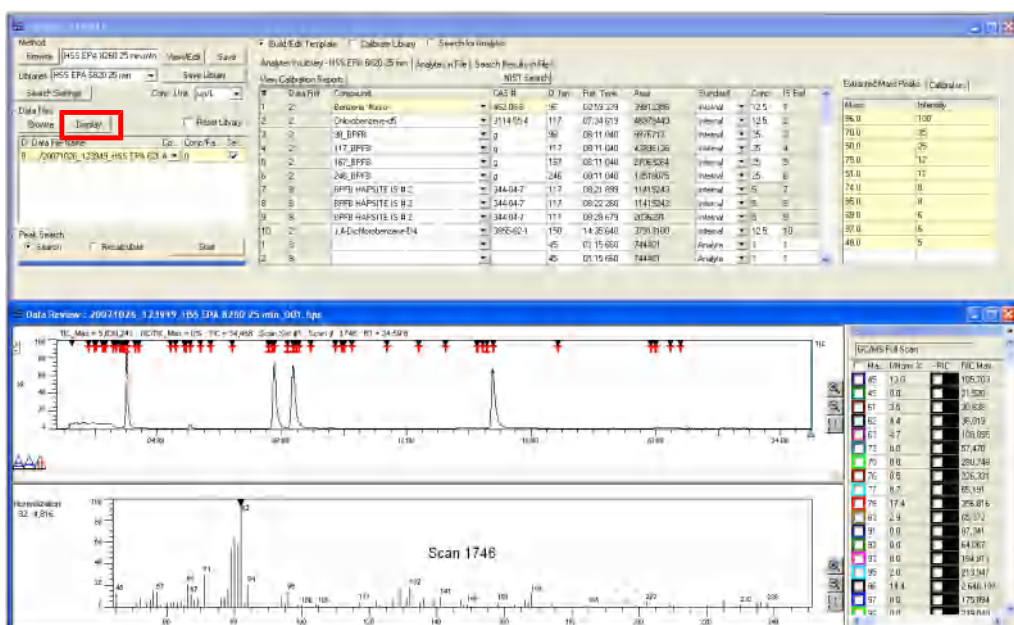


Conc	Shows the concentration of the analyte or internal standard in the displayed file.
IS Ref	Displays the internal standard reference number for analyte quantization.

The field is not used if the concentration flag is set to Global.

## 16.7 Display Function

The **Display** button in the **Data Files** section of both **Calibrate** and **ID Unknowns** shows the chromatogram and spectrum of the selected data file. This feature is beneficial when reviewing and revising identifications, selecting spectral peaks, adding to a library and manually integrating peak areas.



# 17 Maintenance

## 17.1 Introduction

This chapter outlines basic maintenance and troubleshooting procedures. It also provides an overview of common errors.

## 17.2 HAPSITE Symptom - Cause - Remedy Chart

Symptom	Cause	Remedy
HAPSITE ER is not powering on.	The battery is not charged.	Verify that the battery is charged. Replace the power source if necessary.
	The cable is not delivering power to the unit.	Verify that the cords are plugged into the unit. Do not use two HAPSITE ER units using a Y splitter as this will not deliver sufficient power.
HAPSITE ER periodically shuts off while in Extended Standby.	The power is intermittent or fluctuating too much for AC/DC supply to regulate.	Add a dedicated uninterruptible power supply (UPS) upstream of the AC/DC converter.
There is a N2 Canister Low error.	The canister is nearly empty.	Replace with a new carrier gas canister.
There is an Internal Standard Canister Low error or Internal Standard Expired error.	The canister is nearly empty or expired.	Replace with a new, unexpired internal standard gas canister.
There is sample carryover.	The system has become contaminated.	Run blanks until carryover is no longer present.
There is AutoTune Failure.	The IS canister is expired or empty.	Replace with a new, unexpired internal standard gas canister and repeat AutoTune.
	There is a leak in the fluidic pathway.	Remove and replace all fluidic connections, ensure each is secured at both ends of the concentrator.
	The mass spectrometer parameters are out of range.	Repeat AutoTune. If failure persists after 3 tries, perform a manual tune. Refer to Tune [▶ 276].

Symptom	Cause	Remedy
The concentrator clean out continuously fails.	The concentrator is chipped or broken.	Reinsert the concentrator. Verify that the ferrules are in good condition and correctly oriented..
	The concentrator is improperly seated or installed backwards.	Replace the concentrator with a new one
	The concentrator is contaminated.	Replace the concentrator with a new one.
HAPSITE ER will not properly communicate with the laptop.	HAPSITE ER is not properly configured to the laptop.	Refer to Configuring the Instrument for Communications [▶ 119].
The retention time for BPFb is not within the 3:45±0:05 second range.	The GC pressure flow needs adjustment.	Refer to Pressure Flows and Temperatures [▶ 190].
There is a GC column error.	The concentrator is improperly seated.	Reinsert the concentrator. Verify that the ferrules are in good condition and correctly oriented.
	The nitrogen carrier gas canister is nearly empty.	Replace with a new nitrogen carrier gas canister.
	The concentrator is chipped or broken.	Replace with a concentrator that is in good condition.
The probe is not recognized by HAPSITE ER, but appears to be plugged in into the port.	The probe is not fully inserted into the port.	Insert the probe into the port until it clicks into place.
	There are bent or broken pins on the LEMO plug.	Gently straighten bent pins and reinsert probe.
The probe is plugged in, but registers incorrect temperature.	The RTD of the probe line may be damaged.	Install a different probe in the AM, verify correct function. Install problem probe into different AM, verify defective behavior. Contact INFICON for service support.
There is Elevated Baseline.	There is background contamination, MS leak, or improper MS tune.	Run a noise check in manual tune to verify MS is not leaking. Manually tune unit according to instructions in Chapter 9. Repeat blank run to verify that baseline is less than 10% of BPFb. Contact INFICON for technical support.
	The electronic connection inside the probe is damaged.	Try using a different probe- if this works, contact INFICON for support as the original item will need to be serviced.

Symptom	Cause	Remedy
There is Zero Baseline.	The tune parameters are outside specifications.	Perform manual tune, refer to Performing Manual Tune [▶ 283], and adjust threshold to 300 and baseline to 100.
The IS Canister is not recognized.	The memory chip on the canister is damaged.	Replace internal standard canister.
	The contact pins are damaged.	Repair or replace pins on the inside of the front panel.
There is low sensitivity, or the ionizer has failed.	The ionizer is depleted.	Contact INFICON for support- this component can only be replaced by trained INFICON service personnel.
<ul style="list-style-type: none"> <li>• There is a High Pressure error.</li> <li>• The filament shut off or will not open.</li> <li>• There is an electron multiplier fault.</li> <li>• There is an ion pump failure.</li> <li>• There is a MS emission error.</li> </ul>	The NEG/ion pump is depleted mass or the spectrometer requires service. Please review Vacuum System [▶ 26] for details on the vacuum system.	Attach the unit to the Service Module and pump down for 24 hours. (See Attaching HAPSITE to the Service Module [▶ 406].) Perform an autotune with the unit attached to the Service Module. If the autotune fails after three tries, perform a manual tune. Refer to Tune [▶ 276]. Detach the unit from the Service Module and re-start it. If the problem persists, contact INFICON for technical support. Consider replacing the NEG.

**HAPSITE ER ionizer cannot be replaced in the field- it must be replaced by trained INFICON service personnel.**



### **⚠ WARNING**

**Venting HAPSITE ER with a NEG that has not cooled causes total NEG consumption and may possibly result in severe damage to the HAPSITE ER mass spectrometer components. It may also result in physical injury since extreme heat generation from NEG consumption creates hot surfaces.**

## 17.3 Saturation of the Probe and Probe Line

### 17.3.1 Symptoms

Symptoms of contamination in the probe and probe line include a high continuous base line with the same or similar identification in Survey Mode. It can also be seen as a persistent peak in Analyze (GC/MS) Mode.

### 17.3.2 Decontaminate Saturation

- 1 Remove the probe from HAPSITE ER.
- 2 Hold the probe and probe line in a "U" shape.
- 3 Holding the probe, pour methanol from a squeeze bottle into the probe nut.



#### **WARNING**

**For safety precautions, wear appropriate PPE according to the manufacturer's MSDS.**

- 4 With each end of the probe in a separate hand, move each hand up and down to allow the methanol to flow through the probe.
- 5 Empty the methanol remaining in the probe line by tipping one end of the probe line downward until all of the methanol drains from the probe line. Repeat this procedure to allow the methanol to flush contaminants from the probe line.
- 6 Blow out the probe line with nitrogen to remove any residual methanol that may be left in the probe line. Allow the probe to fully dry.
- 7 Reattach the probe line to HAPSITE ER.



#### **WARNING**

**Continue to wear PPE while blowing out probe and be sure that both ends of the probe are facing away from the user when blowing out occurs.**

## 17.4 NEG Troubleshooting

A high pressure warning indicates that the on-board NEG and ion pump cannot maintain appropriate vacuum, and that loading the unit on a Service Module to re-create the vacuum may be necessary. For instructions on how to load the instrument onto a service module, please see Attaching HAPSITE to the Service Module [▶ 406].

The high pressure error may also indicate that the NEG pump is worn and needs replacing. Please continue reading for information on how to troubleshoot NEG pumps.



To view the MS pressure:

- 1 Touch **HAPSITE** icon.
- 2 Touch the **Tune** icon.
- 3 Locate the MS pressure. In order for HAPSITE ER to properly operate, the pressure must be below 6 e-03. If pressure is too high, ionizer will not activate.

If the NEG pump has 150 hours or less, consider trying a bakeout to extend the life of the NEG pump. To check the NEG pump hours, refer to NEG Status [▶ 191].



If the NEG pump has more than 250 hours, a bakeout can be tried, though the results are likely to be limited.

## 17.5 Attaching HAPSITE to the Service Module



### **⚠ CAUTION**

Prior to attaching HAPSITE ER to the Service Module, unplug the black NEG cable inside the HAPSITE ER front panel. This will ensure that the NEG will not heat when using the Service Module to provide vacuum.



### **⚠ WARNING**

Venting HAPSITE ER with a NEG that has not cooled causes total NEG consumption and may possibly result in severe damage to the HAPSITE ER mass spectrometer components. It may also result in physical injury since extreme heat generation from NEG consumption creates hot surfaces.



If HAPSITE ER is turned on with the NEG at 400°C, then the NEG must be cooled before proceeding. Turn off HAPSITE ER and allow it to cool for approximately 24 hours or until the NEG is at room temperature.

If the Service Module has been in storage, refer to HAPSITE ER Service Module operating manual, Chapter 4, section 4.2.1, Setting Up the Service Module, on page 4-2 before continuing.

HAPSITE ER must be turned on before continuing (refer to HAPSITE ER Service Module operating manual, Chapter 5, section 5.4, Starting Up HAPSITE ER on the Service Module, on page 5-9).

Physically attach HAPSITE ER to the Service Module (refer to HAPSITE ER Service Module operating manual, Chapter 5, section 5.2, Placing HAPSITE ER on the Service Module, on page 5-2).

HAPSITE ER can be electronically attached to the Service Module using the IQ Software, or using the HAPSITE ER front panel. Refer to the appropriate HAPSITE ER model operating manual for more instruction on front panel usage.

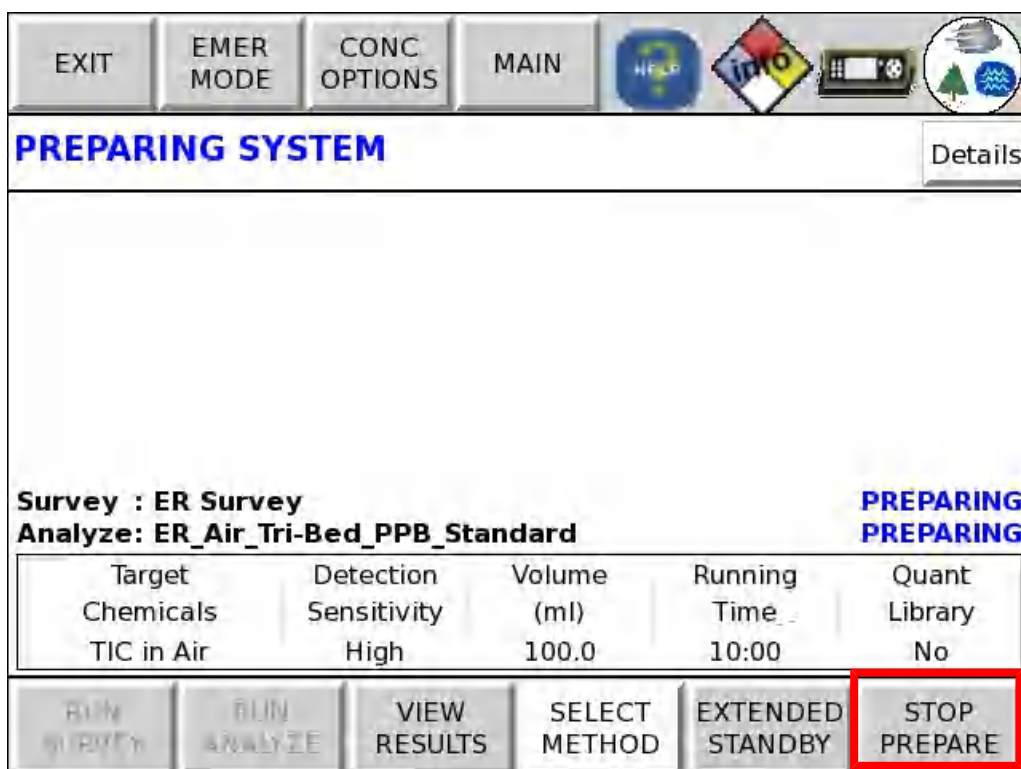


#### CAUTION

**When operating the Service Module, the vents must be kept clear to allow free airflow. Air flows from right to left through the Service Module to allow cooling of the pumps. A blockage can prevent the air from cooling the pumps properly and may cause the over-temperature protection sensor to automatically shut down the pumps.**

### 17.5.1 Attaching HAPSITE to the Service Module Using IQ Software

- 1 Make sure that HAPSITE ER does not heat, or is in the **NOT READY** state. As soon as the HAPSITE ER screen is displayed, tap **STOP PREPARE** or using **◀▲▼▶**, highlight **STOP PREPARE** and tap **OK SEL**.



**PREPARING SYSTEM** Details

**Survey : ER Survey** **PREPARING**  
**Analyze: ER\_Air\_Tri-Bed\_PPB\_Standard** **PREPARING**

Target	Detection	Volume	Running	Quant
Chemicals	Sensitivity	(ml)	Time	Library
TIC in Air	High	100.0	10:00	No

RUN SURVEY RUN ANALYZE VIEW RESULTS SELECT METHOD EXTENDED STANDBY **STOP PREPARE**



### CAUTION

Prior to attaching HAPSITE ER to the Service Module, unplug the black NEG cable inside the HAPSITE ER front panel. This will ensure that the NEG will not heat when using the Service Module to provide vacuum.

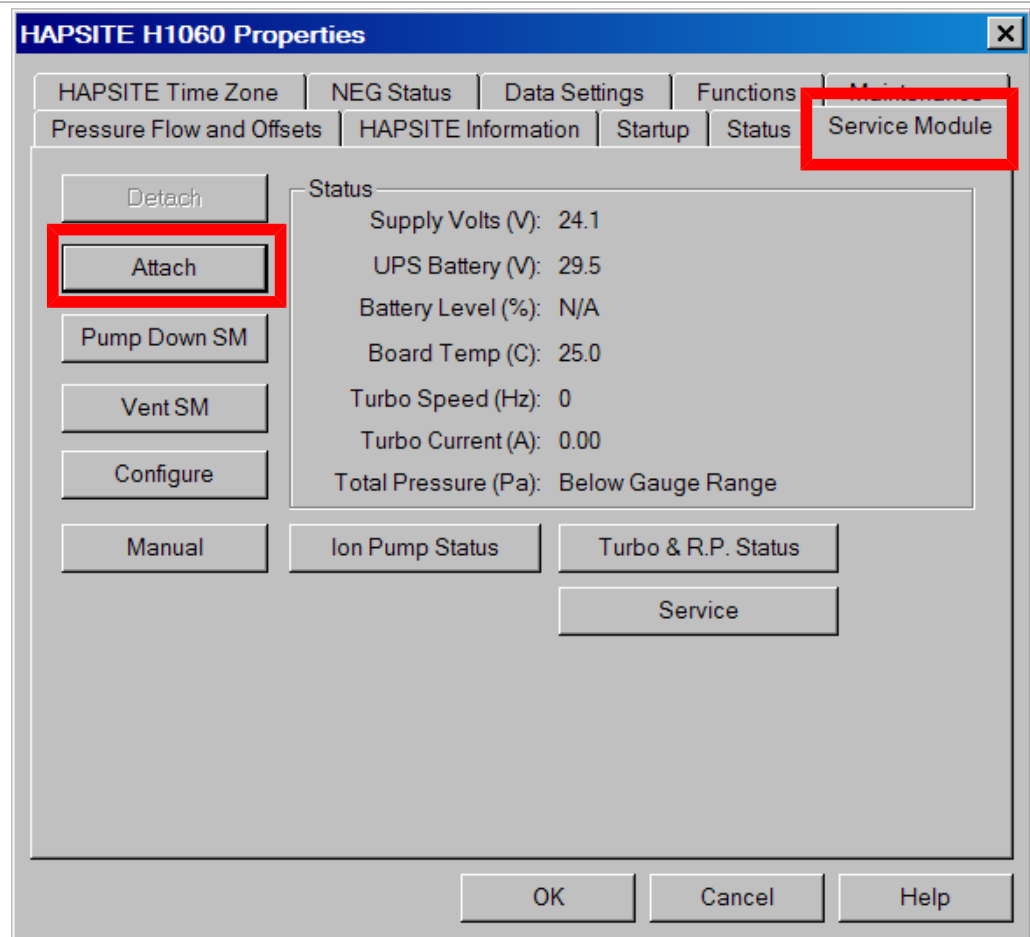
- 2 Connect HAPSITE ER to the computer using wireless communication on the crossover cable.
- 3 Open IQ Software.
- 4 Click the desired HAPSITE ER sensor icon.
- 5 Double-click the **Service Module** icon.



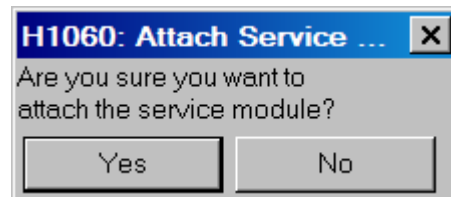
Service  
Module

- 6 The **Service Module** tab on the **HAPSITE Properties** window displays.
- 7 Click **Attach**.





- 8 Are you sure you want to attach the service module? confirmation message is displayed. Click **Yes**.



- 9 The Roughing Pump will start first, then the Turbo Pump will begin, as shown on the Turbo Speed (Hz) line in the figure in step 7. The speed is initially displayed as 0, the increases.



After clicking **Attach**, the **HAPSITE Properties** window can be closed.

- ⇒ The procedure typically takes about five minutes to complete. While attaching, the **Attaching Service Module Please Wait** message is displayed.

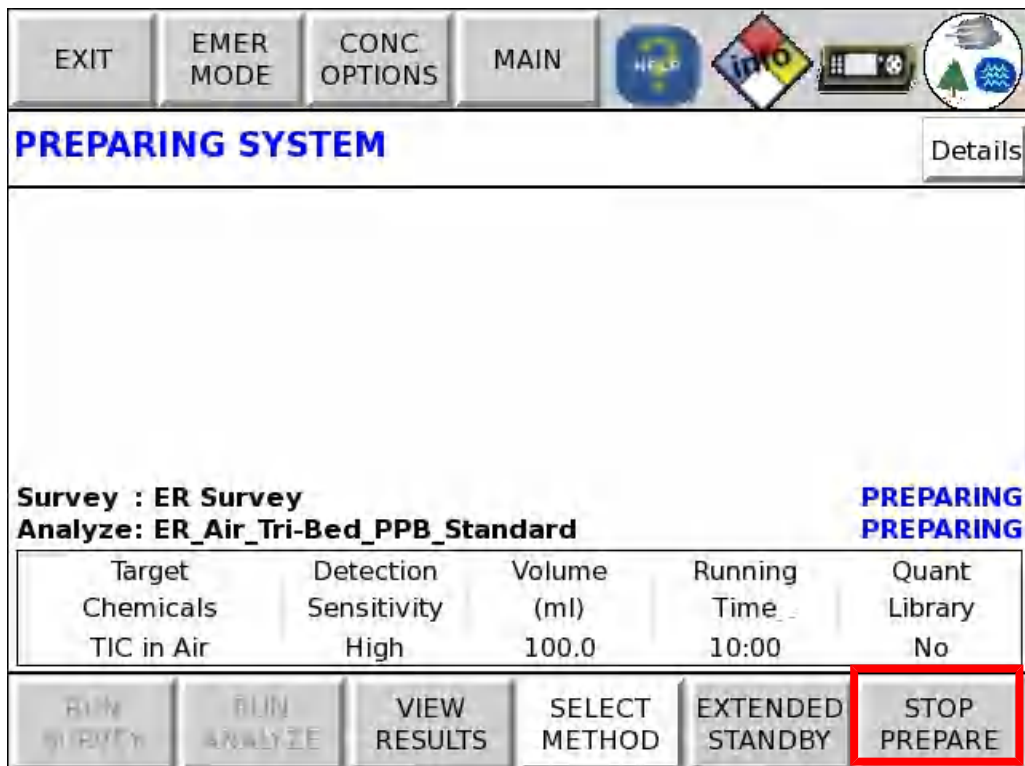


- 10 When the procedure is finished, the **HAPSITE is Attached** message is displayed.



## 17.5.2 Attaching HAPSITE to the Service Module Using the HAPSITE Front Panel Controls

- 1 To avoid running the start up method or AutoTune, tap **STOP PREPARE**.

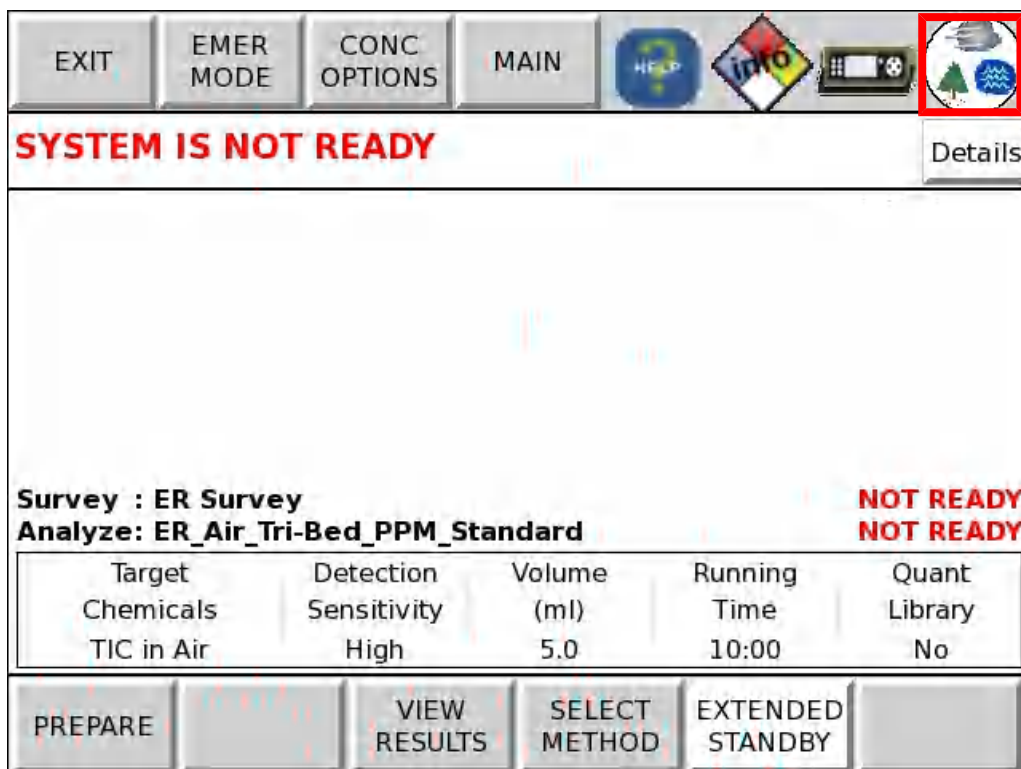


- 2 If using the push button keys, highlight **STOP PREPARE** with ◀▶▼▶. Tap **OK SEL**.



- 3 The **SYSTEM IS NOT READY** message will appear at the top of the screen.
- 4 Tap the **Accessory** icon, or push the **SYSTEM/STAT** button until the accessory page appears.





- 5 Tap the **ATTACH SM** button or using ◀▲▼▶ highlight the **ATTACH SM** button and tap **OK SEL**.
- 6 A status bar displaying the progress of the attach procedure will be displayed.



The **ATTACH SM** button will be grayed out.

- 7 When the Attach has successfully completed, the **Service Module Attached** message will be displayed.

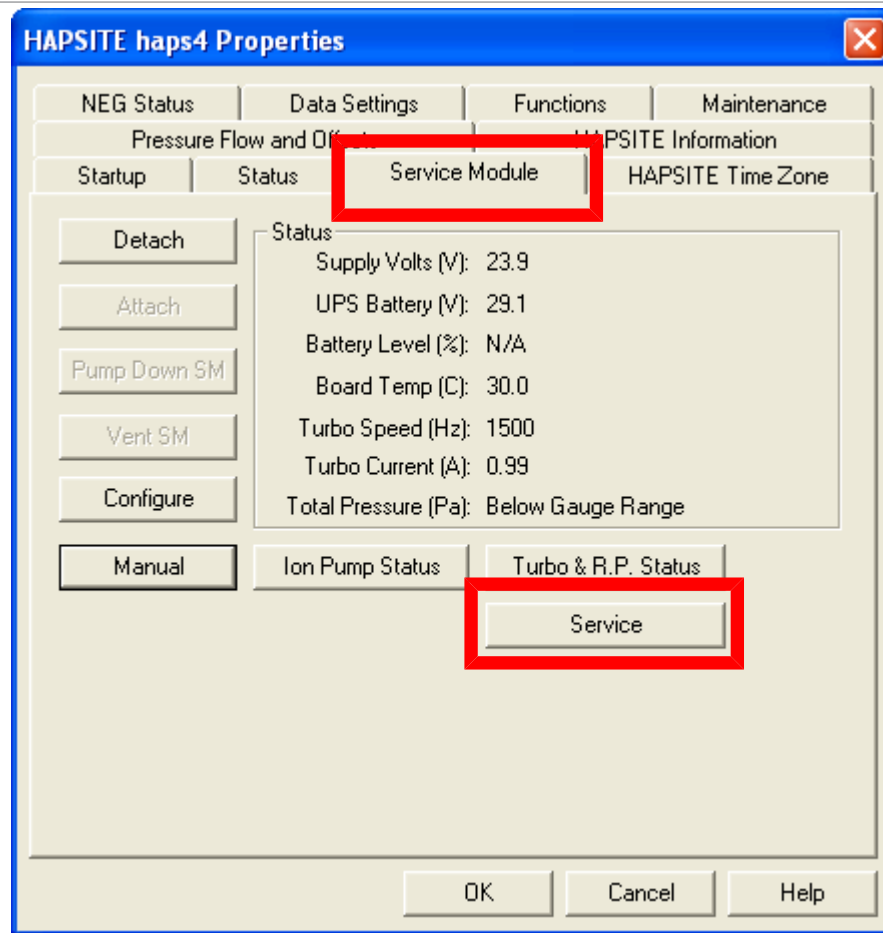


Both **ATTACH SM** and **DETACH SM** buttons will be grayed out immediately after a successful attach while the system prepares.

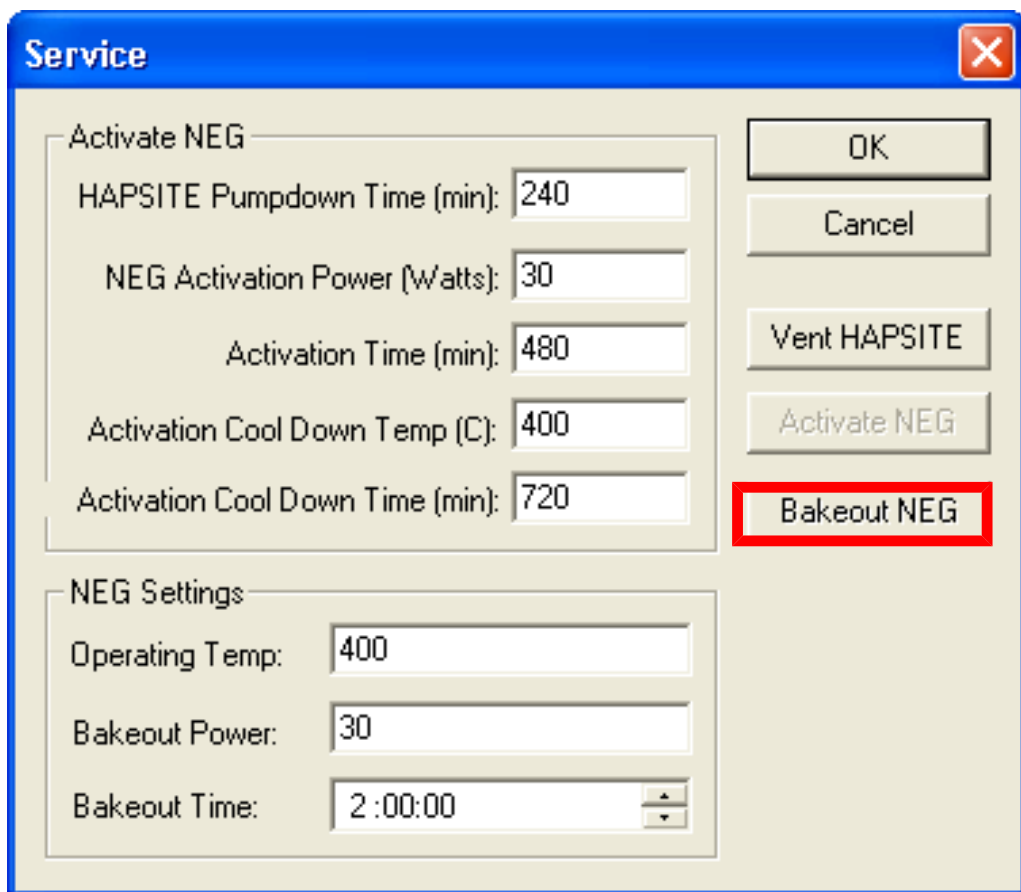
## 17.6 Bakeout Procedure

A bakeout can be performed with or without the use of the Service Module. A bakeout heats the NEG pump to 700°C for a specified length of time. (The default time setting is two hours). Contact INFICON technical support before performing this procedure.

- 1 Click on the **Service Module** tab of the **Properties** menu.



- 2 Click on the **Service** button.
- 3 Verify that the settings match the setting displayed below and click **Bakeout NEG**.

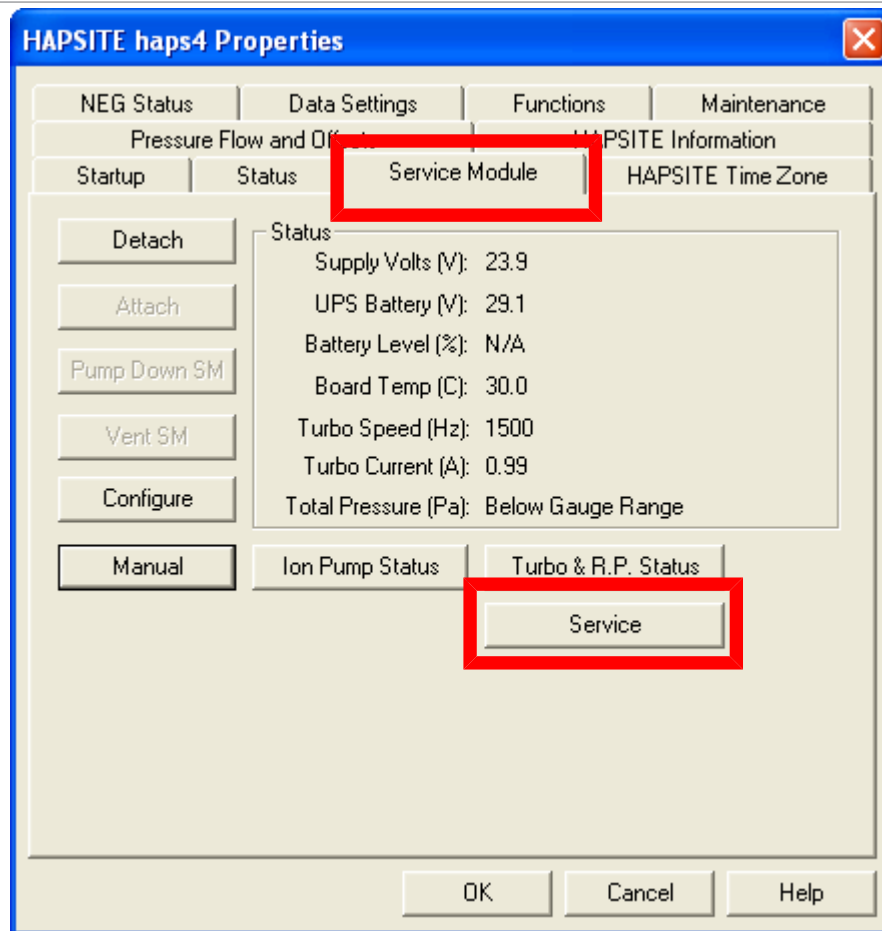


- 4 If the bakeout is complete, run a blank method. If the bakeout was successful HAPSITE ER will be operational. If the bakeout was unsuccessful, a high pressure error will occur.

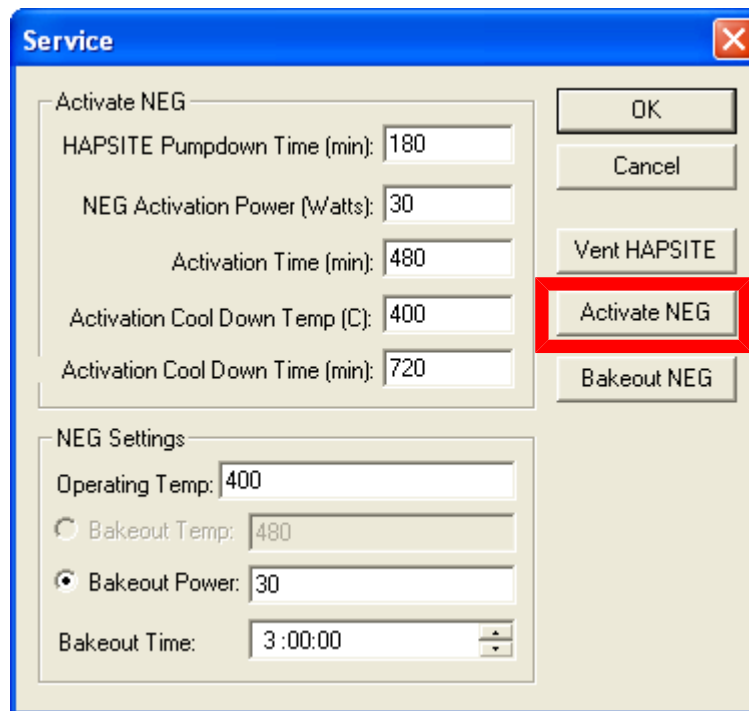
### 17.6.1 Reactivating the NEG Pump

Reactivating the NEG pump requires having the Service Module attached to HAPSITE ER for at least 22 hours. This procedure is the same procedure that is used to activate a new NEG pump.

- 1 Click on the **Service Module** tab of the **Properties** menu.
- 2 Click on the **Service** button.



- 3 Use the **Activate NEG** setting below as a guideline. However, change the HAPSITE ER Pumpdown Time to **180**.



- 4 Click the **Activate NEG** button.

- 5** At the end of the reactivation, the program will detach HAPSITE ER from the Service Module as part of the process.



## 18 Part Numbers

### 18.1 HAPSITE Part Numbers

Part Number	Product Feature Options	HSER
930-2100-G10	HAPSITE analytical module with standard column no NEG	1
930-2100-G11	HAPSITE analytical module with standard column NEG	2
930-850-G5	120V HAPSITE ER	1
930-850-G6	230V HAPSITE ER Europe	2
930-850-G7	230V HAPSITE ER United Kingdom	3
930-850-G8	230V HAPSITE ER Australia/China	4
930-206-G6	Hand control unit (Probe)	1
930-0371-G1	NIST and HAPSITE ER software only. No laptop.	A
930-261-G6	Laptop with Windows	B
930-261-G7	Ruggedized laptop with Windows	C
930-262-G6	Laptop with Windows (Europe)	D
930-262-G7	Ruggedized laptop with Windows (Europe)	E
930-263-G6	Laptop with Windows (United Kingdom)	F
930-263-G7	Ruggedized laptop with Windows (United Kingdom)	G
930-264-G6	Laptop with Windows (Australia/China)	H
930-264-G7	Ruggedized laptop with Windows (Australia/China)	J
930-202-G1	Service module 100-240 V	1
930-035-G1	HAPSITE IQ software, English (installed in laptop and AM)	A

### 18.2 HAPSITE Accessories

931-205-G2	HAPSITE ER Headspace sampling system
932-220-G2	HAPSITE ER SituProbe sampling system
934-290-G1	HAPSITE ER SPME sampling system
934-708-G1	HAPSITE ER TDSS sampling system

## 18.3 HAPSITE Spare Parts

<b>Power</b>	930-469-P1	110V AC - 24V DC HAPSITE Power Supply
	930-469-P2	230V Power Supply (EU)
	930-469-G3	230V Power Supply (UK)
	930-469-G4	230V Power Supply (Australia)
	930-470-G1	Battery Charger
	068-0002	Battery Charger/Service Module Power Cord (US)
	068-0151	Battery Charger/Service Module Power Cord (EU)
	068-0388	Battery Charger/Service Module Power Cord (UK)
	068-0393	Battery Charger/Service Module Power Cord (Australia)
	930-4062-G1	HAPSITE Battery
<b>Cables:</b>	600-1319-G2	Ethernet communication cable (crossed) - black cable (12 ft.)
	930-246-G1	Hot swap cable (battery test bracket)
<b>Kits:</b>	930-021-G1	Gasket kit
	930-0221-G1	Concentrator tube nut and ferrule kit, 10 each
	930-022-G1	Tool kit with torque wrench kit
	930-0231-G1	Probe nut and ferrule kit, 5 each
	930-2020-G2	Decontamination cap plug kit
	930-705-G1	Sample loop tube kit
	930-206-G6	Hand control unit (probe)
	930-249-G2	Concentrator cover
	930-250-G1	Sample loop cover
	<b>Concentrator Tubes:</b>	930-251-G1
930-716-G1		Tri-Bed Kit
<b>Line Insulation:</b>	070-1545	Probe insulation
<b>NIST:</b>	930-4071-G1	NIST version upgrade
	930-4081-G1	NIST (with AMDIS)
<b>Shipping Cases:</b>	930-464-P1	HAPSITE ER
	930-4131-P1	HAPSITE ER accessory case

<b>Miscellaneous:</b>	930-4051-P1	Cold Weather Insulation Bag
	059-0329	Quick Disconnect Stem for N <sub>2</sub>
	930-612-P1	USB Drive
	930-4551-G1	Back, HAPSPACK

## 18.4 HAPSITE Consumables

<b>NEG Pumps:</b>	930-425-P1	Spare NEG pump
<b>Carrier Gas</b>	930-432-P6	Canister, Carrier Gas, 6 each
<b>Canisters:</b>	930-432-P12	Canister, Carrier Gas, 12 each
	930-432-P24	Canister, Carrier Gas, 24 each
<b>Extended Life Carrier Gas Canisters:</b>	930-730-G1	Extended life carrier gas deployment kit (110 liter)
	930-4611-P1	Extended life carrier gas (110 liter cylinder)
<b>Internal Standard Canisters:</b>	930-433-P6	Canister, internal standard gas, 6 each
	930-433-P12	Canister, internal standard gas, 12 each
	930-433-P24	Canister, internal standard gas, 24 each
<b>Combo Pack Canisters:</b>	930-477-P1	Gas combo pack (4 carrier gas and 2 internal standard)
<b>Chemical Kits:</b>	071-747	Air Performance Standard (5 analytes) in Methanol 1.2 mL
	070-860-2	HAPSITE Chemical Standards Kit, 19 part (for training and practice)

## 18.5 Service Module Spare Parts

068-0002	Battery charger/service module power cord, US.
930-0211-G1	Torque wrench kit
930-465-P1	Shipping case, service module
600-1001-P15	RS232 cable (15 ft.)

## 19 Glossary

Air peak	A response by the mass spectrometer to the components of air. This set of compounds typically elutes 1 to 1.5 minutes from the start of analysis.
Alignment	A part of the tuning process which assures that the mass peaks fall at their calibrated position on the mass scale.
AM	Analytical module, also called the HAPSITE ER.
AMDIS	Automated Mass Spectral Deconvolution and Identification System Software
AMU	Atomic mass unit. A unit that is used for indicating mass on an atomic scale
Analyte	That portion of a sample which comprises compounds to be analyzed.
AutoTune	A process that occurs when the instrument is initially started up; it automatically performs mass alignment, resolution adjustment and adjustment of relative intensity of the peaks. AutoTune will take place once the heated zones have reached the proper temperature.
Baseline	A measure of the intensity of the background noise of the mass spectrometer. This is determined using the <b>Noise Check</b> feature in the <b>Tune</b> program.
Carrier gas	The pure inorganic gas used to aid the flow of sample gas through the chromatograph for analysis. VOC-free nitrogen is the carrier gas for the HAPSITE ER.
Column	The column is a long glass capillary which is lined with a material (called the “stationary phase”) with which the analytes interact based on their physical characteristics, slowing their flow. The degree of this interaction progressively separates the different compounds from one another during elution.
DAC	Digital to analog converter. An element of the electronic circuitry which converts the microprocessor’s digital instructions to the analog requirements for control of the instrument.
DOC	Declaration of Contamination document. All chemicals that have been run through the HAPSITE ER must be listed on the form prior to service and repairs.
Elution time	The elapsed time from injection of a specific compound onto the column until the compound exits the column (same as retention time).
ET	Elapsed time of sample run. Used in <b>Survey</b> method instead of retention time.
Filament	A hot wire in the ionizer from which electrons are emitted.
Filament delay	This specifies the amount of time between the start of analysis and the time which the HAPSITE ER turns on the filament. Filament delay allows components of the air peak or solvents to pass through the mass spectrometer before the filament is turned on.
GC	Gas chromatograph
GUI	Graphical user interface

Inlet state	This refers to the valve states in the HAPSITE ER. The states of the valves control sampling, analysis, clean-out of the HAPSITE ER.
Internal standard	A mix of known compounds with known concentrations. They are mixed with the sample analytes to validate the response of the HAPSITE ER.
Ion energy	These settings in the tune program directly affect the intensity of mass peaks. Ion energies are commonly used to set the relative mass intensities of the tuning ions.
Ion volume	The specific space in the ionizer where ionization of the sample takes place.
Ion	An atom or molecule which carries an electric charge due to depletion or addition of one or more electrons.
Ionizer	The assembly of parts in the mass spectrometer into which the sample flows and which projects a beam of mixed ions into the mass filter.
I.S. reference	This section of the <b>Calibrate</b> screen identifies the target ion of the internal standard which will be used for quantification of the chosen compound.
kPa	Kilo Pascal. Unit of pressure measurement which is equivalent to approximately 0.145 PSI.
LCD	Liquid crystal display. This refers to the display screen on the front panel of the HAPSITE ER.
Library	A user compiled list of compounds, which includes both analytes and internal standards (if chosen). The library keeps information such as the name, target ion, concentration, retention time, relative mass intensities, and compound specific search parameters (if selected).
Mass calibration	A function of the HAPSITE ER which uses internal standard gas to check the alignment of masses, and also to check the relative intensities of the tune masses.
Mass fragment	A molecule (or ion) resulting from the break-up of a parent molecule.
Mass defect	The effect on a mass spectrum of the difference between the atomic weight of a compound or fragment and a whole number.
Mass spectrum	A display of the amount of each mass fragment present at the specific time, plotted as amplitude vs. molecular weight.
MDP	Molecular dispersion pump
Membrane isolation valve	The valve which supports the mass spectrometer's inlet membrane and (when closed) interrupts the flow of analyte from the membrane into the mass spectrometer.
Method	A set of instructions for a function of HAPSITE ER
Molecular weight	The amu representation of the total number of protons and neutrons in a specified molecule.
MS	Mass spectrometer
ms	milliseconds

SDS	Safety data sheet
Multiplier voltage	The voltage applied to the multiplier in the mass spectrometer, which directly effects the amplitude of signal and background noise.
NEG	Non-evaporable getter. Used for vacuum maintenance.
NIST library	NIST stands for National Institute of Standards and Technology Mass Spectral Library. This is a library of spectra of compounds which can be searched to tentatively identify unknown compounds.
Noise Check	An option in the <b>Tune</b> program which checks the system for background noise. The results of the noise check are used to discriminate against baseline noise during analysis.
Pascal (pa)	Unit of pressure, equal to 1 dyne per cm <sup>2</sup> . Equivalent to 7.5 x 10 <sup>-3</sup> Torr and 1.45 x 10 <sup>-4</sup> PSI.
PEEK	A contamination resistant material used for a number of fittings in the HAPSITE ER.
Phase	The coating on the inside of the gas chromatograph column by which organic vapors are retained.
PPB	Parts per billion concentration level
PPE	Personal protective equipment
PPM	Parts per million concentration level
PPT	Parts per trillion concentration level
Remote power	Power supplied to the HAPSITE ER and Headspace sample system either from the Service Module (for the HAPSITE ER) or external AC - 24 V(dc) converter.
Resolution	These settings in the tune program affect the way the mass spectrometer resolves peaks. Increasing the resolution narrows the peaks in that mass range, while lowering the resolution will broaden the peaks.
Retention time	The elapsed time from injection of a specific compound onto the column until the compound exits the column (same as retention time).
Reverse search	A function of the NIST search (tentative unknown identification) library which allows compounds which are specified in the user library to be identified as part of the search.
RH	Relative humidity
RIC	Reconstructed ion chromatogram. A presentation of the chromatographic record which extracts from the TIC and displays the intensity of the ion or ions specified.
Round trip time	The amount of time required to complete a scan of all the masses specified in a SIM method. This includes the number of masses, integration time, number of extra measurements, lead in time, and peak width.
RMA	Return material authorization. Returning material cannot be sent back without this assigned number.

%RSD	Percent relative standard deviation. This is a measure of the linearity (using mathematical regression analysis) of the concentration levels in the calibration curve for each compound.
Sample loop	The portion of the gas chromatograph through which the inlet flow is directed and from which the injection is made.
Scan method	This method specifies the masses to be scanned by the mass spectrometer, length of the run, filament delay, and scan and integration times.
Scan time	In <b>Full Scan</b> analysis, this refers to the cumulative time required to make a scan of all the masses in the range specified. The calculation of scan time includes the integration time and the points/amu.
SIM	<b>Selected Ion Monitoring.</b> Mass analysis of one or several ion peaks without scanning the entire spectrum.
Target ion	The specific ion mass which will be used for quantification or primary identification of a compound in the library.
Temperature programmable	Software controlled temperature programming that allows the user to reach temperatures from 55°C to 200°C in a controlled ramp.
Threshold	A measure of the amplitude of the background noise of the mass spectrometer. This is determined using the <b>Noise Check</b> feature in the tune program.
TIC	Total ion chromatogram. A graph of time verses signal intensity.
TMP	Turbo molecular pump
Torr	Unit of sub-atmospheric pressure. Equivalent to 133.3 pa.
Vacuum interconnect valve	The two-part valve which seals the HAPSITE ER manifold, when closed, and opens it to the vacuum pumps in the Service Module, when open. The vacuum interconnect valve is powered by a motor within the Service Module, under direction of the HAPSITE ER.
VSO valve	Voltage sensitive orifice valve. This valve uses voltage applied to the valve to control the size of its orifice. This in turn controls the flow rate of gas through HAPSITE ER.

## 20 Appendix A: HAPSITE Target Compounds

### 20.1 Compounds in Order of Elution

Name	Formula	k	Quantion amu	I.S amu	CAS #
Chloromethane	CH <sub>3</sub> Cl	a 0.08	50	50	74-87-3
Vinyl Chloride	CH <sub>2</sub> =CHCl	a 0.11	62	50	75-01-4
Bromomethane	CH <sub>3</sub> Br	b 0.17	96	9	74-83-9
Chloroethane	CH <sub>3</sub> CH <sub>2</sub> Cl	b 0.19	64	69	75-00-3
Acetone	CH <sub>3</sub> COCH <sub>3</sub>	0.27	43, 58	50	67-64-1
1,1-Dichloroethylene	CCl <sub>2</sub> =CH <sub>2</sub>	c 0.37	98	99	75-35-4
Methylene Chloride	CH <sub>2</sub> Cl <sub>2</sub>	c 0.39	86	99	75-09-2
Carbon Disulfide	CS <sub>2</sub>	0.46	76	69	75-15-0
trans-1,2-Dichloroethylene	CClH=CHCl	0.51	96	69	540-59-0
1,1-Dichloroethane	CHCl <sub>2</sub> CH <sub>3</sub>	d 0.57	65	69	75-34-3
Vinyl Acetate	CH <sub>3</sub> COOC(H)CH <sub>2</sub>	d 0.57	43, 86	50	108-05-4
2-Butanone	CH <sub>3</sub> COCH <sub>2</sub> CH <sub>3</sub>	0.63	43, 58	69	78-93-3
cis-1,2-Dichloroethylene	CClH=CClH	0.73	96	99	540-59-0
Chloroform	CHCl <sub>3</sub>	0.78	83	69	67-66-3
1,3,5Tris(trifluoromethyl)benzene	C <sub>6</sub> H <sub>3</sub> (CF <sub>3</sub> ) <sub>3</sub>	e 0.96	Note 1		729-81-7
1,2-Dichloroethane	CClH <sub>2</sub> CClH <sub>2</sub>	e 0.98	64	69	107-06-2
1,1,1-Trichloroethane	CCl <sub>3</sub> CH <sub>3</sub>	1.07	97	99	71-55-6
Benzene	C <sub>6</sub> H <sub>6</sub>	1.22	78	69	71-43-2
Carbon Tetrachloride	CCl <sub>4</sub>	1.26	117	125	56-23-5
1,2-Dichloropropane	CH <sub>2</sub> ClCHClCH <sub>3</sub>	1.51	63	69	78-87-5
Bromodichloromethane	BrCl <sub>2</sub> CH	f 1.59	83	69	75-27-4
Trichloroethene	ClCH=CCl <sub>2</sub>	f 1.61	130	99	79-01-6
cis-1,3-Dichloropropene	CClH=CCClH <sub>2</sub> (H)	g 2.08	75	69	542-75-6
4-Methyl-2-Pentanone	CH <sub>3</sub> COCH <sub>2</sub> CH(CH <sub>3</sub> )CH <sub>3</sub>	g 2.11	43, 58	69	108-10-1
trans-1,3-Dichloropropene	CClH=C(H)CClH <sub>2</sub>	2.44	75	69	542-75-6
1,1,2-Trichloroethane	CHCl <sub>2</sub> CH <sub>2</sub> Cl	2.56	97	99	79-00-5
Toluene	C <sub>6</sub> H <sub>5</sub> CH <sub>3</sub>	2.8	91	79	108-88-3
2-Hexanone	CH <sub>3</sub> CO(CH <sub>2</sub> ) <sub>3</sub> CH <sub>3</sub>	h 3.08	43, 58	79	591-78-6



Name	Formula	k	Quantion amu	I.S amu	CAS #
Dibromochloromethane	Br2ClCH	h 3.16	127	117	124-48-1
Tetrachloroethylene	Cl2C=CCl2	4.02	129	167	127-18-4
Chlorobenzene	C6H5Cl	5.07	122	117	108-90-7
Bromopentafluorobenzene	C6BrF5	5.59	Note 2		344-4-7
Ethyl Benzene	CH3CH2C6H5	5.91	91	79	100-41-4
Bromoform	CHBr3	i 6.24	173	167	75-25-2
m-Xylene	C6H4(CH3)2	i 6.35	106	117	1330-20-7
p-Xylene	C6H4(CH3)2	i 6.35	106	117	1330-20-7
Styrene	C6H5CH=CH2	7.25	104	117	100-42-5
o-Xylene	C6H4(CH3)2	j 7.52	91	79	1330-20-7
1,1,2,2-Tetrachloroethane	CHCl2CHCl2	j 7.52	83	79	79-34-5

Note 1: 69, 75, 99, 125

Note 2: 79, 117, 167



**k is the partition coefficient of a volatile.**

# 21 Appendix B: Calibrating Gas Mixtures

## 21.1 Acquisition, Preparation, and Handling



### **⚠ CAUTION**

**Failure to calibrate the instrument may give you inaccurate identifications when sampling.**



### **⚠ WARNING**

**When using chemicals, wear the appropriate PPE according to SDS.**

HAPSITE ER (or any GC/MS instrument) must be calibrated at one or more concentration levels of the organic compound(s) of interest for quantitative analysis. In the case of the HAPSITE ER, the compounds of interest must be supplied to the instrument as a gaseous mixture of known volume/volume composition (mole/mole % or ppmv levels in air or nitrogen) and at atmospheric pressure.

There are a number of important factors to consider in acquiring, preparing, and handling gaseous standard calibration mixtures. These can be organized in three groups:

1. How to establish the desired concentrations of the required compounds. See How to Establish the Desired Concentrations [▶ 426].
2. Correct delivery of the mix to the inlet of the HAPSITE ER. See Correct Delivery of the Mix to the Inlet of the HAPSITE [▶ 428].
3. Gas cylinder safety, contamination checks, and corrective steps in equipment. See Gas Cylinder Safety, Contamination Checks, and Corrective Steps [▶ 430].

### 21.1.1 How to Establish the Desired Concentrations

There are two basic ways to obtain several concentrations of a given mix of compounds. The compounds can be bought, premixed to specification, in cylinders containing the several concentrations desired. A master cylinder of the compounds can also be purchased at the highest concentration needed, and diluted to the lower required concentrations. Each of these options is discussed in the following sections.

### 21.1.1.1 Using Cylinders Containing Each Concentration

A gas supplier (such as Airgas<sup>1</sup>) can provide a choice of cylinder sizes with the compounds of interest mixed in a suitable matrix at the requisite concentrations. The matrix (or balance gas) for the mixture should be specified as "VOC-free Nitrogen" or "VOC-free Air," to minimize the level of background VOCs in the calibration mix.

The concentrations for calibration of the various compounds of interest will probably be defined in the method being followed. The method may specify, for example, 0.1 ppm, 1 ppm, and 10 ppm of each compound. Calibrate HAPSITE ER to bracket the concentrations at which the compounds of interest will occur in the samples.

The mixtures received will be tagged with the precise value of the concentration of each compound as delivered. The concentration supplied will generally be within  $\pm 10\%$  tolerance; this is termed the *blend accuracy*.

The precise values should be used in the course of building the calibration libraries and are accurate to  $+2 -20\%$ , depending on the target concentration levels and the certification methods used. This is termed the *analytical accuracy*. The certified concentrations in each cylinder mixture will generally be stable at room temperature conditions for about six months.

The selected gas supplier should be able to advise about the reactivity of the compounds needed, and the materials of cylinder construction to provide the best long term stability of the concentration. The supplier will recommend the use of stainless steel regulators with stainless diaphragms. To minimize stagnant volumes where VOCs can accumulate, the regulator body should be designed with minimum internal dead-volume. Use 1 in. diameter gauges, or eliminate the gauges altogether. The regulators and the tubing following should be rated for high purity, mildly corrosive (or corrosive) service if any halogenated VOCs are to be delivered.



A regulator/transfer line system must be well purged with pure nitrogen or air to remove any residual VOCs prior to use with a cylinder containing a lower concentration mix.

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Transfer fittings should be composed of the stainless steel Swagelok<sup>2</sup> type, and transfer lines should be clean, stainless steel or nickel 1/8 inch tubing. Teflon tubing should be avoided due to its permeability. Ideally, regulators and transfer lines should be heat-traced to maintain above ambient temperatures (35-55°C) and to reduce adsorption of less volatile VOCs.

1. Airgas USA, LLC: 259 North Radnor-Chester Road, Suite 100, Radnor, PA 19087-5283, 1-866-734-2338

2. Swagelock (Crawford Fitting Company): (216)248-4600

### 21.1.1.2 Diluting the Gas On-Site

Guidelines to verify acceptable performance of suitable dynamic gas mixing/dilution systems are suggested in the Federal Register (vol. 59, No. 148, Aug. 3, 1994 Proposed Rules, 40 CFR Part 51 Method 205).

Systems conforming to Method 205 are available commercially from Environics<sup>3</sup> (Series 2014 Computerized VOC Gas Dilution System) and Alltech<sup>4</sup> (GB-2 Gas Blender).

The materials in the flow stream must be inert to the VOC compounds of interest, and heat-traced to prevent condensation and accumulation of any VOCs in the flow channels. A well performing gas mixing system minimizes future outlay in certified cylinder gas standard mixes. In this system, only the cylinders at the highest calibration concentration levels are required. Lower concentrations (by as much as a factor of 1000) can be prepared by serial dilution (with VOC-free Nitrogen or air) of these cylinder mixes to the desired calibration levels with the gas mixing system. This is probably the most economic route for labs which must frequently do multi concentration re-calibrations for known VOC mixtures.

3. Environics: (202)429-5040

4. Alltech: (800)255-8324

### 21.1.2 Correct Delivery of the Mix to the Inlet of the HAPSITE

HAPSITE ER is designed to draw samples at atmospheric pressure. Internal standard gas is mixed with the sample in a ratio which is dependent on the flow rate of the sample gas and the suction of the pump.



#### **WARNING**

**Connecting the inlet of the probe to a sample at a pressure above or below atmospheric will cause the mixing ratio of the internal standards to be incorrect, so the resultant calibration will be invalid.**

There are two basic approaches to assuring that the calibration mix is at atmospheric pressure: a free flow of gas or capture of the gas mixture in an inert sample bag.

#### 21.1.2.1 Free Flow of Gas

The free flow of gas from the regulator of a pressure cylinder is reduced to atmospheric pressure when the impedance to flow is small. This can be achieved by placing a sampling tee at the point where the line becomes large in diameter. The connection of the HAPSITE ER sample probe inlet should be at right angles to the direction of gas flow with 1/8 in. stainless steel Swagelok fittings.

**⚠ WARNING**

**The excess vent flow (overflow) from this sampling tee (in the gas flow direction) should exit through stainless steel fittings of at least 1/4 in. size and a short vent line to fume hood or other exhaust system.**

The smaller "leg" of the sampling tee is coupled to the HAPSITE ER. The total flow to the sampling tee should be approximately 1 liter/min. to allow sufficient excess over the HAPSITE ER sampling flow rate which is approximately 100 cc/min. and to prevent external air from being drawn back into the vent "leg" of the sampling tee which would alter the concentrations delivered from the cylinder or mixer.

### 21.1.2.2 Inert Sample Bag

Ultra clean Tedlar sample bags, dedicated to a given VOC compound mix/concentration level, will be the most economic option for regular calibration (more than once a week) and eliminates the waste of certified gas mix out of the sampling tee vent. The dedicated Tedlar bag can be filled directly from the associated gas cylinder or gas mixing system effluent.

**⚠ WARNING**

**Regulate the gas delivery to avoid overfilling the bag. The bags are not designed to be pressurized.**

Alternatively, a bag can be filled by delivery of a set volume of the diluent gas (via a mass flow meter), then adding a set volume of the certified cylinder VOC gas mix, followed by mixing to homogeneity in the bag to obtain the proper dilution. A 12-liter Tedlar bag will allow about 60 HAPSITE ER samplings of the contents between refills.

The use of properly filled Tedlar bags inherently assures that the gaseous contents are at atmospheric pressure for sampling. The bag should not be filled to the point where the bag appears like a firm "air pillow," as the bag would then be at above atmospheric pressure, and could not be sampled accurately by the HAPSITE ER. In addition, this would lead to eventual leakage along the bag seams, destroying the integrity.

Clean Tedlar bags to be filled with a certified gas mix should be filled once with the gas mix and allowed to stand several minutes for preconditioning, then evacuated with a transfer line and a diaphragm vacuum pump and refilled again with the mix.

Fittings on the Tedlar bags are typically 3/16 in. diameter; the inlet systems for HAPSITE ER are 1/8 in. diameter. Connection of the probe to the Tedlar bag can be made with a stainless steel Swagelok type adapter, 3/16 in. to 1/8 in. The recommended parts for this adapter include:

3/16 in. to 1/8 in. reducer

(Swagelok part# SS-300-R-2)

3/16 in. teflon ferrule set	(Swagelok part# T-300-Set)
1/8 in. nut	(Swagelok part# S-S-202-1)
1/8 in. ferrule set	(Swagelok part# SS-200-Set)

The 3/16 in. O.D. tube on the Tedlar bag valve will slip into and out of the 3/16 in. nut on the adapter, which can be easily finger tightened to seal, leak-free, on the Teflon ferrule set. Care should be taken to not completely unscrew the 3/16 in. nut from the adapter each time a Tedlar bag is removed. This will prevent the dropping of nuts and ferrules. The 1/8 in. end of the adapter is a swaged connection to the 1/8 in. male Swagelok fitting on the end of the HAPSITE ER probe, so wrenches will be required to make a leak free connection.

The Tedlar bag valve should be open only during HAPSITE ER sample taking cycle to save gas usage.

### 21.1.3 Gas Cylinder Safety, Contamination Checks, and Corrective Steps



#### **⚠ WARNING**

**Safety of operations should always take precedence in the working environment. Gas cylinders should be properly affixed to lab benches with clamps, or chained to the wall for safety. A safety certified gas cylinder cart should be available in the vicinity of where the cylinders are normally used, for moving them and replacing empty cylinders. Gas cylinders should never be transported with the regulator attached!**

Tedlar bags may be cleaned for reuse, or replaced with new bags. To clean a Tedlar bag for use with different VOC's or concentrations, partially fill with VOC-free N<sub>2</sub> or VOC-free air, heat it to 40-50°C by wrapping the bag with an electric blanket for several minutes, then evacuate the bag contents through the open valve with a clean transfer line to a diaphragm vacuum pump. This operation should be repeated 10 times for a normal cleaning. Then the bag may be stored filled with VOC free N<sub>2</sub> or VOC-free air until needed.

A supply of clean Tedlar bags can be useful for quick standards preparation by direct liquid injection of VOC's not regularly analyzed into an N<sub>2</sub> or air matrix in the bags. This allows a more convenient and rapid alternative to gaseous cylinder mixes in such uses as new applications development or verification of unknown VOCs by component spiking. Accurate gas standard preparation by direct liquid injection is only recommended at levels greater than 5 ppmv, because the minimum liquid volume deliverable by syringe at an acceptable accuracy and precision is about 0.5 µL. This corresponds to approximately 10 ppmv in a 12 liter Tedlar bag, or approximately 3

ppmv in a 40 liter Tedlar bag. Larger Tedlar bags are available, but convenience in regular handling and the possibility of target compound adsorption on the larger interior surface area may be matters of concern.

## 22 Appendix C: Shipping the HAPSITE and Consumables

### 22.1 Introduction

The HAPSITE ER instrument is designed to ship to remote locations. The instrument can be reshipped in the cardboard boxes (with the same cut-foam inserts) in which it is received. However, these boxes will not suffice for frequent shipping. A heavy-duty fitted shipping case for HAPSITE ER is available from INFICON (part number 930-464-P1). The protection provided by this case will allow the instrument to survive handling by most airline, air freight and trucking handlers.

While there is room for the necessary cables in the case, additional boxing must be used for certain accessories and consumables, as detailed below.



#### CAUTION

**The batteries should be removed from the HAPSITE ER before shipping, as their weight, under the shock-loads of shipment, will damage the respective instrument. They will require their own packaging for shipment. The computer, if required at the remote site, should be hand-carried.**

NEG Pumps can be easily shipped in the box in which they are received. A NEG Pump installed in HAPSITE ER will not be damaged by shipment.



#### WARNING

**When shipping canisters follow DOT regulations for packaging, labeling and methods in which hazardous materials can be shipped.**

### 22.2 Shipping the Canisters

The canisters of carrier gas and internal standards gas are pressurized to 700 kPa (100 psig) or more. The canisters are approved by the Department of Transportation (DOT), but they are considered hazardous cargo because they are pressurized. They are permitted to be transported on passenger aircraft, but not in the passenger compartment, nor checked as luggage. The labeling of the cartons and the paperwork required can be tedious. The easiest approach is to contact INFICON and order the



required gases to be shipped directly to the site. If previously purchased gases are to be shipped, the original cartons can be used. If new cartons must be used, refer to the old shipping packages for the required labeling.

**⚠ WARNING**

**Do not ship canisters installed in the HAPSITE ER; they are still hazardous and can damage the unit during transport.**

The regulations governing shipments of hazardous goods are found in the DOT portion of the Code of Federal Regulations: Part 171, 172 and 173 of 49 C.F.R. The gas canisters, pressurized, are classified as hazardous materials under Section 172.101. When shipped from INFICON, they meet all the packaging requirements set forth in Section 173.

Federal Express, UPS, and the passenger airlines are forbidden to accept such cargo unless it is accompanied with the required "Shipper's Declaration for Dangerous Goods" in four copies. Both FedEx and UPS have their own version and will provide instructions. The generic version, for use with airlines, is shown after page C-3, and for instructions on filling out the form, see below.

In filling out the form, it is important to be precise. In the "Transport Details" box, firmly cross out the term "Cargo Aircraft Only." To the right of the box, cross out the term "Radioactive."

The "Proper Shipping Name" and "UN or ID NO." are either:

- Nitrogen, Compressed, UN 1066, or
- Compressed Gases, n. o. s., UN 1956 respectively (Bromo-pentafluorobenzene, Nitrogen)

The "Class or Division" is 2.2. "Packing Group" and "Subsidiary Risk" are left blank. "Quantity and Type of Packing" for a single six-pack would read: *6 DOT 2M Canisters in Fiberboard Box X 0.04 Kg.*

For two six-packs in a single larger box (which must carry the green diamond and other placarding), this would read: *12 DOT 2M Canisters in 2 Fiberboard Boxes X 0.08 Kg (Overpack Used).* The Kg number refers to the total mass of the gas, not the gross weight.

In the "Packing Inst." column write 200. The "Authorization" column is left blank. The signature section is very important; fill it out completely.

The "Shipper's Declaration for Dangerous Goods" is a "Style F83R" from Label master in Chicago; their phone number is 800 621-5808. They are carbon-less, four-part forms and may be available from local stationary suppliers. The form, and all its copies, must have red markings along the borders; black and white copies will not be accepted.

Although the airline will carry the box of canisters in the same cargo hold as the baggage, they will not accept hazardous materials at the check-in counter. Take the box of canisters with the form filled out to the desk of your airline at the **air freight terminal** at your airport. They will be able to assist you with transporting the gas.

## 22.3 Empty Canisters

It is important to remember that it is the pressure of the gas in the canisters which is considered hazardous. The gases themselves are mostly nitrogen. (The amount of the organic internal standards compounds is 50 ppm and 100 ppm.)

To discard the canisters, simply discharge them outdoors by inserting any small point into the valve. Once they are empty, they can be disposed of as aluminum scrap.



### **WARNING**

**When discharging the canisters, point them away from people and stand upwind of the discharge. Whenever possible, discharge canisters into a hood.**

If the empty canisters cannot be recycled or disposed, they may be shipped back to their point of origin for disposal.

Be certain that the canisters are empty (less than 30 psi), then package them in a plain cardboard box, without a green diamond label. Mark the box as "**Empty Canisters for Destruction.**" Ship them, prepaid, to:

Airgas USA, LLC

259 North Radnor-Chester Road

Suite 100, Radnor, PA 19087-5283

1-866-734-2338.



