

5 Operation

5.1 Starting the BrukerS1 Program

Each analyzer is delivered fully calibrated for the intended application. Therefore, it can be used for normal work without any preparation other than that described in earlier sections. The intuitive user interface makes it easy to begin using the Tracer series instrument right away. The analyzer is operated and maintained through the BrukerS1 analytical program, located in the *Start* menu on the PDA. Alternatively, the device can be activated by pressing the program Calendar button, located on the PDA directly above the communication port. To view the PDA desktop while running BrukerS1, press the *Show Desktop* button, located adjacent to the BrukerS1 *Start* button (Figure 25).



5.1.1 Memory Card

The analyzer ships with a Compact Flash (CF) card of varying capacity. This card contains a backup of the BrukerS1 program and instrument calibration, and is specific to each analyzer. Store the flash card in a safe location; it is required to reinstall the BrukerS1 program. Refer to the Troubleshooting section (page 50) for

instructions on how to reset and reinstall the software from CF card. DO NOT install a memory card from another analyzer in the PDA.



CAUTION: The memory card provided with the analyzer contains settings and calibrations specific to the instrument with which it ships. Using a memory card or PDA from another instrument may produce undesirable results.

The supplied flash memory card is not necessary to operate the analyzer; all components required to operate the analyzer are included on the PDA. Additionally, assays are saved to the internal memory of the PDA. If desired, the program can store these assay files to a memory card. Bruker



Figure 26 Logon Screen

recommends use of a separate memory card for file storage and supplies a Secure Digital (SD) card for this purpose.

After turning the power on to the instrument, select the "BrukerS1" icon from the **Start** menu. The icon is also located in the **Programs** group, (**Start Menu > Programs**). Upon starting the BrukerS1 program, the title screen will display, showing a progress bar. If the instrument connects successfully, the page will show the "Connected – Ready" status.



IMPORTANT: The analyzer arrives from the factory with the default password: 12345. It is highly recommended that the owner <u>immediately</u> change the password upon receipt. See "I forgot my password" in the Troubleshooting section.

Tap the *Exit* button to quit the BrukerS1 program, or the *Login* button to display the login screen, (Figure 26). Enter your personal password and tap *Continue*. When the software has verified the user password, a



Radiation Warning will display (Figure 27). No operator action is possible during this time. After 15 seconds, the *Main Menu* will appear (Figure 28). From the Main Menu, you can access

either the *General Purpose Measure*, or *Utilities*.

5.2 General Purpose Measure

Selecting the General Purpose Measure button displays the *Mode Selection Menu* (Figure 29). The menu is organized into two groups of buttons: *Metals Mode* and *Configuration*.

5.2.1 Metals Mode

By default, the Tracer series instrument is set up to perform an unlimited measurement of materials in *Universal* mode. This feature will detect the type of alloy under test, and make automatic adjustments to the excitation parameters and filter settings during the first second of analysis. This default function is intended to remove the uncertainty in selecting method and analysis type, and make these decisions automatically—just point and shoot. Universal Mode is described in detail on page 37.

Pass/Fail

This useful option allows the user to determine if the material being analyzed matches a specific alloy from the library. Any number of materials can be added to the match list, including those from custom libraries; the program will compare the current analysis to the chemistries of the materials listed and issue a PASS/FAIL result. This is a fast and accurate way of quickly sorting materials based on Grade ID. FP and any



empirical method can be used in *Pass/Fail* Mode; however, the sample must be in the library to receive a PASS result.

Activate **Pass/Fail** analysis by tapping on the associated button, displaying the **Pass/Fail** screen (Figure 30). To test for a specific alloy, scroll down the "Fail" list and highlight the alloy of interest with the stylus. Tap the arrow button underneath to add the selected alloy to the "Pass" list. The Pass list indicates which alloys will be tested against the library. To remove an alloy from the Pass list, highlight the alloy on the Pass list and tap on the arrow button underneath to move the alloy into the Fail list.





During analysis, An icon will appear showing that the instrument is calculating the results.



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Results - Emp

Once the alloys have been selected and testing is ready to begin, pull the trigger. The screen will display

results similar to those shown in Figure 31. This screen displays the Grade ID name, the tested material's chemistry, and whether or not the material passes or fails the match test. As the test progresses, the color of the upper screen will indicate the test status: *green* indicates that the material matches one of the Grade IDs selected; *yellow* indicates a possible match; and *red* indicates that the material does not match any of the selected Grade IDs. The display also includes a *Match Quality* value (in parenthesis). This is a range 0.0 to 10, and indicates how closely the measured chemistry matches the chemistry for the Grade ID found in the library. Higher numbers indicate a closer match. For most standard alloy grades, a value of 8.0 or higher can be expected. If no match is found, the result will say No Match.

The **Results** screen presents additional information in column form: **El** (element), **Min** (the minimum percent value for passing), **Result** (the percent value recorded in the analysis), **Max** (the maximum percent value for passing), and **Err** (2 standard deviations). If the sample analyzed falls between the min and max values, it passes (green); if an element within the sample falls outside of the min and max values, but within the standard deviation, it is uncertain (yellow); if it falls outside the standard deviation, it fails (red). Tap on any column heading to sort that column.

1892) 4130 or 41 Time: 15.0 PASS (9.7) Min Result Max Err 🔺 El 0.80 1.100.05 Mn 0.30 1.00 0.05 Fe 96.00 99.00 0.18Ni 0.13 0.04 Cu Mo 0.13 0.03 • 0.01 0.150.32 Spectra Edit Info Back ←Prev Next→ Figure 31 Pass Fail Results 📌 Analyze # ◀€ 12:17 Ready to Analyze Results Edit Info Back Figure 32 Ready to Analyze Results - Emp # ◀€ 12:38 Hast B or B-2 6) Time: 21.0 Match Qual: 10.0 Date-Time: 11-01-2007 12:37 El Min Result Max Err 0.00 1.00 0.32 Mn 0.00 1.00 0.03 Fe 0.00 2.00 0.09 Co Ni Mo 0.00 1.00 0.02 74 00 0.16 65.00 30.00 26.00 0.18Тa 0.01 0.00 w 0.02 0.01 Spectra ←Prev Next-> Figure 33 Live Results

<u>Analyze</u>

NOTE: If a material does not match one of the alloys in the PASS list, the Tracer series instrument will still attempt to determine a Grade ID

NOTE: If the chemistry of the alloy does not closely match a chemistry in a library, "No Match" will display for Grade ID. The Match Quality threshold below which "No Match" is displayed is set to a default value of 5.0. The Match Quality threshold may be changed from the System Setup Menu (see page 43).

Analyze is the primary tool for obtaining the Grade ID (alloy name) and chemical composition of all materials—alloys, plastics, etc. Selecting Analyze from the menu prompts the **Analyze screen** (Figure 32), indicating that the instrument is ready to analyze. The screen also shows the status of the internal pressure (Vacuum Status). Depending on the selected method, a good, bad, or N/A status will be displayed. Near the bottom of

the screen is the **Results button** which opens the **Results Viewer**. Next to the Results button is the **Edit Info button**, which allows the operator to change file names and add extra information. The **Back button** returns to the previous menu.



5.2.2 <u>Taking a Measurement</u>

To begin a measurement, place a sample over the examination window and IR proximity sensor and pull the

trigger. During a measurement, the *Live Results* screen (Figure 33) will display the assay number, Grade ID of the alloy, the match quality (confidence) number, and chemistry in weight-percent (wt%). As measurement time increases, the results will become more precise. At the bottom of the screen is a small spectral display that shows the energy lines in real time. It may be brought to the foreground by tapping on the *Spectra* button. Release the trigger at any time to halt the measurement and display the results (Figure 34).

<u>Grade ID</u> – If the material being measured is an alloy found in the sample library, the name will be displayed at the top of the screen. Materials not found in the library will be named "No Match."

<u>Match Quality</u> – This is a range 0.0 to 10 and indicates how closely the measured chemistry matches the chemistry for the Grade ID found in the library. Higher numbers indicate a closer match. For most standard alloy grades, a value of 8.0 to 10 can be expected.

<u>Chemistry List</u> - The concentration of each element in the sample is compared to the allowable range of concentrations for that element in the reported Grade ID. Concentrations that fall within the allowable range are highlighted in green. Those elements outside of the range, but within the error limits of their respective ranges, are highlighted yellow. If an element falls outside the range beyond error, the concentration is highlighted red.

Edit Info - Information related to an assay may be added to the record by using this function. Tap on the **Edit Info** button on the **Results** screen to display the **Edit Info** dialog (Figure 35). From here, the user can enter the name of the test, the name (ID) of the material being tested, and other optional information in the two provided fields. To enter information in any field, tap on the field to display the cursor, activate the keyboard, and enter the desired information. When a particular field is complete, repeat the procedure for the other fields as needed. To save this information, tap **Continue** at the bottom of the screen. Tap the **Back** button to return to the Results. The data will be stored with each assay until they are changed again.



NOTE: The information will be saved with the next assay, not the current results.







Spectra - This function allows the user to evaluate more closely the spectra stored on the PDA. Toggle back to the Results screen by tapping the **Results** button. The spectra (Figure 36) can be manipulated by dragging the stylus along the XY axis of the screen. Dragging the stylus up and down will stretch and compress the y-axis (count rate) scale. Dragging the stylus left and right will move the x-axis (keV) scale so that the entire spectrum can be viewed.

The spectrum can also be manipulated through the spectral menu. Press and hold the stylus anywhere on the spectrum to bring up the *Spectral Menu*.

The following options are available:

X+: Stretches the x-axis (keV) scale to zoom in on the spectrum.

X-: Compresses the x-axis (keV) scale to zoom out from the spectrum.

X0: Re-centers and returns the spectrum to the original x-axis scale.

Cent.: Re-centers the spectrum on both the x- and y-axes.

Y+: Stretches the y-axis (count rate) scale.

Y-: Compresses the y-axis (count rate) scale.

YO: Returns the spectrum to the original scale along the y-axis.

Def.: Restores the spectrum to its default setting; the spectrum is re-centered and the original scale along both axes is restored.

To highlight specific peaks, tap anywhere on the screen to mark the region of interest with two red vertical lines (Figure 36). These lines correspond to the spectral energies of each element. Tap the *element button* and an element list appears (Figure 37). Select an element of interest and tap continue to see the spectral lines for that element.

To identify which spectral energy lines correspond to a particular element, tap on the *Results* button to return to the results page. Highlight the element of interest by tapping on the element name. Tap on the *Spectra* button to return to the spectrum. The spectral energy lines associated with the element of interest will be displayed by two red lines (the K and L energy lines).

Back - Returns to the *Ready to Analyze* screen (Figure 32).



Previous and Next allow the user to scroll through the current list of recorded spectra.

To return to the *Ready to Analyze* screen from *Results*, tap the *Back* button. From the *Ready to Analyze* screen, you may begin another measurement; edit information for subsequent measurements; or view results. Once at the *Ready to Analyze* screen, tap the *Main* button to open the *Main Menu*, where



additional configuration options can be selected to further detail each subsequent measurement and alter the overall behavior of the analyzer.

5.2.3 Configuration

The *Configuration* group contains four buttons: *Analysis Type, Test Params, Method*, and *Library* (see Figure 29). The text displayed on each reflects the function of the button and the current selection.

<u>Analysis Type</u>

This button allows the operator to change the type of analysis for the selected *Method* (see page 38). The analysis types available are defined below. Changing the analysis type will affect general behavior of the analyzer and the accuracy of the results. Tapping this button will reveal the menu (Figure 38).

<u>Universal</u>

The **Universal** mode is the default analysis type (Figure 38), bringing together the benefits of Empirical and FP calibrations, automatic Method detection, and Dual Energy excitation. In the first second of a measurement, the analyzer determines the best excitation voltage, anode current, and beam filter based primarily on the matrix element, and automatically switch to it. In the next five seconds, the algorithm determines if the measurement would benefit from a second analysis at a lower energy (Dual Mode). Typically, at the end of a 10 - 15 second assay, the appropriate calibration will be chosen (Empirical or FP) and results will display. Analysis will halt at anytime by releasing the trigger.

Empirical (EMP)

The *Empirical* function (Figure 39) calculates elemental concentrations *empirically* based on valid count data. If the type of material is generally known (e.g., steel alloy, copper alloy), the Empirical analysis will identify the results more quickly than the FP type, and will often report more accurate analytical results.

Dual (Tracer IV-SD only)

The **Dual** function (Figure 40) is a subset of the Empirical and FP Analysis types that measure samples with two different excitation energies. It is available only on models containing light-element calibrations.

Some alloys contain critical light elements that define them, and are difficult to quantify with a 40kV source. With **Dual** enabled, the

analyzer will drop to 15kV after five (5) seconds and continue analysis until the trigger is release or the measurement concludes. Dual Mode is a toggle function and can be selected when EMP or FP are







active. Figure 40 shows the EMP analysis type activated with Dual Mode enabled. Tapping the **Dual** button will turn off Dual and enable the original 40 kV Empirical analysis.

Fundamental Parameters (FP)

This function (Figure 41) analyzes valid counts for each element and computes concentrations. FP should be selected if the composition of the material is generally unknown. It can analyze the composition of a broader range of materials, but will typically take longer to display results, and the results may not be as accurate as those obtained using the Empirical analysis type.

<u>Auto</u>

Auto mode (Figure 42) automatically switches from Empirical analysis to Fundamental Parameters analysis if a grade ID cannot be determined within 10 seconds and/or the material under test is not defined in the empirical calibration.

Methods Menu

The *Methods menu* allows the user to choose instrument settings optimized for measurements of certain sample types to obtain more accurate results. These settings establish different voltage, current, and filter settings. The number of methods available will vary based on the purchased configuration. Simply select a one of the following methods and tap *Continue*:

Standard Alloys

This setting is the de facto standard method and is used for the general alloy analysis of steel, nickel, cobalt, and copper.

Aluminum FP Alloys

This setting is used for Grade ID and general chemistry of Aluminum alloys.

Additional methods for RoHS, Mining, Precious metals and other special calibrations are available; discuss these options with your sales representative.

Spectrum Acquisition

With Bruker S1 software version 1.0.2.9 or later, spectral data may be captured on the PDA. To use this feature, the instrument tube must first be set using X-Ray Ops (see the X-Ray Ops User Guide for details on tube pre-sets).

Tube settings are selected from the Methods window (Figure 43). These settings are created and saved using X-Ray Ops. See the X-Ray Ops User Guide for more detail on how to save tube settings.



Figure 41 FP Analysis Type

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Set Analysis Type:	Auto
Universa	al Mode 🗌
FP	Emp
Auto	Dual
	Continue
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Figure 42 Auto Analysis Type





Using pre-set tube settings, spectra will be displayed as in Figure 44. Each acquisition is named SPECTRUM, auto-incremented, and stored as a PDZ file.

For operation of the *Results* window, see Spectra, page 36.

<u>Test Parameters</u>

This menu (Figure 45) allows the user to define minimum and maximum measurement time, trigger behavior, and Dual Mode reaction times. By default, the measurement time is Unlimited and Manual, which allows the analysis to continue as long as the trigger is pulled and safety criteria are satisfied.

Trigger Options

By default, the Tracer series instrument will run unlimited measurements (i.e., it will continue to collect data as long as the trigger is pulled and safety criteria are satisfied). Selecting the *Trigger Options* button will toggle this option to *Timed Measurement*. Once set, the operator will be able to change the Test Time and toggle the Manual/Auto trigger.

<u>Manual Trigger</u> – The analyzer requires physical contact with the trigger. It must be depressed completely to take a measurement. The measurement will continue for the set minimum time, up to the maximum time, or until the trigger is released or safety criteria are disturbed.

<u>Auto Trigger</u> – If the trigger is pulled for 2 seconds and released, the analysis will begin. Analysis time is controlled by the contents of the **Set Test Time** fields. Due to regulatory restrictions, this feature is not available in all locales.

IMPORTANT: Fields that appear grayed out are unavailable with the current configuration. Changing the Analysis Type or Trigger options will alter the availability of certain menu items.

Set Test Time

By entering minimum and maximum values, the measurement time is set. This feature is only available if *Timed Measurement* is active (see Trigger Options above and Figure 46). When set, the analysis will continue until the trigger is released or the maximum measurement time has been reached. If the trigger is released before the maximum time is reached, the measurement will stop. If the trigger is held beyond the maximum time, the measurement will stop at the set time. If an assay runs for less than the minimum time, no data will be stored and the file index will not be incremented. Note that if any of the safety criteria are disturbed, the measurement will stop.





Dual Mode Reaction Time

Entering values into the **Dual T1** and **Dual T2** fields controls how Dual Mode operates. Used only when Dual analysis type is selected, Dual T1 sets the duration (in seconds) that a measurement will run at 40kV, and Dual T2 sets the duration for the 15kV measurement. It is unlikely these will ever need to be changed, but results may vary.

<u>Library</u>

The Library feature allows the operator to create custom libraries and add new samples unique to his/her application. In the context of the Tracer series instrument, a library is a file residing in memory on the PDA that defines the names (Grade ID) and allowable ranges of concentration for each element for a particular alloy. By default, the Standard factory library of alloys is used by the calibration for Grade ID. User Libraries are custom user-created libraries that contain definitions of alloys other than those contained in the Standard Library. From the Library menu, the operator

may add/delete individualized libraries and/or samples, and even exclude the factory library entirely.



CAUTION: Deleting a user library is PERMANENT; however, the standard factory library cannot be deleted.

Adding a Library

Tap the Library button to open the Selection Screen (Figure 47). By default, only the Standard factory library is included.



To add a new library, tap the *Lib Maint* button to open the menu. Tap *Create Library* and the *New User Library* screen will display (Figure 48).

Enter the name of your library and tap **OK**. The newly created library will open, showing an empty sample list (Figure 49).

Adding Samples to a Custom Library

From the sample list of the *User Library Maintenance* screen (Figure 50), tap the *Add New* button to display the *User Grade Entry* screen (Figure 50). Tap on the text field at the top and enter the name of the sample.

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Edit Library Delete Library		Element Min % Max % ▲ Mg 0.00 0.00 ≡ AI 0.00 0.00 ≡ Si 0.00 0.00 □ F 0.00 0.00 □ Ti 0.00 0.00 □ V 0.00 0.00 □ Cr 0.00 0.00 ▼
Figure 48 Library	Figure 49 New library (empty)	Save Cancel



NOTE: To expose or hide the virtual keyboard, tap the keyboard icon at the bottom of the screen.

Using the stylus, scroll down to the defining elements and highlight them. Enter the ranges in wt% by tapping on the *Min* and *Max* value and entering proper percentage with the stylus and keyboard. Tap the *Save* button to commit the sample to the library and return to the *Library Sample* list. Enter additional samples (up to 100 entries per library) as required. Tap the *Back* button to return to the

Library Maintenance menu. Determining the minimum and maximum concentrations for each material is beyond the scope of this document. Use caution when selecting a range of values for a particular element that overlaps the ranges for that element in another material. Overlapping ranges may result in ambiguous Grade Identification.

The newly created library displays the list of available libraries (Figure 51). Additional libraries may be added at any time (the recommended limit is 100), and samples can be added to existing user-created libraries, but not the standard library. User libraries may also be deleted.

To return to the main *Library* menu, tap the *Back* button. Figure 51 shows the Standard factory library (highlighted) and the newly created library beneath it. To include the new library in future analysis, highlight it by tapping on the name and tap *Continue*. Notice the text on the *Library* button (Figure 52) changed from "Library Standard" to "Library Multiple," as multiple libraries were selected. To exclude a library, tap the *Library* button then tap the undesired library to remove the highlight, and tap *Continue*.

IMPORTANT: Including multiple libraries, large ones in particular, will increase analysis time, as each library must be searched individually





5.2.4 View Results

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El	Min	%	Max	+/-
Fe	61.85	68.82	72.00	0.27
Cr	16.00	16.64	18.00	0.19
Ni	10.00	10.80	14.00	0.24
Mo	2.00	2.10	3.00	0.05
Mn	0.00	1.12	2.00	0.12
Cu	Cu 0.24 0.04			
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Sp	ectra	Edit I	nto	Back
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gure 54 Results explore				

The final button in the *Configuration* group is *View Results*. This feature, which

can be accessed from numerous locations throughout the program, allows the user to sort and review prior assays for a more detailed analysis.

Tap the *View Results* button to open the *View Readings* screen (Figure 53). This window displays every assay stored in memory, ordered by index. The five checkboxes to the left represent the modes used to collect the data stored on the PDA. Check the box corresponding to the assays to be viewed (e.g., to display assays collected in *Analyze Mode*,

check the box labeled *Analyze*). To view the results of a prior assay, highlight it with the stylus and tap the box at the bottom having that index number. The *Results* screen (Figure 54) appears and displays the results from that assay. Three buttons are available from this screen.

Spectra – See page 35 for description of this function.

Back – Returns to the View Results screen.

Edit Info – see page 35 for use of this feature.

5.3 Utilities

The *Utilities* menu contains a variety of tools for viewing and managing data, and manipulating system level functions. From the main *Mode Selection* menu, tap the *Utilities* button to display the screen (Figure 55).

5.3.1 View Readings

The View Readings tool performs identically to the View Results function previously detailed (see page 42).

5.3.2 View Energies

The View Energies tool (Figure 56) is a periodic table that contains pertinent information for each element. The table consists of:

- Atomic number
- Atomic Symbol
- Atomic Name
- Atomic Weight
- Spectral Line Energies
- Spectral line energies









5.3.3 Library Maintenance

Selecting the *Library Maintenance* button opens a menu that allows manipulation of certain aspects of the library system. Two options are available.

View Standard Library Utility

The *View Standard Library* utility allows the operator to view all alloys identified by the Tracer series instrument, as well as the allowable ranges by weight percent and the UNS designation (Unified Numbering System for Metals and Alloys). This library is installed at the factory and cannot be edited or deleted from within the BrukerS1 program (Figure 57). Advanced users may wish to import the library from the KTILIB.CSV in the System folder of the flash card.

Maintain User Libraries Utility

The *Maintain User Libraries* utility allows the user to create custom libraries and manage the contents by defining the chemistry of special materials. This Utility is identical to the *Library...* function within the *Mode Selection* menu. Refer to page 40 for details.

5.3.4 System Setup

The System Setup screen (Figure 58) enables the user to alter various settings for use during subsequent testing. In summary, the user may select which data files to record, where the data files will be written, which COM port to use for communication with the analyzer, and the threshold for Match Quality used in Pass/Fail testing. The user password may also be changed beginning from the **System Setup** screen. Whenever a system setting is changed, tap **Continue** and the system will prompt you to restart the program.

Saving Output Data

By default, all data is saved to the Data folder on the PDA in the root of My Device. When PDA memory

has been completely filled with assay data, it will begin overwriting the files with the oldest time/date stamp. If a blank CF or SD card is inserted into the PDA, and the *Removable Media* box is check, all assay data will be stored to the card, rather than PDA memory.

Results – Enabled by default. Uncheck this box to discard the results from all assays. The output options 'Spectra' and 'Save CSV' are ignored if this box is unchecked.

Spectra – Enabled by default. Spectra and results are stored in the .PDZ file format. They can be opened from within the **View Results** utility, or with a Windows Compatible PC running S1PXRF.

Save CSV – Enabled by default. The resulting Grade ID and chemistry of every alloy tested is appended to the RESULTS.CSV file in the Data folder. It can be imported into Microsoft Excel[®] for later evaluation.



Removable Media – Disabled by default. This option requires installation of a blank, formatted Compact Flash or SD Card into the PDA. Once enabled, all output files are stored in a Data folder residing



on the card(s). When the card is removed, the default is reset. It is recommended to use a separate media card when using the *Removable Media* feature.



CAUTION: DO NOT use the compact flash card provided with the analyzer during normal operation. This card contains the files required for installation of the BrukerS1 program and will overwrite the contents of the PDA.

<u>Lanquaqe</u>

Select available languages are from this drop-down menu. If a language is not available, contact a sales representative to discuss when it will become available. This option only changes the language of the BrukerS1 program. The language of the Windows environment is changed from within the PDA control panel under "regional settings."

Instrument Port

By default, the PDA communicates to the Tracer series instrument on communications Port 1. Some special applications may require the use of another port. In most cases, the default value is applicable.

Match Quality Threshold

To change the threshold for Match Quality used in Pass/Fail calculations, enter the new value in the *Match Quality Threshold* box. For most Pass/Fail measurements, the default value is applicable. Changing this threshold is not recommended when using the Standard Library. Generally, the Match Quality Threshold should only be changed if a User Library is active (see *User Libraries, page 40*).

Simple Mode

Simple Mode allows the user to limit the functions available, simplifying the analysis process. When checked, Simple Mode will disable all functions except those in Utilities, Edit Info, and Results. Ensure that the method you want to use as default has been selected <u>BEFORE</u> selecting Simple Mode (see 0 for details on selecting methods). Once Simple Mode is selected, tap Continue and the program will reboot in the General Measure mode using settings active when Simple Mode was selected.

When *Simple Mode* is selected, the *Ready to Analyze* window will be reconfigured (Figure 61) to include the *Utilities* button. When you want to return to *Normal Mode*, use the *Utilities* button to return to Instrument Setup.

System Password

The Tracer series instrument arrives from the factory with the default password (12345). It is highly recommended that the owner immediately change the password upon receipt.

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Current Password
New Password:
Verify Password:
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Utilities
Results Edit Info LogOff
Figure 61 Simple Mode
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Tap the *Change Password* button to display the *Password Management* dialog box (Figure 59). Enter the current password, then the new password, then re-enter the new password. Select *OK* to submit the new password. If successful, a dialog box will appear, indicating a successful change.

If the current password was entered incorrectly, a dialog box will appear stating that the New and Verify passwords do not match. In this case, carefully re-enter the new and verify passwords and try again.



IMPORTANT: The password scheme in the BrukerS1 software is casesensitive. Be sure you record your selected password in a safe place away from the analyzer, as Bruker Elemental cannot recover a lost user password. See "I forgot my password" in the Troubleshooting section.

Display Settings

This function (Figure 60) allows the setting of display units, % or PPM (parts per million) and number of displayed decimals. Use Color coding and Grade Limits checkbox allows to choose whether grade color coding and grade limits are displayed in result screen or not. Color codes are enabled by default.

5.3.5 Backup Data

The Backup Data utility (Figure 62) will copy or move the results of every assay stored in local memory to another location, be it a Compact Flash, SD card, or another folder within PDA memory. If moving data, the operator is given the option to **Reset the Assay Filename Counter** (index). The next assay stored will begin with the index 1.

Select *Copy* to leave data on the PDF, or select *Move* to remove the data from the PDA. In either case, select the file destination and tap *Execute*.

5.4 Shutting Down

From any menu, continue tapping either the **Back** or **Main** buttons until the **Login** screen appears. Tap the **Exit** to return to the PDA desktop. Turn the PDA power off by depressing the power button in the upper right of the PDA. Depress the pushbutton switch to turn the instrument **OFF**.

5.5 Viewing and Exporting Stored Data

The Tracer series instrument saves and appends to the file RESULTS.CSV the chemistry of each material tested. Test results may be viewed outside the BrukerS1

program by exporting the stored results to a Windows Compatible PC running Excel 95 or later. Results can also be viewed individually on the PDA by accessing the *View Readings* screen in the Utilities menu (See page 42).

Windows[™] PC

To view test data on a Windows Compatible PC running Excel 97 or later, you must first export the test data to the PC by one of two methods.

Media Card

If the BrukerS1 program was instructed to save files to Removable Media, simply remove the card from the PDA (Compact Flash or SD) and insert it into a media card reader attached to the Windows PC. Using File Explorer, browse to the Data Folder on the card. The folder contains two file types, PDZ and CSV.





Double-click on the file RESULTS.CSV to open the file in Excel. Viewing PDZ files requires S1PXRF to be installed. Refer to the S1PXRF User Guide for details.

If the BrukerS1 Program was NOT instructed to save files to Removable Media, it is still possible to transfer them to a PC using this method. Insert a media card into the PDA and open File Explorer. Browse to the Data folder in the root of My Device. Scroll down and select the file RESULTS.CSV with the stylus. Tap Menu->Edit->Copy to copy the file to the clipboard. Next, browse to the media card. Tap Menu->Edit->Paste to paste the file from the clipboard to the media card. Remove the card from the PDA and insert it into a media card reader in the same manner.

Alternatively, data can be moved to a media card by using the Backup utility from within the BrukerS1 program (see page 45).

<u>ActiveSync®</u>

ActiveSync is a program that synchronizes files from frequently used applications to both PDA and PC. Every Pocket PC device is compatible with ActiveSync, but to use it, it must be installed on the PC.

Installing ActiveSync

- 1. Turn on the PC and log on to Windows.
- 2. A copy of ActiveSync has been provided for convenience. It is a software product distributed freely by Microsoft (following EULA) and updated frequently. There is no guarantee that the copy provided is the most current.
- 3. Insert the ActiveSync CD-ROM into the CD/DVD-ROM drive. Follow the instructions that appear on the screen.



NOTE: The most current version of ActiveSync may be downloaded from the Microsoft website: http://www.microsoft.com/windowsmobile/activesync/activesync45.mspx

Transferring Files

- 1. Connect the PDA cradle to the PC with the supplied USB cable.
- 2. Insert the PDA into the cradle. ActiveSync will start and ask if a Partnership should be established. This is not necessary and, in fact, not recommended. Click Cancel.
- 3. In the ActiveSync window, click on Explore from the toolbar. A File Explorer window will open to display the contents of the PDA memory.
- 4. Double-click the icon at the top labeled "My Windows Mobile-Based Device."
- 5. Select the Data folder, and then click Edit->Copy to copy the folder to the clipboard.
- 6. Browse to a location on the PC hard drive (such as My Documents) and click Edit->Paste. The entire Data folder will appear in the new location.
- 7. Open the new Data Folder to view the Spectra files (PDZ) and RESULTS.CSV.
- 8. Scroll down to the file RESULTS.CSV and double-click to open it in Excel.



5.6 Checking Calibrations

Each Tracer series instrument ships with two calibration check samples and documentation for each. Locate these in the shipping case:

- A stainless steel duplex 2205 check sample (used to verify general alloy calibration)
- An aluminum AA5083 or AA7075 check sample (used to verify the light-element and/or aluminum calibration)
- A calibration sheet for each
- A CD-ROM with a copy of the calibration files

All Tracer XRF analyzers are calibrated with NIST traceable alloy standards unless the client application is not intended for alloys or the library contains proprietary materials.

To verify the calibration of the analyzer, set the analyzer up to operate and run five 30-second assays. Calculate the average of the chemistry results (shown from within the RESULTS.CSV file). The results for each element should be within the tolerance range specified on the corresponding calibration sheet.

Contact Bruker Elemental if you suspect your calibration is invalid.

5.7 Coefficient Setup

5.7.1 Introduction to Coefficients

Coefficients enable the user to fine tune methods by setting up offset and slope corrections. This feature is intended for mining and specialty applications where site specific calibration optimization is required.

Coefficients are available in both General Measure and Pass-Fail Measure mode. Generally, coefficients should not be used for standard alloy application. Coefficients are specific to selected method and are applied only to selected method or method group.



Caution! Use of coefficients will change the results and if they are incorrectly used may lead to erroneous results. Use of coefficients is intended only for the advanced users. If in doubt how to correctly use this feature, don't use it!

Methods	# # € 7:43	
Select Method: Standard Alloys Aluminum FP Alloys MiningOxidesHD Mining Oxides Mining Elements*		
Coefficients	Continue	
E		
with coefficient highlighted		
highli Coefficients	ghted #* ≪€ 7:39	
highli Coefficients Select Coefficient S Ni ore A Ni ore B	ghted #* ◀€ 7:39 Set:	
highli Coefficients Select Coefficient S Ni ore A Ni ore B	ghted #	
highli Coefficients Select Coefficient S Ni ore A Ni ore B Coef Maint	ghted ﷺ ◀€ 7:39 Set: Itinue None	

Once a coefficient set has been defined for a specific method, it will be applied to that method in all instances when the method is used, including in Universal or Auto mode. An asterisk after the Method name indicates that a coefficient set has been applied to that method (Figure 63).

Coefficient sets are applied to the final measurement result of specific element and can contain slope and offset correction for multiple elements. It is possible to create and save multiple coefficient sets to one calibration method, but only one coefficient set can be active at a time.



Once a coefficient set has been activated, the adjusted results are reported on the PDA screen and in Results.CSV file. The original, uncorrected results are not saved.

5.7.2 Applying a Coefficient

From the *Main Menu*, select the Methods button to open the *Methods Menu* (Figure 63). Highlight the method for which you wish to apply a coefficient set, and then tap on the *Coefficients* button. The *Coefficient Menu* (Figure 64) will open. Highlight the coefficient set you wish to apply to the selected method, and then tap *Continue*. You will return to the *Methods Menu*. Ensure an asterisk now shows next to the selected method. Select the method and tap *Continue* to activate the adjusted method.

If a coefficient set needs to be adjusted, or a new coefficient added to the existing list, tap the *Coef Maint* button on the *Coefficients Menu* (see Section 5.7.3).

Tap *None* to return to the *Methods Menu* with no coefficient set selected.

5.7.3 Maintaining Coefficients

The *Coefficient Maintenance* window (Figure 65) allows the user to edit, delete, or add a new coefficient set for application to methods. See Section 5.7.4 for details on calculating slope and offset for coefficients.

To delete an existing coefficient set from the list, highlight the coefficient set and tap **Delete**.

To add a new coefficient set, tap *Add New* to open the *Coefficient Entry* window (Figure 66). Highlight the element of interest that you wish to adjust and the keyboard will open. Enter the *Coefficient Name* in the field provided, then change the offset and slope for each element you wish to adjust. Tap the *keyboard icon* at the bottom of the window to close the keyboard. Check the appropriate box for Empirical (*Emp*) and/or Fundamental Parameters (*FP*). Tap *Save* to set the new coefficient, or *Cancel* to discard the changes and return to the *Coefficient Maintenance* menu.

5.7.4 Slope and Offset Calculations

If a simple offset or slope correction is required (e.g., result are always relative 10% too low, slope coefficient is 1.1), the value can be determined without calculation. If, however, the relation between measured values and reference values (expected correct values) is more complex, multiple

Coefficient Maintena Ni ore A Ni ore B	ince # 4 7:49		
Figure 65 Coefficient Maintenance			
Coefficient Entry Coefficient Name Mining test1	₩ 4 € 8:03		
El Offset Mn 0.0000 Fe 0.0000 Ni 0.237 Cu 0.0000 Zn 0.0000 Ga 0.0000	Slope ▲ 1.0000 ■ 1.0000 ■ 1.0000 1.124 1.0000 1.0000 1.0000 ■		
Emp Save	✓ FP Cancel		
Figure 66 Co	efficient Entry		

samples should be used to define the slope and/or offset correction. A sample Excel sheet (Figure 67) is included on the operator's disk provided by Bruker. This Excel sheet contains the required formulae for proper calibration.

To use this sheet to calculate coefficients, select a set of samples which are representative of the matrix of the unknowns and for which you have reliable analysis. These samples must cover the range of concentrations of interest. Measure each sample with sufficient measurement time (e.g., 60-300 sec) and



record the values reported by the analyzer. Using the spreadsheet, enter the known values in the column marked "Reference Values" and the measured values in the column marked "S1 Meas. Results". When all samples have been entered, examine the correlation – the closer to 100% the better; if this value is greater than 80-85%, there is reasonable correlation between the measured value and the known value. Repeat this process for each element of interest. Once all the data has been input, create a coefficient set using the values in the Slope and Offset rows in the sheet.

Input Reference values and S1 Measurement results to BLUE cells. Estimated measurement result after Coefficients are applied is indicated in "Adjusted S1 Result" column.

Element 1	Ni
SLOPE	1.0407
OFFSET	0.4396
CORRELATION	99.7%

Reference	S1 Meas.	Adjusted S1	
values	Results	Result	
2.3	1.8	2.31	
2.3	1.77	2.28	
4.5	3.92	4.52	
4.5	3.99	4.59	
6.4	5.75	6.42	
6.4	5.54	6.21	
7	6 1 2	G 91	

Element 2	Cu			
SLOPE	0.6214			
OFFSET	0.0752		0.0752	
CORRELATION	99.1%			
Reference	S1 Meas.	Adjusted S1		
values	Results	Result		
0.17	0.22	0.21		
0.17	0.22	0.21		
0.93	1.22	0.83		
0.93	1.34	0.91		
1.11	1.57	1.05		
1.11	1.66 1.11			
1.4	2.31	1.51		

Element 3	Со
SLOPE	1.2355
OFFSET	-0.4575
CORRELATION	95.6%

Reference	S1 Meas.	Adjusted S1
values	Results	Result
2	1.9	1.89
3.1	3.2	3.50
4.4	3.7	4.11
		-0.46
		-0.46
		-0.46
		-0.46

Figure 67 BrukerS1 Calibration Coefficient Calculation