ORTEC®

GammaVision®
Maestro-PRO®

Gamma-Ray Spectrum Analysis and MCA Emulators for Microsoft® Windows® 7, 8.1, and 10 Professional

A66-BW
A66SV-BW
A66MP-BW
Software User's Manual

Software Version 9

Printed in U.S.A. ORTEC Part No. 783620 0220
Manual Revision M

Advanced Measurement Technology, Inc.

a/k/a/ ORTEC®, a subsidiary of AMETEK®, Inc.

WARRANTY

ORTEC* DISCLAIMS ALL WARRANTIES OF ANY KIND, EITHER EXPRESSED OR IMPLIED, INCLUDING, BUT NOT LIMITED TO, THE IMPLIED WARRANTIES OF MERCHANTABILITY AND FITNESS FOR A PARTICULAR PURPOSE, NOT EXPRESSLY SET FORTH HEREIN. IN NO EVENT WILL ORTEC BE LIABLE FOR INDIRECT, INCIDENTAL, SPECIAL, OR CONSEQUENTIAL DAMAGES, INCLUDING LOST PROFITS OR LOST SAVINGS, EVEN IF ORTEC HAS BEEN ADVISED OF THE POSSIBILITY OF SUCH DAMAGES RESULTING FROM THE USE OF THESE DATA.

Copyright © 2020, Advanced Measurement Technology, Inc. All rights reserved.

*ORTEC® is a registered trademark of Advanced Measurement Technology, Inc. All other trademarks used herein are the property of their respective owners.

NOTICE OF PROPRIETARY PROPERTY —This document and the information contained in it are the proprietary property of AMETEK Inc., ORTEC Business Unit. It may not be copied or used in any manner nor may any of the information in or upon it be used for any purpose without the express written consent of an authorized agent of AMETEK Inc., ORTEC Business Unit.

TABLE OF CONTENTS

Installation — page 7
Tutorial — page 17

NOTE!

If you are not fully acquainted with the Windows environment, we strongly urge you to visit the Microsoft website as well as familiarize yourself with a few simple applications before proceeding.

The convention used in this manual to represent actual keys pressed is to enclose the key label within angle brackets; for example, **<F1>**. For key combinations, the key labels are joined by a + within the angle brackets; for example, **<Alt + 2>**.

INSTALLATION AND STARTUP

Refer first to the instructions in the accompanying CONNECTIONS Driver Update Kit (Part No. 797230).

For information on installation and configuration, hardware driver activation, network protocol configuration, and building the master list of instruments accessible within **GammaVision**, see Chapter 2 (page 7). If installing Chinese GammaVision on an English Windows computer, you must change the Windows Regional Settings to the Chinese language.

You can use **GammaVision**, with access to all features, for 60 days without entering its registration key (see Section 2.5).

The tutorial begins on page 17.

MAESTRO-PRO NOTATION

Maestro-PRO and **GammaVision** share much of the same functionality. In fact, **Maestro-PRO** has all of the functionality of **GammaVision**, except for the advanced analysis capability. All descriptions within this user manual for **GammaVision** functionality is also applicable to **Maestro-PRO**. Functionality that is only applicable to **GammaVision** will be denoted with a superscript Greek gamma character within parenthesis (ã) throughout this document.

Following are the major differences between **Maestro-PRO** and **GammaVision**:

- The installation path is **<Program Files>\Maestro-PRO** versus **<Program Files>\GammaVision**.
- The **File/About GammaVision** is changed to **File/About Maestro-PRO**. The **About** screen is changed to show **Maestro-PRO** details instead of **GammaVision**.
- Within the **Analyze/Settings/Sample Type** dialog, Selecting the **Analysis** tab shows **Reserved** for all analysis program engines. All fields are read-only when displaying the contents of sample settings previously defined by GammaVision.
- The Toolbar does not contain the **Analyze Spectrum** icon.
- The application title bar shows **Maestro-PRO for Windows** instead of **GammaVision for Windows**.
- The **ANALYZE**, **ANALYZEFILE**, **ANALYZESPECTRUM**, **ASK_GAMMATOTAL**, **ASK_PBC**, **CREATEPBC**, **QABACKGROUND**, **QASAMPLE**, and **WAIT_QA** JOB functions are disabled.

- The following menu options are not available in Maestro-PRO:
  - Acquire / Start/Save/Clear
  - Acquire / QA
  - Analyze / Entire Spectrum in Memory
  - Analyze / Spectrum on Disk
  - Analyze / Settings / Report Generator
  - Analyze / Settings / Attenuation Coefficients
  - Analyze / Settings / Geometry Correction
  - Analyze / Settings / Peak Background Correction
  - Analyze / Settings / Average Energy
  - Analyze / Settings / Iodine Equivalence
  - Analyze / Settings / DAC (MPC)
  - Analyze / Settings / Gamma Total

1. INTRODUCTION

1.1. General

ORTEC® continues to deliver the finest in germanium-detector gamma-ray spectrum acquisition, analysis, and reporting software with the latest release of GammaVision® — version 9. This release of GammaVision extends the capabilities of our world-standard gamma-ray spectroscopy software to provide even more advanced tools for simplifying and reducing effort in your counting laboratory.

Features and options in GammaVision v9 include:

- Operating System Compatibility — GammaVision operates on computers running Microsoft® Windows® 7, 8.1, and 10 Professional.

- English, French, Chinese, and German User Interface — During installation, choose the GammaVision language interface that matches your computer operating system language.

- **Spectrum Analysis Capability** — GammaVision was originally designed for HPGe spectrum analysis with adjustable analysis settings and engines that can be tailored for specific applications. The NAI32 analysis engine introduced in Version 8 supports Low Resolution spectrum analysis for use with Sodium Iodide detectors and similar types.

- Support for ORTEC instruments that operate in *List Mode* (such as the DSPEC®-50/502, digiBASE®, and DSPEC® Pro), which streams spectroscopy data are directly to the computer, event-by-event, without the data "dead periods" associated with the acquire-store-clear-restart cycle of standard spectrum acquisition.

- Extensive automation using JOB files.

- An optional multi-detector interface that allows you to simultaneously start, stop, and monitor up to eight multichannel buffers (MCBs); and view up to eight live spectra and eight buffer windows at a time.

- Automatic and Manual calibration processes to meet different application needs.

- ISO NORM Compatibility — Optional report data compatible with ISO/DIS 11929.[1]

---

[1]ISO/DIS 11929, "*Determination of characteristic limits (decision threshold, detection limit, and limits of the confidence interval) for measurements of ionizing radiation — Fundamentals and applications*," http://www.iso.org/iso/iso_catalogue/catalogue_tc/catalogue_detail.htm?csnumber=43810.

- Gamma Total(ã) Support — This is available to generate specific results and reports[2] as defined by EDF (Électricité de France). (Gamma Total users, be sure to see the system configuration note on page 11.)

- An enhanced analysis results display, and a revised and expanded histogram plotting program, GVPlot.

- **Spectrum File Types** — GammaVision is compatible with the 2006 and 2012 ANSI N42 file formats implemented with ORTEC's Detective and Spectroscopy portal products.

GammaVision combines the latest advances in analytical accuracy with user friendliness and the widest range of tools and corrections available to the spectroscopist. These include true coincidence correction (TCC), absorption correction, a calibration wizard, an enhanced source certificate file editor, and the ability to use nuclide libraries in either GammaVision or NuclideNavigator® III (Microsoft® Access®) format. In addition, all hardware setup including presets, acquisition settings, and MCB settings, is performed in one dialog.

For the ORTEC DSPEC® family of instruments, GammaVision takes full advantage of the hardware's zero-dead-time (ZDT[3]) method for loss-free counting correction with uncertainty propagation. Our newer MCBs also support a multi-nuclide MDA preset.

Regulatory compliance is easy with GammaVision. The software's quality assurance (QA) features monitor system performance and store the results in an Access database. All hardware and analysis parameters are saved with the spectral data to ensure traceability.

GammaVision's extensive menus and toolbar let you operate all aspects of data acquisition and analysis including calibration, library editing, computer-controlled hardware setup, and analysis parameter setup; as well as numerous onscreen data manipulation, comparison, and analysis tools.

Password protection lets you lock Detector controls (Section 5.7.4) and menus (Section 5.7.3)

---

[2]"*Protocole d'échange d'informations entre les logiciels EFFLUENTS/ENVIRONNEMENT et un analyseur GAMMA TOTAL*" — ref : D 5870/GDMI/BRY/SG/000211, and "*Protocole d'échange d'informations entre les logiciels EFFLUENTS/ENVIRONNEMENT et un analyseur de SPECTROMETRIE GAMMA*" — ref : D 5870/GDMI/BRY/SG/000211.

[3]U.S. Patent 6,327,549.

1.1.1. Automation for High-Throughput Environments

GammaVision has numerous automation features, including powerful automated command sequences or "job streams." You can even create a desktop icon for a particular data collection and analysis job stream — one double-click that runs the entire procedure. All sample analyses can be controlled from a single screen, even across a network. Remote workstations can control, analyze, and view the data being gathered in the counting room.

1.1.2. Analysis and Display Tools

GammaVision is designed to analyze spectra generated by any ORTEC MCB, directly from the spectrum on display or from spectrum files on disk, in any of several file formats including the advanced and archivable .SPC format. In addition, GammaVision can directly read and write spectral data files in the .SPE ASCII file format.

GammaVision offers six analysis engines and three major analysis methodologies. In the primary analysis method, a library-directed peak search delivers lower detection limits than can be achieved by "unguided" peak searches. This method is ideally suited for the determination of low-level and ultra-low-level samples (where statistics might be poor) for a specified list of nuclides. For analysis of true unknowns (e.g., emergency-response samples), an "Auto Isotope Identification" mode allows efficient, accurate use of large libraries while maintaining reasonable analysis times. The interactive re-analysis mode lets you repeatedly re-fit the spectrum while monitoring the fit residuals. This is invaluable for highly complex spectral analyses such as certain neutron-activation and reactor-coolant spectra. A "directed fit" option lets you report negative activity values if calculated, as required for some effluent analysis requirements. An enhancement to directed fit allows this option to be used in the deconvolution of overlapping peak areas.

After analysis, evaluate the results using the flexible, easy-to-read GammaVision report or a variety of onscreen, informative plotting routines. For custom-configured reports, we offer the optional GammaVision Report Writer (A44-BW), which uses an Access-format database and SAP® BusinessObjects Crystal Reports™. In addition, we offer Global Value™, which provides custom reporting capability, data management and integration tools, advanced quality assurance, and automation for routine measurement processes.

1.2. MCA Emulation

An MCA, in its most basic form, is an instrument that sorts and counts events in real time. This sorting is based on some characteristic of these events, and the events are grouped together into bins for counting purposes called *channels.* The most common type of multichannel analysis, and the one of greatest interest to nuclear spectroscopists, is *pulse-height analysis* (PHA).

PHA events are signal pulses originating from a detector,[4] and the characteristic of interest is the pulse height or voltage, which is proportional to the particle or photon energy. An *analog-to-digital converter* (ADC) is used to convert each pulse into a channel number, so that each channel corresponds to a narrow range of pulse heights or voltages. As pulses arrive over time, the MCA will collect in memory a distribution of the count of pulses with respect to pulse height (a series of memory locations, corresponding to ADC channels, will contain the count of pulses of similar, although not necessarily identical, height). This distribution, arranged in order of ascending energies, is commonly referred to as a *spectrum.* To be useful, the acquired spectrum must be available for storage and/or analysis, and is displayed on a graph whose horizontal axis represents the height of the pulse and whose vertical axis represents the number of pulses at that height, also referred to as a *histogram.*

GammaVision, combined with *multichannel buffer* (MCB) hardware (Detector interface) and a Windows computer, emulates an MCA with remarkable power and flexibility. The MCB performs the actual pulse-height analysis, while the computer and operating system make available the display facility and data-archiving hardware and drivers. GammaVision software is the vital link that marries these components to provide meaningful access to the MCB via the user interface provided by the computer hardware.

The GammaVision MCA emulation continuously shows the currently acquiring spectra, the current operating conditions, and the available menus. All important operations that need to be performed on a spectrum, such as peak location, insertion of *regions of interest* (ROIs), display scaling, and sizing are implemented with both the keyboard (accelerators) and the mouse (menus and toolbars). Spectrum peak searching, report generation, printing, archiving, calibration, and other analysis tools are available from the drop-down menus. Some menu commands have more than one accelerator so that both new and experienced users will find the system easy to use.

GammaVision maintains *buffers* in the computer memory to which spectra can be moved for display and analysis, either from Detector memory or from disk, freeing the Detector for another spectrum acquisition. As much as possible, these buffers duplicate in memory the functions of the Detector hardware on which a particular spectrum was collected. Data can also be analyzed directly in the Detector hardware memory, as well as stored directly from the Detector to disk. GammaVision allows you to open up to eight Detector windows and eight buffer windows at a time.

[4]In this manual, “Detector” (capitalized) means the transducer (high-purity germanium, sodium iodide, silicon surface barrier, or others) plus all the electronics including the ADC and histogram memory. The transducers are referenced by the complete name, e.g., high-purity germanium (HPGe) detector.

GammaVision also uses the network features of Windows so you can use and control supported ORTEC MCB hardware anywhere on a network. See the next section for more information on support for legacy ORTEC instruments in Microsoft Windows 7, 8.1 and 10.

1.3. Computer Requirements and Operating System Cautions

GammaVision is designed for use on computers that run Windows 7, 8.1, and 10 Professional. In 32-bit Windows operating systems, the GammaVision program files are installed in the \Program Files folder; in 64-bit Windows, GammaVision installed in the \Program Files (x86) folder.

1.4. MCB Support in GammaVision v9

Your computer's processor and operating system will determine which MCBs, instrument-to-computer interfaces, and network protocols can be used. For detailed information, see the accompanying CONNECTIONS Driver Update Kit Instruction (P/N 932721) or consult your ORTEC representative. For setup of pre-2005 MCBs, ORTEC can supply an electronic copy of the *ORTEC MCB CONNECTIONS-32 Hardware Property Dialogs Manual* (p/n 931001).

Adding more MCBs to your system is fast and easy; see the accompanying CONNECTIONS Driver Update Kit Instruction (P/N 932721) for instructions.

1.5. Detector Security

GammaVision allows you to protect your Detectors from destructive access by setting a password with the **Lock/Unlock Detector** command (Section 5.7.3). Once a password is set, no user or application can start, stop, clear, change presets, change ROIs, or perform any command that affects the data in the detector if the password is not known; however, the current spectrum and settings for the locked device can be viewed read-only. The password is required for any destructive access, whether local, on a network, or via .JOB file commands. This includes changing instrument ID numbers and descriptions with the MCB Configuration program.

1.6. List Mode Support

GammaVision now supports our instruments that operate in *List Mode* (such as the digiBASE®, DSPEC®-50/502, and DSPEC® Pro). In List Mode, spectroscopy data are streamed directly to the computer, event-by-event, without the data "dead periods" associated with the acquire-store-clear-restart cycle of standard spectrum acquisition. New commands on the menus and toolbar allow you to switch between PHA and List modes, and view all or part of a list mode acquisition. In addition, our automated JOB streams support the new List Mode capabilities.

NOTE GammaVision samples the list mode data stream every 250 milliseconds of real time, and can display the data with a granularity of 1 second. To extract data at a higher resolution, use our A11-B32 Programmer's Toolkit in conjunction with your instrument's firmware commands (documented in the hardware manual) to write your own applications.

The first time you start a Detector in List Mode, GammaVision creates a Detector-specific .LIS file in C:\User\Cxt that stores the accumulating list mode data. The file is closed each time you stop data acquisition. If you leave the Detector in List Mode and the Detector window open, you can stop and restart acquisition and the new data will be appended to the Detector-specific .LIS file. These data are retained until the next time this Detector is switched from PHA to List Mode, either manually or by closing and reopening the Detector window (at which point the old data will be cleared). Most users will save the data as soon as acquisition is stopped and before switching back to PHA Mode. However, any time *before the next list mode acquisition is started*, you can use the **Recall...** command to open the Detector-specific .LIS file from the \Cxt folder to a buffer window and save it in .LIS format under a new filename. In addition to the list-mode data, GammaVision adds the Detector's current calibration and sample description to this file.

Note that List Mode allows you to clear the data during acquisition; however, regions of interest (ROIs) cannot be marked in a List Mode window.

The **List Data Range...** command on the toolbar and the **Calculate** menu (Section 5.4.2) allows you to view a specific time slice of the list mode data. It is active only in a buffer window in which a .LIS file has been retrieved. You can optionally save list mode time slices in any supported file format.

The specific List Mode implementation and data structure for supported ORTEC MCBs differs from model to model; see your instrument's hardware manual.

2. INSTALLING GAMMAVISION

You must have Administrator access in Windows to install GammaVision.

2.1. Step 1: Installing CONNECTIONS

The GammaVision CD is accompanied by a CONNECTIONS Driver Update Kit (Part No. 797230). *You must install CONNECTIONS before GammaVision will install.* If you attempt to install GammaVision before CONNECTIONS, an error message will be displayed. If a "program compatibility assistant" dialog then opens saying "this program may not have installed correctly," click **Cancel** to close it, install CONNECTIONS, then install GammaVision.

Be sure to read the Update Kit instruction guide completely! It describes how to install CONNECTIONS, enable/disable the drivers for your ORTEC MCB(s), share ORTEC instruments across a network, and control the MCB Configuration program. It also points you to information on selecting the proper network protocol for older, direct-to-Ethernet units. At the end of installation, you will be directed to restart the computer.

2.2. Step 2: Installing GammaVision

1) Insert the GammaVision CD, navigate to the CD drive, then locate and open \Disk1\Setup.exe. One or more security dialogs will open. Choose the "continue" or "install anyway" option, then the installation wizard will start. Click **Next** to begin moving through the wizard screens.

2) Select the **English**, **French**, **Chinese**, or **German** language interface; and continue to the end of installation.

   NOTE *If installing Chinese GammaVision on an English Windows computer, you must change the Windows Regional Settings to the Chinese language.*

3) The wizard will offer you the option of installing the new example files in their own folder, C:\User\V9 Examples. These demonstration/tutorial files including spectra, calibrations, libraries, analysis results files, derived air concentration (DAC) correction files, etc. If you unmark this checkbox, the files will not be installed. This option allows you to keep example files from different GammaVision versions from being overwritten.

4) If you are upgrading from an older version of GammaVision, a backup of its analysis settings file will be created (b30winds.ini.bak and n30winds.ini.bak). GammaVision will install new b30winds.ini and n30winds.ini files containing the new factory default settings.

NOTES Version 7 and 8 analysis settings (.SDF) and geometry correction (.GEO) files are not

compatible with earlier versions of GammaVision.

Also, beginning with v7, the GammaVision analysis engines are installed separately from the software application. This is transparent during installation. However, the Windows software install/uninstall utility now lists these two GammaVision entities separately (Fig. 1). They can be installed and uninstalled separately.

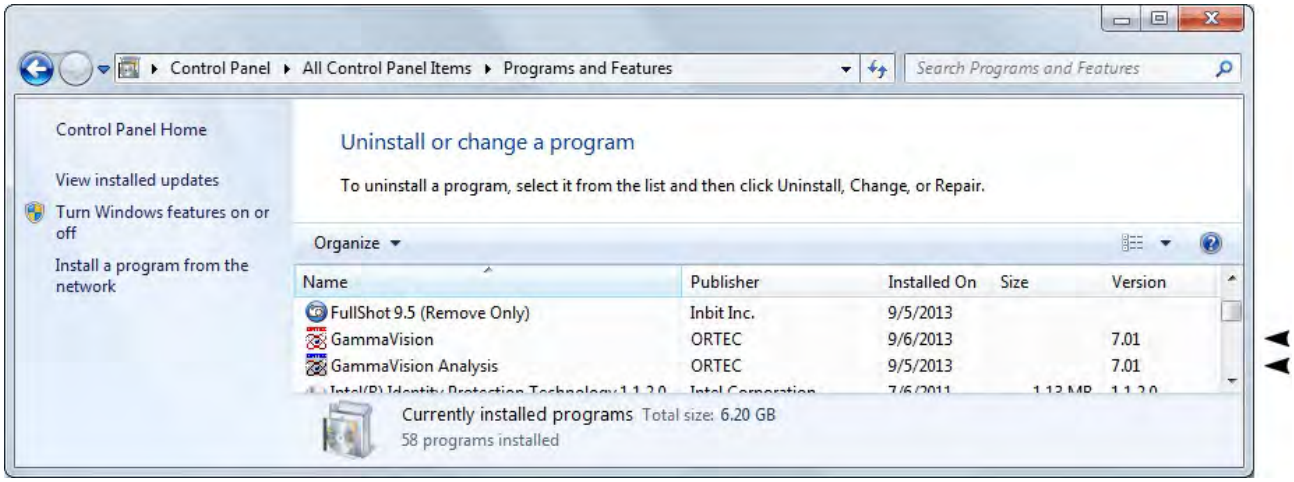


Figure 1. GammaVision Program and Analysis Engines in Control Panel.

5) File installation locations are as follows:

- The \GammaVision folder contains the GammaVision executable, all analysis engines, user manual PDFs, help files, language support files, and the b30winds.ini/n30winds.ini analysis engine parameter files.

- The QA database is installed in C:\User and all context files are in C:\User\Cxt.

- GVPlot, CONNECTIONS, and the library editor are stored in the program files folder under \Common Files\ORTEC Shared.

- The default storage folder for all spectrum, analysis, report, and graphics files generated by GammaVision is C:\User. You can change this on the Directories tab under **File/ Settings...** as discussed in Section 5.1.1.4.

2.3. Step 3: Establishing Communication With Your ORTEC MCBs

1) If you have purchased new ORTEC spectroscopy hardware, connect it and power it on according to its accompanying hardware manual.[5]

2) Connect and power on all local and network ORTEC instruments that you wish to use, as well as their associated computers. Otherwise, the MCB Configuration program will not detect them during installation. Any instruments not detected can be configured at a later time.

3) To start the software, enter the letters mcb in the "*search programs and files*" box at the bottom of the Windows Start menu, then click the **MCB Configuration** search result; or open the Windows Start menu and click **GammaVision**, then **MCB Configuration**. The MCB Configuration program will locate all of the powered-on ORTEC Detectors on the local computer and the network, and display the list of instruments found (the *Master Instrument List*; Fig. 2). If you wish, you may enter customized instrument ID numbers and descriptions (Section 2.3.2). When you close the dialog, any changes you have made to an ID number or description will be written back to the corresponding Detector.

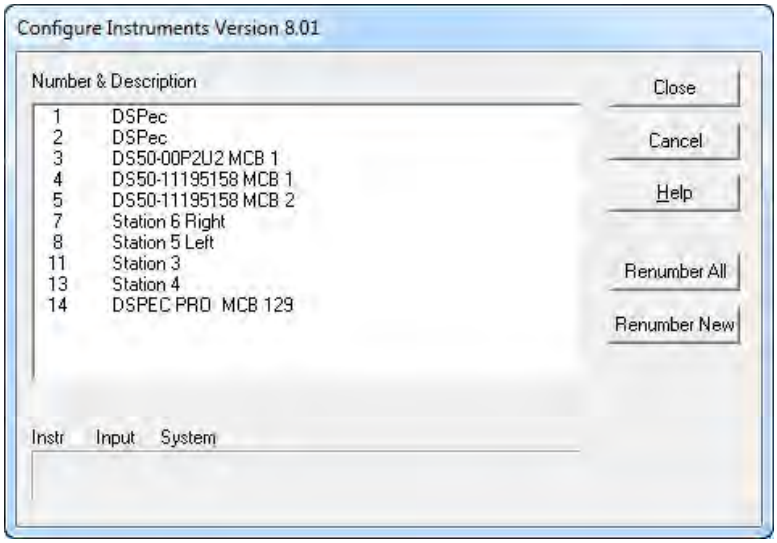


Figure 2. Detector Numbering and Descriptions.

[5]The first time a particular MCB model is connected, a"found new hardware" wizard will start up. Choose *not* to "search the internet for a driver" option, then choose to automatically search for the driver.

2.3.1. Configuring a New Instrument

The first time a new instrument is detected, the dialog shown in Fig. 3 will remind you that all new instruments must be assigned a unique, *non-zero* ID number.[6] Click **OK**. You can either manually change the ID Number and Description as described in the next subsection, or you can click the **Renumber New** button to renumber only the new instruments.

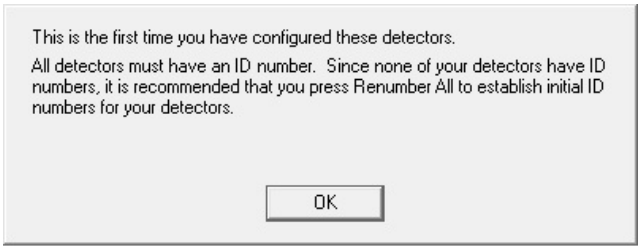


Figure 3. New Instruments Must Have a Non-Zero ID Number.

NOTE *We recommend not using the* **Renumber All** *button*. In addition, we strongly recommend ***not*** renumbering Detectors that "belong" to other users, as this could affect the interaction between their Detectors and their ORTEC software, for instance, if they control their Detectors with .JOB files (e.g., the .JOB file command SET_DETECTOR 5), or use the GammaVision or ISOTOPIC spectroscopy applications. See also the following NOTE and the NOTES in the next section.

NOTE FOR MULTIPLE USERS ON A NETWORK

There are two ways to reduce the chance that other users will renumber your Detectors:

- Add the -I flag to their MCB Configuration command line, as described in Section 2.4.2. This will allow you to assign whatever ID Numbers you wish, regardless of the numbers assigned by other users on your network. (Ideally, everyone using ORTEC instruments on your network should make this change.)

- To prevent others from renumbering your Detectors (or performing any other actions except read-only viewing), password-lock your Detectors with the **Lock/Unlock Detector** command (Section 5.7.3). If you lock a detector that will be controlled by a JOB stream, remember to include the proper password-unlock commands in your .JOB file (Section 10.1.1.4).

[6] If this is a first-time installation of ORTEC products, all your instruments will be "new."

2.3.2. Customizing ID Numbers and Descriptions

If you wish, you can change the instrument ID Numbers and Descriptions by double-clicking on an instrument entry in the Configure Instruments dialog. This will open the Change Description or ID dialog (Fig. 4). It shows the physical Detector location (read-only), and allows you to change the **ID** Number and **Description**.

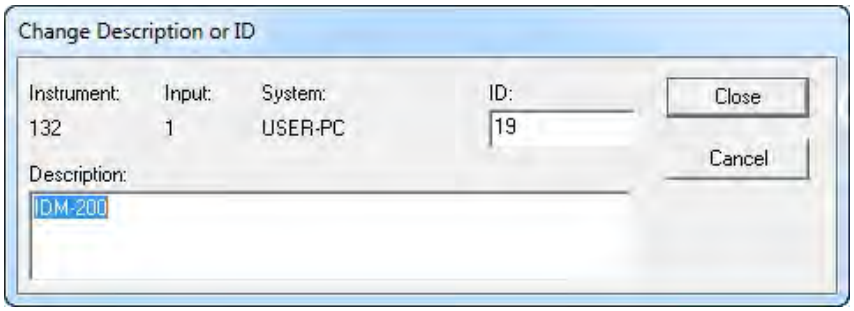


Figure 4. Change Detector Number or Description.

NOTE FOR GAMMA TOTAL USERS

The filenaming conventions for EDF's **Gamma Total** effluent reports (Section 5.5.1.9) are based on a single-digit identifier for the MCBs used for data acquisition. When first setting up GammaVision, be sure to choose instrument **ID** numbers that each end with a unique digit, e.g., 0–9 (for instance, 90**1**, 2**2**, 1**3**, **4**, 37**5**, and so on). Note that in Fig. 2, two of the instruments in the list share **1** as the final digit of their **ID** number, and two share **4** as the final digit. To avoid having two MCBs that generate reports with the same device identification number, two of these MCBs should ideally be reassigned ID numbers with unique final digits.

Make the desired changes and click **Close**. Any changes you have made to an ID number or description will then be written back to the corresponding Detector.

If a modified description has already been applied to a particular instrument, you can restore the default description by deleting the entry in the **Description** field and re-running MCB Configuration. After MCB Configuration runs, the default description will be displayed.

2.4. Caution: Running the MCB Configuration Program Can Affect Quality Assurance

Detector identification in GammaVision is based on the *instrument ID number and description* assigned to a Detector by the MCB Configuration program. Instrument **ID** number and description are assigned when MCB Configuration polls the local computer and network for attached ORTEC MCBs and then builds a Master Detector List of the instruments found. This instrument identification is then used for all QA measurements.

Once you have established QA settings for those detectors and subsequently *collected data using them*, if you then re-run the MCB Configuration program for any reason, you must ensure each instrument is still assigned its previous instrument **ID** number and description *before collecting any more data.* Allowing the MCB Configuration program to assign a new instrument identification to a detector, and then *using* that new identification, interrupts the orderly accumulation of QA records. This is because GammaVision treats the renumbered detector as new, with zero "previous QA measurements" and with potentially incorrect QA settings.

If you must re-run the MCB Configuration program, you can avoid any renumbering problems either by not renumbering instruments or by manually editing the instrument numbers for all of the Detectors on the Master Detector List for your computer. Doing so requires that you keep a separate record of the ID and Description for each MCB on your system. ***Note spelling, spacing, and uppercase/lowercase;*** *these details will be necessary when recreating the* ***Description*** *text string.* Let us use the following example to illustrate the process:

Suppose you are using two MCBs for your GammaVision measurements and in your original MCB Configuration you configured them as **1 DSPEC PRO 1** and **4 DSPEC PRO 4**. This is depicted in Fig. 5. The numerical prefixes **1** and **4** are the **ID**s and the corresponding text strings are the **Description**s.

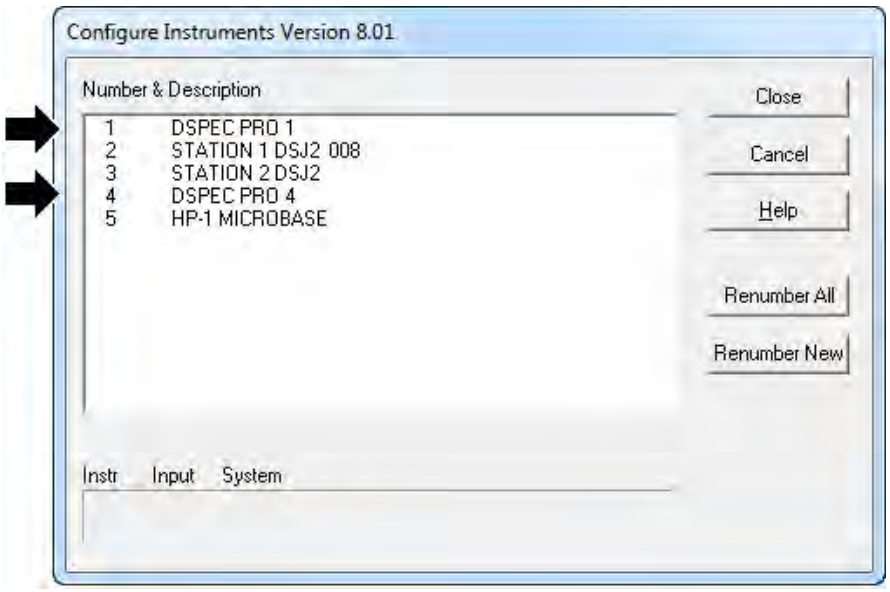


Figure 5. Original MCB Configuration Showing Our Two DSPEC Pro MCBs.

Suppose we add one new MCB to the system and remove two. We must then manually re-run MCB Configuration to add the new instrument to the Master Detector List. Suppose we then find that our two DSPEC Pro units, originally assigned IDs of **1** and **4**, have been renumbered with IDs of **2** and **3**, respectively. ***Before*** closing the Configure Instruments dialog, double-

click the MCB entries that must be renumbered and/or renamed. This will open the Change Description or ID dialog. Restore the original instrument number in the **ID** field and click **OK**, as shown in Fig. 6.

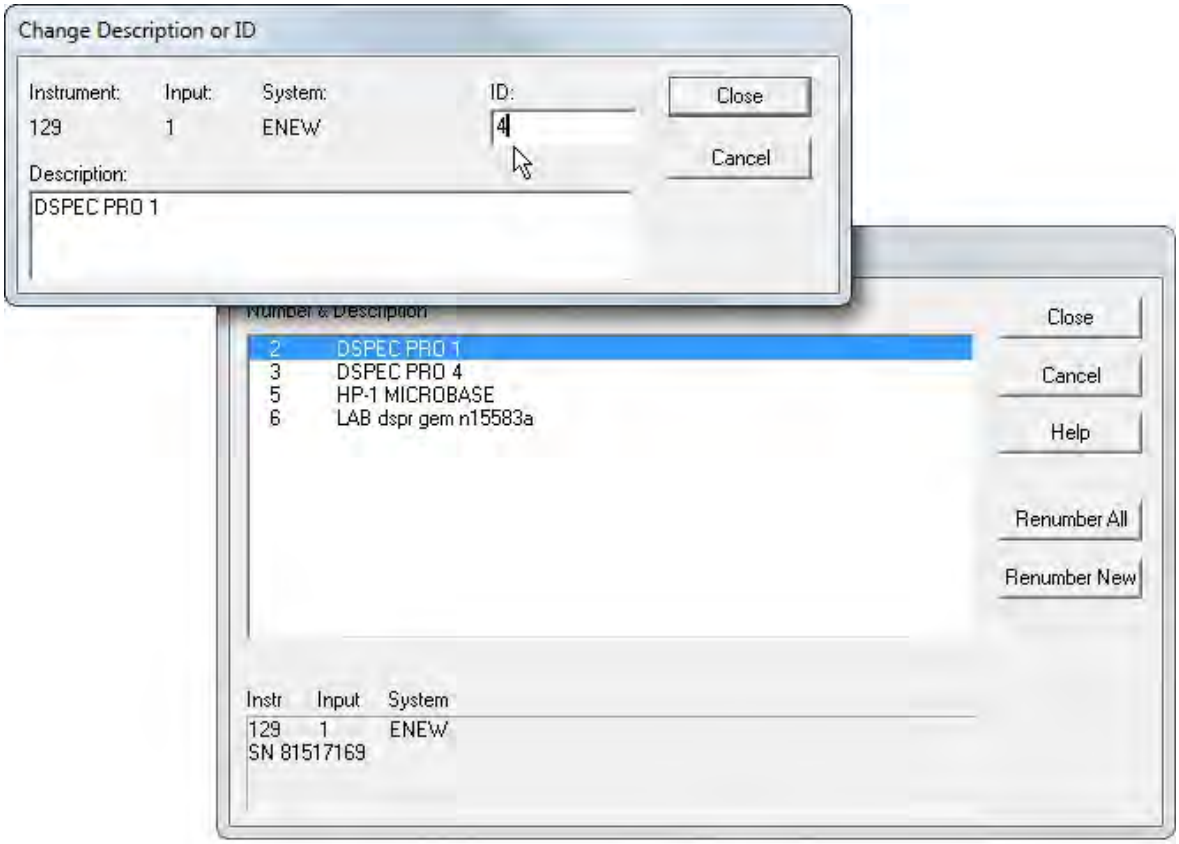


Figure 6. Manually Renumbering and/or Renaming Detectors to Maintain QA Integrity.

Repeat for all Detectors that must be renumbered and/or renamed. When you are finished, click **Close**.

2.4.1. Confirming the MCB Identification to Maintain QA Integrity

To confirm that the original QA **Settings...** are still in effect, run background and sample QA measurements and check the results dialogs to confirm that the MCBs are being properly tracked.

2.4.2. Editing the MCB Configuration Command Line

The command line for the MCB Configuration program is:[7]

"C:\Program Files\Common Files\ORTEC Shared\UMCBI\mcbcon32.exe"

You can modify the way the MCB Configuration program runs by adding one or more of the following flags to the command line. You can use any combination of flags or none, and the flags are not case-sensitive.

-I Ignore duplicate IDs. MCB Configuration allows you to accept an instrument list with duplicate detector ID numbers; no renumbering is required. Useful for customers using our QA tools, JOB commands, and "Gamma Total" function; and when sharing a network with other users of ORTEC MCBs.

-L Configure only local instruments (i.e., no discovery of ORTEC instruments across a network except "attached" digiBASE-E units). This can significantly reduce the time it takes to run MCB Configuration, if you have only local MCBs.

-P Append all newly discovered instruments to the existing list (i.e., don't clear the existing list before starting discovery). Useful when you don't have all your instruments connected or powered-on at the same time but wish to configure new detectors.

There are two ways to modify the MCB Configuration command line:

- To retain the flags from use to use, right-click **MCB Configuration** in the Start menu, select **Properties**, then in the **Target** field, add the flags *outside* the right-hand quotation mark and click **OK**. For instance:

  "C:\Program Files\Common Files\ORTEC Shared\UMCBI\mcbcon32.exe" -I -L

- To temporarily change the command line, open the Windows Start menu's **Run...** dialog, browse to locate the MCB Configuration file, mcbcon32.exe, add the flags *outside* the right-hand quotation mark, and click **OK**.

You are now ready to register your copy of GammaVision, as discussed in the next section.

[7] As noted earlier, 32-bit Windows uses the \Program Files folder and 64-bit Windows uses \Program Files (x86).

2.5. Product Registration

GammaVision requires product registration within 60 days after installation. Until registered, the dialog shown in Fig. 7 opens each time you start the program. Click the **Register Later** button to bypass registration and access the full-featured GammaVision application. Once you enter the registration key and click **Register Now**, this dialog will no longer be displayed. After 60 days of unregistered use, the **Register Later** option will be disabled and GammaVision will shut down when you close this dialog.

Figure 7. Register GammaVision.

To obtain your registration key and activate your copy of GammaVision, you may call the ORTEC telephone extension listed on the GammaVision Registration dialog. You will need the serial number for your copy of the software (located on the box). Enter the registration key on the GammaVision Registration dialog and click **Register Now**.

Alternatively, you may fill out and submit the registration form as follows:

1) Click **Generate ORTEC Registration Form** to open the ORTEC Registration Form dialog shown in Fig. 8.

2) Enter the **Serial Number** for the software (located on the box) and all other fields as applicable.

3) Click the **Write ORTEC Registration File** button to create a text file containing your registration information. A standard file-save dialog will open. Enter a filename and location, and click **Save**. Email this file to the ORTEC address listed on the GammaVision Registration

dialog. We will respond promptly with your registration key.

4) Enter the registration key on the GammaVision Registration dialog and click **Register Now**.

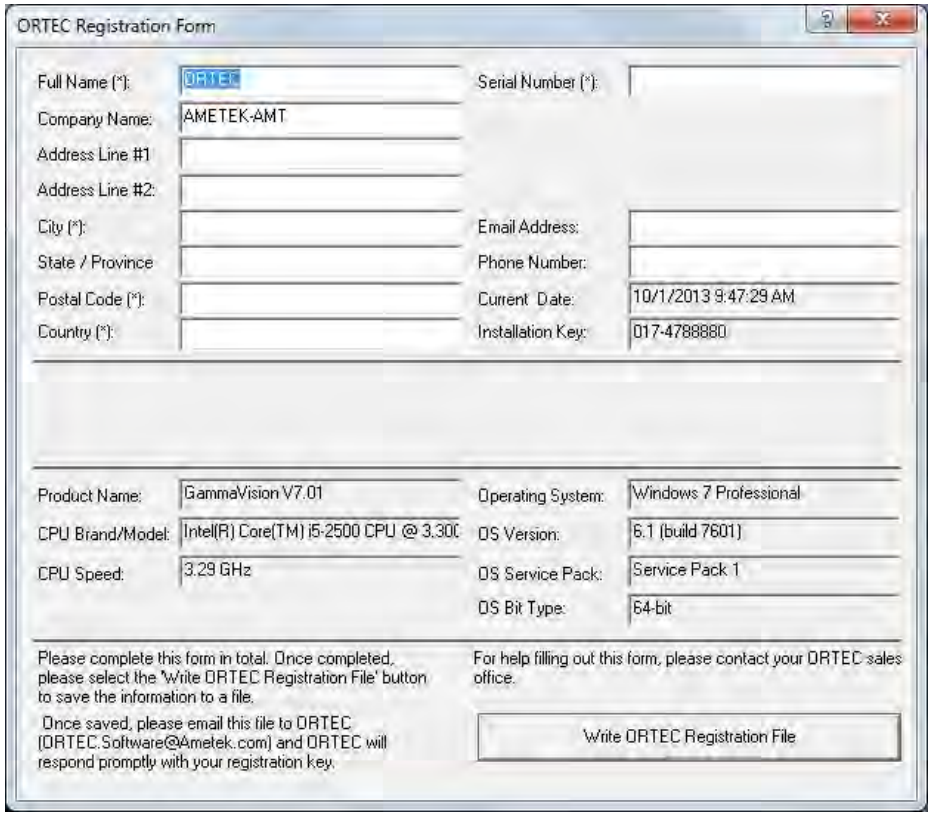


Figure 8. Create a Registration File.

2.6. Enabling Additional ORTEC Device Drivers and Adding New MCBs

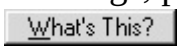
You can enable other device drivers later with the Windows **Add/Remove Programs** utility on the Control Panel. Follow the instructions in the CONNECTIONS Driver Update Kit.

3. GETTING STARTED — A GAMMAVISION TUTORIAL

3.1. Introduction

This chapter provides a series of straightforward examples to help you become familiar with GammaVision's basic operations and move on quickly to full use. We will cover the following basic functions:

- Recalling a spectrum file from disk
- Performing a simple analysis of the spectrum
- Loading a nuclide library
- Using the library editor
- Energy calibration
- Efficiency calibration
- The calibration wizard
- Getting a Detector ready for data acquisition

To display help for any of the dialogs, put the mouse pointer on the item and click the right mouse button to display the 

button. Now click the left mouse button to display the help message. After reading the help message, click the left mouse button to close the message box.

To make the discussion easier and more realistic, the optionally installed sample files in C:\User \V9 Examples will be used in the remainder of the chapter.[8] You may either leave them in the examples folder or copy them to C:\User.

GVDEMO.SPC	GVDEMO.EFT
GVDEMO.LIB	GVDEMO.ENT

Before we actually begin, here is a short note on the *Detector and buffer concept* used in GammaVision.

A spectrum can exist in three places in GammaVision:

- In an MCB (which we call a Detector)
- In computer memory (a buffer window in GammaVision)
- In a file on disk

[8] If you chose not to install the example files, you may wish to reinstall GammaVision and choose to install the files.

The Detector is where the data are gathered from the HPGe detector. Data can be displayed and manipulated directly in the Detector memory or in a buffer window. They can be copied from the Detector to either the buffer or disk. Data can also be copied from disk to the buffer. Copying data will overwrite the existing buffer contents. A warning message is displayed before any data are overwritten and lost. Actions on the data in the buffer have no effect on data acquisition taking place in a Detector — GammaVision maintains separate calibrations and viewing settings for each Detector and buffer window.

GammaVision's multi-detector interface allows you to open up to eight Detector windows and eight buffer windows at a time. If you try to open a ninth window, the program will ask if you wish to close the oldest window. If you answer **Yes**, the oldest window will close and the new Detector or buffer window will open. To cancel and keep that oldest window open, click **No**.

In addition, the Acquisition Settings dialog (**Acquire/Acquisition Settings...**) now gives you the choice of starting all displayed Detectors simultaneously (**All MCBs**) or one Detector at a time (**Current MCB**); or **Prompt**s you to either start all MCBs or start only the current MCB.

3.2. Starting GammaVision

To start GammaVision, enter `gamm` in the "*search programs and files*" box on the Windows Start panel, then click the **GammaVision** search result; or open the Windows Start menu and click **GammaVision**, and **GammaVision** (Fig. 9). You can also start GammaVision by entering **run** in the search box and choosing the **Run** option; or (in XP) by selecting **Run** from the Start menu. The Run option allows you to start up from the command line, with or without arguments, as described in Section A.1.

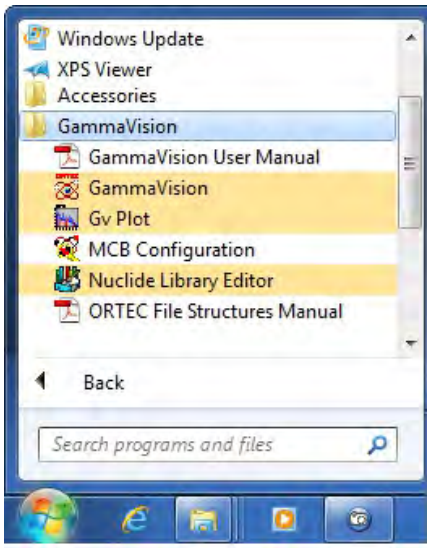


Figure 9. GammaVision Menu.

If you have not yet entered the **Registration Key** for your copy of GammaVision, the registration dialog will open, as discussed in Section 2.5. You may either enter the Registration Key (after which the registration dialog will not be displayed again); or, for 60 days after installation, you may bypass registration by clicking on **Register Later**.

GammaVision will check for Detectors, then display a screen similar to Fig. 10.

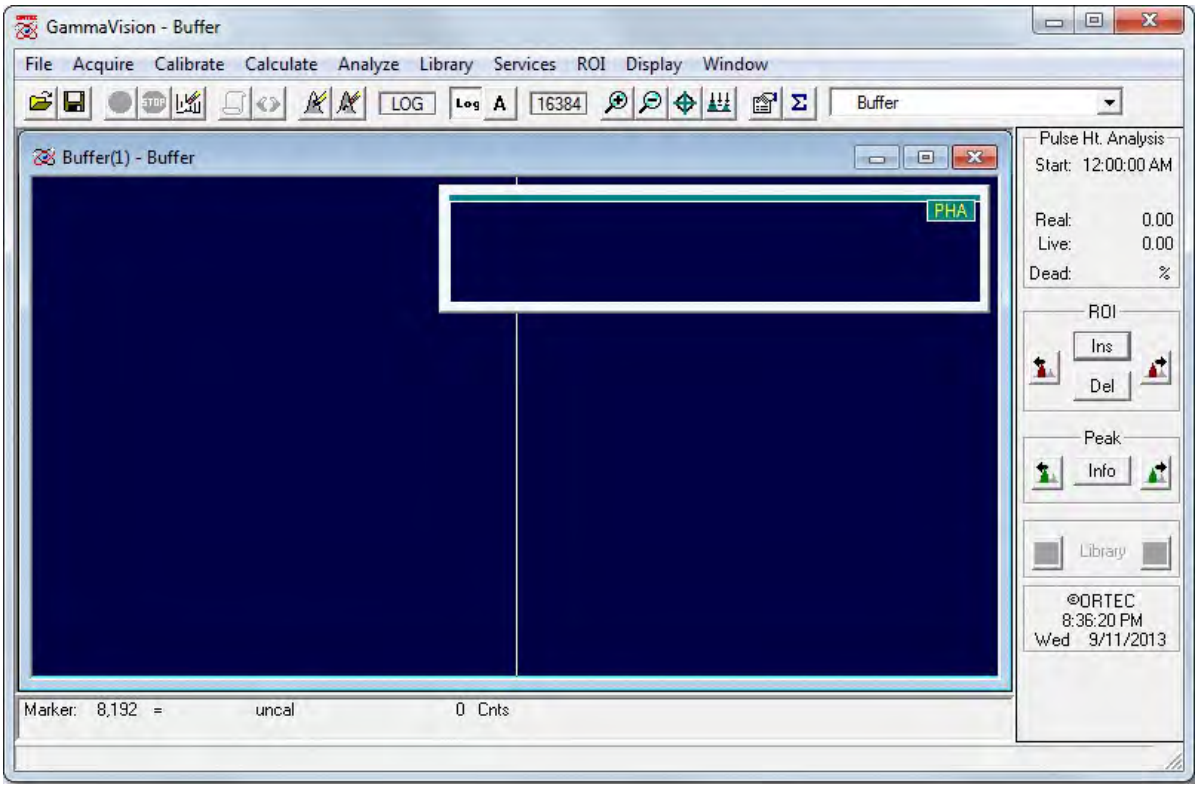


Figure 10. Example GammaVision Opening Screen.

3.2.1. Recalling a Spectrum

If a Detector or buffer window is already open, click its Close box ( ). Next, recall GVDEMO.SPC from the the menu bar by clicking on **File**, then **Recall...**. This will open a dialog showing the list of spectrum files in the C:\User folder. If you did not copy the example files into this folder, look in the \V9 Examples folder, as shown in Fig. 11. From the list of files, double-click GVDEMO.SPC, or click once on the file name and then **Open**.

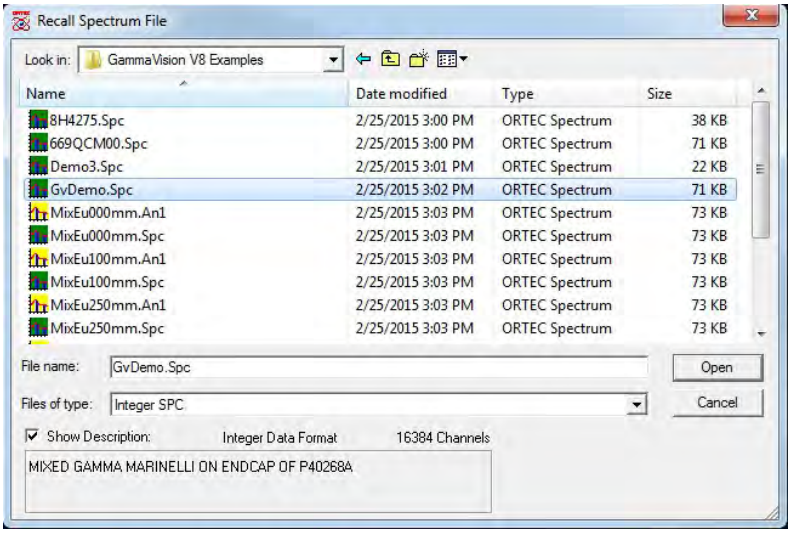


Figure 11. Recalling a Spectrum File.

A buffer window will open, displaying GVDEMO.SPC (Fig. 12). The *Status Side-bar* on the right of the screen will now show details about this spectrum.

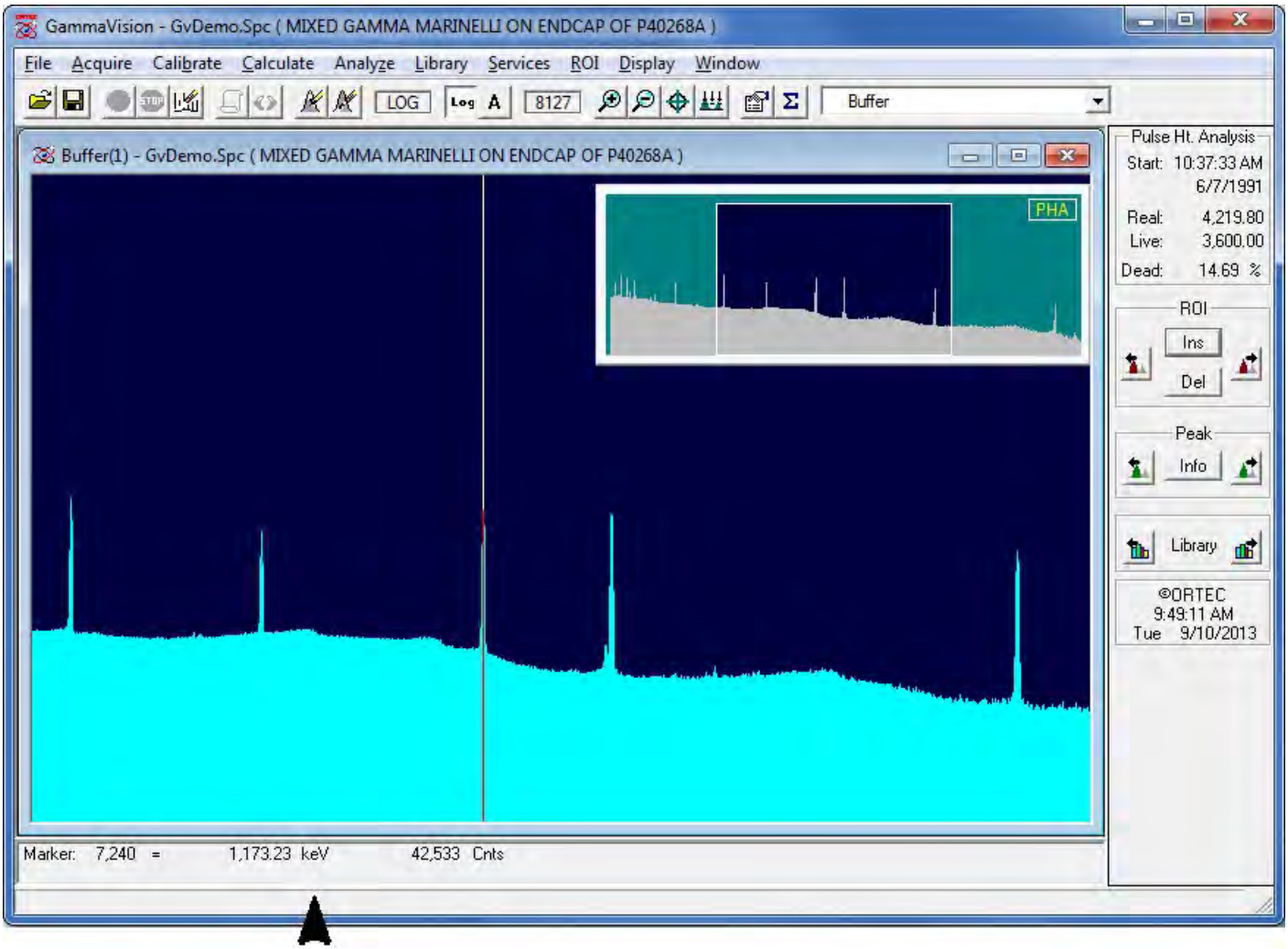


Figure 12. Calibrated Spectrum Recalled from Disk File.

Note the vertical *marker* line, which you can move by left-clicking the mouse on a different part of the spectrum. The *marker information line* at the bottom of the display reflects the channel contents at the marker's location. You can tell that this spectrum is already calibrated because the information about the marker reads in units of energy, keV. (An uncalibrated spectrum would instead display the word uncal.)

3.2.2. The Simplest Way To Do An Analysis

Select a portion of the GVDEMO.SPC spectrum for analysis by positioning the mouse on or near the 122 keV peak in the *Full Spectrum View* (Fig. 13), which will be located near the left edge of the window, and clicking the left mouse button. This will move the marker to the mouse pointer. The *Expanded Spectrum View* will now show this part of the spectrum.

Now expand this part of the spectrum by clicking on the **Zoom In** button ( ) on the toolbar one or more times. As you zoom in, the Full Spectrum View will show which portion of the spectrum is expanded, and the Expanded Spectrum View will display this part of the spectrum (see Fig. 12). If the 122 keV region is not on the screen, point the mouse in the Full Spectrum View and try again.

On the menu bar, click **Analyze**, and select **Interactive in viewed area...** (see Fig. 14). GammaVision will automatically analyze the selected region and display the results. The *Analysis Sidebar* will open, superimposed on the Status Sidebar, the peak fit(s) will be shown graphically, and the numerical results will be displayed in an *Analysis Results Table* window, as shown in Fig. 15.

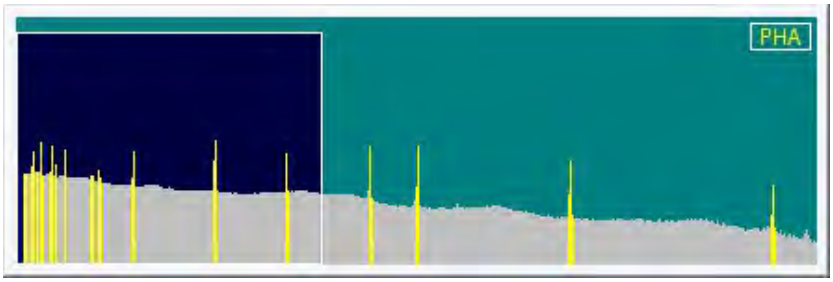


Figure 13. Full Spectrum Window.

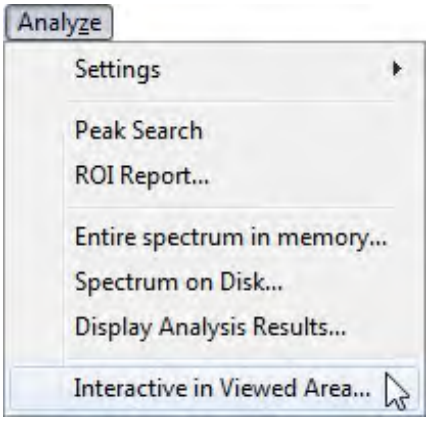


Figure 14. Analyze/Interactive in Viewed Area.

That's all it takes to do an analysis!

There are several functions that you can access at this point, but first we will load a *working nuclide library* and check some parameters. Exit this analysis session by clicking on the Analysis Sidebar's Close button ( ). This will close the Analysis Sidebar and the table window.

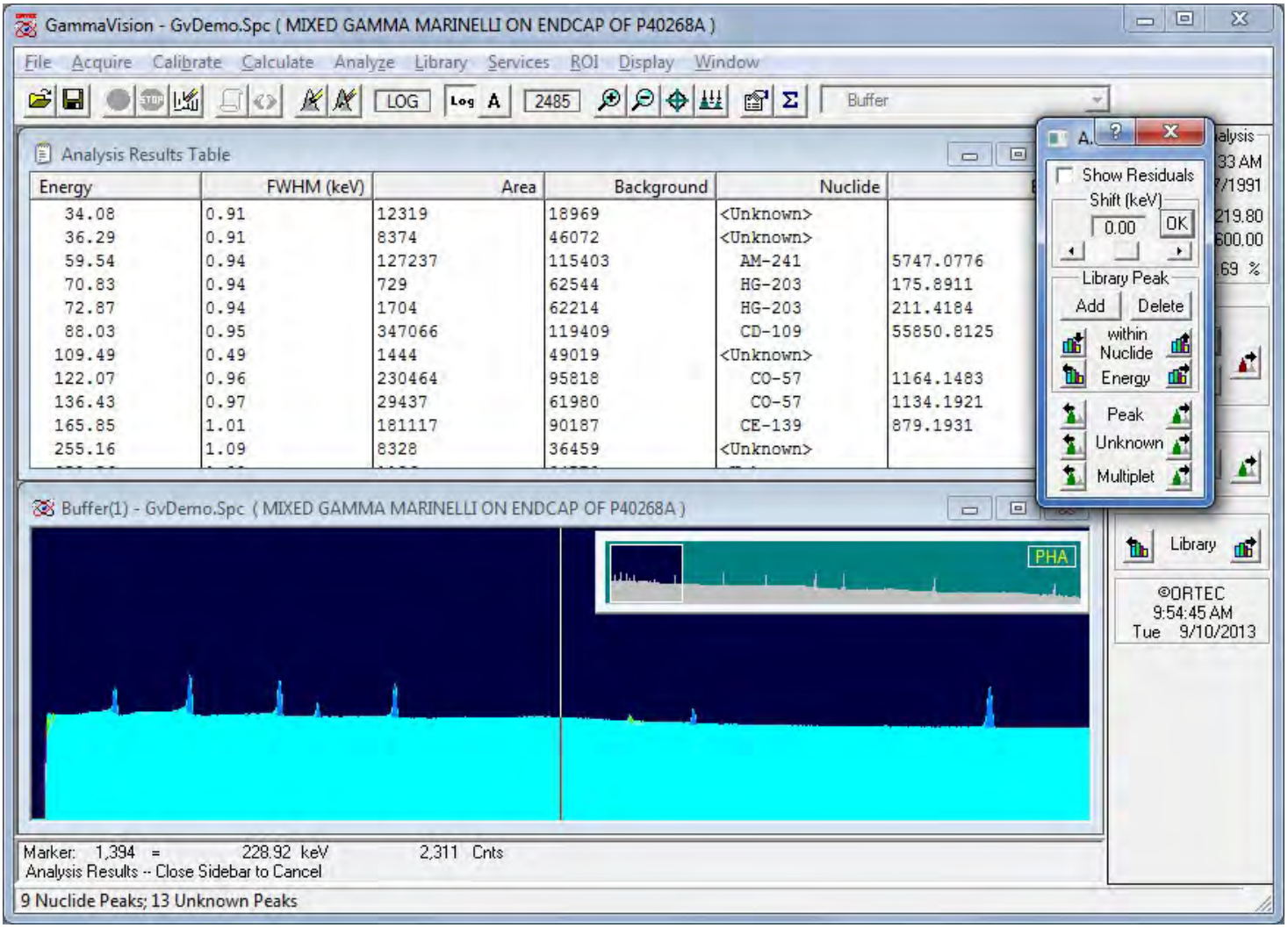


Figure 15. Completed Analysis, Showing Results Table and Analysis Sidebar.

3.2.3. Loading a Library

From the menu bar, select **Library**, then **Select File...** as shown in Fig. 16. This will open a list of nuclide libraries in the current directory.

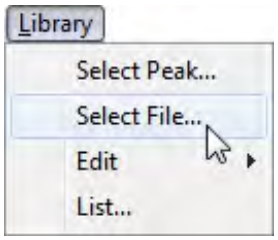


Figure 16. Load a Library from Menu.

Select the library file GVDEMO.LIB and click **OK** to load it. The following message will appear on the *Supplemental Information Line* at the bottom of the GammaVision window:

GVDEMO.LIB: 1024 Bytes; 9 Nuclides /9 alloc.; 16 Peaks /16 alloc.

This message describes the library just loaded. GVDEMO.LIB is 1024 bytes in size, has 9 nuclides with space for 9, and has 16 peaks with space for 16.

This library, GVDEMO.LIB, is now loaded into the computer memory as the *working library*, and is the library that GammaVision will use for all analyses until you change it (by recalling another library from the **Library** menu or from within a *sample defaults file* as discussed later). It is automatically reloaded each time GammaVision is started.

3.2.4. Setting the Analysis Parameters

Click **Analyze**, then **Settings** to open the submenu shown in Fig. 17. Select **Sample Type...**. This will open the Sample Type Settings dialog shown in Fig. 18, which allows you to specify the parameters that control analysis of the currently displayed spectrum. For routine measurements, the analysis settings and sample description may be established using prompts configured from the **Acquisition Settings...** command under the **Acquire** menu.

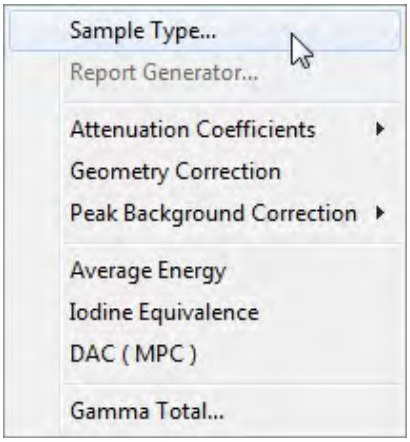


Figure 17. Choose Sample Type... Command.

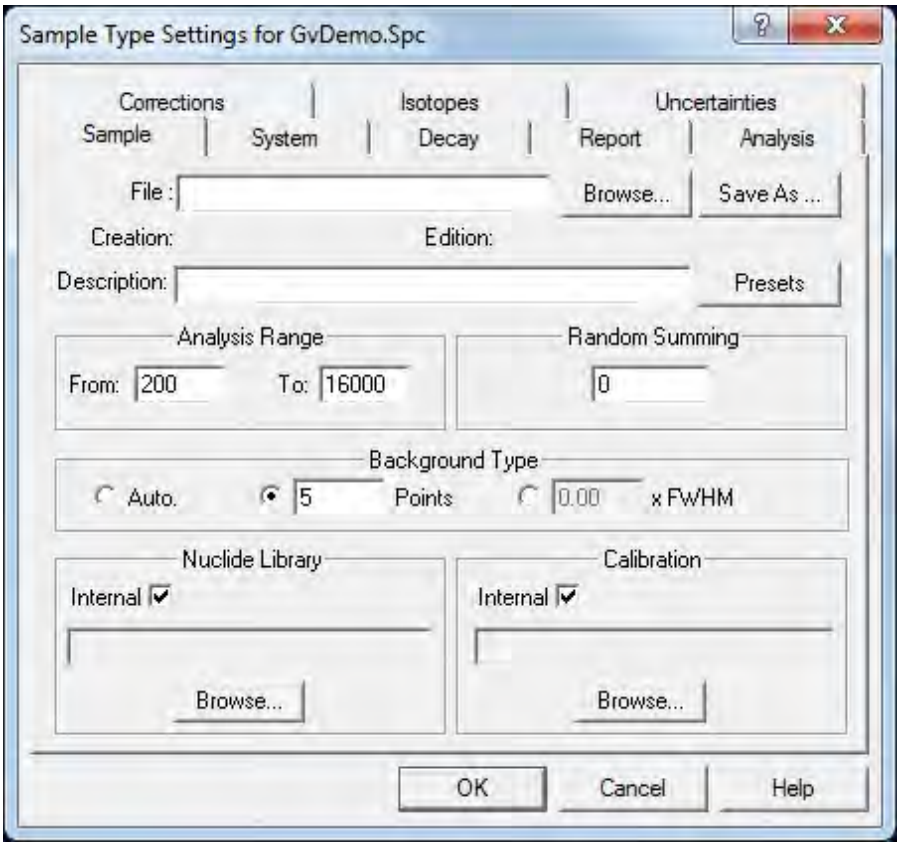


Figure 18. Sample Type Settings Dialog, Sample Tab.

We will use the **Nuclide Library** just loaded in computer memory by leaving the **Internal** checkbox marked. Similarly, to use the **Calibration** that was saved with the spectrum in GVDEMO.SPC, leave this **Internal** checkbox marked also.

Select the **Report** tab to view the reporting, uncertainty reporting, and output options (Fig. 19).

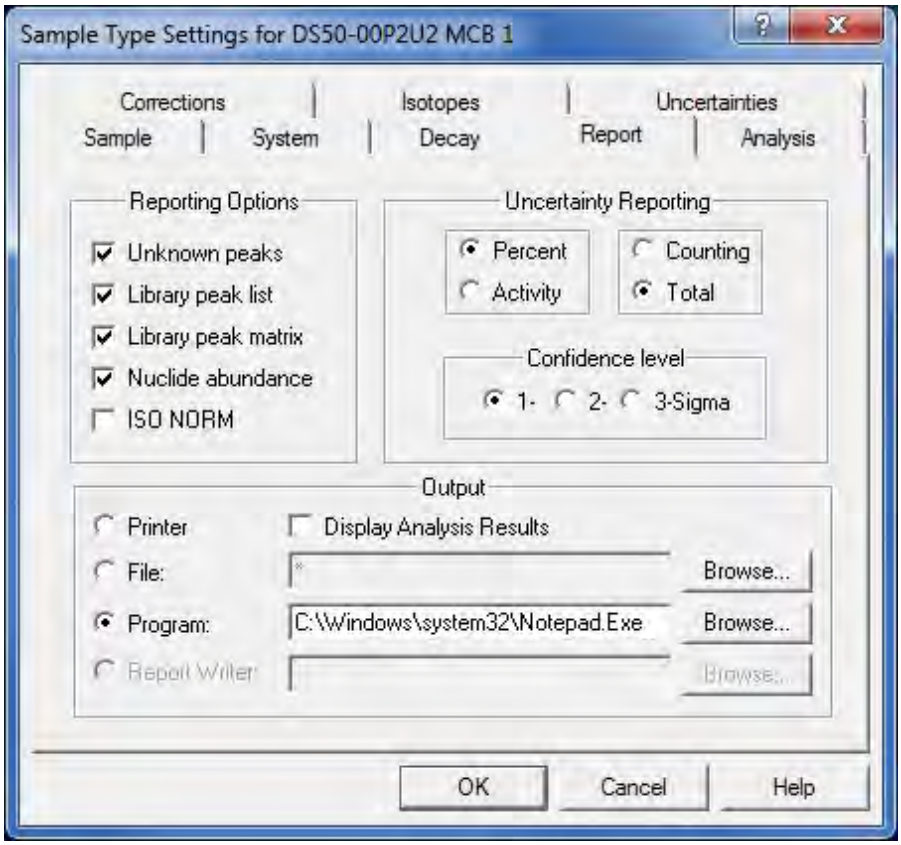


Figure 19. Report Tab.

Mark all of the **Reporting Options** except **ISO NORM**, and make sure the **Total** option is selected in the **Uncertainty Reporting** section.

To send the output to a printer, go to the **Output** section of the screen and click the **Printer** radio button to mark it with a dot.

To send the output to a file instead, click the **File** radio button, and leave the asterisk (*****) as the filename. Leaving the asterisk ensures that the report file will have the same filename as the spectrum (however, it will have the extension .RPT). You can, however, enter a path and file-name in this field to force the report to be saved to the filename you specify.

To send the output to a text processing program, such as Windows Notepad (which is the default), click the **Program** radio button.

Click all four checkboxes in the **Reporting Options** section of the screen, then click **OK**.

Select **Analyze** and **Entire spectrum in memory....**[(ã)] Spectra can be analyzed in the buffer (as we have done here), directly from disk, or in the Detector memory (when the Detector is not

counting). For spectra in the Detector memory or a buffer, the displayed spectrum is the one being analyzed.

When the analysis is complete, the results will be printed or saved to disk, according to your selection on the **Report** tab on the **Sample Type Settings** dialog (the report is covered in Chapter 7). They can also be graphically displayed by selecting **Analyze** and **Display Analysis Results...**, then clicking on **Open** to load the analysis results file, GVDEMO.UFO. This will overlay the peak shapes on the spectrum data, open the Analysis Results Table for the spectrum, and display the Analysis Sidebar superimposed over the Status Sidebar, as shown in Fig. 20. Zoom in to see more details.

Click on the peak at 136 keV and expand the display horizontally with **Zoom In**. Put the mouse on the ^{241}Am (59.6 keV) entry in the peak list table and click. The marker will move to that peak in the display. You can use the scroll bars on the peak list window to show other energies, and then when you click the energy, the display will show that peak.

In this mode, you can also use the buttons on the Analysis Sidebar to move the marker in the spectrum. For example, click ^{241}Am in the peak table, then click 

(the right-hand **Energy** button in the **Library Peak** section of the Analysis Sidebar) to put the marker on the next-highest-energy library peak, which is the 70.8 keV line of ^{203}Hg.

Now click 

to go to the next-highest-energy peak in the library for ^{203}Hg, then click again to get to the 279 keV peak. The **within Nuclide** buttons are useful for checking if other peaks for the nuclide exist so that you can confirm their identity. The 

button moves the marker in reverse order through the peaks for the selected nuclide.

The 

buttons are used to select the spectrum peaks that are not associated with a library energy. This is useful to see if there are any unidentified spectrum peaks that should be considered in the complete analysis.

The 

buttons are used to select the regions with overlapping peaks. With these, you can easily check how the analysis of complicated regions was handled.

Now, select **Library** and **Select Peak...** to show a list of the peaks in the current library.[9] You can use this list of peaks to move around in the spectrum. Click the Library List window's down arrow to scroll down to 88 keV ^{109}Cd. Now click this entry and the display will update to this peak.

[9]This can be a different library than the one used in the analysis of the spectrum.

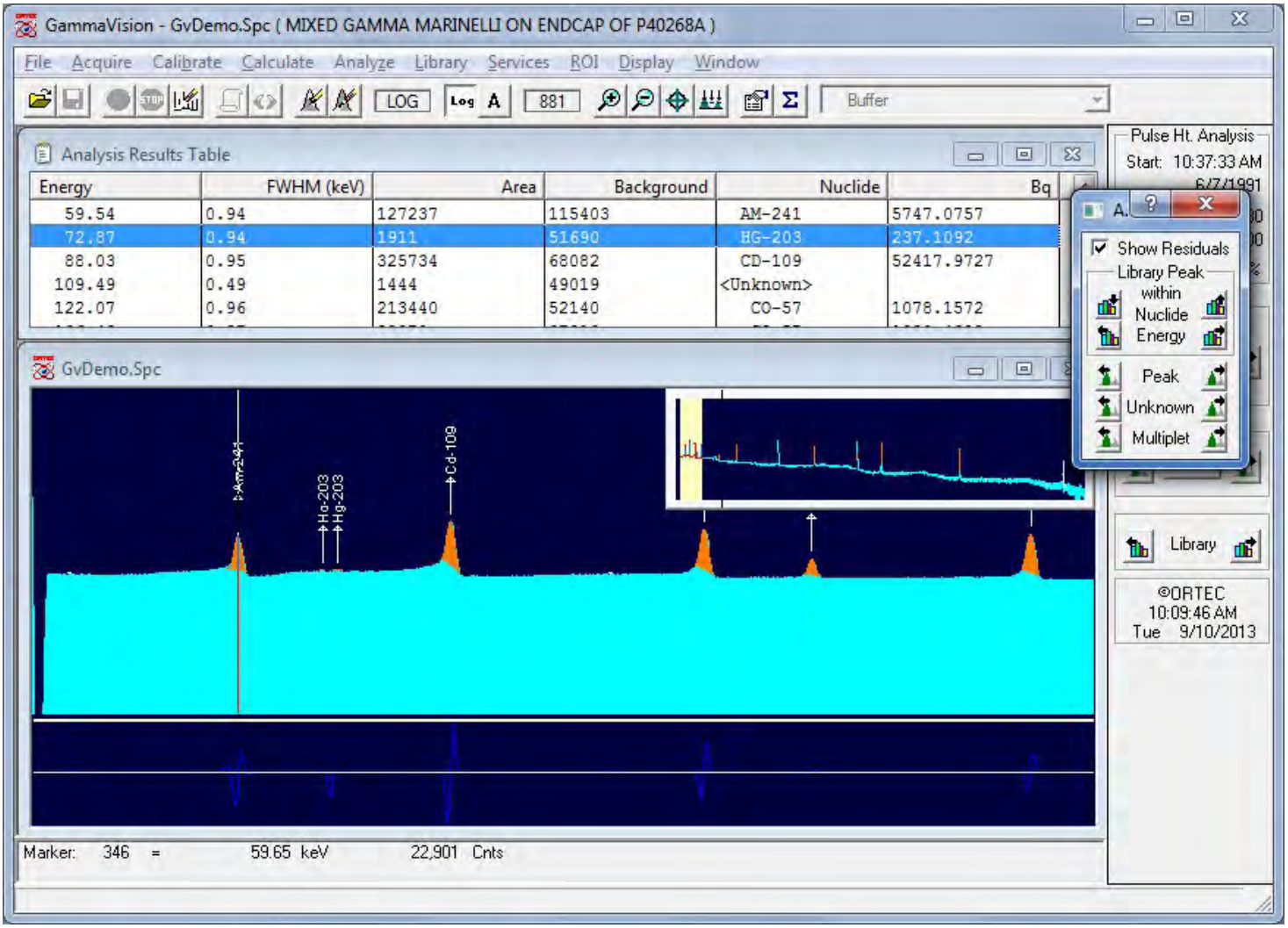


Figure 20. Display Analysis Results.

Exit this analysis session by clicking on the Analysis Sidebar's Close button ( ) to close the Analysis Sidebar and Analysis Results List window. Also close the Library List window.

3.2.5. Energy Calibration

For this example, we will use the spectrum files supplied with GammaVision to recalibrate the buffer. The same procedure is used to calibrate the Detector spectrum. The buffer window containing GVDEMO.SPC should still be displayed.

From the **Calibrate** menu (Fig. 21, 320), select **Energy...**. The *Energy Calibration Sidebar*, shown in Fig. 22, will open to the right of the spectrum area. You can move the sidebar by clicking on the titlebar and dragging as you would in any Windows application.

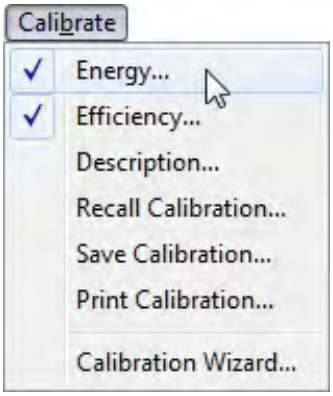


Figure 21. Start Energy Calibration from Menu.

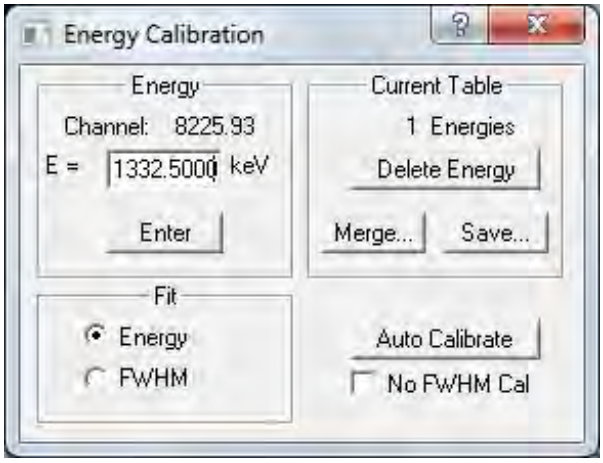


Figure 22. Energy Calibration Sidebar.

This time, so that we start from the very beginning, clear the current energy calibration by clicking on the icon to the left of the "**Energy Calibration**" title. This will open the *control menu* shown in Fig. 23. Click on **Destroy**. The Marker Information Line now shows the legend **uncal**.

Figure 23. Energy Calibration Sidebar Control Menu.

Move the cursor to channel 8226, the location of the upper ^{60}Co peak, at 1332.5 keV. Do this directly in the full window or by using the Peak buttons until you get there. Click once in the **E=** field at the top of the Energy Calibration Sidebar, enter the correct energy for this peak (1332.5 keV), and click **Enter**. The system will automatically perform a simple calibration based on this peak and the assumption that channel zero is energy zero. The graphs of the calibration and the table of values will be shown on the display, as in Fig. 24.

If the screen becomes too visually crowded, you can either move one or more windows until they are nearly "stacked" atop each other (leave at least an edge or corner of each window showing); or close one or more windows by clicking on their Close box ( ). However, do not close the Energy Calibration Sidebar or you'll end the calibration session. Rearrange and/or resize the windows as needed.

Now we can use the library; click **Library/Select Peak** to reopen the Library List window. Double-click the 122.07 keV peak of ^{57}Co in the library list. The marker will move close to, but not precisely on, that peak in the spectrum based on our current "one-point calibration."

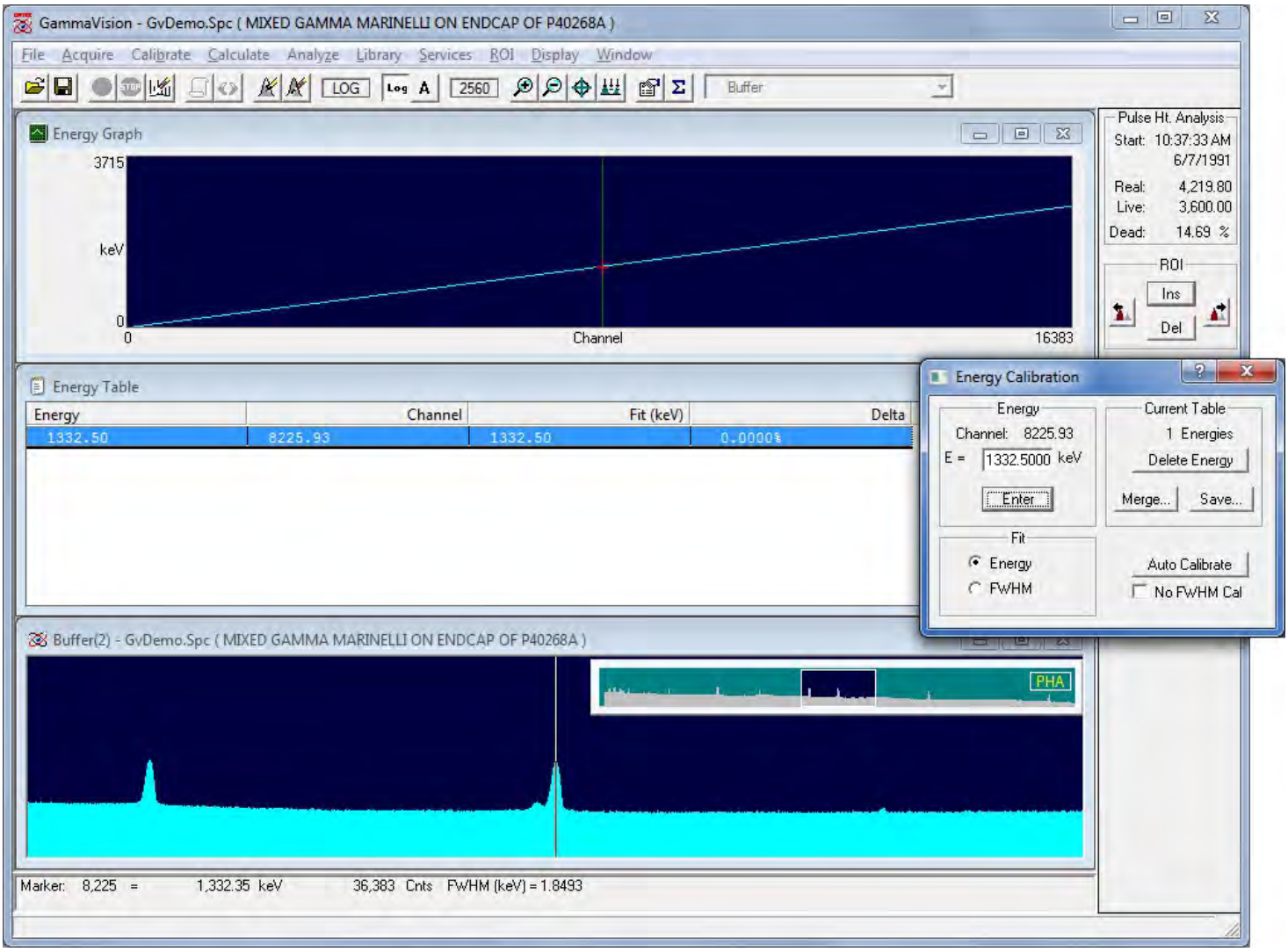


Figure 24. Energy Calibration Display.

Use the Peak buttons to put the cursor on the peak, then click once on the 122 keV entry in the library list. Note that the **E= 122.07 keV** in the Energy Calibration Sidebar already has the appropriate energy from the library, and you need only accept it by clicking on **Enter**. The refitted calibration curve is automatically displayed.

Proceed through the library list in Table 1 adding the peaks (in any order) into the calibration. To do this, double-click within 2 channels of the peak center, then click **Enter**.

If you decide that you don't want one of the peaks, you can delete it at will by clicking on the **Delete Energy** button on the Calibration Sidebar.

Now examine the **Energy Table** and note that the **Delta**s (the differences between data points and the fit to the data points) are small. Next, bring the **Energy** plot window to the front and

visually inspect the calibration curve, resizing the windows as needed to allow a closer examination of the graphical fit.

Click the **FWHM** (full width at half maximum) radio button on the lower section of the Calibration Sidebar to display the table of FWHM results and the FWHM graph (which is shown in Fig. 25). The FWHM fit uses the peaks specified in the energy fit. If FWHM of any peak has a deviation of more than 25% between the actual and fitted values, a warning message is displayed.

Table 1. Source Energies.

Nuclide	Energy (keV)
^{88}Y	1836.01
^{57}Co	122.07
^{60}Co	1173.2
^{60}Co	1332.51
^{88}Y	898.02
^{137}Cs	661.66
^{113}Sn	391.69
^{203}Hg	279.17
^{109}Cd	88.03
^{241}Am	59.54

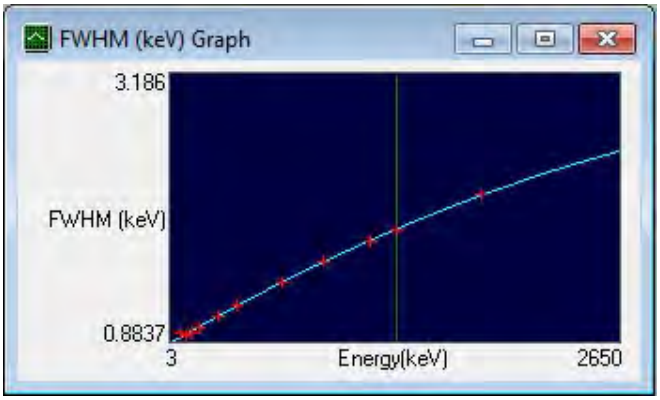


Figure 25. FWHM Fit Selection.

Save the energy table for later use: click the Calibration Sidebar's **Save** button, enter a name such as GVDEMO for the table filename, and click **Save**. GammaVision will append the extension .ENT to the filename.

To examine the Energy Table, open the Calibration Sidebar's control menu and select **Edit File**. This table is a list of peak energies and the associated channel and FWHM values used for the calibration.

The energy calibration is complete; we shall consider this to be a "good" energy calibration for the purposes of this demonstration. Close the calibration session by selecting the system menu in the calibration and selecting the **Close** option. This new energy calibration is now held in memory but is not yet stored on disk.

3.2.5.1. Auto Calibration

The **Auto Calibrate** button is the fastest and easiest way to do the energy calibration. Just click **Auto Calibrate** to use the working library to calibrate the displayed spectrum with no other inputs. The current calibration is erased before the new calibration is started.

Select **Close** from the sidebar's control menu.

3.2.6. Efficiency Calibration

Select **Calibrate** from the menu bar, then **Efficiency**. This opens the *Efficiency Calibration Sidebar*, shown in Fig. 26 (note its similarity to the Energy Calibration Sidebar).

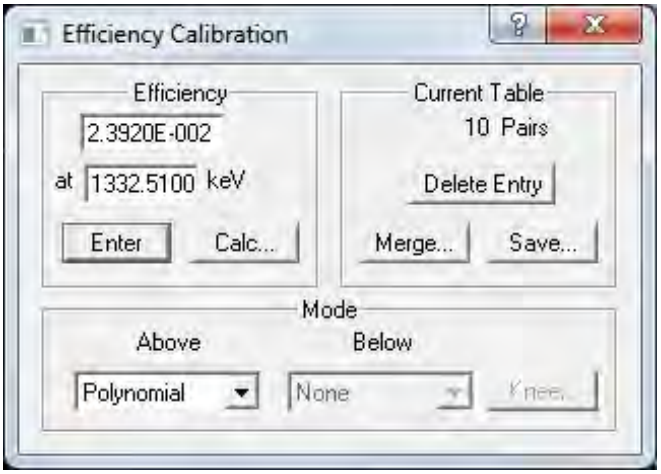


Figure 26. Efficiency Calibration Sidebar.

We want to start from the beginning of the process, so open the sidebar's control menu (click the icon on the left of the title bar) and select **Destroy**.

The Library List window should be visible, but if not, click **Library/Select Peak...** to reopen it.

From the library, double-click the 1332.5 keV peak of ^{60}Co. The marker will move to the corresponding peak and GammaVision will enter the energy in the top section of the Efficiency Calibration Sidebar.

In the upper section of the sidebar, click the **Calc...** button to open the Efficiency Calculation Worksheet (Fig. 27).

Enter the date and the time from the calibration certificate (see Table 2), as Oct-01-90 12:00. Enter the gammas per second (5838) from the calibration certificate for ^{60}Co at 1332.5 keV. Select **GPS** from the units droplist. Note that the **from Library** box is checked; this shows that the half-life came from the library.

At this point, the **Calculate Efficiency=** button at the top of the worksheet should be active (black rather than gray). If it is disabled (gray), one or more of the data inputs is either incorrect or has not been entered. When you have completed all fields and **Calculate Efficiency=** is activated, click it to obtain the efficiency value at this energy. Click **OK** to insert the value in the efficiency table. You will see that the value appears in the Efficiency Table window.

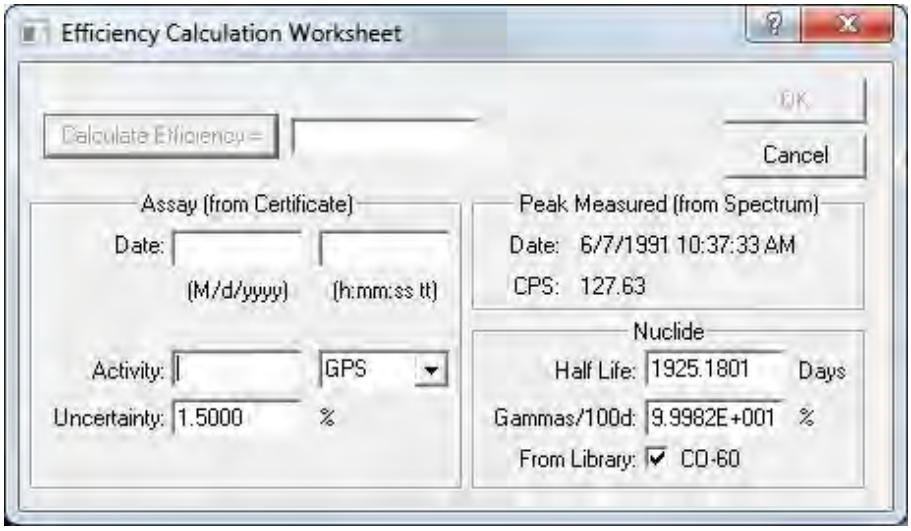


Figure 27. Efficiency Worksheet.

You could repeat this process for all other peaks in the calibration certificate data, but there is an easier way. All of the information from the calibration certificate can be stored in an efficiency calibration (.EFT) file (see Section 5.3.3.12 for instructions on creating and editing this file).

Using this file to direct the calibration is easy. On the Efficiency Calibration Sidebar, click the **Merge...** button, then select the file GVDEMO.EFT. GammaVision will use the data in the table to calculate the efficiency at each energy from the spectrum and fill in the efficiency table. You can see the marker jump from peak to peak in the spectrum as the peak areas are calculated.

Table 2. List of Peak Energies.

Reference Time: 12:00 GMT 01 Oct 1990		
Nuclide	**Energy (keV)**	**Gammas/second**
^{241}Am	59.54	2078
^{109}Cd	88.03	2967
^{57}Co	122.1	1813
^{139}Ce	165.9	2550
^{113}Sn	391.7	4263
^{137}Cs	661.63	4198
^{88}Y	898.02	10120
^{60}Co	1173.2	5818
^{60}Co	1332.5	5838
^{88}Y	1836.01	10640

When the data points are all calculated, the fit **Mode** stored in the file is used to make the fit. You can select another fit **Mode** from the Calibration Sidebar. In the **Above**-the-knee list, choose the **Polynomial** option. This will automatically produce a single-function polynomial fit of the entire energy range, as shown in Fig. 28. The other modes use separate fits above and below the “knee” of the detector efficiency curve.

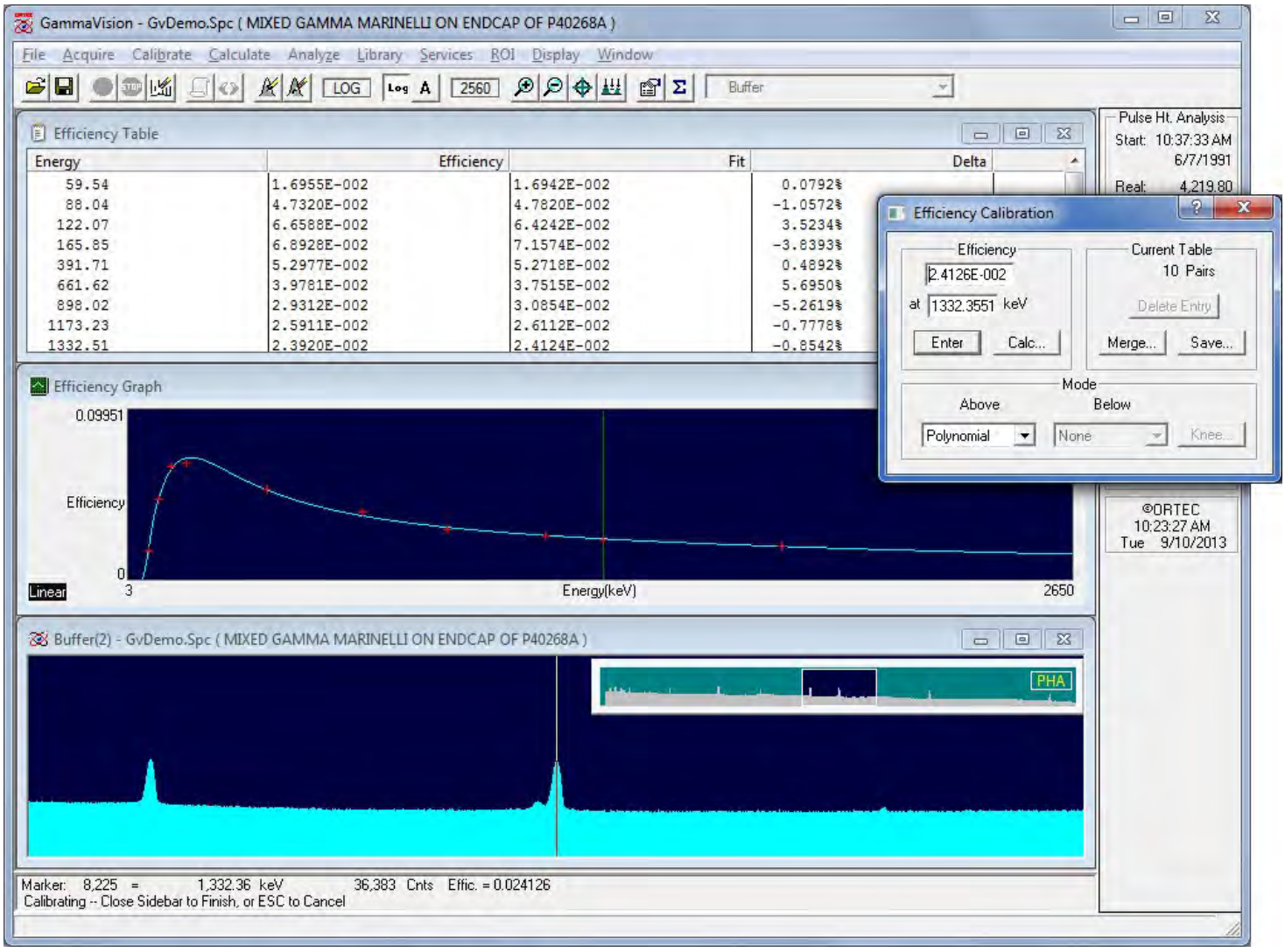


Figure 28. Polynomial Efficiency Fit.

The fit will take place automatically. You can then view it by bringing the **Efficiency** calibration fit window forward. Click the window's control menu to choose scaling and grid display options (see Fig. 29). The marker line in the efficiency graph window will be at the energy of the peak selected in the Library List or the Efficiency Table window.

We will accept this calibration and close the calibration session by clicking the Calibration Sidebar's **Close** button. Now save this calibration to disk by selecting **Calibrate** and **Save Calibration...**. Give the calibration file the name GVDEMO. GammaVision will attach the default .CLB extension to the filename.

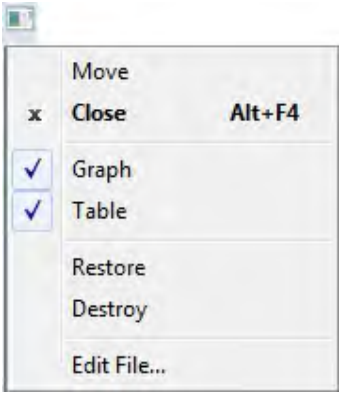


Figure 29. Control Menu.

3.2.7. Energy and Efficiency Calibration Using the Calibration Wizard

GammaVision has a calibration wizard to help you with energy and efficiency calibration, as well as *total coincidence correction* (TCC) calibration. To start the wizard, go to the **Calibrate** menu and select **Calibration Wizard...**. This will open the dialog shown in Fig. 30.

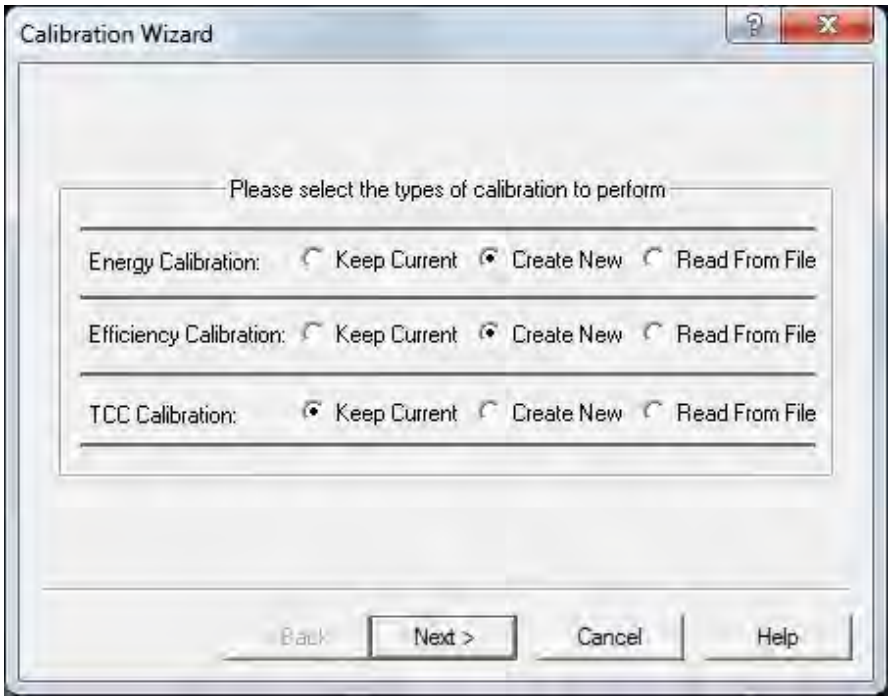


Figure 30. Select One or More Calibrations to Perform.

For this demonstration we will perform only the energy and efficiency calibrations. Go to **Energy Calibration** and click **Create New**, then do the same under **Efficiency Calibration**. Click **Next**.

In the next dialog (Fig. 31), go to the **Library** field and enter GVDEMO.LIB, then click **Next**.

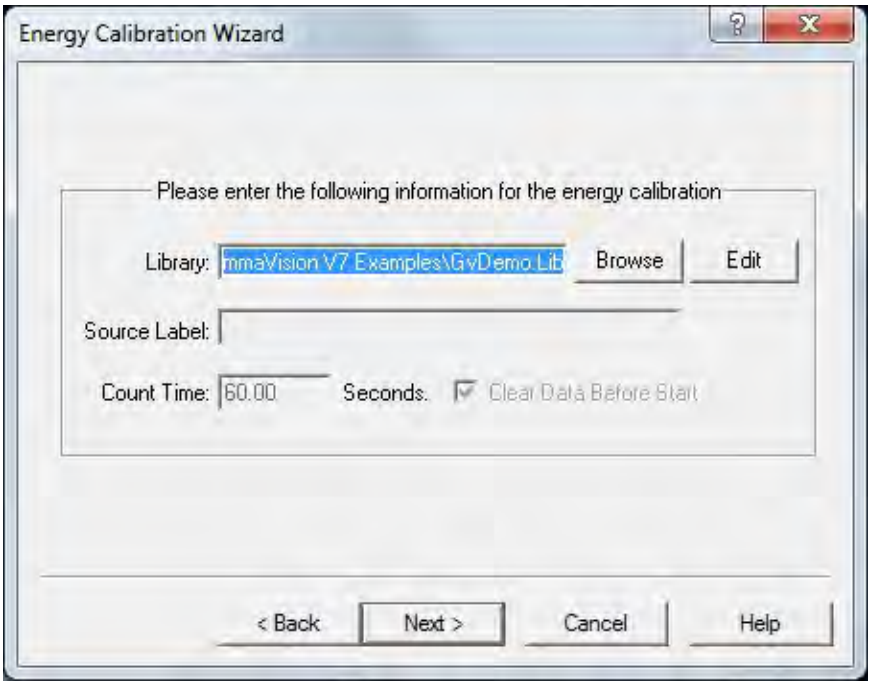


Figure 31. Enter the Library File to be Used in the Energy Calibration.

On the third wizard screen (Fig. 32), enter GVDEMO.EFT as the **Certificate File** to be used in the efficiency calibration.

Figure 32. Enter the Certificate File to be Used in the Efficiency Calibration.

Now click **Next**. GammaVision will now perform the two calibrations. The results are shown in Fig. 33. The **Fit vs. Energy** display on the lower right refers to the true-coincidence correction calibration. Since this example does not use the TCC calibration, its display is marked Uncalibrated.

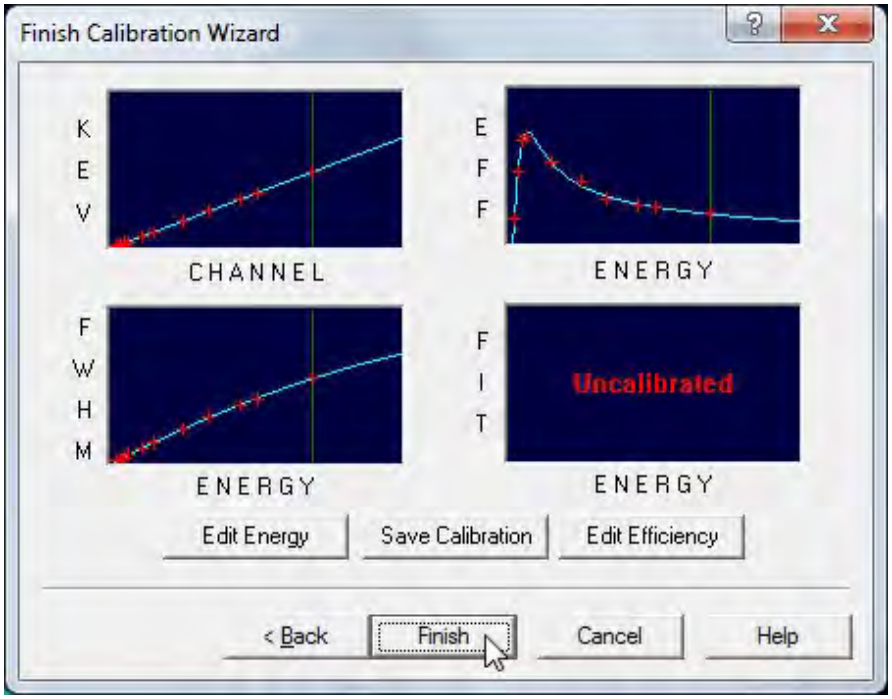


Figure 33. Energy and Efficiency Calibration Results.

Click **Save Calibration** and assign the filename GVDEMO.CLB. Finally, click **Finish** — *that's all there is to it!*

3.2.8. Changing a Library

Select **Library/Edit/GammaVision Editor...** from the menu bar. This will open the **Editing** dialog (Fig. 34), which allows you to change, add, or delete nuclide and gamma-ray values in the currently loaded nuclide library file.

Select the nuclide ^{60}Co from the left-hand section of the dialog. All the gamma-ray energies or peaks for this nuclide will then appear in the **Peaks** section; select the 1332.5 keV peak. Click **Edit...** in the **Peaks** section. This will open the **Edit Library Peak** dialog (Fig. 35), which will show the current values and allow you to change the energy and gammas-per-disintegration of the 1332.5 keV line.

Click the **Gammas per 100 disintegrations** field and change the value, then click **OK**. You will see that the **Gammas per 100 Disintegrations** value for this peak has been changed to the number you just entered.

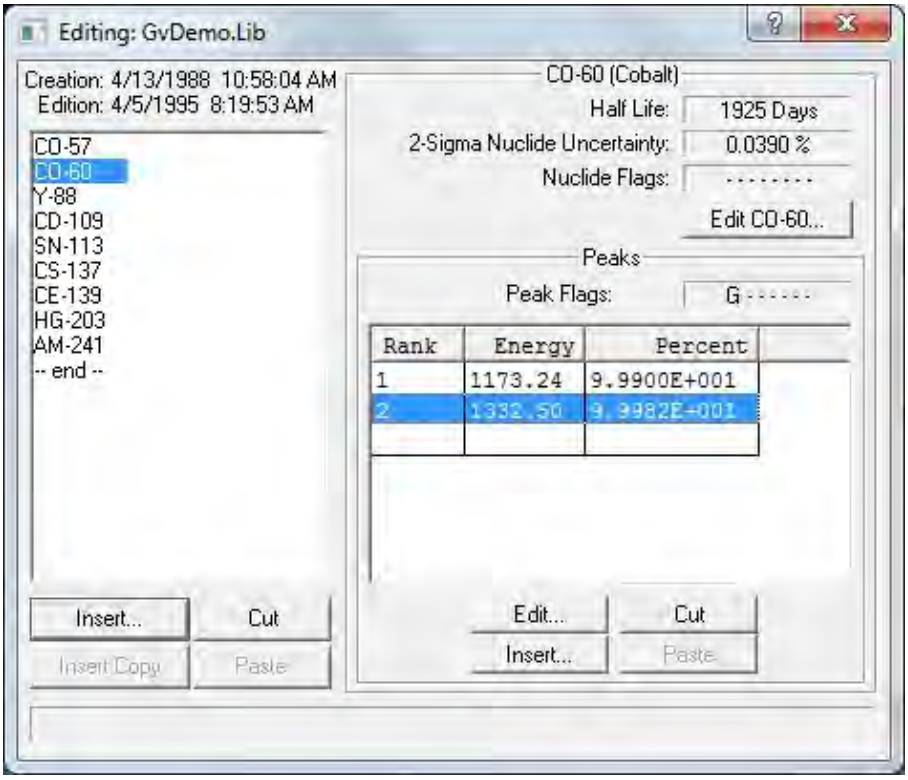


Figure 34. Edit Nuclide Library with GammaVision Editor.

Now click the Editing dialog's **Close** button to leave the library editor. When asked if you want to save the modified library, click **No** to ignore the change you just made in the **Gammas per 100 Disintegrations** field.

The GammaVision library editor is explained in detail in Section 5.6. Note that GammaVision can also use NuclideNavigator III libraries, and that you can access NuclideNavigator III directly from the GammaVision **Library/Edit** submenu.

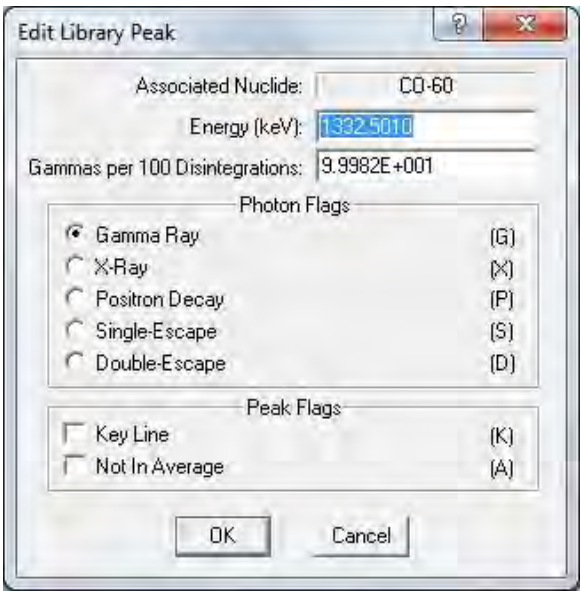


Figure 35. Edit Nuclide Peak.

3.2.9. Detector Setup

Before starting data collection, make sure the detector, analog electronics (if any), and MCB are connected and powered on according to their respective hardware manuals. Before the germanium detector's high voltage is applied, the detector must be cooled for the time listed in the detector manual, otherwise the unit could be damaged.

The GammaVision installation program will have already located the Detectors available to this computer. Click the Detector pick list on the right of the toolbar and select a Detector. The spectrum displays will update to show the data in this Detector.

In the simplest mode of operation, data acquisition is started from the toolbar; simply click the **Start** button. You can use the **Acquire** menu (Fig. 36) to check the analysis settings while data is being gathered. After acquisition stops, the analysis can proceed.

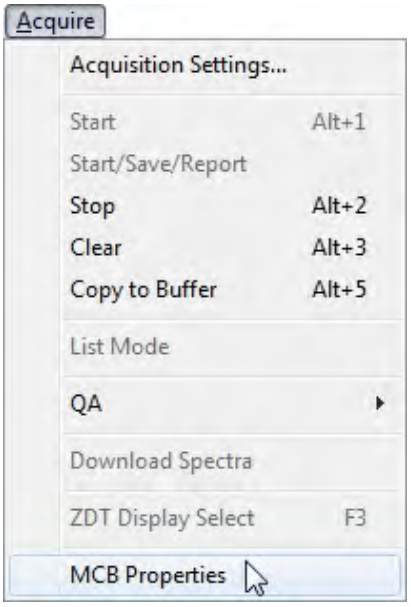


Figure 36. Acquire Menu.

All of GammaVision's hardware setup controls are now in *one, MCB-specific dialog.* Depending on your Detector, this might include controls for conversion gain, amplifier, high voltage, shaping, data acquisition presets, and more. To access this dialog, click **Acquire/MCB Properties...**, or right-click the mouse anywhere in the spectrum window to open its menu and select **MCB Properties**.

Some of the Detector's internal parameters can only be changed when the Detector is not acquiring data. To see if the Detector is in acquisition mode, open the **Acquire** menu look at the menu items. If **Stop** is black and **Start** is gray (see Fig. 36), the Detector is in acquisition mode (even if no counts are accumulating in the MCB at the moment). If this is the case, select **Stop** from the menu or toolbar.

3.2.9.1. Conversion Gain

If you wish to change the conversion gain, click **Acquire/MCB Properties...**, select the ADC tab (Fig. 37), then change the **Conversion Gain** field. The ADC gain is stored in the MCB and automatically recalled from the MCB the next time you restart GammaVision. Note that in this example, we are using a DSPEC-50, and that the Properties dialog automatically displays only data fields that are applicable to this MCB.

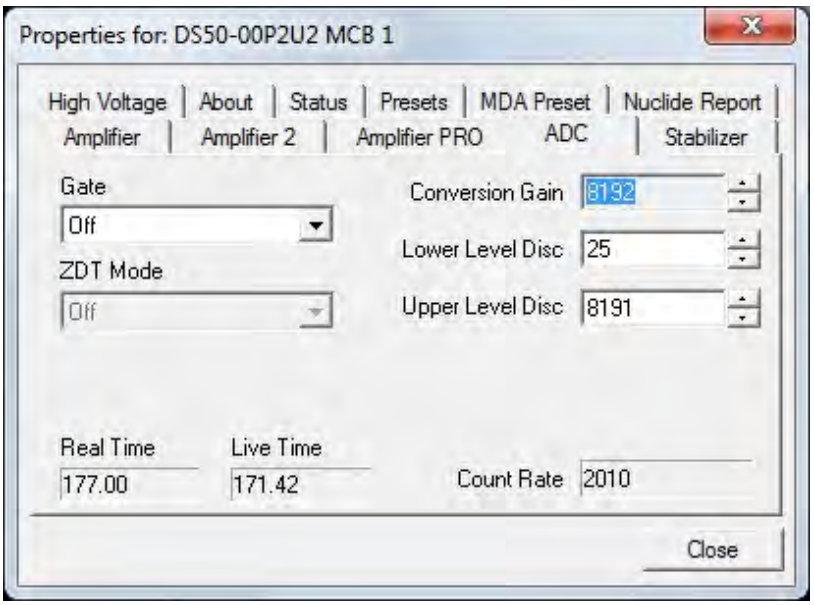


Figure 37. Setting the DSPEC-50 Conversion Gain.

If you have software-controlled hardware (as distinguished from NIM units with front- and rear-panel hardware adjustment controls), skip to Section 3.2.9.3.

3.2.9.2. Detectors Set Up Manually

Adjust the spectroscopy amplifier gain, shaping time, and pole zero. This is a manual operation which should be carried out according to the instructions given in the amplifier manual. A source with only one or two lines (e.g., ^{137}Cs or ^{60}Co) should be used for the initial test spectrum so you'll be able to easily see the correct pattern of the peaks. The amplifier gain should be adjusted to align known energy peaks to the respective channel based on the energy range of interest. For example, if the energy range of interest is up to 2 MeV at 4000 channels, then the Co-60 1332.5 kev peak would be centered on channel 2665. With a 2 MeV range at 8000 channels the 1332.5 kev peak would be centered on channel 5330.

3.2.9.3. Computer-Controlled Hardware Setup

In this section, we will use GammaVision to enable the DSPEC-50's high voltage and adjust the spectroscopy amplifier gain and shaping constants.

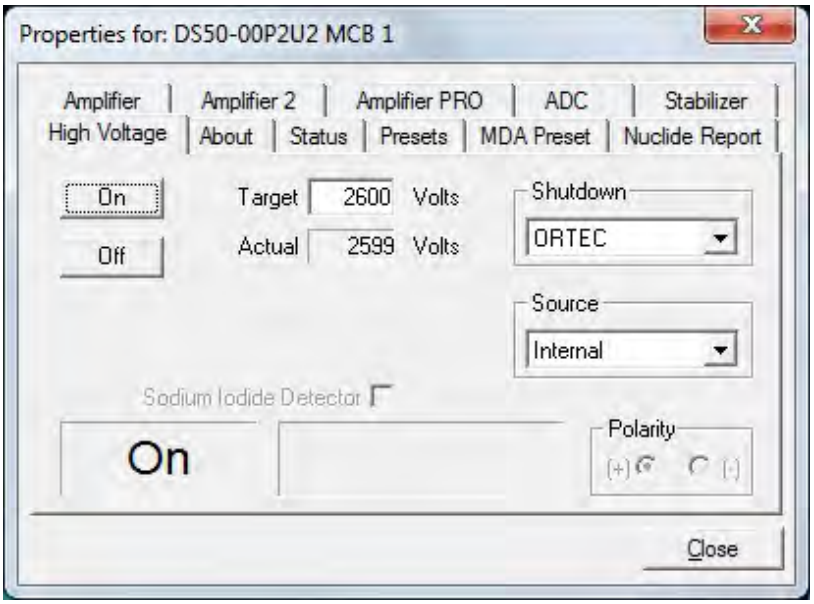


Figure 38. Monitoring the DSPEC-50 Bias Setting on the High Voltage Tab.

Click **Acquire/MCB Properties...** to open the Properties dialog for this MCB, and click the High Voltage tab (see Fig. 38). Set the **Target** bias. When the value of the detector bias matches that shown on the detector's Quality Assurance data sheet (also given on the endcap label), click the **On** button and note the **Actual** voltage readout. If the On/Off indicator reads **Shutdown**, the detector is most likely warm. (The detector might require 3–6 hours after filling before it is cold enough to take bias.)

3.2.9.4. Amplifier Settings

The Amplifier tab (Fig. 39) lets you set the amplifier shaping time to either **Long** or **Short**. The **Long** shaping time is the recommended choice for low to moderate count rates. The value of the shaping time (in ì s) is given in the hardware manual.

If you have a transistor-reset preamplifier (Plus Series), select it from the **Preamplifier Type** droplist.

Click **Close** to apply the new MCB hardware settings.

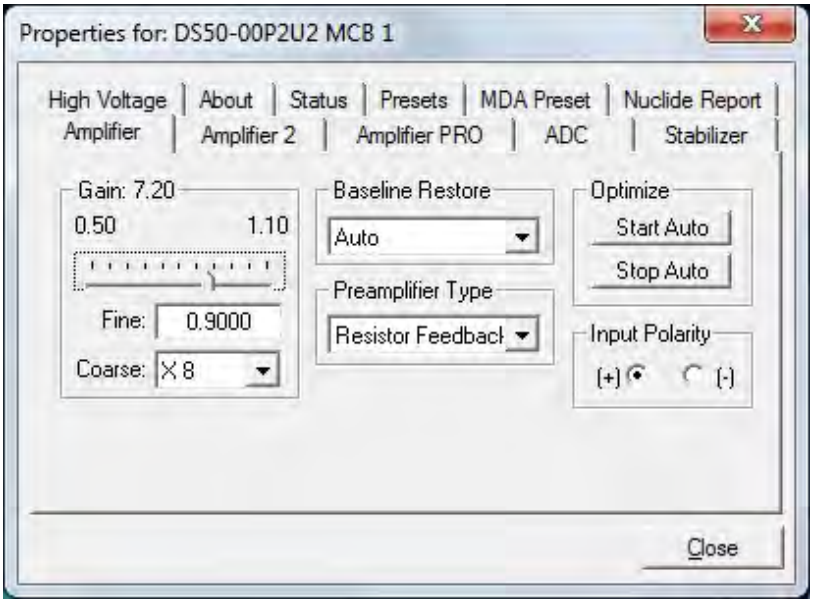


Figure 39. The DSPEC-50 Amplifier Tab.

Automatic Optimization

Select **Acquire**, then **Start**, to start the Detector counting. Next, position a source such as ^{60}Co such that the detector's input count rate (1) satisfies the count rate guidance instructions on the bottom-left corner of the Amplifier tab or (2) is ~5000 CPS. During data collection, the **Dead** time will be displayed at the top of the Status Sidebar to the right of the spectrum window (Fig. 40).

Return to **Acquire/MCB Properties...** and click the Amplifier tab. Go to the **Optimize** section of the dialog and click **Start Auto**. This will tell the Detector to automatically adjust the amplifier's shaping constants. While optimization is in progress, you will hear a periodic beep and see the message "**Optimize in progress....**" This process typically takes about 5 minutes. Remember that if you change the shaping time, you must pole zero the Detector again.

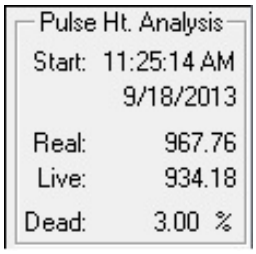


Figure 40. Dead Time.

Click **Close** to apply the new MCB hardware settings.

Adjusting Amplifier Gain

Adjust the amplifier gain to achieve the desired energy range across the Detector display. A source with only one or two lines (e.g., ^{137}Cs or ^{60}Co) should be used for the initial setup to easily identify the applicable peaks. Figure 41 shows the 1332.5 kev peak centered on channel 7348 for an energy range of approximately 2.9 MeV at channel 16000.

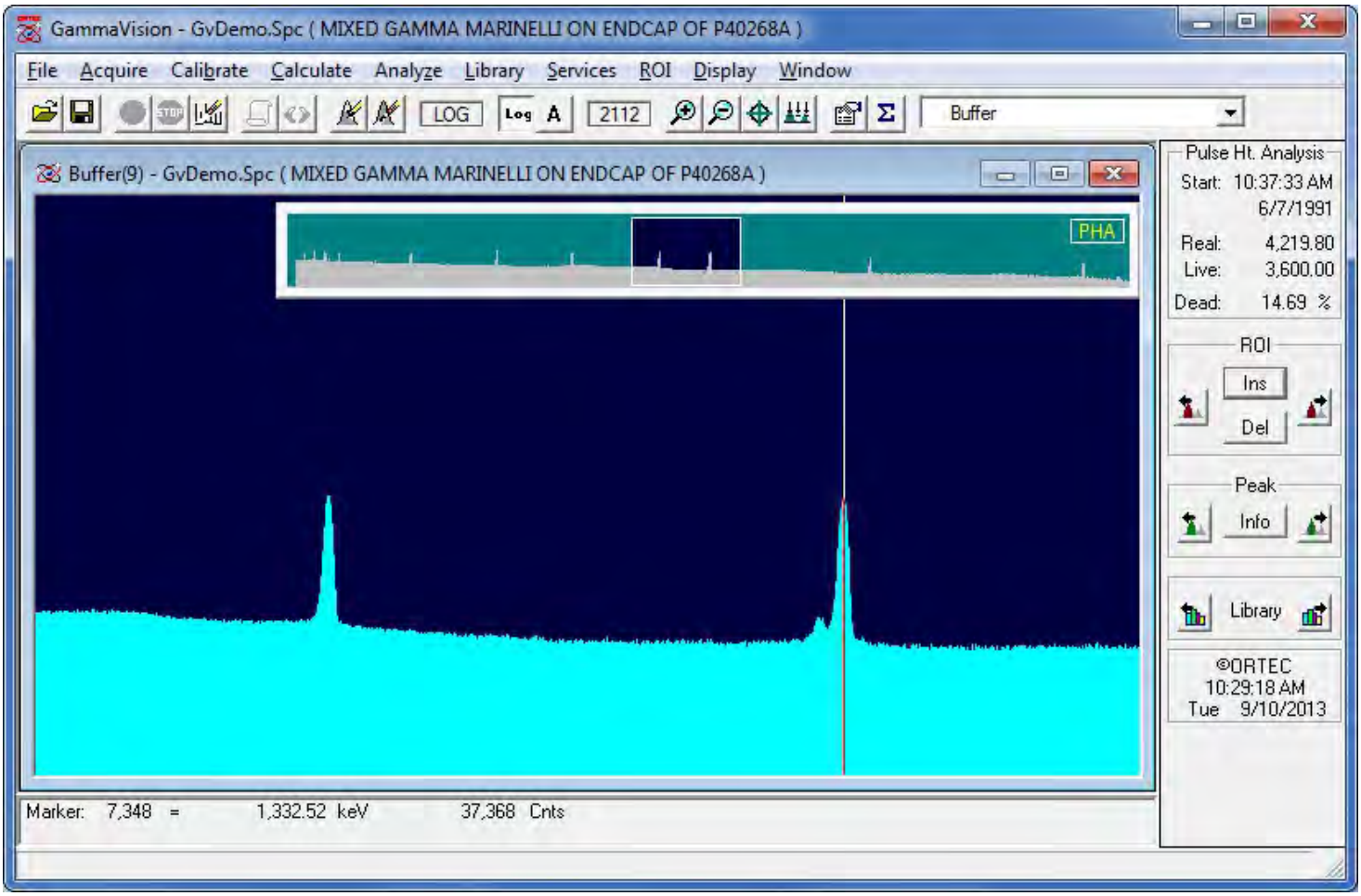


Figure 41. Spectrum with ^{60}Co.

To set the gain for the DSPEC-50 (and all other software-controlled ORTEC MCBs):

1) Start data collection by clicking on the **Start** toolbar button or by selecting **Acquire/Start** from the menu bar.

2) Select **Acquire/MCB Properties...** and click the Amplifier tab (Fig. 39).

3) Select the **Coarse Gain** setting from the droplist (if present), then move the slider to the fine gain desired. The spectrum display updates continuously, even while the Properties dialog is open.

4) Once the gain is *approximately* correct, click **Close** to close the control dialog, then use **<Alt + +>** and **<Alt + ->** to make fine gain adjustments until the peak is in the desired channel. To make coarser gain adjustments, use **<Alt + Shift + +>** and **<Alt + Shift + ->**. (These keyboard commands are discussed in Chapter 9.)

GammaVision will retain all of these settings and adjustments on exit, and will reload them from the MCB on restart.

**** You are now ready to acquire spectral data, calibrate, and analyze your own sample data. ****

[Intentionally blank]

4. DISPLAY FEATURES

This chapter describes how to start GammaVision, explains its display features, discusses the role of the mouse and keyboard, covers the use of the toolbar and sidebars, and shows how to use additional features such as Help.

4.1. Startup

To start GammaVision, open the Windows Start menu and click **GammaVision** folder, then the **GammaVision** icon (Fig. 42). You can also start GammaVision using the **Run** option from the Start menu or by creating Windows shortcuts to GammaVision in order to use the command line option, with or without arguments, as described in Section A.1.

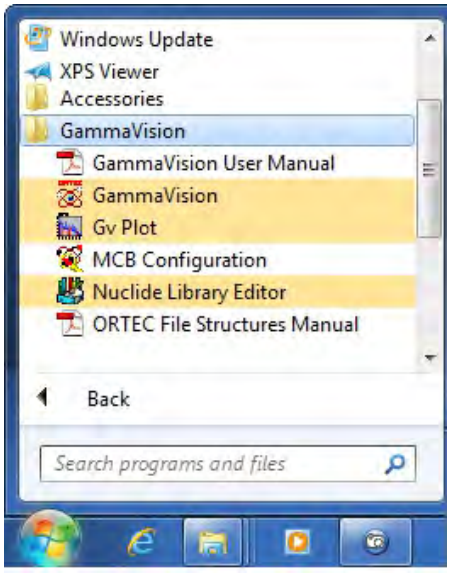


Figure 42. GammaVision Menu.

Figure 43 shows GammaVision's principal screen features.

1) **Title bar**, showing the program name and the source of the currently active spectrum window. There is also a title bar on each of the spectrum windows showing the source of the data: either the Detector name or the word "Buffer" with the spectrum name. On the far right are the standard Windows Minimize, Maximize, and Close buttons.

2) **Menu Bar**, showing the available menu commands (which can be selected with either the mouse or keyboard); these functions are discussed in detail in Chapter 5.

3) **Toolbar**, beneath the menu bar, containing icons for recalling spectra, saving them to disk, starting and stopping data acquisition, adjusting the vertical and horizontal scale of the active spectrum window, and accessing the analysis parameters.

4) **Detector List**, on the toolbar, displaying the currently selected Detector (or the buffer). Clicking on this field opens a list of all Detectors currently on the computer's GammaVision Detector pick list, from which you can open Detector and/or buffer windows. When you select the buffer or a Detector from the list, a new spectrum window opens, to a limit of eight Detectors and eight buffers. (If a Detector is already displayed, selecting it from the list does not open a duplicate window for that instrument.) If you select a Detector, the spectrum in its memory (if any) is displayed. The droplist shows the name of the most recently selected Detector or buffer.

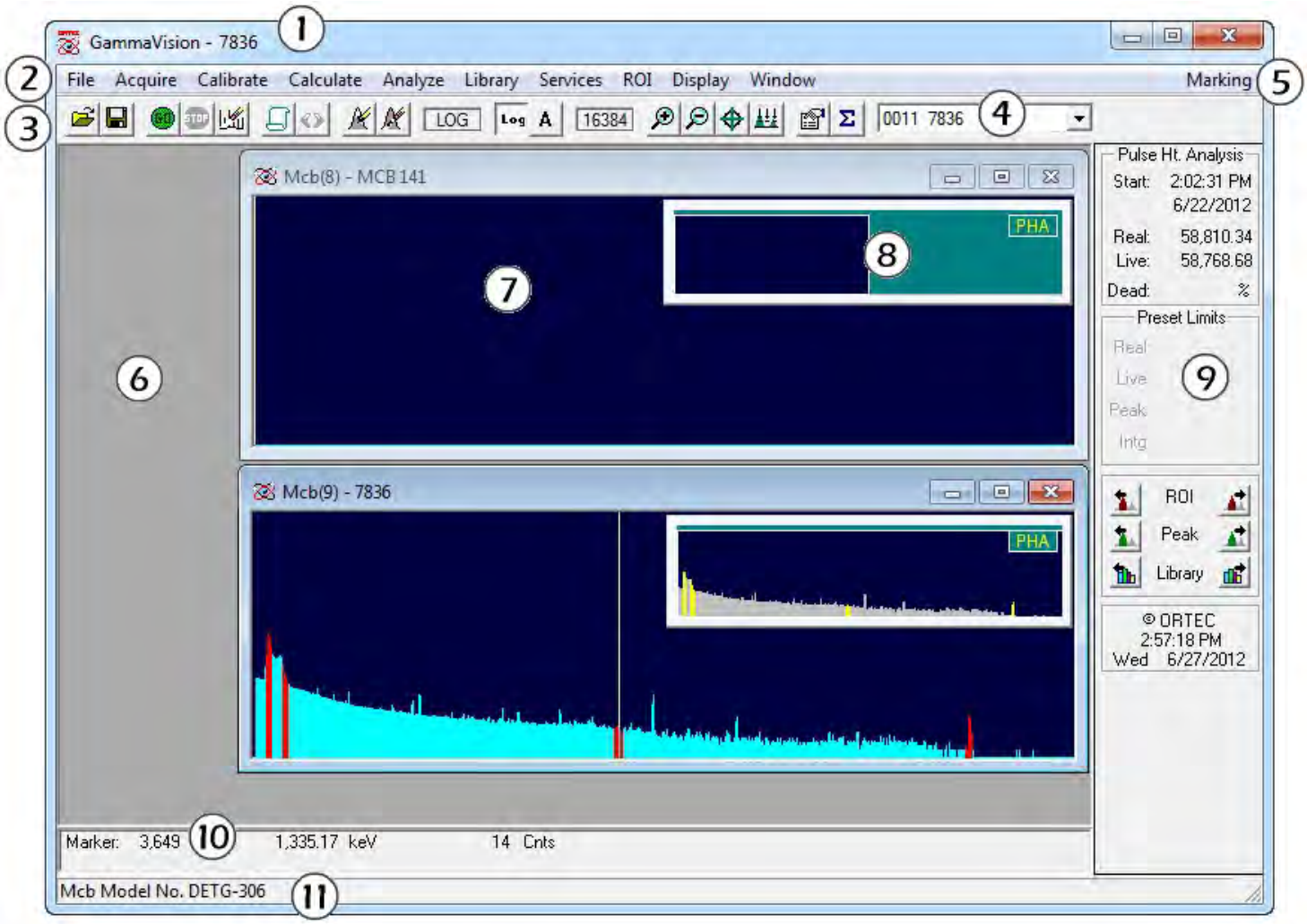


Figure 43. Main GammaVision Screen Features.

5) ROI Status Area, on the right side of the menu bar, indicates whether the ROI marking mode is currently **Mark** or **UnMark**. This operates in conjunction with the **ROI** menu commands and arrow keys (see Section 5.8).

6) Spectrum Area, which displays multiple *spectrum windows* — up to eight Detector windows and eight buffer windows simultaneously. When you attempt to open a ninth spectrum or buffer window, GammaVision will ask if you wish to close the oldest window of that type. Alternatively, you can turn off the **Multiple Windows** feature and run in the original one-window-at-a-time mode.

Spectrum windows can be moved, sized, minimized, maximized, and closed with the mouse, as well as tiled horizontally or vertically from the **Window** menu. When more than one window is open, only one is active — available for data manipulation and analysis — at a time. The title bar on the active window will normally be a brighter color than those on the inactive windows (the color scheme will depend on the desktop colors you have selected in

Windows Control Panel). Detector windows or buffer windows containing a spectrum from an MCB will display the Detector name on the title bar. If you have opened a spectrum file into a buffer window, the title bar will display the filename. To switch windows, click the window you wish to activate, use the **Window** menu (see Section 5.10), or cycle between windows by pressing **<Ctrl + Tab>**.

Each spectrum window contains an **Expanded Spectrum View** and a **Full Spectrum View** (see items 7 and 8 below).

7) The **Expanded Spectrum View** shows all or part of the full histogram; this allows you to zoom in on a particular part of the spectrum and see it in more detail. You can change the expanded view vertical and horizontal scaling, and perform a number of analytical operations such as peak information, marking ROIs, or calibrating the spectrum. This window contains a vertical line called a *marker* that highlights a particular position in the spectrum. Information about that position is displayed on the Marker Information Line (see item 10 below).

8) The **Full Spectrum View** shows the full histogram from the file or the Detector memory. Note the indicator in the upper-right corner, which indicates the unit's current data collection mode, e.g., pulse-height analysis mode (PHA), list mode (LIST), or one of the three zero-dead-time modes (ZDT, LTC, or ERR; see Fig. 76, page 76). The vertical scale is always logarithmic, and the window can be moved and resized (see Section 4.4.4). The Full Spectrum View contains a rectangular window that highlights the portion of spectrum now displayed in the Expanded Spectrum View (see Fig. 44). To quickly move to a different part of the spectrum, just click on that area in the Full Spectrum View and the expanded display updates immediately at the new position.

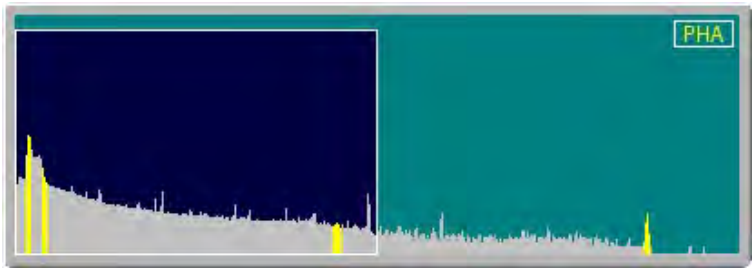


Figure 44. Full Spectrum View with Expanded Spectrum View Area Highlighted.

9) **Status Sidebar**, on the right side of the screen, provides information on the current Detector presets and counting times, the time and date, and a set of buttons for moving easily between peaks, ROIs, and library entries (see Section 4.5).

10) **Marker Information Line**, beneath the spectrum, showing the marker channel, marker energy, channel contents and in some modes, other details about the marker channel, such as the efficiency at this energy.

11) Supplementary Information Line, below the Marker Information Line, used to show library contents, the results of certain calculations, warning messages, or instructions.

4.2. Spectrum Displays

The Full and Expanded Spectrum Views respectively show a complete histogram of the current spectrum (whether from a Detector or the buffer) and an expanded view of all or part of the spectrum. These two windows are the central features of the GammaVision screen. All other windows and most functions relate to the spectrum windows. The **Display**/**Preferences** menu lets you adjust the color and fill type of the various spectrum features (e.g., background, spectrum, ROIs).

- **Full Spectrum View** — This view is embedded in the Expanded Spectrum View, and shows all channels of Detector data memory as configured with the **MCB Properties...** command on the **Acquire** menu. It includes a rectangular area showing the portion of spectrum currently displayed in the Expanded View, and a data acquisition mode indicator (refer to item 8 on the preceding page). The vertical scale in the Full Spectrum View is always logarithmic.

- **Expanded Spectrum View** — The Expanded Spectrum View contains a reverse-color marker line at the horizontal position of the pixel representing the marker channel. This marker can be moved with the mouse pointer, as described in Section 4.4.1, and with the **<←>/<→>** and **<PgUp>/<PgDn>** keys. Information about the marked channel is displayed on the Marker Information Line.

  — Use the menu commands, accelerator keys, and toolbar buttons to choose between logarithmic and linear scales, zoom in and out, and select which region of the spectrum to view.

  — You can also zoom in to any horizontal and vertical scale with the click-and-drag *rubber rectangle* tool (see Section 4.4.3). The baseline or "zero level" at the bottom of the display can also be offset with this tool, allowing the greatest possible flexibility in showing the spectrum in any detail.

  — Note that the marker can be moved by no less than one pixel or one channel (whichever is greater) at a time. The **<→>** and **<←>** keys make it easy to perform these small changes. If true single-channel motions are required, you must zoom in on the desired portion of the spectrum until a single press of the **<→>** and **<←>** keys changes the readout on the Marker Information Line by one channel or one energy unit (e.g., keV).

4.3. The Toolbar

The row of buttons below the menu bar provides convenient shortcuts to some of the most common GammaVision commands.

The **Recall** button retrieves an existing spectrum file. This is the equivalent of selecting **File/Recall** from the menu.

Save copies the currently displayed spectrum to disk. It duplicates the commands **File/ Save** or **File/Save As...** (depending on whether the spectrum was recalled from disk, and whether any changes have been made to the spectrum window since the last save).

Start Acquisition starts data collection in the current Detector. This duplicates **Acquire/Start** and **<Alt + 1>**.

Stop Acquisition stops data collection. This duplicates **Acquire/Stop** and **<Alt + 2>**.

Clear Spectrum clears the detector or file spectrum from the window. This duplicates **Acquire/Clear** and **<Alt + 3>**.

List Mode toggles the current Detector between PHA and LIST modes. This duplicates **Acquire/List Mode**. An indicator in the upper right of the Full Spectrum View shows the current data acquisition mode.

List Data Range lets you retrieve a specified time slice of data from a .LIS file in a buffer window (Section 5.4.2). This duplicates **Calculate/List Data Range...**.

Mark ROI automatically marks an ROI in the spectrum at the marker position, according to the criteria in Section 5.8.4. This duplicates **ROI/Mark Peak** and **<Insert>**.

Clear ROI removes the ROI mark from the channels of the peak currently selected with the marker. This duplicates **ROI/Clear** and **<Delete>**.

The next section of the toolbar (Fig. 45) contains the buttons that control the spectrum's vertical scale. These commands are also on the **Display** menu. In addition, vertical scale can be adjusted by zooming in with the mouse (see Section 4.4.3).

Figure 45. Vertical Scaling Section of Toolbar.

Vertical Log/Lin Scale switches between logarithmic and linear scaling. When switching from logarithmic to linear, it uses the previous linear scale setting. Its keyboard duplicate is **Keypad</>**.

Vertical Auto Scale turns on the *autoscale* mode, a linear scale that automatically adjusts until the largest peak shown is at its maximum height without overflowing the display. Its keyboard duplicate is **Keypad<*>**.

The field to the left of these two buttons displays **LOG** if the scale is logarithmic, or indicates the current vertical full-scale linear value.

The horizontal scaling section (Fig. 46) follows next. It includes a field that shows the current window width in channels, and the **Zoom In**, **Zoom Out**, **Center,** and **Baseline Zoom** buttons. These commands are also on the **Display** menu. In addition, horizontal scale can be adjusted by zooming in with the mouse (see Section 4.4.3).

Figure 46. Horizontal Scaling Section of Toolbar.

Zoom In decreases the horizontal full scale of the Expanded Spectrum View according to the discussion in Section 4.2, so the peaks appear "magnified." This duplicates **Display/Zoom In** and **Keypad<+>**.

Zoom Out increases the horizontal full scale of the Expanded Spectrum View according to the discussion in Section 4.2, so the peaks appear reduced in size. This duplicates **Display/Zoom Out** and **Keypad<–>**.

Center moves the marker to the center of the screen by shifting the spectrum without moving the marker from its current channel. This duplicates **Display/Center** and **Keypad<5>**.

Baseline Zoom keeps the baseline of the spectrum set to zero counts.

The remaining buttons allow you to access the principal sample analysis functions.

Sample Type Settings opens the dialog that controls the current analysis settings (see Section 5.5.1.1). This duplicates the **Sample Type...** command on the **Analyze/Settings** submenu.

Analyze Spectrum(γ) duplicates the **Entire Spectrum in Memory...**(γ) command on the **Analyze** menu (see Section 5.5.4).

The right-most part of the toolbar is a drop-down list of the available Detectors (Fig. 47). To select a Detector or the buffer, click in the field or on the down-arrow beside it to open the list, then click the desired entry. The sidebar will register your selection. Finally, note that as you pause the mouse pointer over the center of a toolbar button, a pop-up *tool tip* box opens, describing the button's function (Fig. 48).

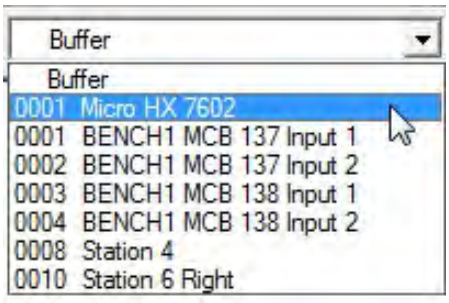


Figure 47. Drop-Down Detector List.

Figure 48. Roll-Over Toolbar Tool Tips.

4.4. Using the Mouse

The mouse can be used to access the menus, toolbar, and sidebars; adjust spectrum scaling; mark and unmark peaks and ROIs; select Detectors; work in the dialogs — every function in Gamma-Vision except text entry. The following sections describe specialized mouse functions.

4.4.1. Moving the Marker with the Mouse

To position the marker with the mouse, move the pointer to the desired channel in the Expanded Spectrum View and click the left mouse button once. This will move the marker to the mouse position. Click in the Full Spectrum View to move the expanded view to that place. This is generally a much easier way to move the marker around in the spectrum than using the arrow keys and accelerators, although you might still prefer some keyboard functions for specific motions.

4.4.2. The Right-Mouse-Button Menu

Figure 49 shows the right-mouse-button (context) menu. To open it, position the mouse pointer in the spectrum display, click the right mouse button, then use the left mouse button to select from its list of commands. Not all of the commands are available

Figure 49.

at all times, depending on the spectrum displayed and whether the rubber rectangle is active. Except for **Undo Zoom In**, all of these functions are on the toolbar and/or the menus (**Peak Info, Input Count Rate,** and **Sum** are only on the Menu Bar, under **Calculate**). See Section 5.11 for more information on the commands.

4.4.3. Using the "Rubber Rectangle"

The *rubber rectangle* is used for selecting a particular area of interest within a spectrum. It can be used in conjunction with the toolbar and right-mouse-button menu commands for many functions. To draw a rubber rectangle:

- Click and hold the left mouse button; this anchors the starting corner of the rectangle.
- Drag the mouse diagonally across the area of interest. As you drag, the mouse will be drawing a reverse-color rectangle bisected by the marker line to form a "crosshair" (Fig. 51). This makes it easy to select the center channel in the area of interest — for instance, the center of an ROI you wish to mark or unmark, a portion of the spectrum to be summed, or a peak for which you want detailed information.
- Release the mouse button to anchor the ending corner of the rectangle.
- Once the area of interest is marked, select the applicable command from the toolbar, menus, right-mouse-button menu, Status Sidebar, or keyboard.

4.4.4. Resizing and Moving the Full Spectrum View

- **Resizing** — Roll the mouse pointer over the side edge, bottom edge, or corner of the window until the pointer changes to a double-sided arrow (see Fig. 50). Click and drag the edge of the window until it is the size you want, then release the mouse button.
- **Moving** — Roll the mouse pointer onto the top edge of the window until the pointer changes to a four-sided arrow (see Fig. 50). Click and drag the window to its new location, and release the mouse button.

4.5. Buttons and Boxes

This section describes GammaVision's radio buttons, indexing buttons, and checkboxes. To activate a button or box, just click it.

- **Radio buttons** (Fig. 53) appear on many GammaVision dialogs, and allow only one of the choices to be selected.

- **Checkboxes** (Fig. 52) are another common feature, allowing one or more of the options to be selected at the same time.

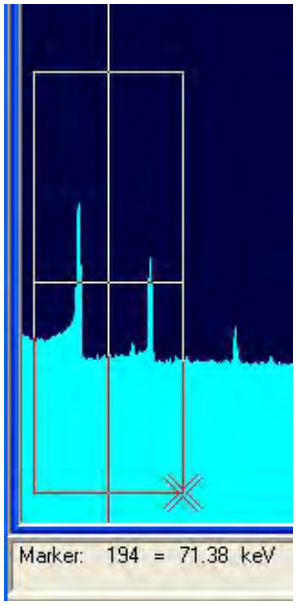


Figure 51. Rubber Rectangle Crosshair.

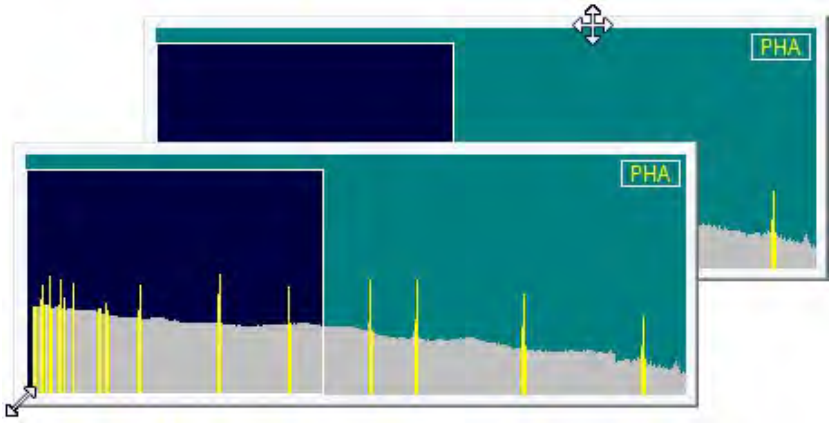


Figure 50. Two-Sided Pointer for Sizing Full Spectrum View, and Four-Sided Pointer for Moving Window.

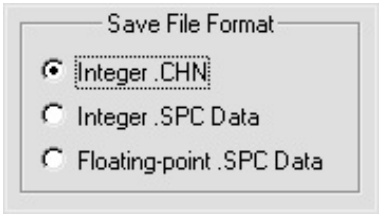


Figure 53. Radio Buttons.

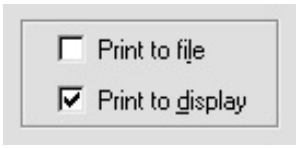


Figure 52. Checkboxes.

- The **ROI**, **Peak**, and **Library** indexing buttons on the Status Side-bar are useful for rapidly locating ROIs or peaks, and for advancing between entries in the library. When the last item in either direction is reached, the computer beeps and GammaVision posts a no more entries message on the Supplementary Information Line.

- The indexing buttons are displayed in two different ways, depending on whether Gamma-Vision is in Detector or buffer mode, as shown in Fig. 54. However, they function the same way in both modes. In buffer mode, the additional features are the ability to insert or delete an ROI with the **Ins** and **Del** buttons, respectively (located between the **ROI** indexing buttons); and to display the peak information for an ROI with the **Info** button (located between the **Peak** indexing arrows).

- The **Library** buttons are useful after a peak has been located to move forward or backward through the library to the next closest library entry. Each button press advances to the next library entry and moves the marker to the corresponding energy. If a library file has not been loaded or the Detector is not calibrated, these buttons are disabled.

HINT Instead of using the **Peak** buttons to move from a previously identified peak, click the marker anywhere in the spectrum then click the **Library** buttons to locate the entries closest in energy to that point. If a warning beep sounds, it means that all library entries have been exhausted in that direction or that the spectrum is not calibrated. In any case, if an appropriate peak is available at the location of the marker, peak data are displayed on the Marker Information Line at the bottom of the screen.

Figure 54. Detector mode, top; buffer mode, bottom).

The **ROI** and **Peak** indexing buttons are duplicated by **<Shift+ ←>/ <Shift+ →>** and **<Ctrl+ ←>/ <Ctrl+ →>**, respectively. The **Library** buttons are duplicated by **<Alt+ ←>/<Alt+ →>**. The **Del** button function is duplicated by the **<Delete>** key and **Clear ROI** on the menus and toolbar. The **Ins** button has the same function as the **<Insert>** key and **Mark ROI** on the menus and toolbar. The **Info** button duplicates the **Calculate/Peak Info** command, **Peak Info** on the right-mouse-button menu, and double-clicking in the ROI.

The Spectrum navigation section of the sidebar is displayed when N42 files are loaded into a Buffer window. Individual spectra from an N42 file containing multiple spectra can be accessed using the navigation buttons or by entering the spectrum index in the current spectrum field. The drop down list allows the list of spectra in a multi-spectrum N42 file to be filtered by the spectrum type available in N42 files including Any (all spectra), Background, Time Slice, Long Count, Known Sample, and Blank Sample.

4.6. Opening Files with Drag-and-Drop

GammaVision lets you open ORTEC spectrum (.SPC, .AN1, .CHN), library (.LIB), and region of interest (.ROI) files by dragging and dropping them from Windows Explorer into the GammaVision window. A spectrum file opens in a buffer window, a library file is loaded as the working library, and the ROIs saved in an .ROI file are set in the currently active spectrum window.

4.7. Associated Files

Installing GammaVision registers the spectrum files in Windows so they can be opened from Windows Explorer by double-clicking the filename. The spectrum files are displayed in GVPlot. These files are marked with a spectrum icon ( ) in the Explorer display. .JOB files ( ) are also registered, and open in Windows Notepad.

5. MENU COMMANDS

This chapter describes all the GammaVision menu commands and their associated dialogs. The accelerator(s) (if any) are shown to the right of the command. The underlined letter for each command indicates the (English version) quick-access key that can be used with the **<Alt>** key (e.g., the **Recall...** command on the **File** menu can be selected with **<Alt + F>**, **<Alt + R>**.) The ellipsis (**...**) following a command indicates that a dialog is displayed to complete the function. Finally, a small arrow ("▸") following a menu selection means a submenu with more selections will be shown. The menus and commands, in the order they appear on the menu bar, are:

File (page 56)

- Settings...
- Recall...
- Save
- Save As...
- Export
- Import
- Print
- Compare...
- Save Plot...
- Exit
- About GammaVision... (or About Maestro-PRO...)

Acquire (page 70)

- Acquisition Settings...
- Start <Alt + 1>
- Start/Save/Report(ã)
- Stop <Alt + 2>
- Clear <Alt + 3>
- Copy to Buffer <Alt + 5>
- List Mode
- QA(ã)
  - Settings...
  - Measure Background
  - Measure Sample
  - Status...
  - Control Chart...
- Download Spectra
- ZDT Display Select <F3>
- MCB Properties...

Calibrate (page 103)

- Energy...

- Efficiency...
- Description...
- Recall Calibration...
- Save Calibration...
- Print Calibration...
- Calibration Wizard

Calculate (page 143)

- Settings...
- List Data Range...
- Peak Info
- Input Count Rate
- Sum
- Smooth
- Strip...

Analyze (page 149)

- Settings ▸
  - Sample Type...
  - Report Generator...
  - Attenuation Coefficients ▸
    - Coefficient Table
    - Calculate from Spectra
  - Geometry Correction
  - Peak Background Correction ▸
    - Create PBC
    - Select PBC...
    - Edit PBC...
    - Print PBC...
  - Average Energy
  - Iodine Equivalency
  - DAC (MPC)
  - Gamma Total...
- Peak Search
- ROI Report...
- Entire Spectrum in Memory...(ã)
- Spectrum on Disk...(ã)
- Display Analysis Results...
- Interactive in Memory...

Library (page 206)

- Select Peak...

Select File...
Edit ▸
GammaVision Editor...
Nuclide Navigator...
List...

Services (page 215)
Job Control...
Sample Description...
Menu Passwords...
Lock/Unlock Detector...
Edit Detector List...

ROI (page 221)

Off	<F2> or <Alt + O>
Mark	<F2> or <Alt + M>
UnMark	<F2> or <Alt + U>
Mark Peak	<Insert>
Clear	<Delete>
Clear All	
Auto Clear	
Save File...	
Recall File...	

Display (page 223)

Detector...	Ctrl + <Fn>
Detector/Buffer	F4 or Alt + 6
Select Spectrum...	
Logarithmic	Keypad(/)
Automatic	Keypad(*)
Baseline Zoom	
Zoom In	Keypad(+)
Zoom Out	Keypad(-)
Center	Keypad(5)
Full View	Alt + F7
Isotope Markers	
Preferences ▸	

Points
Fill ROI
Fill All
Fill Singlets
Fill Multiplet Peaks

Fill Multiplet Composites
Spectrum Colors...
Peak Info/Font Color...

Window (page 228)

Cascade
Tile Horizontally
Tile Vertically
Arrange Icons
Auto Arrange
Multiple Windows
[List of open Detector and buffer windows]

Right-Mouse-Button Menu (Spectrum/Buffer Windows) (page 229)

Start
Stop
Clear
Copy to Buffer
Zoom In
Zoom Out
Undo Zoom In
Mark ROI
Clear ROI
Peak Info
Input Count Rate
Sum
MCB Properties

5.1. File

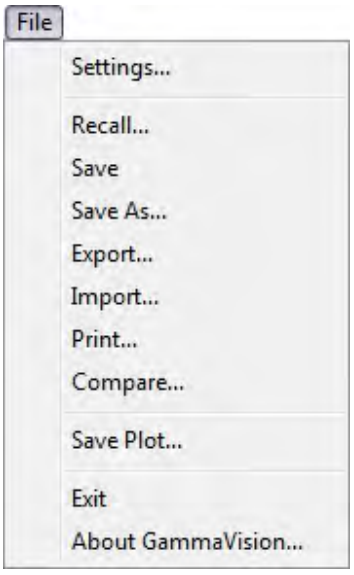


Figure 55. File Menu.

5.1.1. Settings...

The File Settings dialog allows you to specify how the spectrum data are saved, exported, and imported; and set the directories for all the major file types used by GammaVision.

5.1.1.1. General

The entries on this tab (see Fig. 56) control the default spectrum file format and the default sample descriptors to be saved with the spectrum. If you also activate the ask-on-save feature for one or more of these sample descriptors, they will be presented to the

operator before each spectrum is saved.

When you finish setting the parameters in this dialog and click **OK**, these settings will be used until changed. For other adjustable parameters, see **Acquire/Acquisition Settings...** (Section 5.2.1) and **Analyze/Settings/Sample Type...** (Section 5.5.1.1).

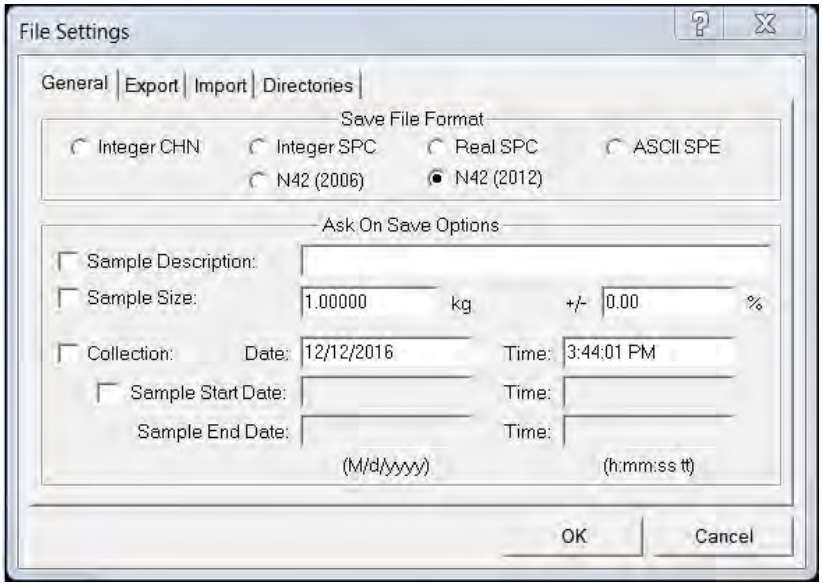


Figure 56. File Settings Dialog, General Tab.

Save File Format

The file types are integer .CHN, integer.SPC, real (floating-point) .SPC, ASCII .SPE, and .N42 (2006 and 2012 format). The .CHN and .SPC files are binary structures described in the *ORTEC Software File Structure Manual for DOS and Windows® Systems* (P/N 753800, hereinafter called the *File Structure Manual*), available on the GammaVision start menu.

The .CHN file format contains basic acquisition information including the live time, real time, acquisition start time, MCB and sample descriptions, and energy calibration (if any); but does not contain the analysis parameter data, the complete calibration, or other data needed for nuclide analysis.

The two .SPC formats contain all of the parameters from the .CHN files as well as the complete calibration records, analysis parameters, hardware parameters, and other data needed for spectrum analysis. The two formats are identical except for the format of the spectrum data. The integer format is the current standard and stores the spectrum as 4-byte integers. The floating-point format is for backward compatibility with legacy software and uses the 4-byte exponential format.

The ASCII .SPE format is used by the Comprehensive Test Ban Treaty Organization (CTBTO).

The .N42 format is XML with tags and descriptions taken from the respective ANSI N42.42 standards.

NOTE Before using the **Acquire/Download Spectra** command, or the **Move** feature on a supported instrument's Field Data tab, be sure to select the **Save File Format** you wish to use for the downloaded spectra.

Ask On Save Options

Use these fields to enter the default sample descriptors to be saved with the spectrum. If you also mark the corresponding **Ask on Save** checkbox, the default value entered here will be presented for acceptance or modification when the spectrum is saved.

Sample Description allows you to designate the default sample description to be saved with the spectrum (128-character maximum for .SPC files; 63 characters for .CHN files). Marking the **Ask on Save** checkbox lets you enter the common descriptors for a group of samples ahead of time, then add the unique descriptors sample-by-sample after each acquisition.

If the output activity is to be normalized to a volume or weight (or any other factor), the default **Sample Size** can be entered here along with the reporting units and an optional 1-sigma uncertainty (+/-) between 0% and 1000%. This will normalize the activity, and the report will be in normalized units. This normalization is in addition to the normalization done by the **Multiplier** and **Divisor** fields on the System tab of the Sample Type Settings dialog (**Analyze/Settings/Sample Type...**).

The **Collection Date** and **Time** are the time used in the decay correction. If the decay correction is enabled (see the Sample tab of the Sample Type Settings dialog), this is the date used in the correction formula.[10]

Sample Start/End Time

These dates/times are the start time of the sample collection and the stop time of the sample collection. For example, for air filters, the start time is the time when the air flow is started, and the stop time is when the air flow is stopped. These times are used to calculate the buildup of the activity in the sample. It is assumed that the spectrum is not collected during the buildup time. The correction for the buildup is given in Section 5.8.4.

5.1.1.2. Export

The Export tab (Fig. 57) lets you specify the program, arguments, and file directory to be used when the **Export...** command is selected. If this computer has the DataMaster Spectrum File

[10]If the collection date and time is before that of the spectrum acquisition, the spectrum will be activity corrected back to the sample collection time. While this is the normal use of this input, if the collection date and time is after the acquisition time, the decay correction will be made forward in time.

Format Translator (A49-B32) installed, the **Use DataMaster** and **Export As** fields will be active and you can use the DataMaster export (and import) functions.

Choose any **Export Program**[11] that can accept the spectrum filename as an argument on the command line. Click on **Browse...** to automatically select the complete proper path for the program.

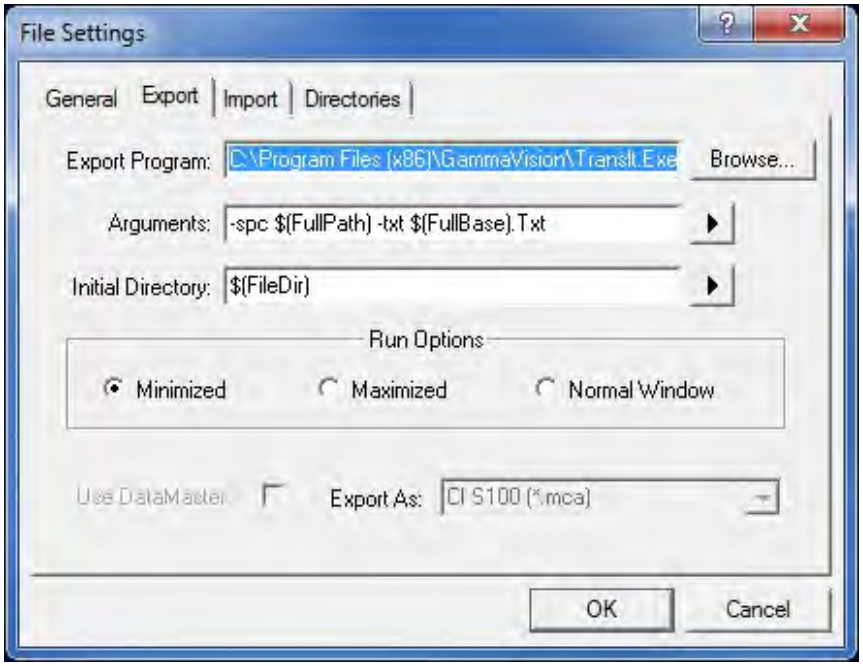


Figure 57. Export Tab.

Arguments

The **Arguments** to the program can be entered as character strings or you can select from the list of "macros" shown in Fig. 58. The list is displayed by clicking on the arrow button to the right of the **Arguments** field. Entries (macros or direct) must be separated by spaces to be read as separate arguments.

- **File Path Name** — This will insert the complete file pathname (e.g., c:\user \spectrum\ test.chn) into the dialog box. This filename is the one chosen in the **Export** command's file-recall dialog.

- **File Base Name** — This will insert the file path name *without* the extension (e.g., c:\user\ spectrum\test) into the dialog. The filename is the name selected in the **Export** command's dialog. The extension can be entered manually after the macro (e.g., $(FullBase).CHN) into the dialog. *Note that the "dot" (.) must also be entered*. Related filenames can also be made by adding characters before the "dot" (e.g., $(FullBase)A.CHN).

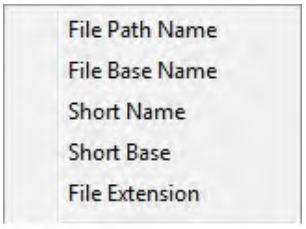


Figure 58. Export Argument Macros.

- **Short Name** — This will insert the filename (e.g., test.CHN) into the dialog box. The filename is the name selected in the **Export** command's dialog. File names can be constructed as $(file base).$(file extension).

[11]Any executable program that can be executed from the Windows **Run** command can be selected, including DOS batch commands.

- **Short Base** — This will insert the base filename (e.g., test) into the dialog box. The file base name is the name selected in the **Export** command's dialog.

- **File Extension** — This will insert the file extension (e.g., CHN) into the dialog box. The file extension is the file type for the file chosen in the **Export** command's dialog. *Note that the "dot" is not included*. Any manually inserted input of the macro form ($(xxx)) will be included in the argument list without changes.

Initial Directory

The initial directory for the program to use can be specified as directly entered character strings or the user can select from the list of macros in Fig. 59. The list is displayed by clicking on the arrow button to the right of the **Initial Directory** field.

Figure 59. The Initial Character Macros.

- **File Directory** — This is the directory in which the file selected with the **File/Export** command is located (e.g., c:\user\spectrum\).

- **Program Directory** — This is the directory for the conversion program. It is shown in the first entry of this dialog.

- **GammaVision Directory** — This is the directory where the GammaVision program is stored. By default, this is C:\Program Files\GammaVision[12] (C:\Program Files\Maestro-PRO for Maestro-PRO).

- **Current Directory** — This is the current default directory for Windows.

Run Options

These three radio buttons (**Minimized**, **Maximized**, and **Normal Window**) are used to select the window for the program. If the program does not have any user dialogs, any option can be selected. If the program needs user inputs, **Normal Window** should be selected.

Use DataMaster

To use DataMaster as the export program, mark the checkbox then select the file type to be exported

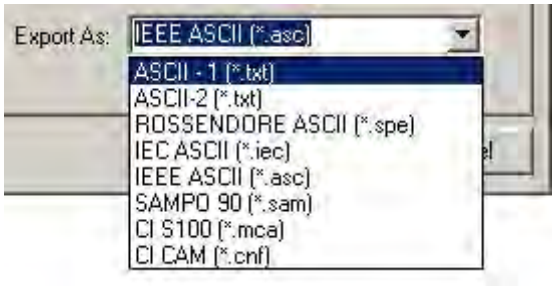


Figure 60. Choose the DataMaster Export File Type.

[12] C:\Program Files (x86) on 64-bit Windows computers.

from the Export As list. Figure 60 shows the list of supported file types. To use the **Export Program** specified in the upper half of the dialog, just unmark the **Use DataMaster** box.

5.1.1.3. Import

The Import tab (Fig. 61) lets you specify the program, arguments, file directory, and default file extension to be used when the **Import...** command is executed. If this computer has the DataMaster Spectrum File Format Translator installed, the **Use DataMaster** and **Default File Type** fields are active and you can use the DataMaster import (and export) functions.

Figure 61. Import Tab.

Choose any **Import Program** that can accept the spectrum filename on the command line. Click **Browse...** to select the complete proper path for the program.

Arguments:

The arguments to the program can be specified as directly entered character strings or you can select from the list of macros shown in Fig. 62. The list is displayed by clicking on the arrow button to the right of the **Arguments** field. The entries (macros or direct) must be separated by spaces to be read as separate arguments. The arguments on this menu are described in Section 5.1.1.2 under "Arguments" (page 59), except that here they refer to the file-name selected for importation with the **File/Import** command.

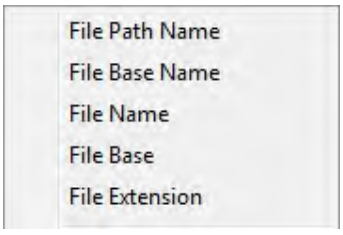


Figure 62. Import Arguments.

Initial Directory

Specify the initial directory for the program to use either with directly entered character strings or by selecting from the list of macros shown in Fig. 63. The list is displayed by clicking on the arrow button to the right of the **Initial Directory** field. The directories on this menu are described in Section 5.1.1.2 under "Initial Directory" (page 60), except that the reference to file-name applies to the file selected for importation with the **File/Import** command.

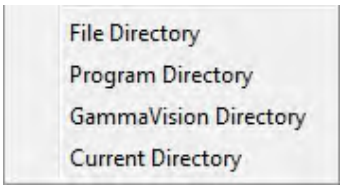


Figure 63. Import Macros.

Default

The default extension entered here is used as the extension for the filename in the filename entry dialog. For example, if TXT is entered, then the name list in the entry dialog will be *.TXT.

Run Options

These three radio buttons (**Minimized**, **Maximized**, and **Normal Window**) are used to select the window for the program. If the program does not have any user dialogs, any option can be selected. If the program needs user inputs, **Normal Window** should be selected.

Use DataMaster

To use DataMaster as the import program, mark the checkbox then select the file type to be imported from the **Default File Type** list. Figure 64 shows the list of supported file types. To use the **Import Program** specified in the upper half of the dialog, just unmark the **Use DataMaster** box.

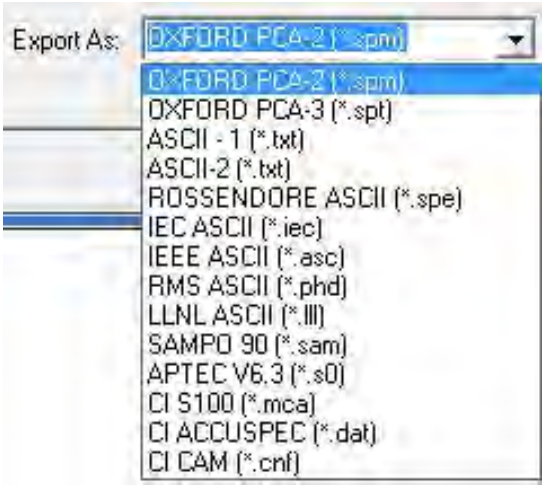


Figure 64. Choose the DataMaster Import File Type.

5.1.1.4. Directories

This tab (Fig. 65) gives you the option of designating where GammaVision's various file types should be stored. Otherwise, all spectra, .ROI files, libraries, .JOB files, reports, correction table files, sample type files, and calibrations will be stored in C:\User. When you generate any of GammaVision's many **File Type**s, the program reads the file extension and stores it according to the location(s) specified on this tab. For instance, if you specify a location for the **Spectra** file type, all .SPC, .CHN, .SPE and .N42 files will be saved there by default. Similarly, if you specify a

location for the **Table Files** file type, GammaVision will save your energy (.ENT) and efficiency (.EFT) calibration tables and table for DAC (.DAC), geometry (.GEO) and other corrections in that folder.

To change the path (**Location**) of a particular **File Type**, click the desired file type, then **Modify...**. This will open a standard file-recall dialog. Choose the desired location, creating a new folder if necessary, and click **Open**. When all path changes have been completed, click **OK** to put them into effect or else **Cancel** to retain the previous settings.

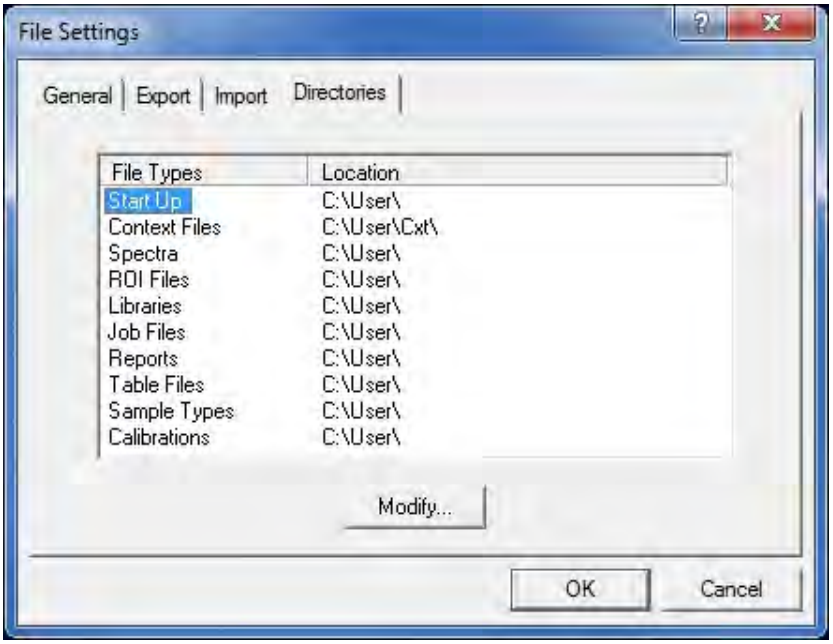


Figure 65. Directories Tab.

5.1.2. Recall...

This command reads a spectrum or List Mode file into a new buffer window. It opens a standard Windows file-open dialog (Fig. 66), allowing you to select the file to be recalled. The spectrum files are created by GammaVision's **Save** and **Save As...** functions and by any other programs that can produce the .CHN, .SPC, .SPE, .N42, or .LIS format (e.g., MAESTRO). The buffer is resized to the memory size of the recalled spectrum.

Note the **Show Description** checkbox on the lower left of the dialog. Mark this to display the sample description, format, and spectrum size of each file without having to open it.

If the maximum eight buffer windows are currently open, GammaVision will ask if you wish to close the oldest buffer. Answering **No** will cancel the recall operation and the oldest buffer will remain onscreen. Answering **Yes** will close the oldest buffer and open a new buffer containing

the recalled file. If the oldest buffer contains data that have not been saved, a warning dialog will first ask if the data should be saved. Click **Yes** to save and **No** to close without saving.

When the spectrum is successfully recalled, GammaVision loads its descriptors (start time, live time, real time, Detector and sample descriptions) and calibration information (if any), and displays the filename on the title bar. For spectrum files containing multiple spectra (such as ZDT mode in supported ORTEC instruments), both spectra are automatically recalled.

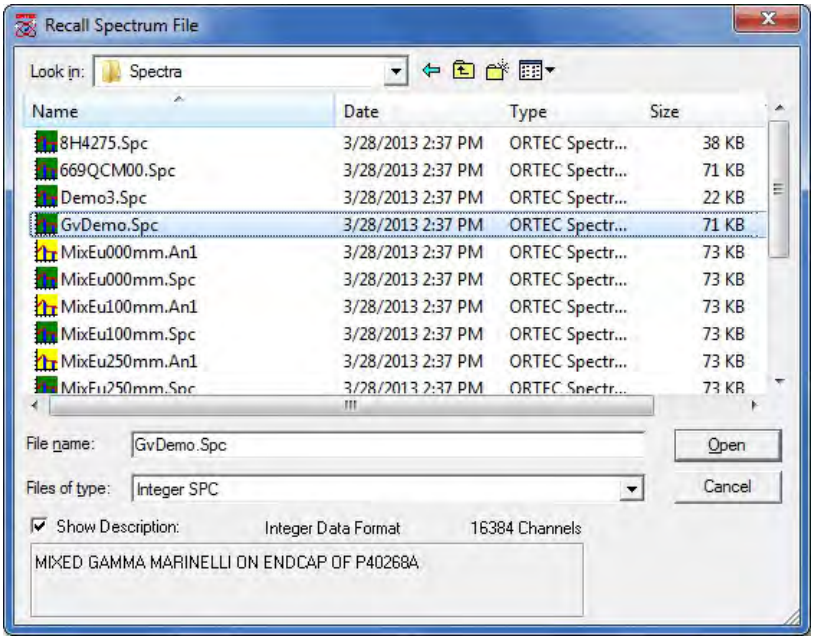


Figure 66. Recall a Spectrum File.

5.1.3. Save/Save As...

These functions open a standard Windows file-save dialog (Fig. 67) so you can save the current spectrum to disk. Use **Save As...** to rename an existing spectrum. If you attempt to overwrite an existing filename, a message box opens asking you to verify the entry or cancel the save. Clicking **OK** overwrites the existing file. After the disk file has been saved, its filename is displayed on the title bar.

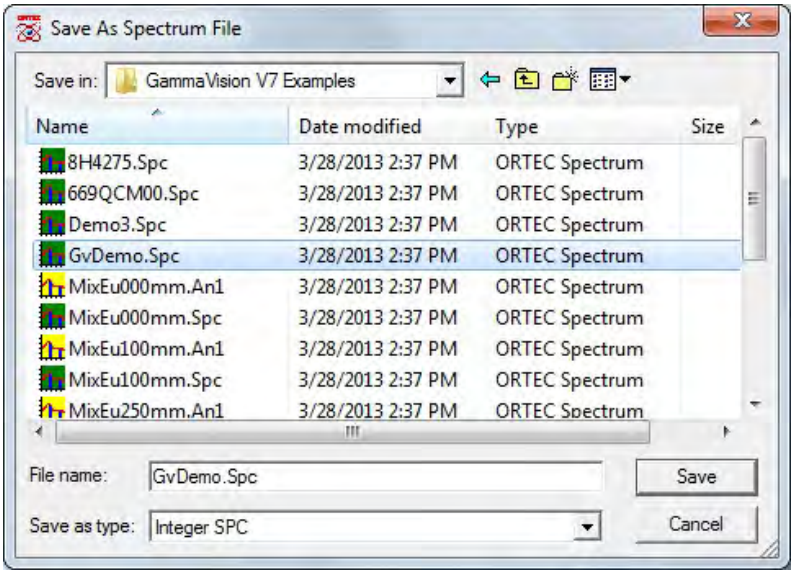


Figure 67. Save As.

PHA Mode Spectra — The default format is specified on the General tab under **File/Settings...** (Section 5.1.1.1); see that section for a brief description of the .CHN, .SPC, .SPE, and .N42file types. Note that you can select any of these file types at the time you save the file, and the save dialog will remember the most recent file type used. or hardware with multiple spectra (such as ZDT mode in the DSPEC Pro), both spectra will be saved in the file. PHA mode spectra cannot be saved in the .LIS (List Data) format.

List Mode Spectra — By default, the **Save** and **Save As...** commands offer to save List Mode spectra in .LIS format, however, you can also save this data in any of the other file formats. Note that the structure and contents of .LIS files is instrument-dependent (see the associated hardware manual for more information), but includes the Detector's current calibration and sample description.

5.1.4. Export...

The **Export...** function is used to write spectra in formats other than the usual formats, or to perform other functions such as plotting or printing the spectrum directly. The export program is specified on the Export tab under **File/Settings...**, as discussed in Section 5.1.1.2. The program can be one of the programs supplied or can be user-supplied. When selected, the **Export Spectrum File** dialog, shown in Fig. 68, is displayed. Choose the filename of the spectrum to be exported.

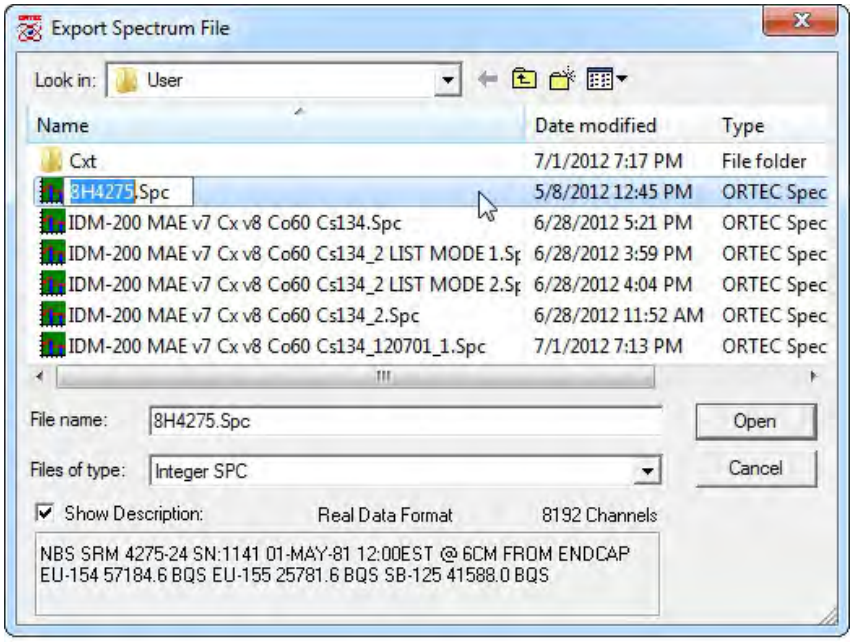


Figure 68. The Export Spectrum File Dialog.

The currently displayed spectrum must be saved to disk before it can be exported. If the currently displayed spectrum has already been stored to disk, that filename is the default. Any file can be selected. The file is then read and the output file is written by the program.

The **Export...** function is not available for a second file until the first file has been exported and the export program has stopped execution.

Export... can also be used to generate hardcopy plots. To do this, select the GVPlot program (supplied with GammaVision) as the export program. When **Export...** has been selected, the GVPlot program will be executed. If the -P switch is specified on the command line (see Sections 5.1.1.2 and 11.1.5), the program will plot the spectrum and exit automatically.

5.1.5. Import...

The **Import** function is used to read spectrum files that are not in one of the usual formats (e.g., .CHN or .SPC). The import program is specified on the Import tab under **File/Settings...**, as discussed in Section 5.1.1.3. The program can be one of the programs supplied or can be user-

supplied. This command opens a standard Windows file-open dialog so you can select the file-name. The file is then read and a spectrum file is written to the specified directory. GammaVision attempts to read this file (in .CHN or .SPC format) and displays the spectrum. If the Import program does not generate a file that GammaVision can read, no spectrum is displayed.

5.1.6. Print

The **Print** function does one of the following:

- If the marker is in an ROI, the data contents of the ROI channels are printed.
- If the marker is not in an ROI, the contents of channels in the expanded view are printed.

A standard file-print dialog opens, allowing you to print the output or save it in a disk file (mark the **Print to file** box). The data are formatted at seven channels per line with the channel number on the left.

5.1.7. Compare...

This function allows you to compare the currently displayed spectrum with an existing spectrum file. When the file-recall dialog opens, select the desired spectrum file. Both spectra will be displayed together as illustrated in Fig. 69, and the title bar will list both spectrum filenames.

The Compare spectrum is offset from the starting spectrum, and can be moved up and down incrementally with the **<Shift + ↑>** and **<Shift + ↓>** accelerators. In addition, the vertical scale of both spectra can be simultaneously changed with <↑> and <↓>. Note that the Compare spectrum's ROIs (if any were saved with the file) are not marked in this mode.

Figure 70 portrays a zoomed-in portion of two comparison files. In this illustration, the starting spectrum is displayed in color **(1)**, the Compare spectrum is shown in color **(2)**, the starting spectrum's ROIs are marked in color **(3)**, and the portion of the starting spectrum that exceeds the Compare spectrum is indicated by color **(4)**. These colors — called **Foreground**, **Compare**, **ROI**, and **Composite**, respectively — are chosen on the **Color Preferences** dialog discussed in Section 5.9.12.2.

Press **<Esc>** to leave Compare mode.

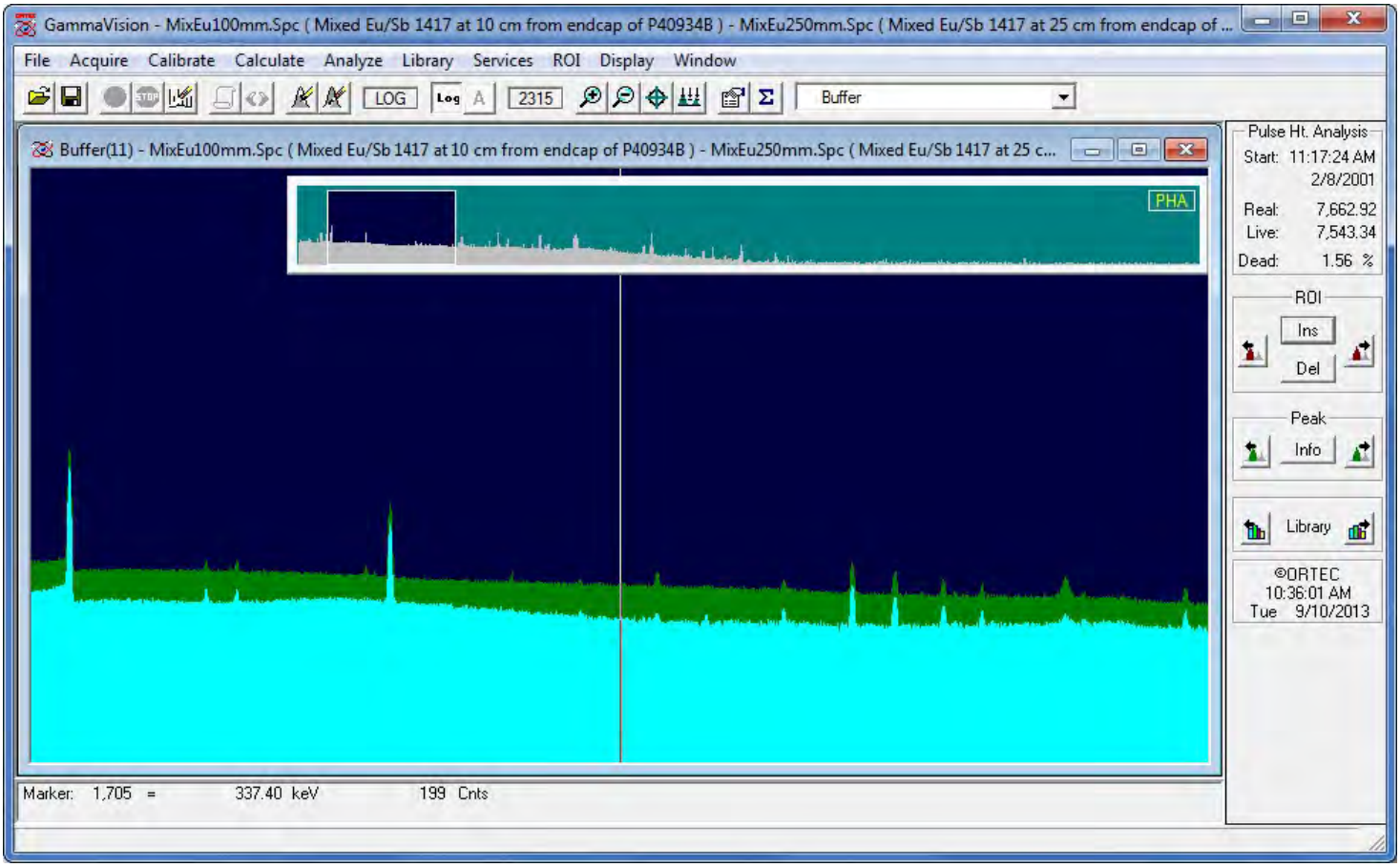


Figure 69. Compare Mode Screen.

5.1.7.1. Comparing ZDT Spectra with <Shift + F3>

The **Compare** feature also works for MCBs that support the Zero Dead Time (ZDT [3]) correction, which generates two spectra per acquisition; and for ZDT spectrum files, which store the two spectra.[13] You can also compare a ZDT Mode spectrum to a non-ZDT spectrum file, however, note that the ZDT MCB or file must be opened *first* to enable the **View ZDT Corrected** command (which allows you to toggle between the CORR and ERR spectra in the file; the shortcut key is **<F3>**). Then use the **Compare** command to open the non-ZDT file.

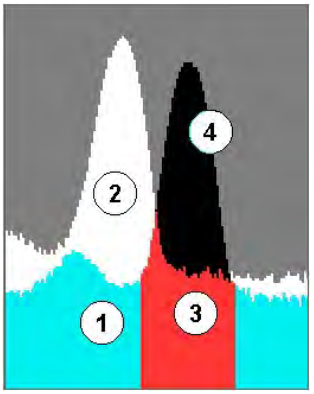


Figure 70. Spectrum Colors in Compare Mode.

[13]See Sections 5.2.11.4 and 5.2.10 for explanations of ZDT mode and the **View ZDT Corrected** command, respectively.

When you issue the **Compare** command and select another ZDT spectrum file, that file opens in the current mode of the starting spectrum, so you are viewing ERR/ERR or ZDT/ZDT. Use **View ZDT Corrected** to toggle both spectra in unison between ERR/ERR and ZDT/ZDT. To hold the starting spectrum in the current view mode and switch the Compare spectrum to the opposite view, use **<Shift + F3>**. **View ZDT Corrected** then allows you to switch between the ERR/ZDT and ZDT/ERR comparisons. (It is also possible to do this with a non-ZDT Compare spectrum, in which case **<Shift + F3>** toggles between the single live-time-corrected spectrum and an empty spectrum baseline.)

5.1.8. Save Plot...

This command is active for buffer and Detector windows when spectrum data is present. Using the current color, titling, and x-/y-axis scaling options set in GVPlot (Section 11.1), it saves either a native bitmap (.BMP) or JPEG (.JPG) image of the currently displayed spectrum (Fig. 71).

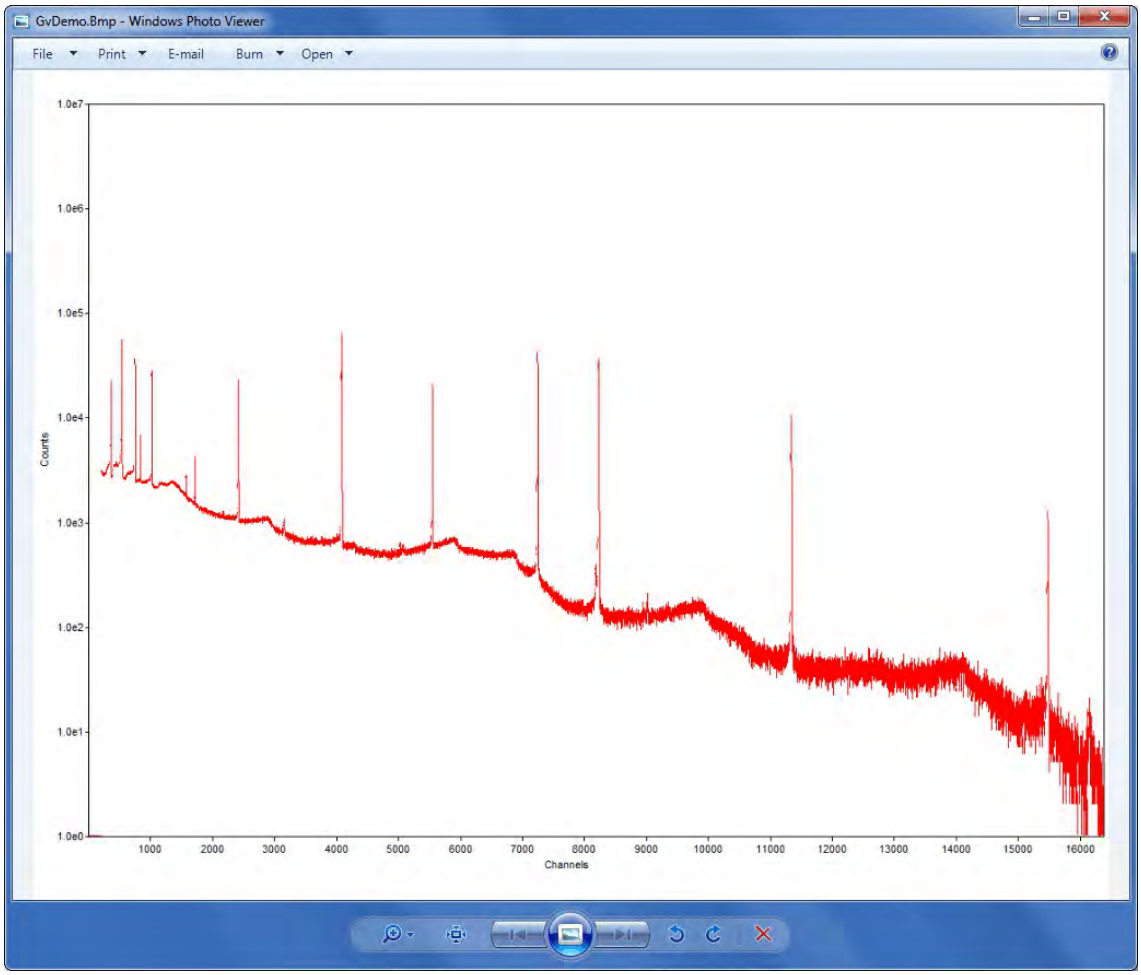


Figure 71. Spectrum Bitmap Image.

The entire spectrum is saved (to save or print a zoomed portion, use the GvPlot program). A standard file-save dialog opens allowing you to choose the image format and file name and location. The image is scaled to fit on 8.5 in. × 11 in. paper in landscape orientation. GvPlot creates the images with a resolution of 100 D.P.I. so the full image resolution is 1100 × 850 pixels.

5.1.9. Exit

This terminates the GammaVision program. If the buffer contains a spectrum that has not been saved, a warning message gives you a file-save option. Any JOBs are terminated. All active MCBs continue to acquire data until the presets are met.

5.1.10. About GammaVision... / About Maestro-PRO...

Figure 72 shows the **About** box for GammaVision (or Maestro-PRO). It provides software version information that will be useful should you need customer support.

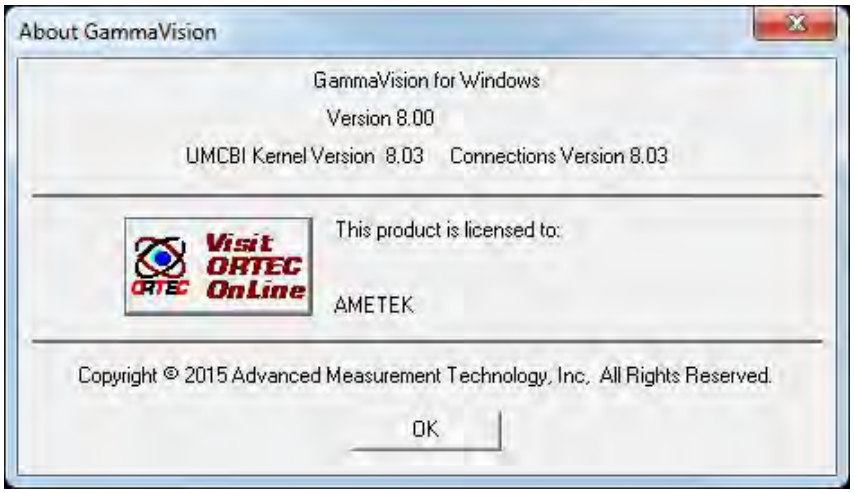


Figure 72. About GammaVision.

Click the **Visit ORTEC OnLine** button to browse our website includes our product catalog, application notes, technical papers, information on training courses, and access to our Global Service Center.

5.2. Acquire

The **Acquire** menu is shown in Fig. 73. Access to the various functions depends on whether the a Detector or buffer window is currently active (for example, if a buffer window is active the Detector controls are disabled and **MCB Properties...** is read-only). The **List Mode**, **Download Spectra** and **View ZDT Corrected** commands are available only for supported hardware (which is listed in the discussion for each of these functions).

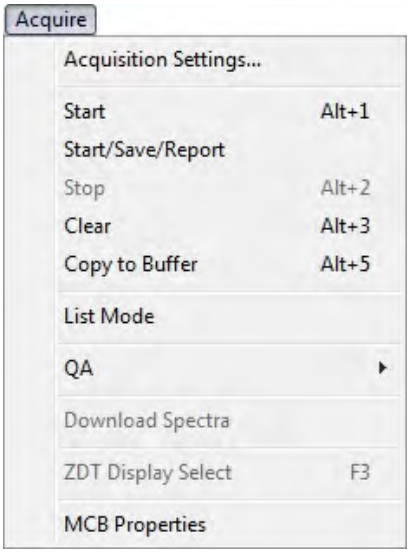


Figure 73. Acquire Menu.

NOTE In some cases, a Detector option might be disabled because it is not supported by the current Detector (while it might still be valid for some other Detector in the system, or for this Detector under different conditions).

5.2.1. Acquisition Settings...

This command opens the Acquisition Settings dialog (Fig. 74), which allows you to control a number of questions that can be "asked on start" (when a Detector is started) and their default values.

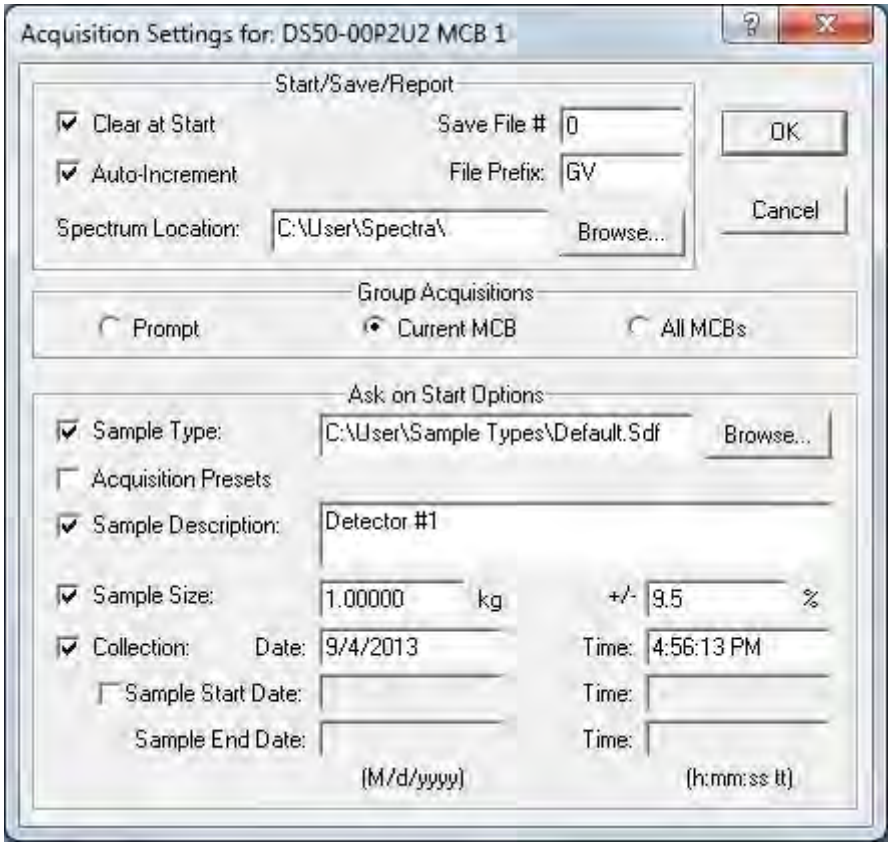


Figure 74. Acquisition Settings.

To take advantage of the multi-detector capability, the **Group Acquisitions** settings apply to the **Start**, **Stop**, **Start/Save/Report**(γ), and **Clear** commands. You can control acquisition in all displayed Detectors simultaneously (**All MCBs**) or one Detector at a time (**Current MCB**); or be asked if you wish to apply an acquisition command to one or all displayed Detectors (**Prompt**).

The **Spectrum Location** field gives you the option of saving each Detector's spectra to different folders (in the example in Fig. 74, this Detector's spectra will be stored in C:\User\EDF Det 1\). If you leave this field blank, all spectra for this Detector are stored in the folder designated on the Directories tab under **File/Settings...** (Section 5.1.1.4).

NOTE To start all Detectors simultaneously, you must turn off all **Ask on Start Options**. This is explained in Section 5.2.1.2.

5.2.1.1. Start/Save/Report(γ)

For the **Start/Save/Report**(ã) function, you must select **Clear at Start**, which automatically clears the Detector before acquisition starts, specify the base filename of the save file (**File Prefix**), and decide whether the filename is to be automatically incremented after each use (**Auto-Increment**). The **File Prefix** can be up to eight alphanumeric characters. However, if **Auto-Increment** is specified, the limit is seven characters. The first one to seven characters of the filename are the file prefix. The remaining characters are the sequence numbers. This starts with the number entered in the **Save File #** field. The number increments to the number of allowed characters (e.g., AAAAAA99) then restarts at zero (e.g., AAAAAA00). The prefix must be short enough to accommodate the number of expected files. The filename is expanded to eight characters with zeros. If the **Auto-Increment** box is checked, the filename will be incremented by 1 each time the **Start/Save/Report**(ã) is done. For example, if 0 were entered for prefix GVX, the first filename would be GVX00000, the second would be GVX00001, and so on.

If the **Auto-Increment** box is not checked, the same file is used for every analysis and the previous data are overwritten with each **Start/Save/Report**(ã). The analysis uses the settings from **Analyze/Settings/Sample Type...** (Section 5.5.1.1).

5.2.1.2. Ask on Start Options

Each Detector has its own suite of **Ask on Start** parameters. When you start a Detector, GammaVision prompts for any **Ask on Start** options that have been turned on. As soon as the prompts for a specific Detector are satisfied, that Detector begins acquisition. If you choose **Cancel** for any of these parameters, the remaining ask-on-start sequence for that Detector terminates and ***acquisition for that Detector is canceled***.

This also applies when starting all Detectors simultaneously (**All MCBs**). If the **Ask on Start Options** have been turned on for any Detector in the group, GammaVision steps through the list of Detectors to be started, and if any ask-on-start parameters are active, the software prompts for them. As soon as the ask-on-start prompts are satisfied for a particular Detector, acquisition in that Detector begins immediately. Therefore, to start all Detectors simultaneously, you must turn off all ask-on-start options.

Note - these settings are stored within the detector specific context files which are stored in the folder specified on the Directories tab under **File/ Settings...** as discussed in Section 5.1.1.4. The user can segregate context settings between GammaVision and Maestro-PRO if desired by changing the location of the context files.

Sample Type Defaults

The sample type file, which contains many of the parameters needed for analysis and acquisition, can be specified here. The file is created in the Sample Type Settings dialog, Section 5.5.1.1. When specified, the file is read and the values in it are the defaults for this dialog. If the **Ask on Start** box is checked, GammaVision will ask for the sample type when Detector acquisition starts, and the values in that file will be used. Click **Browse...** to show the available files.

Acquisition Presets

If the **Ask on Start** box is checked, the presets are asked when the Detector is started; the dialog is the same as the Preset tab for this Detector's MCB Properties dialog. Only the non-zero presets can be changed during the start.

Sample Description

The sample description can be entered here, and it can also be asked for when the spectrum is saved. If the **Ask on Start** box is checked, the description entered here will be presented as the default at the start of data acquisition. This feature is handy when processing a number of similar samples; the common part of the description can be entered here, and the unique descriptors can be added on start.

Sample Size

If the output activity is to be normalized to a volume or weight (or any other factor), the sample quantity can be entered here, along with an optional 1-sigma uncertainty (+/-) between 0% and 1000%. The reporting units are entered, according to the sample type, on the System tab under **Analyze/ Settings/Sample Type...** (page 152). This will normalize the activity and the report will be in normalized units. This normalization is in addition to any normalization done by the multiplier and divisor on the Analysis tab under **Analyze/Settings/Sample Type...** (page 152).

Collection Date and Time

If the decay correction is enabled (see the Sample tab under **Analyze/Settings/Sample Type...**,

Section 5.5.1.1), the collection date and time are used in the correction formula.[14]

Sample Start/Stop Time

These dates/times are the start time of the sample collection and the stop time of the sample collection. For example, for air filters, the start time is the time when the air flow is started and the stop time is when the air flow is stopped. These times are used to calculate the build-up of the activity in the sample. It is assumed that the spectrum is not collected during the build-up time. The correction for the build-up is given in Section 5.8.4.

5.2.2. Start

Based on the **Group Acquisitions** setting in the Acquisition Settings dialog, **Start** simultaneously begins acquisition in all displayed Detectors (**All MCBs**) or one Detector at a time (**Current MCB**); or asks if you wish to begin data collection in one or all displayed Detectors (**Prompt**), as shown in Fig. 75.

Figure 75. Start One or All Displayed Detectors.

Any warnings arising from problems detected at the hardware level will appear in a message box or on the Supplemental Information Line at the bottom of the display. The Detector can also be started with the **<Alt + 1>** accelerator, the **Start Acquisition** button on the toolbar, or the **Start** command on the right-mouse-button menu. If the Detector is already started or if GammaVision is in buffer mode, this command is disabled.

See Section 5.2.1.2 for a discussion of how ask-on-start options can affect the start of data acquisition.

5.2.3. Start/Save/Report(ã)

This command performs all three functions without user intervention. The **Start** is the same as the **Start** above, **Save** is the same as **File/Save** (using the filename in the **Acquire/Acquisition Settings...** dialog), and **Report** is the same as **Analyze/Entire spectrum in memory**. Based on the **Group Acquisitions** setting in the Acquisition Settings dialog, **Start/Save/Report**(ã) simultaneously begins acquisition in all displayed Detectors (**All MCBs**) or one Detector at a time (**Current MCB**); or asks if you wish to begin data collection in one or all displayed Detectors (**Prompt**).

[14]If the collection date and time is before that of the spectrum acquisition, the spectrum will be activity-corrected back to the sample collection time. While this is the normal use of this input, if the collection date and time is after the acquisition time, the decay correction will be made forward in time.

5.2.4. Stop

Stop terminates data collection in the active Detector window. The Detector can also be stopped with the accelerator **<Alt+ 2>,** the **Stop Acquisition** button on the toolbar, and the **Stop** command on the right-mouse-button menu. Based on the **Group Acquisitions** setting in the Acquisition Settings dialog, **Stop** simultaneously halts acquisition in all displayed Detectors (**All MCBs**) or one Detector at a time (**Current MCB**); or asks if you wish to stop data collection in one or all displayed Detectors (**Prompt**).

5.2.5. Clear

Clear erases the spectral data and the descriptors (e.g., real time, live time, start time) for the currently active Detector or buffer window. The presets are not altered. Because the **Group Acquisitions** setting in the Acquisition Settings dialog applies to Detector windows only, this command operates differently in Detector windows than in buffer windows. If a buffer window is active, **Clear** erases only that buffer window, regardless of how many buffer windows are open. However, if a Detector window is active, **Clear** simultaneously clears all displayed Detectors (**All MCBs**), erases only the active Detector window (**Current MCB**); or asks if you wish to clear one or all displayed Detectors (**Prompt**).

This command might not operate on some types of Detectors when they are collecting data. The data can also be cleared with **<Alt+ 3>**, the **Clear Spectrum** button on the toolbar, or the **Clear** command on the right-mouse-button menu.

5.2.6. Copy to Buffer

The **Copy to Buffer** function transfers the data and descriptors (e.g., live time, real time), from the active Detector window to a new buffer window. This function can also be performed with **<Alt + 5>** or the **Copy to Buffer** command on the right-mouse-button menu.

5.2.7. List Mode

This toggles the current Detector's data acquisition mode between PHA mode and list mode (Section 1.6). This function can also be performed with the **List Mode** toolbar button.

5.2.8. QA(γ)

This is explained in Chapter 8, "Quality Assurance."

5.2.9. Download Spectra...

This command supports standalone MCBs such as Detective®-family instruments, trans-SPEC®, digiDART®, and the legacy DART®, and is used to download the spectra from the MCB to the

computer disk. Note that downloading the spectra does not erase them from the MCB.

The files are stored in the directory and spectrum file format specified in the dialog under **File/ Settings** (Section 5.1.1), and are named according to this format:

sss iiiiiiii ddddddddd ttttttttt.ext

where:

sss	is the sequence number as shown on the digiDART spectrum list display or the storage sequence in other supported MCBs.
iiiiiiii	is the ID string entered on the digiDART when the spectrum was saved and shown on the digiDART spectrum list display or the text string from the barcode reader in the DART.
ddddddddd	is the date the spectrum was collected, as recorded in the MCB.
ttttttttt	is the time the spectrum was collected, as recorded in the MCB.
ext	is the extension for the file type selected.

If any **Ask on Save Options** are set in the File Settings dialog, they are asked for each spectrum individually. Note that if you cancel an ask-on-save prompt for a particular spectrum, any remaining ask-on-save prompts for that spectrum are not displayed, and the spectrum is not saved to disk.

NOTE Before downloading, make sure the current conversion gain setting for this MCB (see the ADC tab under **Acquire/MCB Properties...**) is the same as or greater than the conversion gain of the stored spectra; otherwise, the downloaded spectra will be truncated at the current conversion gain setting. For example, if a digiDART was used to acquire 8k spectra in the field and the current conversion gain setting is 4k, only the first 4096 channels of data in each spectrum will be downloaded. See also the spectrum file format NOTE on page 58.

5.2.10. ZDT Display Select

This command is active (1) for a Detector that supports ZDT Mode and has one of the **ZDT** modes enabled on the ADC tab under **Acquire/MCB Properties...**, and (2) a ZDT spectrum file recalled into a buffer window.

When the Detector is in the **CORR_ERR** ZDT mode (the NORM_CORR mode is typically not used), two spectra are collected: the uncertainty spectrum, labeled **ERR**; and the zero-dead-time

corrected spectrum, labeled **ZDT** (see the discussion in Section 5.2.11.4 for more information). The spectrum label is displayed in the upper-right corner of the Full Spectrum View, as shown in Fig. 76.

The **View ZDT Corrected** command (duplicated by the shortcut **<F3>**) allows you to toggle between the two spectra. Note that in the CORR_ERR ZDT mode, the status sidebar does not display a live-time readout for either the ERR or ZDT spectra.

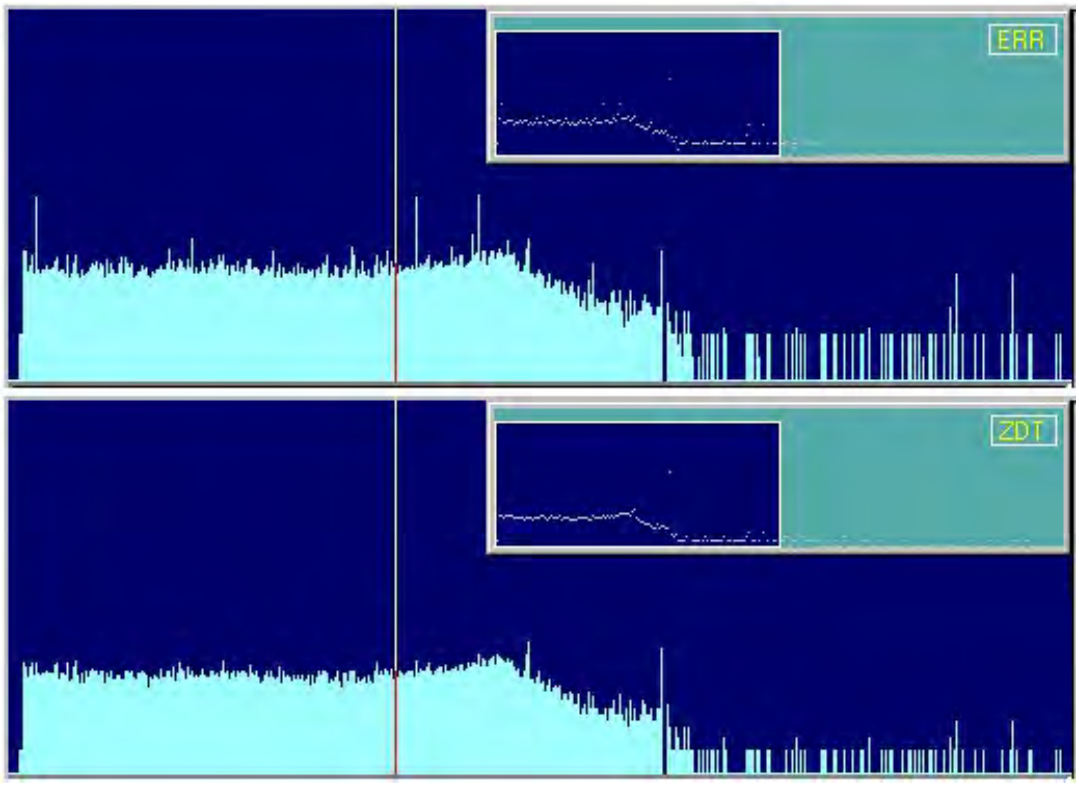


Figure 76. Comparison of Uncertainty and ZDT Spectra Showing Labels in Full Spectrum View.

5.2.11. MCB Properties...

CONNECTIONS applications use a uniform dialog for data acquisition setup, accessed with the **Acquire/MCB Properties...** command. The property pages for the DSPEC-50 are described here. To see the Properties dialog for other CONNECTIONS MCBs, refer their respective hardware manuals.

Depending on the currently selected Detector, the Properties dialog displays several tabs of hardware controls that may include ADC setup parameters, acquisition presets, high-voltage controls, amplifier gain adjustments, gain and zero stabilizers, pole-zero and other shaping controls, the InSight™ Virtual Oscilloscope, digital noise-suppression filters, and radionuclide detection reports. In addition, some MCBs monitor conditions such as detector temperature, external input

status, alpha chamber pressure, charge remaining on batteries, and the number of spectra collected in remote mode, which are reported on a Status tab. Simply move from tab to tab and set your hardware parameters, then click **Close**. Note that as you enter characters in the data entry fields, the characters will be underlined until you move to another field or until 5 seconds have lapsed since a character was last entered. During the time the entry is underlined, no other program or computer on the network can modify this value.

IMPORTANT

The MCB Properties dialogs are part of the standard CONNECTIONS tools available in all ORTEC application software. As such, this interface is available only in English, although our higher-level applications such as GammaVision support other languages. If you use comma delimiters instead of decimal points in these dialogs, you may encounter unexpected results or other problems.

If the Detector is password-locked (see Section 5.7.3), you must know the password before you can modify its MCB properties. To view a locked Detector's properties in read-only mode, click **Cancel** when the Unlock Password dialog opens.

5.2.11.1. DSPEC-50

Amplifier

Figure 77 shows the Amplifier tab. This tab contains the controls for **Gain**, **Baseline Restore**, **Preamplifier Type**, **Input Polarity**, and **Optimize**.

NOTE Be sure that all of the controls on the tabs have been set *before* clicking the **Start Auto** (optimize) button. The changes you make on most property tabs *take place immediately*. There is no cancel or undo for these dialogs.

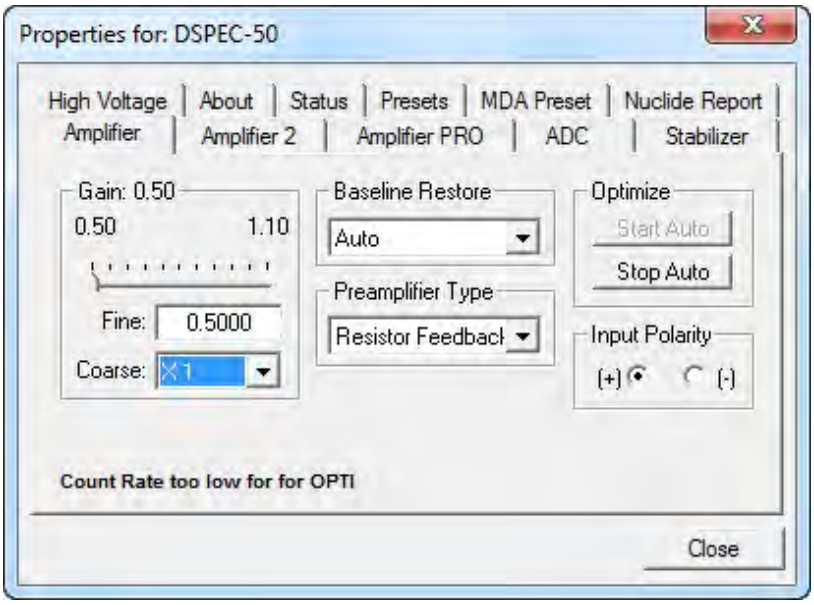


Figure 77. DSPEC-50 Amplifier Tab.

Gain — Set the amplifier coarse gain by selecting from the **Coarse** droplist, then adjust the **Fine** gain with the horizontal slider bar or the edit box, in the range of 0.5 to 1.1. The resulting effective gain is shown at the top of the **Gain** section. The two controls used together cover the entire range of amplification from 0.5 to 140.8.

Input Polarity — These buttons select the preamplifier input signal polarity for the signal from the detector. Normally, GEM (p-type) detectors have a positive signal and GMX (n-type) have a negative signal.

Baseline Restore — This is used to return the baseline of the pulses to the true zero between incoming pulses. This improves the resolution by removing low frequency noise from dc shifts or mains power ac pickup. The baseline settings control the time constant of the circuit that returns the baseline to zero. There are three fixed choices (**Auto**,[15] **Fast**, and **Slow**). The fast setting is used for high count rates, the slow for low count rates. **Auto** adjusts the time constant as appropriate for the input count rate. The settings (**Auto**, **Fast**, or **Slow**) are saved in the DSPEC-50 even when the power is off. The time constant can be manually set on the InSight display (see the discussion beginning on page 98).

You can view the time when the baseline restorer is active on the InSight display as a **Mark** region (see the Marks discussion, p. 100). In the automatic mode, the current value is shown on the InSight sidebar. For a low-count-rate system, the value will remain at about 90.

Preamplifier Type — Choose **Transistor Reset** or **Resistive Feedback** preamplifier operation. Your choice will depend on the preamplifier supplied with the germanium detector being used.

Optimize

The DSPEC-50 is equipped with both automatic pole-zero logic[16] and automatic flattop logic.[17] The **Start Auto** (optimize) button uses these features to automatically choose the best pole-zero and flattop tilt settings. Note that if you selected **Transistor Reset** as the **Preamplifier Type** for this DSPEC-50, optimization does not perform the pole zero.

NOTE You cannot optimize with LFR mode enabled; see Section 5.2.11.1.

As with any system, the DSPEC-50 should be optimized any time the detector is replaced or if the flattop width is changed. For optimization to take place, the DSPEC-50 must be processing pulses. The detector should be connected in its final configuration before optimizing. A count rate guidance message on the lower-left of the Amplifier page will help you position a radioactive source to deliver the correct count rate for optimization. The **Start Auto** optimization button will be disabled (gray) until the count rate is suitable.

---

[15]U.S. Patent 5,912,825.

[16]U.S. Patent 5,872,363.

[17]U.S. Patent 5,821,533.

Select either the **Resistive Feedback** or **Transistor Reset** option and click on **Start Auto**. The optimize command is sent to the DSPEC-50 at this time and, if the DSPEC-50 is able to start the operation, a series of short beeps sounds to indicate that optimization is in progress. When optimizing is complete, the beeping stops.

During optimization, pole zeroes are performed for several rise-time values and the DSPEC-50 is cycled through all the rise time values for the determination of the optimum tilt values. All values for all the combinations are then saved in the DSPEC-50, so you do not need to optimize for each possible rise time. Optimization can take from 1 to 10 minutes depending on count rate, but typically takes 5 minutes.

NOTE Be sure to repeat the optimization if you change the flattop width.

The effect of optimization on the pulse can be seen in the InSight mode, on the Amplifier 2 tab. Note, however, that if the settings were close to proper adjustment before starting optimization, the pulse shape may not change enough for you to see. (In this situation, you also may not notice a change in the shape of the spectrum peaks.) The most visible effect of incorrect settings is high- or low-side peak tailing or poor resolution.

Amplifier 2

Figure 78 shows the Amplifier 2 tab, which accesses the advanced shaping controls including the InSight Virtual Oscilloscope mode.

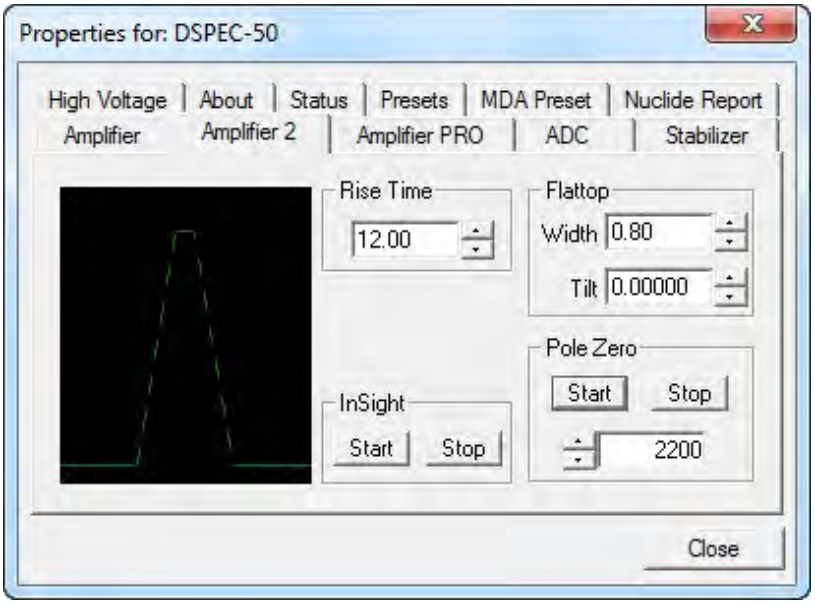


Figure 78. DSPEC-50 Amplifier 2 Tab.

The many choices of **Rise Time** allow you to precisely control the tradeoff between resolution and throughput. The value of the rise time parameter in the DSPEC-50 is roughly equivalent to twice the integration time set on a conventional analog spectroscopy amplifier. Thus, a DSPEC-50 value of 12 ì s corresponds to 6 ì s in a conventional amplifier. Starting with the nominal value of 12.0, you should increase values of the rise time for better resolution for expected lower count rates, or when unusually high count rates are anticipated, reduce the rise time for higher throughput with somewhat worse resolution.

The DSPEC-50 **Rise Time** ranges from 0.8 ì s to 23.0 ì s. Once the unit has been optimized according to Section 5.2.11.1, you can use any **Rise Time** without having to re-optimize. The most recent settings are saved in the DSPEC-50 firmware even when the power is turned off.

For the more advanced user, the InSight mode allows you to directly view all the parameters and adjust them interactively while collecting live data. To access the InSight mode, go to the **InSight** section on the Amplifier 2 tab and click on **Start**. The InSight mode is discussed in more detail in Section 5.2.11.5.

The **Rise Time** value is for both the rise and fall times; thus, changing the rise time has the effect of spreading or narrowing the quasi-trapezoid symmetrically.

The **Flattop** controls adjust the top of the quasi-trapezoid. The **Width** adjusts the extent of the flattop (from 0.3 to 2.4 ì s). The **Tilt** adjustment varies the "flatness" of this section slightly. The **Tilt** can be positive or negative. Choosing a positive value results in a flattop that slopes downward; choosing a negative value gives an upward slope. Alternatively, the optimize feature on the Amplifier tab can set the tilt value automatically. This automatic value is normally the best for resolution, but it can be changed on this dialog and in the InSight mode to accommodate particular throughput/resolution tradeoffs. The optimize feature also automatically adjusts the pole-zero setting.

The dead time per pulse is approximately $(3 \times \textit{Rise Time}) + (2 \times \textit{Flattop Width})$.

In the **Pole Zero** section, the **Start** button performs a pole zero at the specified rise time and other shaping values. Unlike the optimize feature, it performs a pole zero for only the one rise time. The pole-zero **Stop** button aborts the pole zero, and is normally not used.

When you are satisfied with the settings, **Close** the Properties dialog and prepare to acquire data.

Once data acquisition is underway, the advanced user may wish to return to **MCB Properties...** and click on the **Insight** section's **Start** button to adjust the shaping parameters interactively with a "live" waveform showing the actual pulse shape, or just to verify that all is well.

Amplifier PRO

This tab (Fig. 79) contains the controls for the **Low Frequency Rejector** (LFR) filter, high-frequency **Noise Rejection Level**, **Resolution Enhancer**, and **Enhanced Through-put Mode**. To enable a particular feature, mark the corresponding checkbox. Any or all of these features can be used at one time, however, the LFR and Enhanced Throughput modes must be set up before the Resolution Enhancer is configured, as discussed below. Note that once an MCB is "trained" for the Resolution Enhancer (see the following section), it must be "retrained" if any settings

are changed that can affect peak shape or position (e.g., bias, gain, rise time, flattop, pole-zero).

Low Frequency Rejector — This filter is designed to minimize low-frequency noise, and is discussed in detail in the hardware manual. You *cannot* optimize or pole-zero the DSPEC-50 while in LFR mode. The **Optimize** feature must be used with the LFR filter *off.* Subsequent measurements can then be taken with the LFR filter on. Also, LFR mode affects the available range of protection times in **Enhanced Throughput Mode**, as discussed in the next paragraph.

Noise Rejection Level — This setting adjusts a filter that rejects high-frequency noise from the ambient environment. It ranges from 0 to 4. The default setting, **2**, will be suitable for most applications.

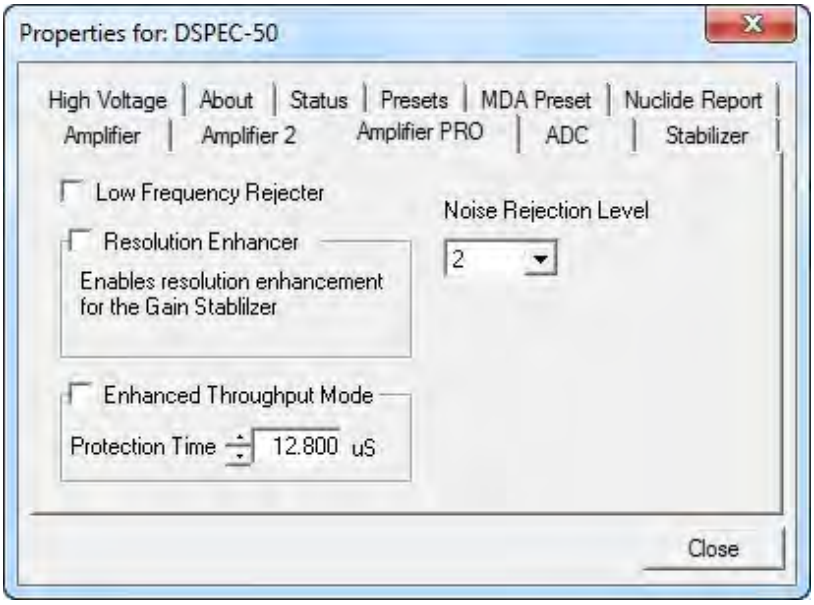


Figure 79. DSPEC-50 Amplifier PRO Tab.

If the system is exhibiting high dead time with no source on the detector, the noise may be induced by nearby RF interference or a result of a ground loop. If possible, resolve the source of the noise by physical means such as common grounding between detectors and instruments, shielding cables, removing nearby motors/generators, etc. If you cannot eliminate the noise, increase the rejection level setting until the dead time returns to the expected low value.

- Note that higher values may reduce the effectiveness of the pile-up rejector when processing very low-energy pulses.

- On systems for which very high dead times are expected (i.e., >60%), especially with very-low-energy sources (e.g., ^{241}Am), decreasing this setting can improve the performance of the spectrometer with respect to live-time correction and the ability to process signals at higher input rates.

Enhanced Throughput Mode — This feature can help reduce the low-side peak tailing that results from increased charge trapping; see the discussion in the hardware manual for more details. This function will *not* improve poor resolution due to other causes. The valid **Protection Time** settings, in 25-ns increments, range as follows:

LFR Mode	Highest Throughput (minimum Protection Time)	Lowest Throughput (maximum Protection Time)
Off	(Rise Time + flattop)	(2 × Rise Time + Flattop)
On	(3 × Rise Time + 2 × Flattop)	(6 × Rise Time + 3 × Flattop)

Turning on this feature automatically sets the minimum protection time (highest throughput rate) based on your current **Rise Time** and **Flattop** settings, however, you can adjust this value at any time. Each time you change the rise time or flattop, the DSPEC-50 will automatically set itself to the new minimum protection time.

"Training" the Resolution Enhancer

The Resolution Enhancer operates by measuring the rise time (collection time) of the pulses and adjusting the gain based on the rise time. This is done on each pulse. The gain adjustment value for the rise time is stored in a table. The values in the table must be set by "training" the Resolution Enhancer. Marking the **Resolution Enhancer** checkbox enables/disables the "learning" mode. Note that, once trained, the enhancer operates continuously until disabled as discussed in Step 13 below. To train the enhancer:

1) Set the bias, gain, rise time, flattop, and PZ as you would for data collection.

2) If you wish to use LFR Mode, turn it on.

3) If you wish to use Enhanced Throughput Mode, turn it on and either accept the automatically calculated, highest-throughput protection time, based on the current rise time and flattop; or enter the desired setting. (The latter might require one or more data acquisitions. When finished, proceed to Step 4).

4) Clear the MCB and acquire a well-isolated peak.

5) Mark the **Resolution Enhancer** checkbox to turn on the learning mode.

6) You will now use the gain stabilization section of the Stabilizer tab to configure the Resolution Enhancer (the gain stabilizer is disabled in the learning mode). Enter the **Center** channel and **Width** of the peak acquired in Step 4; the maximum **Width** is 255 channels. If you wish, use the **Suggest** button. The selected region should be as narrow as possible but should completely include the peak.

7) Click on **Initialize** to clear all the Resolution Enhancer settings. Initialization does not change the current **Center** channel and **Width**.

8) Clear the MCB, re-start acquisition, and monitor the FWHM of the target peak, using the **Peak Info** command (available by right-clicking in the spectrum window) to show the FWHM and peak counts. Collect about 5000 counts in the peak and record the FWHM. Clear the data and collect another 5000 counts, recording the FWHM. Repeat until the FWHM no longer changes. Typically, the more charge trapping exhibited by the detector, the longer the data collection time.

9) When you are satisfied that the FWHM has reached the best possible value, clear the MCB and collect another spectrum for confirmation.

10) At this point, the Resolution Enhancer is now "trained" for the current peak shape parameters and the learning mode should be turned off by returning to the Amplifier PRO tab and unmarking the **Resolution Enhancer** checkbox. The table of adjustments will be stored in the DSPEC-50's memory.

11) If you change any parameters that affect peak shape, you must repeat this "training" procedure.

12) Once the Resolution Enhancer has been trained and its checkbox has been unmarked, the Stabilizer tab once again operates on the gain stabilizer (that is, it no longer adds values to the table of adjustments).

    NOTE The peak selected for the gain stabilizer can be different from the peak used for training the Resolution Enhancer.

13) To turn off the Resolution Enhancer, mark its checkbox to turn on the learning mode, go to the Stabilizer tab and click on the **Initialize** button for the gain stabilizer. This will set the adjustment to zero. Now return to the Amplifier PRO tab and unmark the **Resolution Enhancer** box.

ADC

This tab (Fig. 80) contains the **Gate**, **ZDT Mode**, **Conversion Gain**, **Lower Level Disc**riminator, and **Upper Level Disc**riminator controls. In addition, the current real time, live time, and count rate are monitored at the bottom of the dialog.

Gate — This allows you to select a logic gating function. With this function **Off**, no gating is performed (that is, all detector signals are processed); with the function in **Coincidence**, a gating input signal *must be* present at the proper time for the conversion of the event; in **Anti**

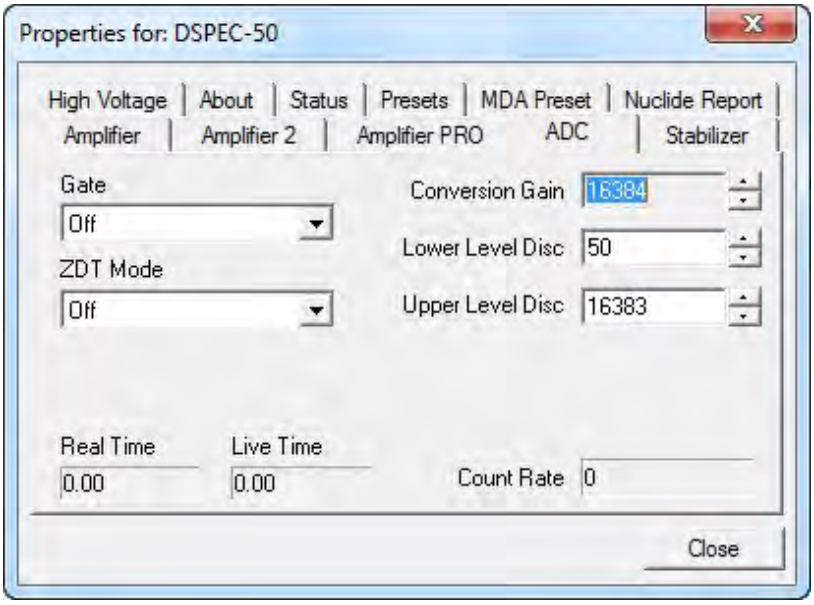


Figure 80. DSPEC-50 ADC Tab.

coincidence, the gating input signal *must not be* present for the conversion of the detector signal. The gating signal must occur prior to and extend 500 ns beyond peak detect (peak maximum).

ZDT Mode — Use this droplist to choose the **ZDT Mode** to be used for collecting the desired zero dead time spectrum (see Section 5.2.11.4). The three modes are **Off** (LTC only), **NORM_ CORR** (LTC and ZDT), and **CORR_ERR** (ERR and ZDT). If one of the ZDT modes is selected, both spectra are stored in the same spectrum (.SPC) file. If you do not need the ZDT spectrum, you should select **Off**. In GammaVision, the display can show either of the two spectra. Use **<F3>** or **Acquire/ZDT Display Select** to toggle the display between the two spectra. In the Compare mode, **<F3>** switches both spectra to the other type and **<Shift+F3>** switches only the compare spectrum. This allows you to make all types of comparisons.

Conversion Gain — This sets the maximum channel number in the spectrum. If set to 16384, the energy scale will be divided into 16384 channels. The conversion gain is entered in powers of 2 (e.g., 8192, 4096, 2048). The up/down arrow buttons step through the valid settings for the DSPEC-50.

Upper- and Lower-Level Discriminators — The **Lower Level Disc**riminator sets the level of the lowest amplitude pulse that will be stored. This level establishes a lower-level cutoff by channel number for ADC conversions. The **Upper Level Disc**riminator sets the level of the highest amplitude pulse that will be stored. This level establishes an upper-level cutoff by channel number for storage.

Stabilizer

The DSPEC-50 has both gain and zero stabilizers (see Section ?). This tab (Fig. 81) shows the current stabilizer settings. Each **Adjustment** section shows how much adjustment is currently applied. The **Initialize** buttons reset the adjustment to 0. If the value approaches 90% or above, adjust the amplifier gain so the stabilizer can continue to function — when the adjustment value reaches 100%, the stabilizer cannot make further corrections in that direction. The **Center Chan**nel and **Width** fields show the peak currently used for stabilization.

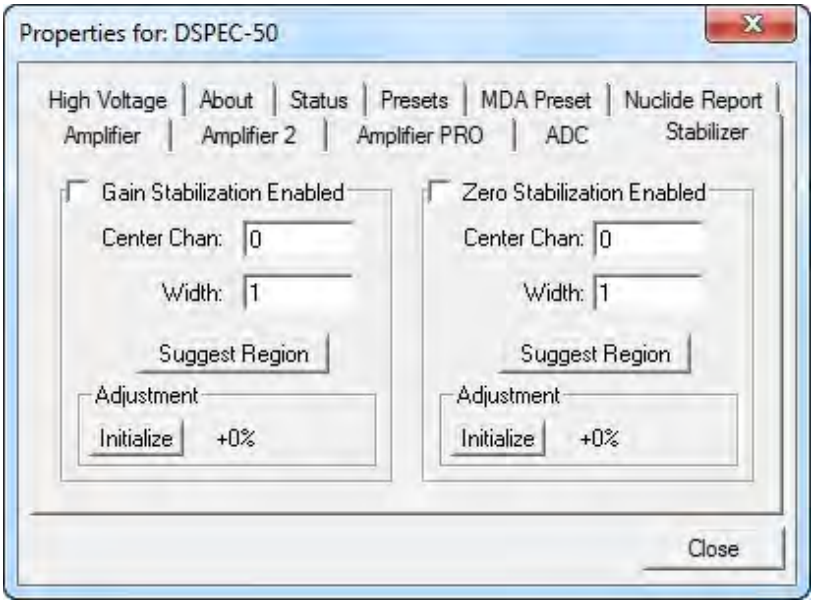


Figure 81. DSPEC-50 Stabilizer Tab.

To enable the stabilizer, enter the **Center Chan**nel and **Width** values manually or click on the **Suggest Region** button. **Suggest Region** reads the position of the marker and inserts values into the fields. If the marker is in an ROI, the limits of the ROI are used. If the marker is not in an ROI: for calibrated spectra, the center channel is the marker channel and the width is 3 times the FWHM at this energy; and for uncalibrated spectra, the region is centered on the peak located within two channels of the marker and as wide as the peak. Now click on the appropriate **Enabled** checkbox to turn the stabilizer on. Until changed in this dialog, the stabilizer will stay enabled even if the power is turned off. When the stabilizer is enabled, the **Center Chan**nel and **Width** cannot be changed.

High Voltage

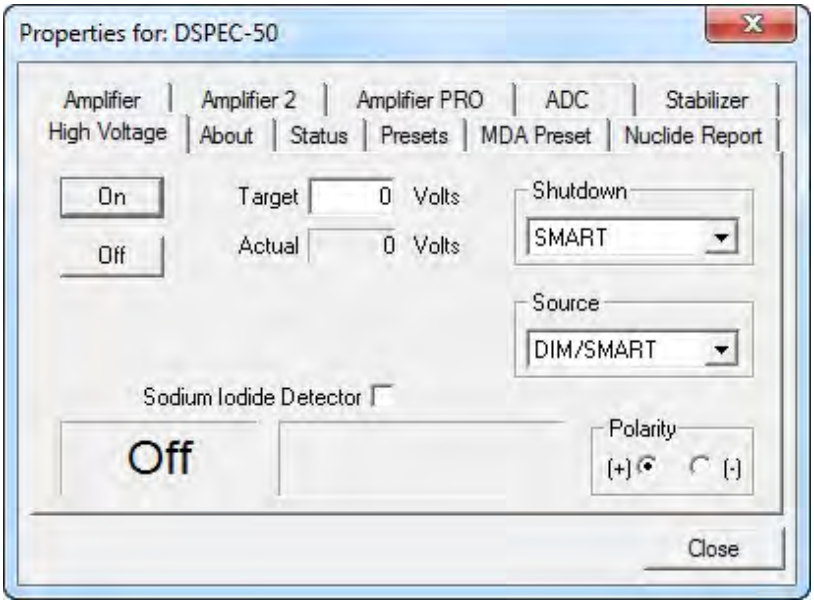


Figure 82. DSPEC-50 High Voltage Tab.

Figure 82 shows the High Voltage tab, which allows you to turn the HV on or off; set and monitor the voltage; select the HV **Source** and **Shutdown** mode; and indicate the detector type; and **Polarity**. Note that if the detector is attached via the rear-panel **DIM** connector, some of these options may be disabled or auto-selected. For example, the detector polarity is determined by the SMART-1 or DIM module.

The **Source** is **Internal** for conventional, non-DIM detectors; **DIM-296** for the Model 296, and **DIM/SMART** for all other DIM-based detectors.

NOTE NaI detectors require the DIM-POSNAI interface and the **DIM/SMART** source selection.

Enter the **Target** high voltage, click **On**, and monitor the voltage in the **Actual** field. Click **Off** to turn off the high voltage.

The HV will not turn on if the detector is sending a remote shutdown or overload signal. The Overload indicator means there is a bad connection in your system. The Shutdown indicator means that either the detector is warm or you have chosen the wrong **Shutdown** or **Source** mode.

The shutdown types are **ORTEC**, **TTL**, and **SMART**. The **ORTEC** mode is used for all ORTEC detectors except SMART-1 (**SMART**) detectors. Most non-ORTEC detectors use the **TTL** mode; check with the manufacturer.

Choose the detector **Polarity** (SMART-1 detectors auto-select this setting). Normally, GEM (p-type) detectors have a positive signal and GMX (n-type) detectors have a negative signal.

To use a **Sodium Iodide Detector**, mark the checkbox. This changes the gain and zero stabilizers to operate in a faster mode.

About

This tab (Fig. 83) displays hardware and firmware information about the currently selected DSPEC-50 as well as the data **Acquisition Start Time** and **Sample** description. In addition, the **Access** field shows whether the Detector is currently locked with a password (Section 5.7.4), **Read/Write** indicates that the Detector is unlocked; **Read Only** means it is locked.

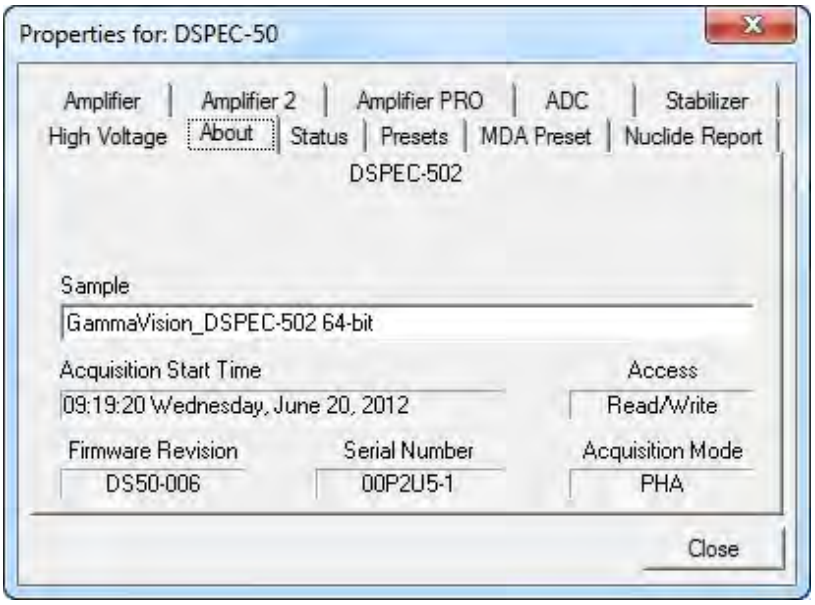


Figure 83. DSPEC-50 About Tab.

Status

Figure 84 shows the Status tab.
You can select any six of these to be displayed simultaneously on the Status tab. The parameters you choose can be changed at any time, so you can view them as needed. Two types of values are presented: **OK** or **ERR**, and numeric values. The SOH parameters return either **OK** or **ERR**.

If the state is **OK**, the parameter stayed within the set limits during the spectrum acquisition. If the parameter varied from the nominal value by more than the allowed limit, the **ERR** is set until cleared by the program. The numeric values are displayed in the units reported by the DSPEC-50. **Security**, **Detector temperature**, and **Live detector temperature** are available only for SMART-1 detectors. For non-SMART-1 detectors, they display **N/A**.

Detector State of Health
Returns OK or an error message describing a problem with detector power or bias.

+24 volts
This is the current value of the +24 volt supply.

+12 volts
This is the current value of the +12 volt supply.

−12 volts
This is the current value of the −12 volt supply.

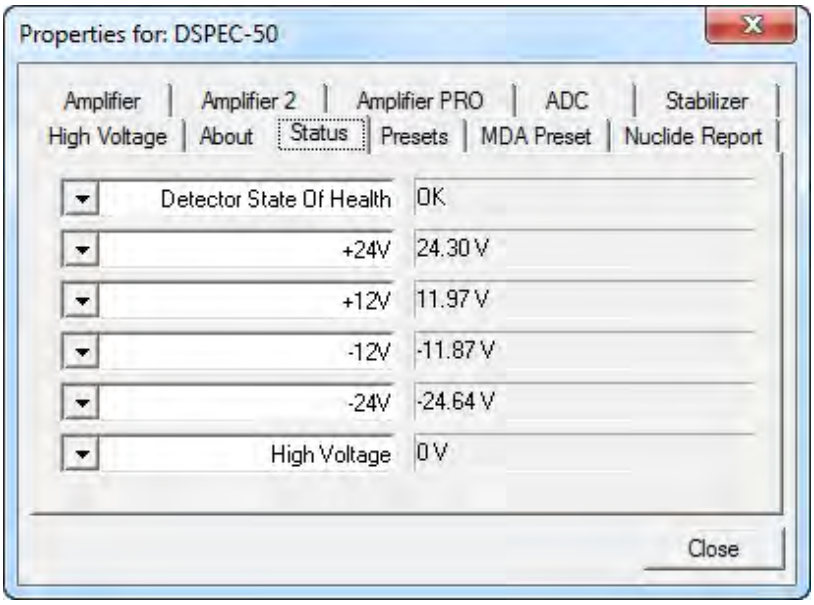


Figure 84. DSPEC-50 Status Tab.

−24 volts
This is the current value of the −24 volt supply.

High Voltage
This is the current value of the high voltage bias supply.

Note that, as of this release, the **Detector temperature** and **Live detector temperature** monitors are listed, but return only N/A.

Presets

Figure 85 shows the Presets tab. MDA presets are shown on a separate tab.

The presets can only be set on an MCB that is not acquiring data (during acquisition the preset field backgrounds are inactive [gray]). You can use any or all of the presets at one time. To disable a preset, enter a value of zero. If you disable all of the presets, data acquisition will continue until manually stopped.

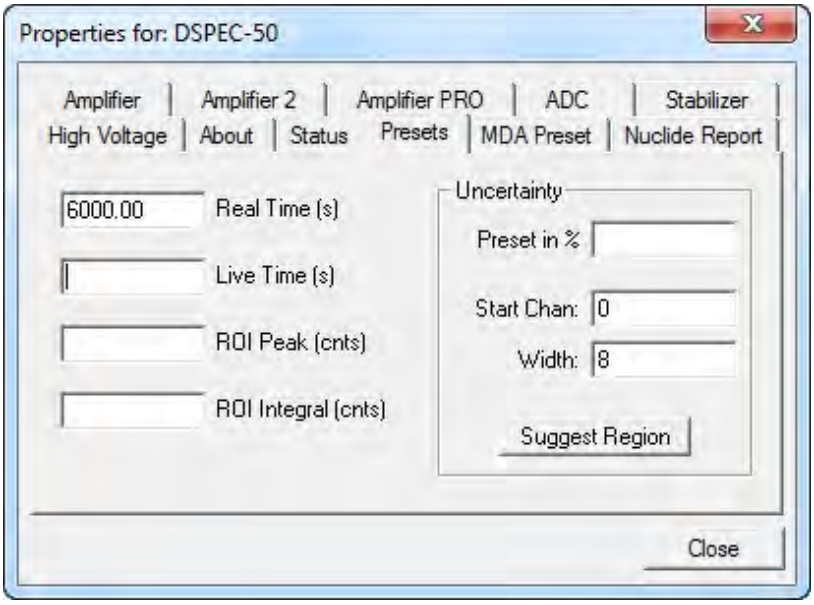


Figure 85. DSPEC-50 Presets Tab.

When more than one preset is enabled (set to a non-zero value), the first condition met during the acquisition causes the MCB to stop. This can be useful when you are analyzing samples of widely varying activity and do not know the general activity before counting. For example, the **Live Time** preset can be set so that sufficient counts can be obtained for proper calculation of the activity in the sample with the least activity. But if the sample contains a large amount of this or another nuclide, the dead time could be high, resulting in a long counting time for the sample. If you set the **ROI Peak** preset in addition to the **Live Time** preset, the low-level samples will be counted to the desired fixed live time while the very active samples will be counted for the ROI peak count. In this circumstance, the **ROI Peak** preset can be viewed as a "safety valve."

The values of all presets for the currently selected MCB are shown on the Status Sidebar. These values do not change as new values are entered on the Presets tab; the changes take place only when you **Close** the Properties dialog.

Enter the **Real Time** and **Live Time** presets in units of seconds and fractions of a second. These values are stored internally with a resolution of 20 milliseconds (ms) since the MCB clock increments by 20 ms. *Real time* means elapsed time or clock time. *Live time* refers to the amount of time that the MCB is available to accept another pulse (i.e., is not busy), and is equal to the real time minus the *dead time* (the time the MCB is not available).

Enter the **ROI Peak** count preset value in counts. With this preset condition, the MCB stops counting when any ROI channel reaches this value unless there are no ROIs marked in the MCB, in which case that MCB continues counting until the count is manually stopped.

Enter the **ROI Integral** preset value in counts. With this preset condition, the MCB stops counting when the sum of all counts in all ROI channels (regardless of the number of ROIs) reaches this value. This has no function if no ROIs are marked in the MCB.

The **Uncertainty** preset stops acquisition when the statistical or counting uncertainty of a user-selected net peak reaches the value you have entered. Enter the **Preset in %** value as percent

uncertainty at 1 sigma of the net peak area. The range is from 99% to 0.1% in 0.1% steps. You have complete control over the selected peak region. The region must be at least 7 channels wide with 3 channels of background on each side of the peak. Note that GammaVision calculates this preset once per 40 seconds. Therefore, the software will continue data acquisition up to 40 seconds after the preset has been reached, and the uncertainty achieved for a high count-rate sample may be lower than the preset value.

Use the **Start Chan**nel and **Width** fields to enter the channel limits directly, or click on **Suggest Region**. If the marker is positioned in an ROI around the peak of interest, **Suggest Region** reads the limits of the ROI with the marker and display those limits in the **Start Chan** and **Width** fields. The ROI can be cleared after the preset is entered without affecting the uncertainty calculation. If the marker is not in positioned in an ROI: for calibrated spectra, the start channel is 1.5 times the FWHM below the marker channel, and the width is 3 times the FWHM; for uncalibrated spectra, the region is centered on the peak located within two channels of the marker and as wide as the peak. The net peak area and statistical uncertainty are calculated in the same manner as for the **Peak Info** command.

MDA Preset

The MDA preset (Fig. 86) can monitor up to 20 nuclides at one time, and stops data collection when the values of the minimum detectable activity (MDA) for *all* of the user-specified MDA nuclides reach the needed value. Presets are expressed in Bq, and are evaluated every 40 seconds. The detector must be calibrated for energy in all spectroscopy applications, and for efficiency in all applications but MAESTRO.

The MDA presets are implemented in the MCB (i.e., the entries you make on this screen are saved in the MCB memory), and have no direct link to MDA methods selected in the analysis options for applications such as ScintiVision™, ISOTOPIC, etc. The MDA preset calculation uses the following formula:

$$MDA = \frac{a + \sqrt{b + c * Counts}}{Live\ time * (CorrectionFactor)}$$

where:

a, *b*, and *c* are determined by the MDA criteria you choose.

Counts is the gross counts in an ROI that is 2.5×FWHM around the target peak energy.

Live time is evaluated in 40 second intervals for the MDA presets.

CorrectionFactor is the product of the calibration efficiency at the specified peak energy and the peak's branching ratio (yield) as listed in the working (active) library.

To add an MDA preset, enter the preset value in the **MDA** or **Correction** field; select the **Nuclide** and **Energy**; enter the desired values for coefficients *a*, *b*, and *c*; then click **Add New**.

To edit an existing preset, click to highlight it in the table. This will load its **Nuclide, Energy**, and coefficients in the lower sections of the dialog. Change as needed, then click **Update**.

To remove a preset, click to highlight it in the table, then click **Delete**.

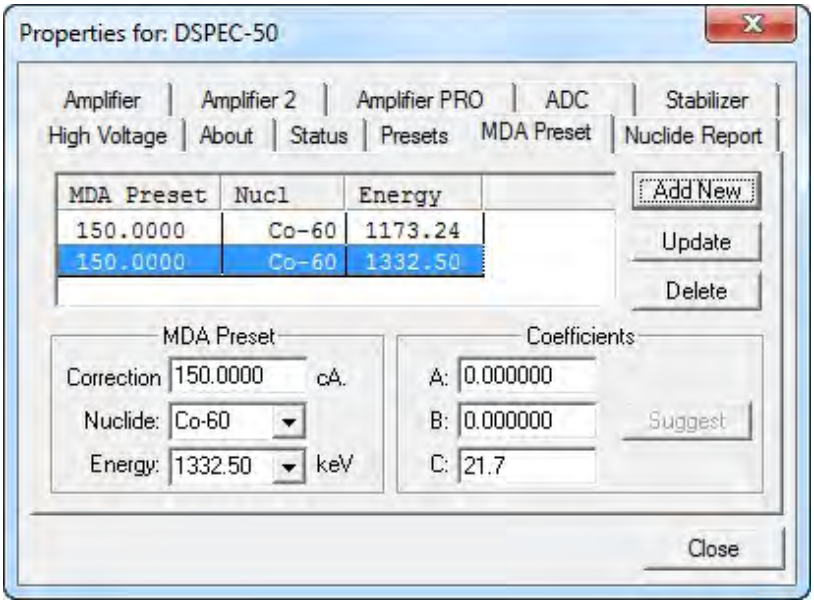


Figure 86. DSPEC-50 MDA Preset Tab.

IMPORTANT These MDA presets *are not dynamically calculated.* Each time you add an MDA preset to this table, its *CorrectionFactor* value is calculated and stored in the MCB's memory. If you then load a different library, change the efficiency calibration, or change the system geometry, the spectroscopy application *will not update* the existing *CorrectionFactor*s, and your MDA presets may no longer be applicable.

Nuclide Report Tab

Figure 87 shows the Nuclide Report tab. The Nuclide Report displays the activity of up to nine (9) user-selected peaks. Once the report is set up, the two lowest-energy ROIs and their respective activity readouts are displayed on the DSPEC-50's Spectrum screen.

The peak area calculations in the hardware use the same methods as the **Peak Info** calculation (Section 5.4.3) so the Nuclide Report display is the same as the **Peak Info** display on the selected peak in the spectra stored in the computer. The calculated value is computed by multiplying the net peak count rate by a user-defined constant. If the constant includes the efficiency and branching ratio, the displayed value is the activity. You enter the nuclide label and the activity units. The report format and calculations are discussed in the next section.

IMPORTANT The entries you make on this screen are saved in the MCB memory, and *are not dynamically calculated.* If you change the energy calibration (i.e., if the peak locations shift), the Nuclide Report may no longer be valid.

Add New

You can add Nuclide Peaks to the report manually or by selecting the peaks from the current working library. The spectrum must be energy calibrated to use the library method.

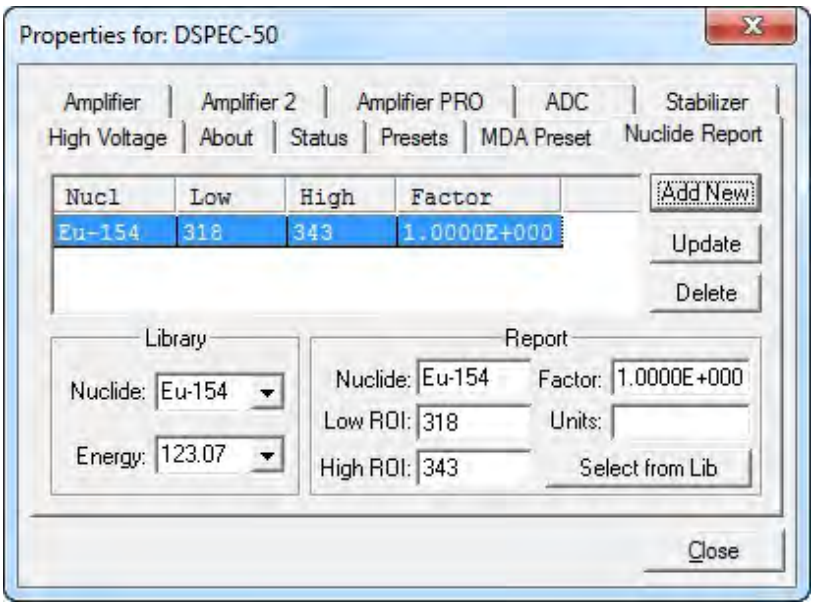


Figure 87. Nuclide Report Tab.

- **Defining Peaks Manually** — To manually define peaks, enter the **Nuclide** name, ROI **Low** (start) and **High** (end) channels, multiplicative **Factor** and **Units** in the Report section; then click **Add New**. All nuclides in the table use the same units, so that value need only be entered once.

- **Selecting Peaks from the Working Library** — To define report peaks using the library, select the **Nuclide** and gamma-ray **Energy** in the Library section. This defines which gamma ray to use. Now, in the Report section, click the **Select from Lib** button. Enter the **Factor** and **Units**, then click **Add New** to add this nuclide to the list. The ROI for this peak will be marked in the MCB's spectrum window, centered on the peak energy and 3 times the width of the calibrated FWHM.

Edit

To change any of the current nuclides, select the nuclide in the list (use the scroll bars if needed). This will show the current settings for this nuclide. Make any changes needed. Any or all of the entries can be changed. When finished with the changes, click on **Update**.

Delete

To remove an entry, select the entry and click **Delete**.

When you close the Properties dialog, all the values entered are written to the DSPEC-50 and the two lowest-energy ROIs and corresponding activity readouts are displayed on the DSPEC-50 screen.

5.2.11.2. Nuclide Report Calculations

The Nuclide Report displays the activity of up to 9 user-selected peaks. Once the report is set up you can view the Nuclide Report at any time. The peak area calculations are the same as the calculations in GammaVision and other ORTEC software, so the Report contents can be duplicated using the spectra stored in the computer. The calculated value is computed by multiplying the net peak count rate by a user-defined constant. If the constant includes the efficiency and branching ratio, the displayed value will be activity. The nuclide label and the activity units are entered by the user.

The report has this format:

Nuclide	keV	uCi/m2	±%
CO-60	1332.5	1.21E+01	10.2
CO-60	1173.2	1.09E+01	12.3
CO-57	122.1	1.48E+00	86.2

Calculations

These are the calculations used to generate the Nuclide Report's **Activity**, **Uncertainty**, and **Peak** values.

Activity is calculated as follows:

$$Activity = \frac{NetCounts \cdot NucCoef}{LiveTime}$$

NucCoef is normally the inverse of efficiency times the branching ratio. Note that the efficiency is the ABSOLUTE counting efficiency for the source/detector geometry being used. Thus, in order to get meaningful activity results, as in any counting situation, you need to have efficiency factors which are appropriate to the actual counting geometry. If *NucCoef* is set to 1, you will get peak count rate on the display.

LiveTime is the current live time.

NetCounts is computed with the following equation:

$$NetCounts = GrossCounts - Background$$

GrossCounts is the sum of the counts in the ROI, excluding the first and last 3 channels of the ROI.

Background is:

$$Background = \frac{AvgCount\ first\ 3\ chan + AvgCount\ last\ 3\ chan}{2} \cdot ROIWidth$$

ROIWidth is:

$$ROIWidth = EndChannel - StartChannel + 1 - 6$$

Uncertainty (in percent) is calculated as follows:

$$Uncertainty = \frac{\sqrt{GrossCounts + Background \cdot \frac{ROIWidth}{6}}}{NetCounts} * 100$$

Peak is the position of the maximum count and is computed with the following equation:

$$Peak = MaximumROIChan * EnergySlope + EnergyIntercept$$

MaximumROIChan is the channel in the ROI with the most counts. If there are no data, the center channel of the ROI is used.

EnergySlope and *EnergyIntercept* are the energy calibration values as entered by keypad (on digiDARTs) or by software. If the values are not present, the result is given in channels.

5.2.11.3. Gain and Zero Stabilization

The gain stabilizer requires a peak in the spectrum to monitor the changes in the gain of the system amplifier. The gain stabilizer controls the amplification factor of a separate amplifier so that the peak will be maintained in its original position.

The zero stabilizer enables you to control the zero-level (or offset) stabilizer. The zero-level stabilizer uses a peak in the spectrum to monitor the changes in the zero level of the system

amplifier. The zero stabilizer controls the offset bias level so the peak will be maintained in its original position.

For both functions, the input pulse-height-to-channel-number relationship is:

$$Channel\ number = Intercept + Gain * pulse\ height$$

where:

Intercept = The channel number of the zero-height input pulse
Gain = The relation between pulse height and channel number (slope of the curve)

Changes in either the intercept or gain can affect the positions of all the peaks in the spectrum. When used with the zero stabilizer, both the zero intercept and the gain (slope) will be monitored to keep all the peaks in the spectrum stabilized. The zero stabilization and gain stabilization are separate functions but both will affect the position of the peaks in the spectrum.

The stabilization operates by keeping a peak centered in an ROI you have defined. The ROI should be made symmetrically about the center of a peak with reasonably good count rate in the higher channels of the spectrum. The ROI should be about twice the FWHM of the peak. If the region is too large, counts not in the peak will have an effect on the stabilization.

Before setting either stabilization peak, the coarse and fine gains should be set to the desired values, and optimization or pole-zero performed.

5.2.11.4. ZDT (Zero Dead Time) Mode

An *extended live-time clock* increases the collection time (real time) of the acquisition to correct for input pulse train losses incurred during acquisition due to system dead time. This corrected time value, known as the live time, is then used to determine the net peak count rates necessary to determine nuclide activities.

As an example, consider the case where the spectrometry amplifier and ADC are 60% dead during the acquisition. The elapsed real time will be:

$$Real\ Time = \left(\frac{Live\ Time}{1 - 0.60} \right)$$

$$= \left(\frac{Live\ Time \times 100\%}{100\% - \%\ Dead\ Time} \right)$$

If the *N* counts in the gamma-ray peak in the spectrum are divided by the elapsed live time, the resulting counting rate, $N / Live\ Time$, is now corrected for dead-time losses. The standard deviation in that counting rate is $\sqrt{N} / Live\ Time$.

Unfortunately, extending the counting time to make up for losses due to system-busy results in an incorrect result *if the gamma-ray flux is changing as a function of time*. If an isotope with a very short half-life is placed in front of the detector, the spectrometer might start out with a very high dead time, but the isotope will decay during the count and the dead time will be zero by the end of the count. If the spectrometer extends the counting time to make up for the lost counts, it will no longer be counting the same source as when the losses occurred. As a result, the number of counts in the peak will not be correct.

When a supported ORTEC MCB operates in ZDT[18] mode, it adjusts for the dead-time losses by taking very short acquisitions and applying a correction in ***real time*** — that is, as the data are coming in — to the number of counts in the spectrum. This technique allows the gamma-ray flux to change while the acquisition is in progress, yet the total counts recorded in each of the peaks are correct. The resulting spectrum has no dead time at all — in ZDT mode, the *data* are corrected, not the acquisition time. Thus, the net counts in a peak are divided by the real time to determine the count rate.

ZDT mode has a unique feature in that it can store both the corrected spectrum and the uncorrected spectrum, or the corrected spectrum and the uncertainty spectrum. Therefore, supported MCBs allow you to choose between three **ZDT Mode** settings on the ADC tab under **MCB Properties...**: **Off**, **NORM_CORR**, and **CORR_ERR**.

- **Off — Uncorrected Spectrum Only**
  In this mode, only the uncorrected spectrum (live time and real time with dead-time losses) — also called the *live-time-corrected* or *LTC* spectrum — is collected and stored in the .SPC file. The LTC spectrum can be used to determine exactly how many pulses at any energy were processed by the spectrometer. The corrected spectrum gives the best estimate of the total counts that would have been in the peak if the system were free of dead-time effects. The uncertainty spectrum can be used to calculate the counting uncertainty, channel by

[18]U.S. Patent 6,327,549.

channel, in the corrected spectrum.

NOTE When the spectrometer is placed in ZDT mode, the throughput of the instrument is reduced somewhat as extra processing must be done on the spectrum; therefore, if the gamma-ray flux is not changing as a function of time, but absolute highest throughput is desirable, you may wish to store only the LTC spectrum in the MCB memory.

- **NORM_CORR — ZDT and Uncorrected Spectra Stored**
  When the ZDT mode is set to **NORM_CORR**, the two spectra stored are the LTC spectrum and the ZDT spectrum (corrected for the dead-time losses; real time only). Unfortunately, in the analysis of the ZDT spectrum, the uncertainty of the measurement cannot be determined using either spectrum.

  NOTE This mode is not useful for quantitative analysis if the counting rate varies significantly during the measurement time, particularly if the user desires an accurate counting rate and standard deviation calculation. *When you select the NORM_CORR mode, GammaVision ignores the ZDT spectrum and analyzes the LTC spectrum as it would for the **Off** ZDT mode.*

- **CORR_ERR — ZDT and Error Spectra Stored**
  In the **CORR_ERR** mode, the estimation of the statistical uncertainty is stored in place of the LTC spectrum, and is referred to as the *error spectrum* (ERR). In this mode, the ZDT spectrum is used to measure the counts in a peak, and the error spectrum is used to determine the uncertainty of the measurement made in the corrected spectrum.

  For example, if the area of a peak is measured in the corrected spectrum by summing channels 1000 to 1100, the variance of the measurement can be determined by summing the counts in channels 1000 to 1100 in the error spectrum. Or, shown another way, the counts in channel i can be expressed as $N(i) \pm \sqrt{V(i)}$ with a 1-sigma confidence limit, where N is the corrected spectral data and V is the variance (error) spectral data.

  The live time is set to the real time within the analysis engine during the analysis of ZDT spectra.

Table 3 shows which spectra are collected in the three possible ZDT modes.

Table 3. ZDT Modes.

Mode	Uncorrected Spectrum	ZDT Corrected Spectrum	ZDT Error Spectrum
Off (ZDT Disabled)	Yes	No	No
NORM_CORR (ZDT–LTC Mode)	Yes	Yes	No
CORR_ERR (ZDT–ERR Mode)	No	Yes	Yes

Choosing a ZDT Mode

When the counting rate is essentially constant during the time required to acquire the spectrum, the standard mode — **ZDT Off** — is the preferred mode; only the uncorrected spectrum is collected and stored in the spectrum file. But, if the counting rate varies significantly during the measurement time, the standard mode will not yield the proper dead-time-corrected counting rate. This can be most easily understood by noting that the uncorrected mode compensates for dead-time losses by extending the real counting time. Hence a sample containing both a short-lived high-activity isotope and a long-lifetime lower-activity isotope will experience very high dead-time losses during the first few seconds of the measurement, as the short-lifetime isotope decays rapidly. This high dead time will cause the counting time to be extended after the short-lived isotope has decayed to zero activity, and the system will count the low-activity isotope for the extra time. Consequently, the average activity of the short-lived isotope will be underestimated.

If you anticipate significantly varying counting rates during the time taken to acquire the spectrum, the **CORR_ERR** ZDT mode should be used. The **CORR_ERR** mode corrects for dead-time losses over minuscule time intervals by adding counts to the ZDT spectrum in proportion to the instantaneous ratio of real time to live time. Thus, the dead-time correction can correctly track rapidly changing counting rates. The **CORR_ERR** mode should be used whenever the counting rate may change significantly during the measurement time. In addition to the rapidly decaying isotope example above, the **CORR_ERR** mode should be used when monitoring cooling water flow from a nuclear reactor. The **CORR_ERR** mode accommodates brief bursts of high-activity in the water flowing past the gamma-ray detector. Both the corrected and error spectra are stored in the resulting spectrum file.

Note that the counts in the ZDT spectrum must be divided by the elapsed REAL time to compute the dead-time corrected counting rate. It is important to note that the standard deviation in the N_{ZDT} counts in a gamma-ray peak in the ZDT spectrum is not $\sqrt{N_{ZDT}}$. Instead the standard deviation is obtained from the N_{ERR} counts in the same peak ROI in the accompanying error spectrum. The standard deviation in this case is $\sqrt{N_{ERR}}$. And the standard deviation in the computed count-

ing rate, $\sqrt{N_{ZDT}} / Real\ Time$, is $\sqrt{N_{ERR}} / Live\ Time$.

The NORM_CORR Diagnostic Mode

Why is there a **NORM_CORR** mode, and why should you avoid using it? This mode simultaneously collects the ZDT spectrum and the conventional uncorrected spectrum. It is useful for demonstrating that the counts in the uncorrected spectrum divided by the live time is the same counting rate as the counts in the ZDT spectrum divided by the real time, in the special case of constant counting rate. Because the error spectrum is not collected in **NORM_CORR** mode, the standard deviation in the ZDT counts cannot be calculated if the counting rate is varying.

GammaVision provides some protection for users if the **ZDT-LTC** mode is inadvertently selected. In this case, GammaVision ignores the ZDT spectrum and presumes you intended to use the uncorrected spectrum in a constant-counting-rate application.

To summarize:

- Use the ZDT **Off** mode when the counting rate is expected to be constant during the time taken to acquire the spectrum.
- Use the ZDT **CORR_ERR** mode when the counting rate is expected to change or might change significantly during the time required to acquire the spectrum.
- Avoid using the **NORM_CORR** mode because GammaVision V9 will default to analyzing the LTC spectrum and will ignore the ZDT spectrum.

More Information

Visit our website or contact your ORTEC representative for more detailed information:

- Application note AN56, "*Loss Free Counting with Uncertainty Analysis Using ORTEC's Innovative Zero Dead Time Technique,*" (http://www.ortec-online.com/pdf/an56.pdf)
- General gamma spectroscopy technical papers (http://www.ortec-online.com/papers/reprints.htm#General)

5.2.11.5. InSight Mode

The **InSight** display (Fig. 88) shows the actual sampled waveform in the digital processing units on a reference graticule. The Properties dialog remains active and can be used to change settings while viewing the pulses. As none of the traditional analog signals are available in digital MCBs, this mode is the only way to display the equivalent amplifier output pulse. Note that at

the bottom of the window the marker channel is displayed in units of time.

To exit the InSight mode and return to the PHA display, press **<Esc>** or go to the **Insight** section on the Amplifier 2 tab and click on **Stop**. The PHA mode is set to STOP when in the InSight mode.

InSight Mode Controls

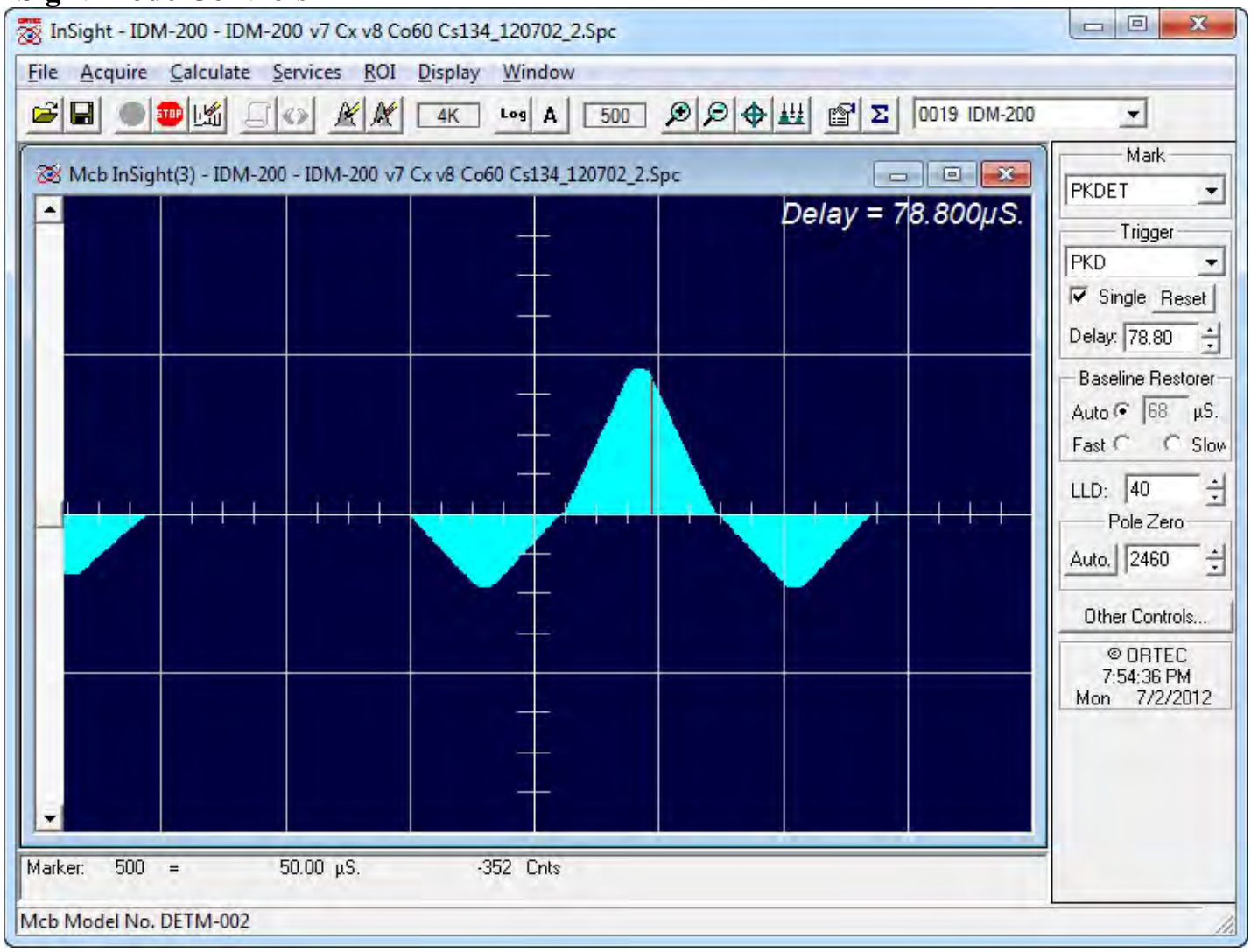


Figure 88. The InSight Mode Display.

The Status Sidebar changes from the PHA mode controls to the InSight controls for adjusting the peak display (Fig. 88) On the left is a vertical scrollbar for adjusting the vertical offset of the waveform. The value of the offset is shown on the display. Double-clicking the mouse in the scrollbar will set the vertical offset to the vertical value of the channel at the marker position. This is to conveniently zoom in on a particular part of the waveform (such as the tail for pole-zeroing).

In the **Auto** trigger mode, the display is updated every time a new pulse exceeds the trigger level. To keep a single pulse displayed, select **Single**. Click on **Reset** to refresh the display to see the next pulse. There will usually be one or two pulses in the "pipeline" that will be displayed before any change entered will be seen. If the trigger is turned off, the display will be redrawn periodically, even if no pulse is there.

The **Delay** setting is the time delay between the pulse shown on the display and the trigger level crossing. The value of the time delay is shown on the display.

Just as for the PHA mode display, the vertical scale can be adjusted with the vertical adjustments. The display can be set to **Log** mode, but the peak shapes do not have a familiar shape in this display. The **Auto** mode will adjust the vertical scale for each pulse. The pulse is shown before the amplifier gain has been applied, so the relation between channel number and pulse height is not fixed.

The horizontal scale extends from 16 to 256 channels. The display is expanded around the marker position which means that in some cases the peak will disappear from the display when it is expanded.

The display can be switched from the current MCB to another Detector or the buffer. The other Detector will be shown in its most recent mode (PHA or InSight). The buffer will always be shown in PHA mode. When you return to the current MCB, the display will return to the InSight mode. This also holds true if you exit GammaVision while in InSight mode; on next startup, this MCB will still be in InSight mode.

The display can include a **Mark** to indicate one of the other signals shown in Fig. 89. The Mark is a solid-color region displayed similarly to that of an ROI in the spectrum. This Mark can be used to set the timing for the gate pulse. It can also be used to set the shaping times and flattop parameters to get the best performance. For example, suppose you need to obtain the best resolution at the highest throughput possible. By viewing the pulses and the pileup reject marker, the rise time can be increased or decreased to obtain a minimum of pileup reject pulses.

Figure 89. Mark List.

Mark Types

For the **Mark,** choose either "points" or "filled" (to the zero line) display. This is controlled by the selection in the **Display/Preferences** menu item. That choice does not affect the PHA mode choice. The colors are the same as for the PHA mode. (Not all DSP MCBs support all marks.)

None No channels are marked in the display.

PUR The region marked indicates when the PUR circuit has detected pileup and is rejecting the marked pulses.

BLN This shows when the negative baseline discriminator has been triggered. Typically this signal only marks the TRP reset pulse. The signal is used internally in the live-time correction, baseline restoration, and pile-up rejection circuits.

BLRG This shows when the baseline restorer is actively restoring the baseline.

BLD This shows when the positive baseline discriminator has been triggered. The signal is used internally in the live-time correction, baseline restoration, and pile-up rejection circuits.

BUSY When the busy signal is active, **Busy** shows in the **Mark** box. It represents the dead time.

GATE This shows when the gate signal is present on the gate input connector. If the **Gate** mode on the ADC tab (see Fig. 88) is set to **Off**, then all regions are marked. If the mode is set to **Coincidence**, then the marked region must overlap the pulse peak (that is, must start before the beginning of the flattop and stop after the end of the flattop) for the pulse to be counted. If the mode is set to **Anticoincidence**, then the marked region will show the pulses that are accepted. That is, the rejected peaks will not be marked. Simply put, in all modes the accepted peaks are marked.

RESV Reserved.

PKDET This is the peak detect pulse. It indicates when the peak detect circuit has detected a valid pulse. The Mark occurs about 1.5 ì s after the pulse maximum on the display.

On the lower right of the InSight display are the shaping parameter controls. The controls are split into two groups, and the **other controls...** button switches between them. (Not all DSP MCBs support all of the controls.)

One group includes **Rise Time**, **Flattop**, **Tilt**, and the **Optimize** button. The **Rise Time** value is for both the rise and fall times; thus, changing the rise time has the effect of spreading or narrowing the quasi-trapezoid symmetrically.

The **Flattop** controls adjust the top of the quasi-trapezoid. The **Width** adjusts the extent of the flattop (from 0.3 to 2.4 ì s). The **Tilt** adjustment varies the “flatness” of this section slightly. The

Tilt can be positive or negative. Choosing a positive value results in a flattop that slopes downward; choosing a negative value gives an upward slope. Alternatively, **Optimize** can set the tilt value automatically. This value is normally the best for resolution, but it can be changed on this dialog and in the InSight mode to accommodate particular throughput/resolution tradeoffs. The **Optimize** button also automatically adjusts the pole-zero setting.

5.2.11.6. Setting the Rise Time in Digital MCBs

To achieve the best results for your application, when using a digital spectrometer, such as a DSPEC-series instrument, we recommend that you set the rise time of the pulses being processed by the digital filter to the minimum value for the resolution needed.

The pulse rise time (and also fall time) is based on the time required for each pulse to reach its peak value. This "peaking time" is about twice that indicated by the conventional time constants displayed on the front panel of commercial analog amplifiers. For example, germanium detectors are often specified at a 6-ì s time constant; this setting is equivalent to 12-ì s peaking (rise) time in our digital spectrometers.

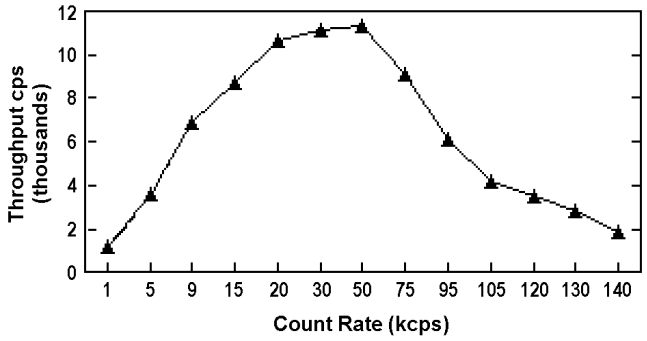


Figure 90. An Example of the Tradeoff Between Throughput and Count Rate.

Up to some value of rise time, one can expect improved resolution with increasing rise time; there will, however, be a tradeoff in maximum throughput to memory. Figure 90 illustrates an example of this tradeoff. ORTEC digital spectrometers operate well above the peak of the throughput curve. Operating there allows these instruments to handle an even higher rate of incoming counts, but with less data into memory and, therefore, a longer count time to the same detection limit. It is possible to move the peak of the curve to the right (more counts to memory with higher input count rate) by reducing the pulse rise (and fall) time, thereby trading off resolution for maximum count rate.

Table 4 is a guide to choosing a count rate that will ensure that the most efficient operation of your digital spectrometer over the range of anticipated input count rates for your application — that is, at or below the throughput peak — while achieving the best resolution obtainable from the detector

Table 4. Rise Time Selection Guide.

Input Count Rate Dynamic Range	Maximum Throughput	Rise Time (µs)
0--->20000	9000	12
0--->50000	12500	8
0--->75000	23500	4
0--->100000	37000	2.4
0--->150000	50000	1.6
0--->200k	70000	0.8
0--->220k	85000	0.6
0--->250k	100000	0.4
0--->300k	120000	0.2

consistent with that requirement. Enter the rise time that best matches your dynamic range of count rate (note that the available rise-time settings will vary by instrument; this chart is a general guide only).

The longest rise time shown in the table is 12 ì s, even though some digital instruments can be set for rise times as long as 23 ì s. If throughput is not an issue because all samples are low rate, increasing the rise time beyond 12 ì s might achieve a small improvement in resolution. For planar detectors, such as ORTEC's GLP, Si(Li), IGLET, and IGLET-X Series, operating at longer rise times frequently gives improved resolution.

5.3. Calibrate

Figure 91 shows the **Calibrate** menu. GammaVision's calibration features include a **Calibration Wizard** to simplify the energy and efficiency calibrations as well as a fully implemented true-coincidence correction (TCC) calibration. This menu also allows you to access the energy and efficiency calibration features directly from the menu rather than stepping through the wizard.

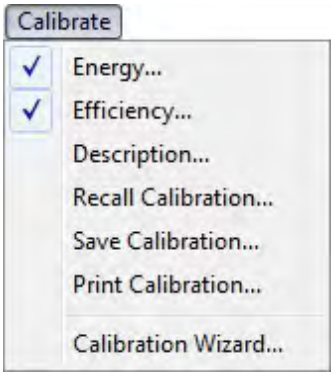


Figure 91. Calibration Menu.

The energy and efficiency calibrations of the spectrum in the Detector, and the calibration wizard are only available if the Detector is not acquiring data. If there is no energy calibration, then all choices except **Energy...**, **Recall Calibration...**, and **Calibration Wizard...** are inactive (gray). If the efficiency calibration exists, there will be a checkmark by the menu item.

5.3.1. General Information, Cautions, and Tips

The calibration of the system defines four relations:

- Spectrum channel numbers and energy
- FWHM of the peak and energy
- Spectrum count rate and activity in becquerels or other units
- True coincidence summing factor and energy

The data collected are in counts/unit time/channel; however, to be most useful, these data need to be converted to activities (i.e., decays/unit time at a given energy). The calibration parameters do this conversion.

These relationships are calculated from spectra, user inputs, and inputs from libraries and tables. The calibration data are merged with the spectrum when it is saved as an .SPC file. The information is used in the analysis section to perform the desired analysis. Spectra saved in the .CHN

format are compatible with older software, however the .CHN format does not contain the efficiency or TCC calibration data.

The energy calibration and the efficiency calibration are separated to make it easier to do these calibrations. The efficiency and TCC calibrations are linked because the TCC depends on the detector/source geometry. If properly chosen sources and libraries are used, the calibration process is simple, quick and accurate. The input values can be saved so that repeated calibrations with the same source are easy and simple.

The energy calibration can be changed without affecting the efficiency calibration. By using the **Recall Calibration...** command, the previously calculated efficiency calibration can be inserted into the new calibration data.

5.3.1.1. For Best Calibration Results

It is important that the energy, efficiency, and TCC calibrations be done correctly because the calibration results will affect all analyses employing them. The energy calibration data is used to define the energies of the peaks in the spectrum. If incorrect, the calculated energies will not correspond to the correct library entry and the peak might be incorrectly identified. The shape parameters are used to define the expected shape for a singlet peak. If incorrect, peaks will be labeled as having a bad shape when they do not, and bad peaks will not be marked. Peaks marked with poor shape might not be included in the activity calculation, resulting in loss of accuracy even for singlet peaks. For deconvolutions, these parameters define the Gaussian shape used for the components of the total peak area. Incorrect peak shapes can result in poor deconvolution results and even incorrect peak height ratios in multiplets.

An incorrect efficiency calibration can cause the nuclide activity to be incorrectly reported. The knee value, if incorrectly chosen, can cause poor results near the knee, especially below the knee.

Using many data points near the knee aids in selecting the correct knee energy. A poor choice of type of fit can result in a good fit to poor data, which will yield a poor efficiency calibration.

NOTES During efficiency calibration, the net peak area calculation can be affected by the library **Match Width** setting in effect at the time the calibration is performed. Before starting an efficiency calibration, go to the System tab under **Analyze/Settings/ Sample Type...** (page 152) and make sure the **Match Width** is set to the same value you will be using during analysis. Most users will keep the default setting, 0.5. If using a different setting, we recommend a value between 0.4 and 0.75.

For TCC calibrations, the library and TCC table should include only the nuclides present in the spectrum. In addition, note that when recalling the TCC calibration from a

File in the Calibration Wizard, *the TCC efficiency calibration from the same file must also be recalled; otherwise, the TCC calibration loaded may not be complete and will not produce accurate results.*

5.3.2. Energy...

5.3.2.1. Introduction

The **Energy...** calibration function calculates two sets of parameters: the energy vs. channel number, and the peak shape or FWHM vs. energy. The inputs to this function are a spectrum or series of spectra with isolated peaks distributed over the energy range of interest, and either a library or table of peak energies. The library referred to here is an analysis gamma-ray library. The creation of a table of peak energies is described in this section.

The formula for energy vs. channel number is:

$$E = a_1 + a_2 C + a_3 C^2 \quad \textbf{(8)}$$

where:

E = energy
a_i = coefficients
C = channel number

The formula for FWHM vs. channels is:

$$F = b_1 + b_2 C + b_3 C^2 \quad \textbf{(9)}$$

where:

F = FWHM in channels
b_i = coefficients
C = channel number

To calculate the FWHM in energy use the following:

$$F(e) = F(c)\,(a_2 + 2a_3 * C) \quad \textbf{(10)}$$

where:

$F(e)$ = FWHM in energy
$F(c)$ = FWHM in channels at channel C
a_2 = energy calibration slope defined in Eq. 8

a_3 = energy calibration quadratic coefficient defined in Eq. 8
C = channel number

When the FWHM fit is made, the fit is automatically checked for validity. If the FWHM curve is negative at any part of the spectrum or the curve bends over (has a maximum and then goes down), a warning message, **Non-physical FWHM fit**, is displayed. Click **OK**, then display the FWHM curve to see why the fit is incorrect. Also, if the delta between the data points and the FWHM fit is greater than 25%, a message is displayed. The curve can be accepted if the warning is due to the fit outside the energy of interest, or some of the data points might need to be deleted. The calibration spectrum should have good peaks with many counts, so counting longer might remedy the poor fit.

The same methods used to calculate the peak centroid and width in the **Calibrate** section are used in the **Analyze** section. This ensures consistency of results.

The energy calibration is done using the spectrum in the buffer or the Detector. The calibration is linked to the spectrum used and is transferred with it when the spectrum is transferred (e.g., from Detector to buffer or disk file).

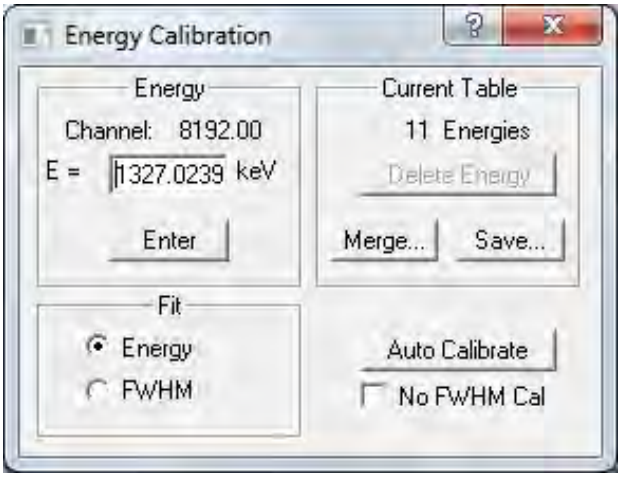


Figure 92. Energy Calibration Sidebar.

The first step in the calibration is to collect a spectrum of a known source with isolated peaks. The spectrum peaks must be well-defined with a small statistical uncertainty. When the Detector has finished collection (i.e., stopped), select **Calibrate** from the menu bar, then **Energy...**. The Energy Calibration Sidebar (Fig. 92) will automatically open. The Calibration Sidebar can be moved by its title bar to another position. It is usually helpful to zoom in on the spectrum so the peaks are clearly displayed.

5.3.2.2. Auto Calibration[19]

The **Auto Calibrate** button will perform a complete energy and FWHM calibration on the displayed spectrum using the working library. This automatic calibration is suitable only for HPGe spectra and requires at least three peaks (five preferred) in the spectrum that are in the library. There can be a different number of peaks in the spectrum than in the library, that is, there can be peaks in the spectrum that are not in the library and peaks in the library that are not in the spectrum. The spectrum can be uncalibrated, calibrated, or even incorrectly calibrated. Spectra such as the mixed gamma standard or uranium ore can be used with the appropriate library.

[19]U.S. Patent 6,006,162.

Auto Calibrate works as follows: the spectrum is searched for all the major peaks, then this peak list is compared to the library peak list to find the calibration that gives the best match.

NOTE If the **No FWHM Cal** checkbox on the Energy Calibration sidebar is marked, the FWHM calibration is not changed during calibration. This might be desirable when decay of short-lived isotopes in a calibration source results in peaks that are adequate for an energy calibration but whose shape might not be optimal for the FWHM calibration.

5.3.2.3. Manual Calibration

NOTE Low Resolution systems (i.e., NaI, LaBr, CsI, etc.) must be calibrated for Energy and FWHM using this Manual Calibration method, and each peak used in the calibration should be marked with a Region of Interest (ROI) that fully covers the entire peak including the background channels.

If there is no energy calibration, the energy of one or two known peaks must be entered. Using the Full Spectrum View, select a peak in the high energy (channel) part of the spectrum. When this part of the spectrum is visible in the expanded display, move the cursor to the known peak. For Low Resolution systems an ROI must be marked around the peak. At this time the centroid of the peak will be calculated and displayed in the upper part of the Energy Calibration Sidebar as, in this example, **Channel: 11342.66**. This is the channel number of the peak centroid. Now click in the **E=** input box and enter the energy of this peak. Click the **Enter** button or press **<Enter>**. A table and graph will appear on the screen (Fig. 93). They can be moved around and sized if they obscure the spectrum.

The table shows one value (the one just entered), and the graph shows a straight line fit from (energy = 0, channel = 0) to the energy and channel just entered. This is an approximate calibration; it should be fairly accurate if the zero offset is small.

The **Energy** and **FWHM** radio buttons at the bottom of the Energy Calibration Sidebar display the table and graph for either energy vs. channel (Fig. 93) or FWHM vs. energy (Fig. 94).

Click **FWHM**. The table shows the one value entered and the graph shows a horizontal line. For a single point, the FWHM is assumed to be a constant.

Using the Full Spectrum View (or the Library List window), select a peak in the low-energy part of the spectrum and move the marker to the centroid of the peak. For Low Resolution systems an ROI must be marked around the peak. Again click in the **E=** field at the top of the sidebar and enter the energy of this peak. Both the energy function and FWHM function, as well as their corresponding tables, will update with the new entry so progress can be monitored.

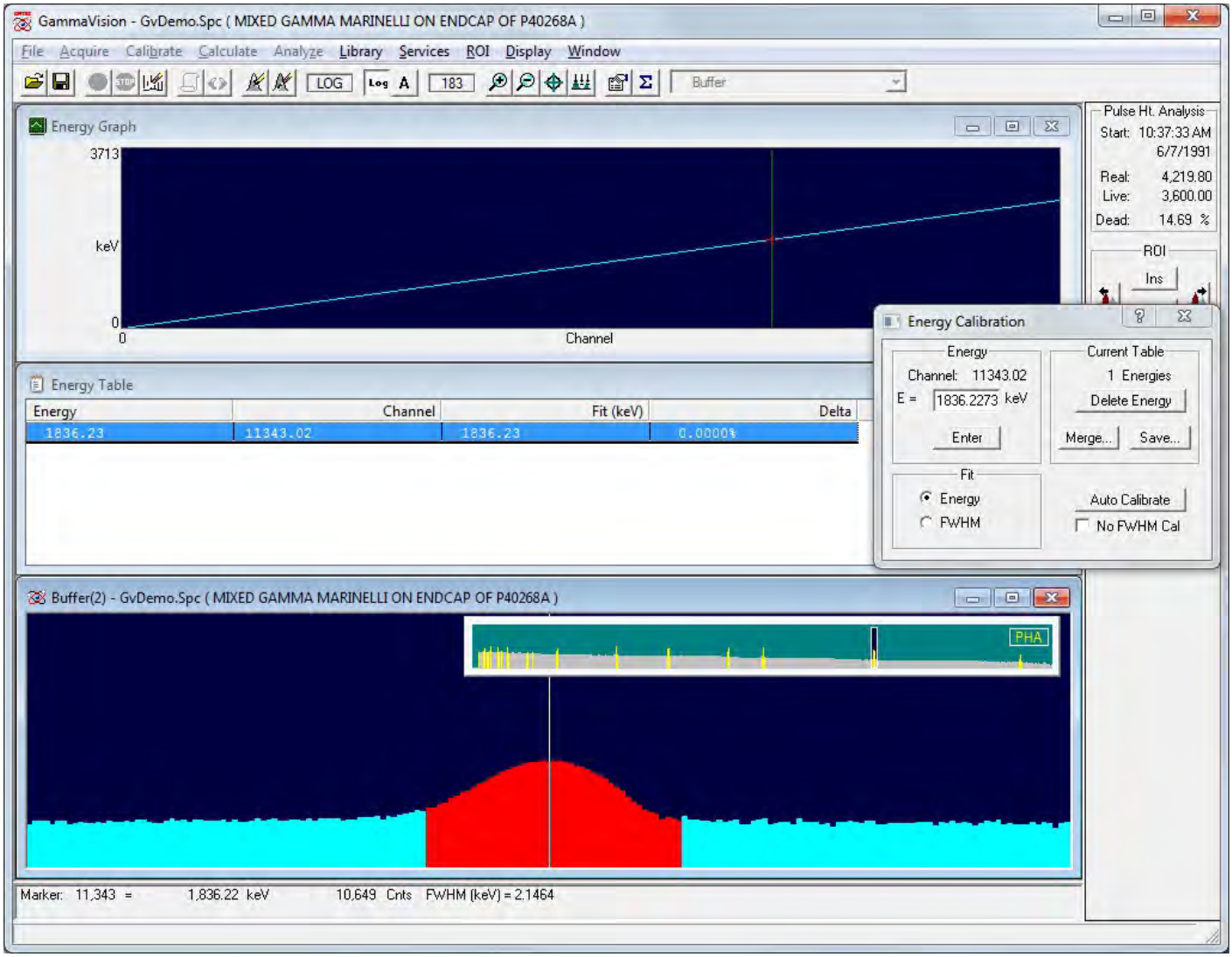


Figure 93. Energy Calibration Display.

At this time, the cursor can be positioned using the calibration graphs, calibration table, Full Spectrum View, or Expanded Spectrum View. The cursor will show the energy based on the calibration up to this point.

The calibration can be refined by adding as many points as desired. For Low Resolution systems an ROI must be marked around each peak. Any point can be deleted by selecting that point in the table of values (**Energy** or **FWHM**) and clicking on the **Delete Energy** button on the calibration sidebar. The fit updates when a point is removed.

NOTE If the **No FWHM Cal** checkbox on the Energy Calibration sidebar is marked, the FWHM calibration is not changed during calibration. This might be desirable when decay of short-lived isotopes in a calibration source results in peaks that are adequate for an energy calibration but whose shape might not be optimal for the FWHM calibration.

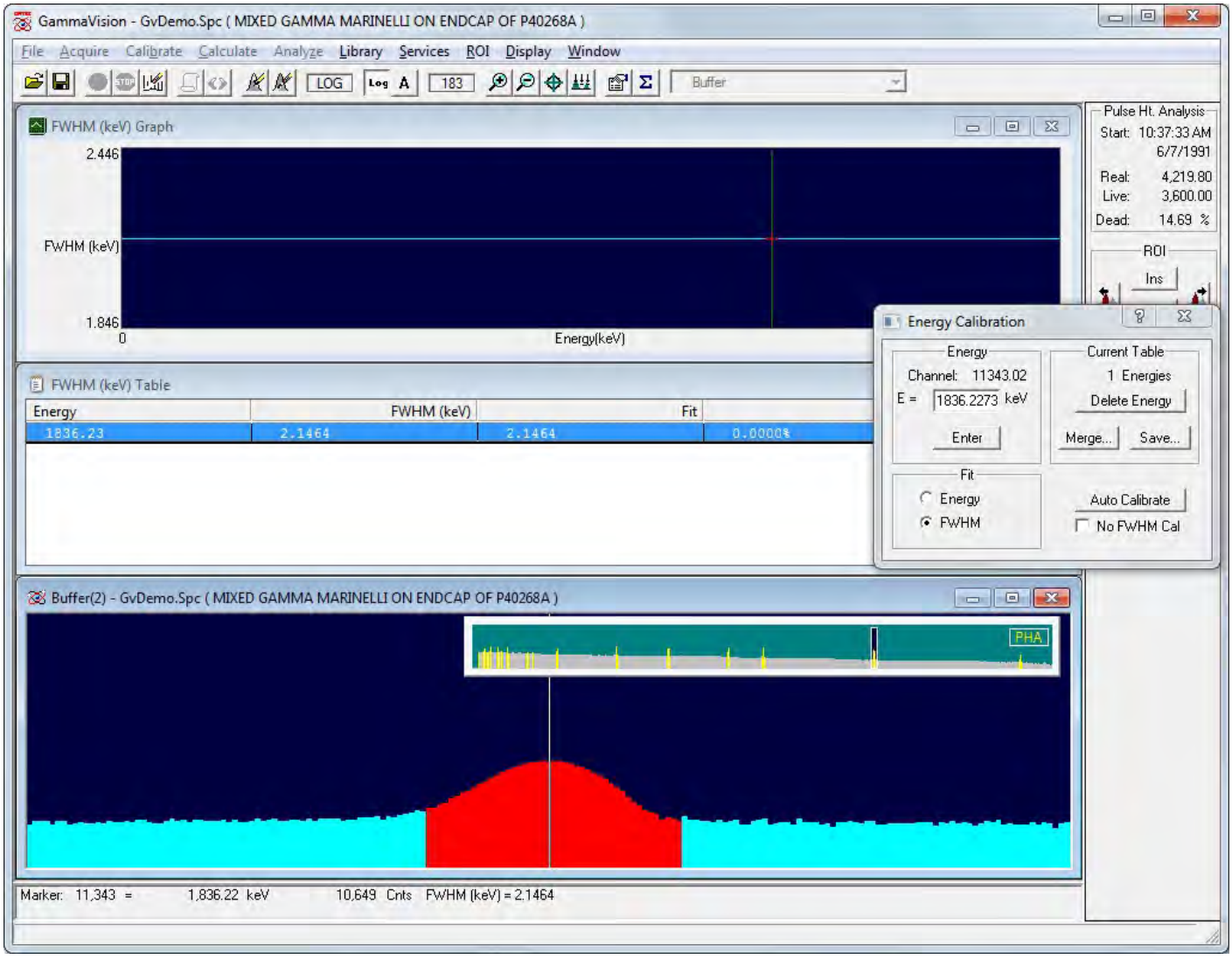


Figure 94. FWHM Calibration Display.

After the desired number of points have been entered, you can save the energy values by clicking the sidebar's **Save...** button. This opens a file-save dialog (Fig. 95).

Assign a filename and GammaVision will append the default energy-calibration extension, .ENT.

The saved table of values now contains the Energy-Channel and Energy-FWHM pairs used in the current calibration. This table can be used for future calibrations using the same nuclides. It can also be edited within GammaVision. To do this, click on the sidebar's title bar icon to open the control menu (Fig. 96). Select **Edit File...** and open the .ENT file to be edited. It will be displayed in the Energy Table Editor dialog shown in Fig. 97.

The Energy Table Editor will list each **Energy** and its associated **Channel** and **FWHM** as determined during the calibration. The values in each column can be edited. In addition, you can **Add New** rows or **Delete** existing ones. This allows you to fine-tune existing calibrations or generate calibrations using data pairs for non-ORTEC spectra. Note that if all **Channel** and **FWHM** values are deleted from the table, the **Energy** list and spectrum data will be used to generate a calibration when the table is **Merge**d as described in the next section.

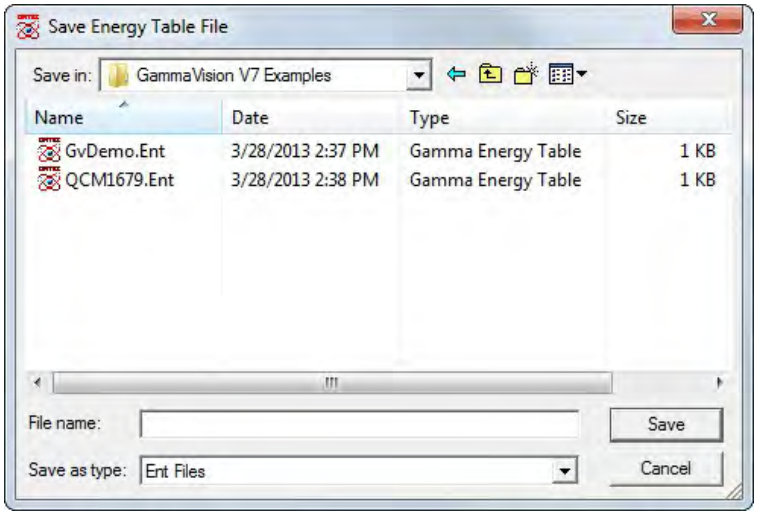


Figure 95. Save Energy Calibration Table.

Figure 96. Calibration Sidebar Control Menu.

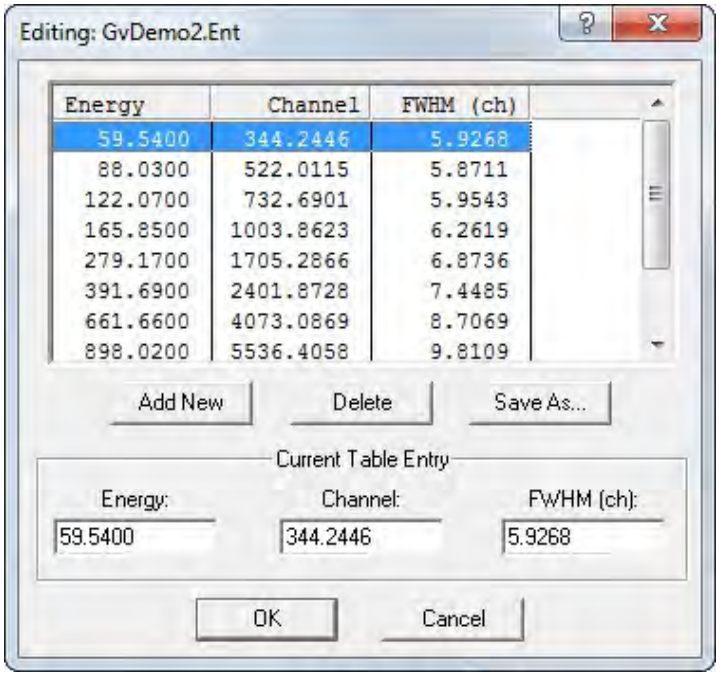


Figure 97. Editing an .ENT File in GammaVision.

After modifying the table, click **OK** to save the table in the current .ENT file, **Save As...** to save it under a different filename, or **Cancel** to close the editor and retain the original values.

5.3.2.4. Easy Recalibration Using An .ENT Table

Using the .ENT table can speed up the calibration process, as follows. For an uncalibrated spectrum, enter one or two energies to establish a basic calibration. Next, click the **Merge...** button on the Energy Calibration Sidebar to open a standard file-recall dialog (Fig. 98). Choose the .ENT file to be used. If any values exist in the **Channel** and **FWHM** columns, you will be prompted to perform a manual calibration (Fig. 99). If you select **Yes**, a calibration will be generated using the **Energy-Channel** and **Energy-FWHM** pairs from the table without regard to spectrum data. If you select **No**, peaks in the spectrum that match the energy list in the table will be evaluated for centroid energy and FWHM to generate a new calibration. When the process is complete, the new fit and table will be displayed.

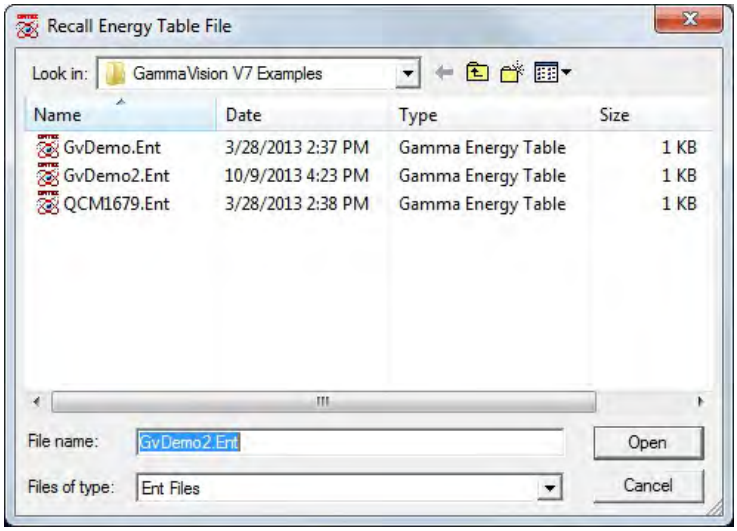


Figure 98. Recall Energy Calibration Table.

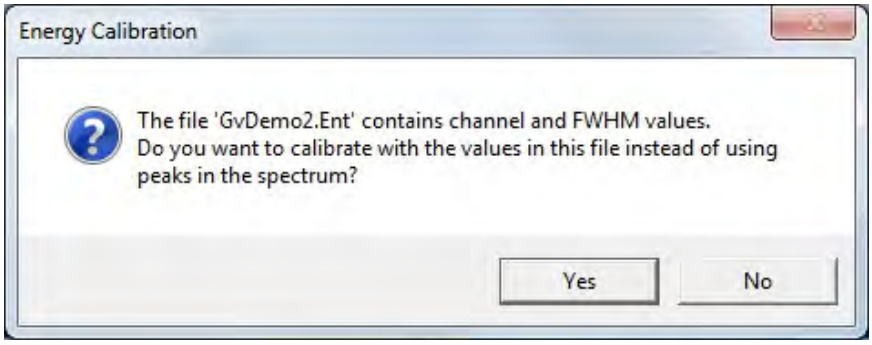


Figure 99. Perform a Manual Energy Calibration?

NOTE If the **No FWHM Cal** checkbox on the Energy Calibration sidebar is marked, the FWHM calibration is not changed during calibration. This might be desirable when decay of short-lived isotopes in a calibration source results in peaks that are adequate for an energy calibration but whose shape might not be optimal for the FWHM calibration.

5.3.2.5. Speeding Up Calibration with a Library

A library can be used to speed up the calibration process as follows. Before entering the calibration process, choose **Library/Select File...** from the menu and open a library file that contains the nuclides in the calibration source. Next, choose **Library/Select Peak...** to show the list of peaks in the library in energy order. Now select **Calibrate/Energy...**. When the table and graph appear, move the table down so the Library List is not covered (see Fig. 100). Rather than manually entering the peak energy in the Energy Calibration Sidebar's **E=** field, *click once* on the peak energy in the Library List to automatically fill the field.

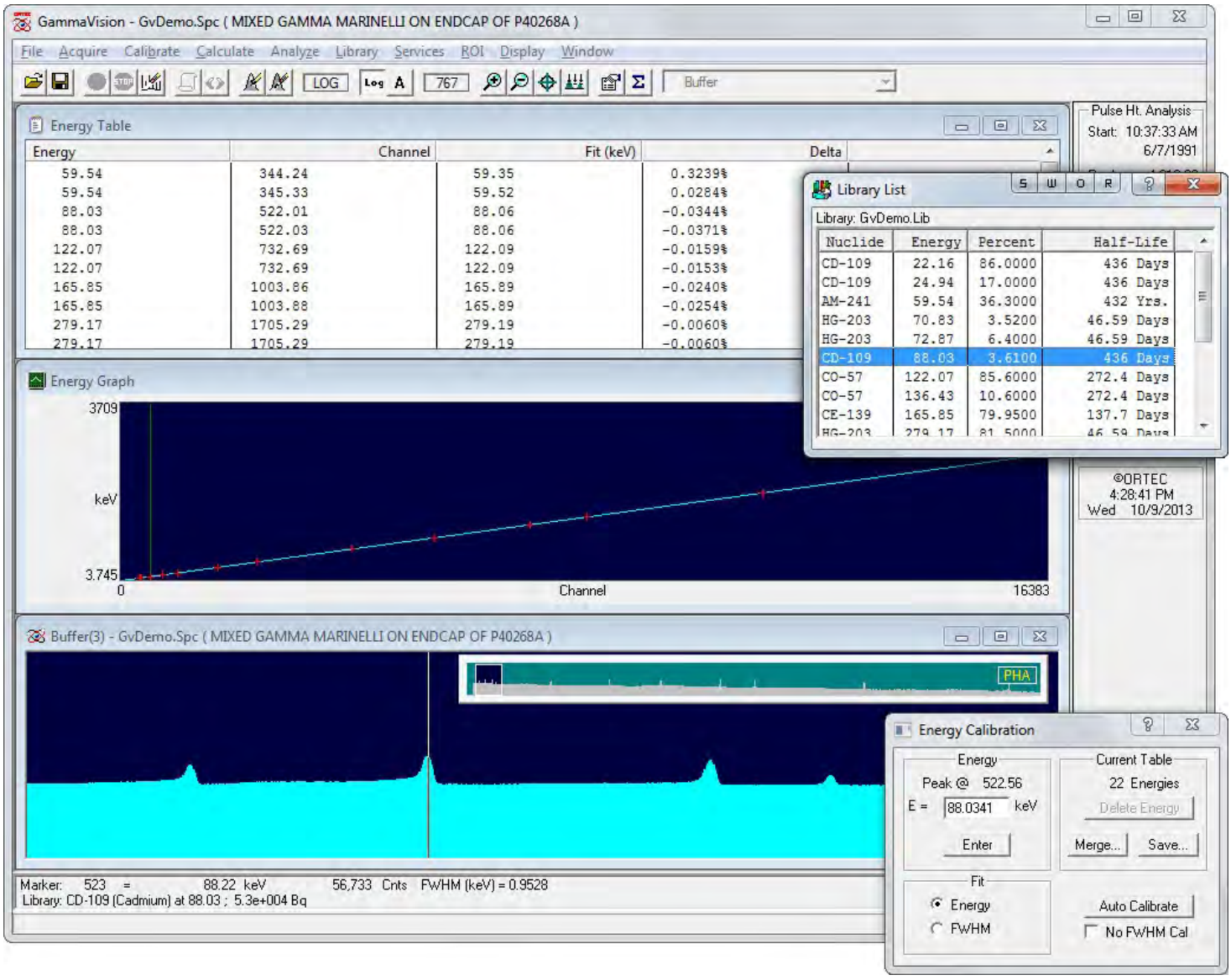


Figure 100. Speeding Up the Energy Calibration with a Library.

For a spectrum with an energy calibration, double-clicking on a library peak will cause the spectrum cursor to jump to the channel corresponding to that energy. If the calibration as it now

stands is not sufficiently accurate, the channel corresponding to that energy might be off by a channel or two. If this is not the correct peak channel, move the cursor to the correct channel, click *once* on the library peak, and press **<Enter>**.

NOTE If the **No FWHM Cal** checkbox on the Energy Calibration sidebar is marked, the FWHM calibration is not changed during calibration. This might be desirable when decay of short-lived isotopes in a calibration source results in peaks that are adequate for an energy calibration but whose shape might not be optimal for the FWHM calibration.

To exit the calibration function, click the Energy Calibration Sidebar's Close button. This will close the calibration function, and the new calibration will be held in memory, available for subsequent spectra gathered on this Detector. To save the calibration to disk, select **Save Calibration...** from the **Calibrate** menu.

5.3.2.6. Other Sidebar Control Commands

The remaining items on the sidebar control menu are **Move**, **Close**, **Restore**, **Clear Table**, and **Destroy**. **Destroy** clears all energy calibration values. **Restore** reinstates the internal energy calibration table to the values stored when the calibration function was entered. **Clear table** erases all the values in the table, but retains the function (energy and FWHM) to be used when the next values are entered. In this way, a recalibration can be done without manual entry of any points. **Close** exits the **Energy...** calibration function and saves the current calibration as the working calibration.

5.3.2.7. Using Multiple Spectra for a Single Calibration

To use more than one source (when simultaneous collection is not possible) to make a single calibration:

1) Collect a spectrum with one source or calibrate with this spectrum.
2) Exit the calibration function.
3) Clear the Detector.
4) Collect the spectrum of the second source.
5) Calibrate by adding the new lines to the existing ones (which are retained).

The process can be repeated for additional sources. When completed, the calibration should be saved on disk. The individual spectra can be saved or used in other application software. In addition, the calibrations in the spectra can be updated by recalling each spectrum in turn, recalling the complete calibration, and re-saving the spectrum.

To use more than one *stored* spectrum to make a single calibration:

1) Calibrate using one spectrum.
2) Exit the calibration function.
3) Save the calibration in a file.
4) Recall the second spectrum.
5) Recall the calibration (because recalling the spectrum has replaced the first calibration with the calibration from the spectrum).
6) Select **Calibrate/Energy...** and enter the peak energies for the second spectrum.

The process can be repeated for additional spectra.

5.3.3. Efficiency...

5.3.3.1. Introduction

The **Efficiency...** calibration function calculates the detection efficiency of the HPGe detector system as a function of energy. The efficiency of the detector system is the relation between the number of gamma rays emitted from the source to the number of gamma rays collected in the full-energy peak.

The HPGe detector system efficiency includes effects from the detector itself, the detector/source geometry, the materials surrounding the detector, and absorption in the source material or matrix (Fig. 101).

In general, it is not good practice to use efficiency calibrations from one detector/source geometry for other geometries. Therefore, different calibration files should be made for all the different detector/source combinations to compensate for the differences between the geometries. It might be useful to assign calibration files names that give some indication of the detector/source geometry to which they apply.

In addition, you should always make sure the library **Match Width** setting (on the System tab under **Analyze/Settings/Sample Type...**; see page 152) in effect during efficiency calibration is the same setting you will be using during sample analysis. This is because the net peak area calculation can be affected by the **Match Width** setting. The default setting is 0.5. If using a different setting, we recommend a value between 0.4 and 0.75.

Since the efficiency is defined as a function of energy, the **Energy...** calibration must be done first. The **Efficiency...** command remains disabled (gray) until the spectrum has been energy calibrated.

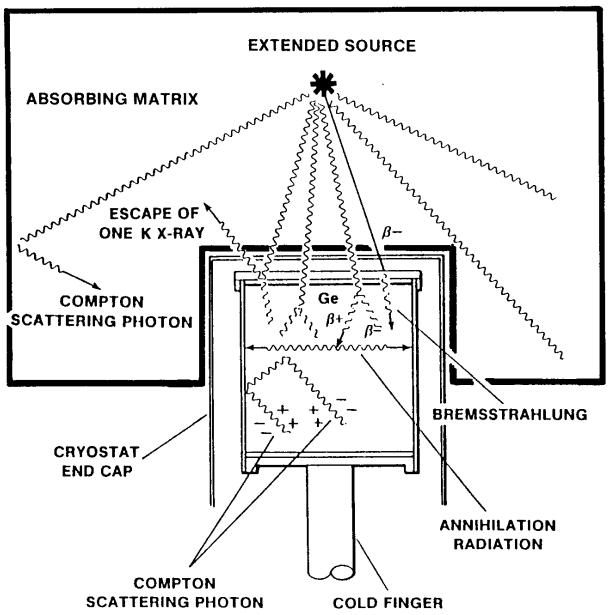


Figure 101. Detector with Extended Source.

The energy recalibration can be redone (to account for gain changes) without the need to redo the efficiency calibration.

P-type germanium detectors, such as the ORTEC GEM Series, have a maximum efficiency at about 150 keV; for n-type detectors, such as the GMX Series, it is about 100 keV. For detectors above about 50% relative efficiency, these values will be somewhat higher (Fig. 102). For both types, these maxima, or knee values, depend on the individual detector. For p-type GEM detectors, the efficiency goes down as the energy goes down from the knee. For n-type GMX detectors, the efficiency is nearly constant at energies below the knee. For both types, the efficiency goes down at energies above the knee.

The efficiency calibration is critically important to the accuracy of the activity results from GammaVision. It is recommended that only calibrated sources traceable to a known standard be used. The time between the calibration of the radionuclide source by its manufacturer and the time the spectrum is collected is important, as this defines the decay correction needed to calculate source strength for the spectrum.

A source should be selected that contains isolated singlets over the entire energy range of interest. If the energy region near the knee is important to the analysis, several points around the knee should be used for both the two-function and polynomial type of fits. If you wish, you can perform the efficiency calibration using one or more spectra to minimize the difficulty of obtaining the required number of singlets.

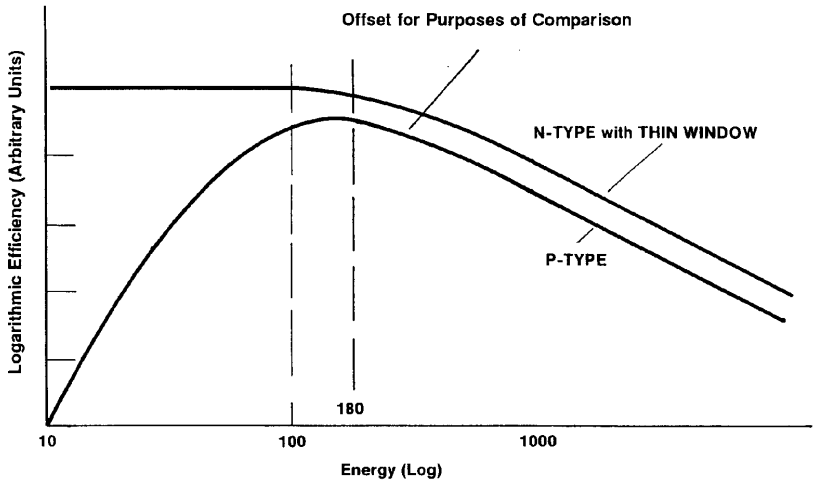


Figure 102. Detector Efficiency as a Function of Energy.

GammaVision calculates and stores the counting uncertainty in the calibration record, similar to the way the fit uncertainty is calculated and stored. There is an above-the-knee counting uncertainty and a below-the-knee counting uncertainty. Above-the-knee counting uncertainty is the averaged counting uncertainty of all the calibration peaks with energy above the knee energy. Below-the-knee counting uncertainty is the averaged counting uncertainty of all the calibration peaks with energy below the knee energy. Both are stored in the calibration data record. See the discussion in Section 6.12.7.

To perform the calibration, you need an energy-calibrated spectrum of the radionuclides and their source strengths and calibration dates. These data are entered into GammaVision in convenient menu-type forms, and you can review the results of each step. Questionable points can be deleted, additional points added, and the fitting process repeated until the desired result is obtained.

If there are many well-separated peaks, GammaVision can use two energy regions for separate fitting. The energy separating the two regions (called the knee) is specified by you. The best fit to the two regions is often obtained by entering a knee energy that corresponds to a region where the efficiency is slowly varying and not at the maximum point. This is usually about 400 keV to 500 keV. By using the calibration plotting feature, the effect of the knee energy can be seen and the best value can be easily determined.

There are several options for the type of fit used to describe the efficiency/energy relationship (see Fig. 103). These are:

Figure 103.

1) **Interpolative** fit.

2) **Linear** fit of the natural logarithm of the efficiency to the natural logarithm of the energy.

3) **Quadratic** fit of the natural logarithm of the efficiency to the natural logarithm of the energy.

4) **Polynomial** fit of the natural logarithm of the efficiency to the energy.[20]

5) **TCC Polynomial**, a different six-order polynomial fit of the natural logarithm of the efficiency to the natural logarithm of the energy.

Options 1, 2, and 3 can be selected separately for two separate energy regions. Either of the two regions might be left uncalibrated by not including any points in the region, but the analysis will report zero activity (in the library peak output) for peaks in the uncalibrated region. If both regions are calibrated, the above-the-knee energy region is fitted first, and the calculated efficiency at the knee is included as a data point in the below-the-knee fit. This means that only one point need be below the knee, but two points are the minimum above the knee for a calibration to be done. Option 4 fits the entire energy range with one function and is best suited to p-type detectors. Option 5 fits the entire energy range with different functions over three energy regions and can be used for p- or n-type detectors. The combination of fit methods above and below the knee that best fit the measured efficiency data points should normally be used.

If you select **None** for the **Above** and/or **Below** energy range, no peak activities are calculated for that range.

5.3.3.2. Interpolative Fit

NOTE The Interpolative Fit method may be the best option for Low Resolution systems as the other methods may not produce a good fit based on the shape of the calibration.

The interpolative fit uses straight lines between the data points and does a linear interpolation between two points (one above and one below) to obtain the efficiency at the selected energy. For energies below the minimum energy data point or above the maximum data point, the efficiency is the straight-line projection of the last two data points at the appropriate end. The interpolative fit is used where the efficiency is recognized to be a complex function of energy that cannot be fit using the other functions.

[20]"Définition de Criteres de Qualité Pour l'Essai des Logiciels Utilisés en Spectrométrie Gamma," Rapport CAE-R-5347, 1986.

If interpolative fit is used over the entire energy range, the knee energy should be set below the minimum energy of interest.

The efficiency/energy formula is:

$$\varepsilon = \varepsilon_1 + (\varepsilon_2 - \varepsilon_1) * (E - E_1) / (E_2 - E_1) \quad \textbf{(11)}$$

where:

- ε = efficiency at energy E
- E = target energy to determine efficiency
- ε_1 = efficiency at energy E_1
- E_1 = the energy point below the target energy
- ε_2 = efficiency at energy E_2
- E_2 = the energy point below the target energy

5.3.3.3. Linear Fit

The linear fit uses a straight-line fit to the data points. This is used when few data points are used or if the data points are all very close in efficiency.

The efficiency/energy formula is:

$$\varepsilon = e^{(a_1 + a_2 \cdot \ln(E))} \quad \textbf{(12)}$$

where:

- ε = efficiency at energy E
- a_i = fitting coefficients
- E = energy

5.3.3.4. Quadratic Fit

The quadratic fit fits a quadratic function to the log (energy) vs. log (efficiency) curve. At least three data points above the knee and two below the knee are required for this fit. With only three points, the fit will be reported as exact for all data points, but the calibration might be inaccurate elsewhere.

If the input points are not well separated, the best fit to the data points might not be an accurate representation of the efficiency outside the fitted region.

The efficiency/energy formula is:

$$\varepsilon = e^{(a_1 + a_2 \cdot \ln(E) + a_3 (\ln(E))^2)} \quad \textbf{(13)}$$

where:

ε = efficiency at energy E
a_i = fitting coefficients
E = energy

5.3.3.5. Polynomial Fit

The polynomial fit uses a 6-term polynomial to fit the natural logarithm of efficiency to the energy. At least five well-separated peaks are required. The function is optimized for p-type detectors. For n-type detectors, the low-energy region (below 60 keV) is not well modeled by this function, and GammaVision performs an interpolative fit instead.

This option is only on the Above knee list, and selecting it disables the knee value and the Below knee fit.

The polynomial efficiency/energy formula is:

$$\varepsilon = e^{\left(\sum_{i=1}^{6} a_i E^{2-i} \right)} \quad \textbf{(14)}$$

where:

ε = efficiency at energy E
a_i = fitting coefficients
E = energy in MeV

The result of the efficiency calibration calculation is one or two sets of coefficients (one for the fit above the knee and one for below the knee, or just one for the polynomial fit), and a set of energy-efficiency pairs. The energy-efficiency pairs are used for the interpolative fit. The pairs might also be used to recalculate the efficiency and to display the efficiency plot.

5.3.3.6. TCC Polynomial Fit

The TCC polynomial fit is several polynomial fits to different energy parts of the spectrum (up to a six-order polynomial). The different energy regions are below 200 keV and above 200 keV. The details of the polynomial fit are given in the papers referenced below.[21,22,23] This fit can be used for p- or n-type detectors, and is used in the GammaVision TCC correction method.

5.3.3.7. Performing the Efficiency Calibration

To efficiency calibrate the system, collect an energy-calibrated spectrum of the known standard for a time sufficient to get well-formed peaks with small uncertainty. The certificate supplied with the source will have the energies, gammas/sec, nuclide names, and measurement date needed in the calibration.

The working library is used in the calculations. Load the library for the calibration source as shown in Section 3.2.3 or 5.6.2.

Expand the spectrum horizontally to show the peaks completely. Select **Calibrate** from the menu, then **Efficiency**. This will open the Efficiency Calibration Sidebar (Fig. 104). If the **Efficiency** item is disabled (gray), the system is not energy calibrated. Because there is yet no efficiency calibration, no graphs or tables are shown. Choose a spectrum peak listed in the source data sheet.

Use the Full Spectrum View (Fig. 105) to approximately locate the peak, or use the Library List and the Expanded Spectrum View to put the marker on the center of the peak. This selects the peak. The peak area and count rate are calculated in the same manner as in the analysis program.

Click the **Calc...** button to open the Efficiency Calculation Worksheet for entering the data about the peak (Fig. 106).

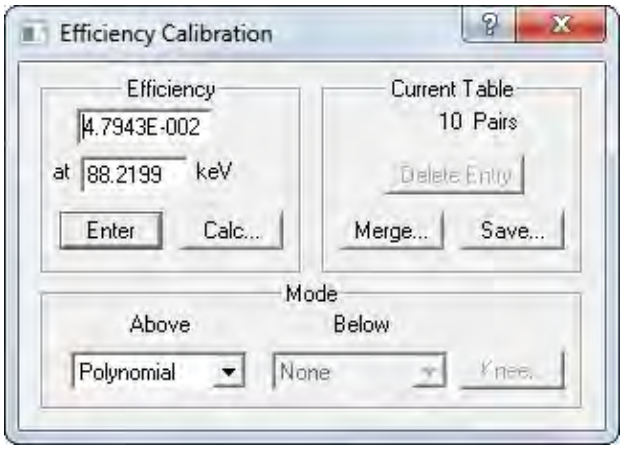


Figure 104. Efficiency Calibration Sidebar.

[21]M. Blaauw, "The use of sources emitting (ã)-rays for determination of absolute efficiency curves of highly efficient Ge detectors," NIM A322, 1993, pp. 483–500.

[22]R. Gunnink, "New method for calibrating a Ge detector by using only zero to four efficiency points," NIM A299, 1990, pp. 372–376.

[23]Gunnink, R., and A.L. Prindle, "Nonconventional methods for accurately calibrating germanium detectors," *J. Radioanalytical and Nuclear Chemistry*, 160(2), 1992, pp. 304–314.

In the **Assay (from Certificate)** section of the dialog, enter the calibration **Date** and **Time** from the source data sheet. Enter the **Activity** from the source and select the units from the droplist.

Figure 105. Select Peak in Full Spectrum Window.

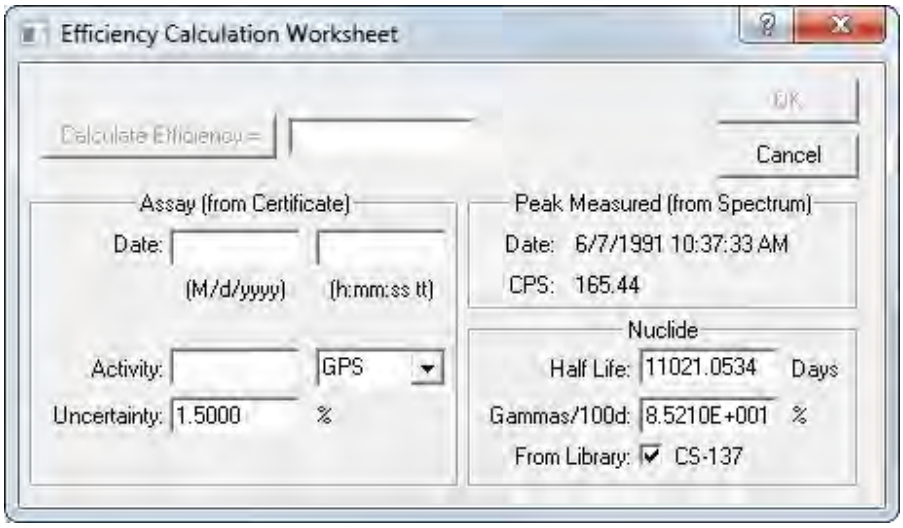


Figure 106. Efficiency Calculation Worksheet.

The source **Uncertainty** is at the 1-sigma confidence level. This uncertainty is used in the total uncertainty calculation.

When the values are correct, click the **Calculate Efficiency =** button at the top of the dialog and the calculated efficiency will be entered in the field beside the button. If this value is acceptable, click **OK** to save the input and efficiency values and leave the worksheet. The graphs and tables will now be displayed.

Select the next peak and repeat the process. The **Date** and **Time** will default to the previously entered values, but the **Nuclide Half-Life** and **Activity** must be entered for each energy.

As each peak (above the minimum) is entered, the table and graph will update and new fits will be made. The fitting mode can be changed at any time to see how the various functions model the data. Note that for quadratic fit, a linear fit is made for one or two points and a quadratic fit is not done until three points are entered. For a polynomial fit, no fit is made until five points are entered. Because of the separate energy regions, the TCC polynomial fit requires more points.

Any point in the Efficiency Table can be deleted by selecting the point then clicking on the sidebar's **Delete Entry** button. Any point in the table can be modified by selecting it and clicking **Calc...**. When the worksheet opens, the previously entered values will be shown. These values can be changed and a new efficiency generated by clicking on **Calculate Efficiency=**. To retain the changes, click **OK**; to discard them, click **Cancel**.

You can change the knee energy by clicking on the **Knee...** button in the calibration sidebar. This will open the Knee dialog (Fig. 107). It will display the energy value for the knee. To change it, enter a new number and click **Apply**. This will move the knee to this energy and update the fit, graph, and table. The value in the Knee dialog field will be set to the marker energy when you move the marker and click in the spectrum or the Efficiency graph window. This is most easily seen in the Efficiency graph window. The knee energy is not changed until you click **Apply**. To close the Knee dialog, click the Close box. GammaVision will use the knee value shown when **Apply** was last clicked.

Figure 107. Set Knee Energy.

The **Merge...** button on the Energy Calibration Sidebar allows you to merge two efficiency tables. Clicking on it opens a standard file-recall dialog. Choose the .EFT file to be used. and click on **Open**. GammaVision will use the efficiency table data to calculate the efficiency at each energy from the spectrum and fill in the efficiency table.

The table of worksheet entries, including the gammas/sec, half-life, and certification date, contains all the information needed to do the calibration. It can be saved by clicking the **Save...** button in the Table area of the sidebar. This opens a standard file-save dialog. Enter a filename and click **Save**; GammaVision will assign a default extension of .EFT.

The worksheet table is saved as an ASCII file that can be edited with the **Edit File...** feature from the calibration sidebar's control menu (Fig. 108) as described in Section 5.3.3.12, or off line with an ASCII text editor.

Figure 108. Sidebar Control Menu.

When the Efficiency graph and table are shown, the marker in the graph window can be moved to an energy by clicking the mouse on the graph, the table, the Full Spectrum View, or the Expanded Spectrum View. The **Peak**, **ROI**, and **Library** indexing buttons on the Status Sidebar can also be used to move the marker to the desired energy.

5.3.3.8. Using The Library

The library can be used to assist in the efficiency calibration in two ways:

- To direct the marker.
- As input for automatic calibration.

To open a library, select **Library/Select File...**. To display the list of library peaks by energy, choose **Library/Select Peak...**. This can be done before or during the calibration process. Arrange the Efficiency Table, graph window, and Library List so the two peak lists are not covered (see Fig. 109).

To select a peak from the Library List, double-click the desired energy in the list. This will move the marker to that energy in the spectrum (updating the view, if necessary), and redisplay the graph and spectrum to reflect the changes.

By clicking on a library peak and then the worksheet, the worksheet is ready for the values for that peak. The half-life is copied from the library to the **Half-Life** field on the worksheet. You need only to enter the **Activity**.

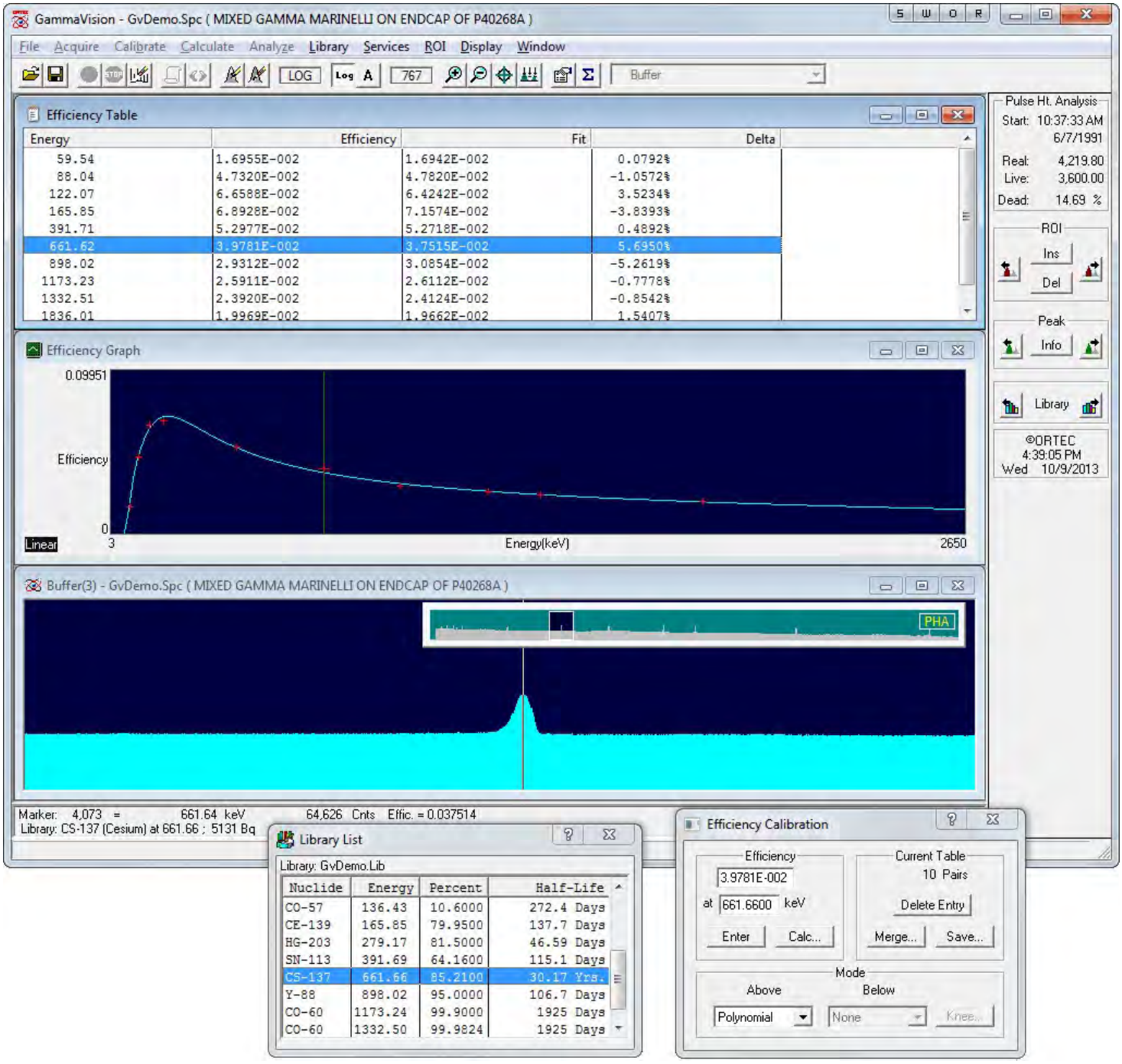


Figure 109. Using the Library in the Efficiency Calibration.

5.3.3.9. Automatic Efficiency Calibration

GammaVision lets you automatically perform the efficiency calibration by using the table in an existing .EFT file. Click the calibration sidebar's **Merge...** button. This will open a standard file-recall dialog (Fig. 110). Select the .EFT file to be used and click **Open**. GammaVision will recall the table of entries and perform a calibration based on the data in the table. When the procedure is complete, the graph and table will be displayed.

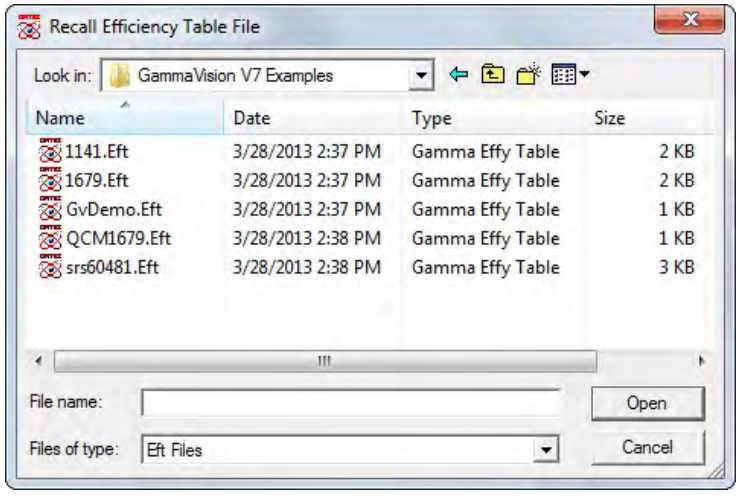


Figure 110. Recall Efficiency Table.

5.3.3.10. Manual Calibration

To perform a completely manual calibration, enter the efficiency and energy in the upper section of the Efficiency Calibration Sidebar, then click **Enter**. The fit, graphs, and table will update after each point is entered.

If the table of values for a manually entered calibration is saved, the only values it will contain are the energy and the efficiency. Doing an automatic recalibration with this table will restore the manual calibration. If the calibration is a mixture of worksheet values and manual entries, the automatic recalibration will use recalculated values for the worksheet entries, and the manual entries will be used as entered.

5.3.3.11. Other Efficiency Sidebar Control Commands

In addition to **Edit File...**, the Efficiency Calibration Sidebar's control menu (Fig. 108) contains the **Move**, **Close**, **Graph**, **Table**, **Restore**, and **Destroy** functions. **Close** saves the efficiency and exits the efficiency calibration function. **Graph** and **Table** are display/hide toggles. Use **Restore** to ignore all calibration inputs made during this calibration session, and **Destroy** to clear the current working calibration and table of values.

5.3.3.12. Editing the Standard (.EFT) Table File

An efficiency standard table file contains all the data input needed to perform a calibration using the standard. This file can be created from the Efficiency Calibration Sidebar by clicking on the **Save** button and assigning a filename, or with an ASCII text editor. The file can be modified with the **Edit File...** function on the sidebar's control menu. Click **File Edit...** to open a standard file-recall dialog. Select the .EFT file to be edited; it will be displayed as shown in Fig. 111.

The table contains the following information (by columns):

- Isotope name (same as library).
- Gamma-ray energy (keV).
- Efficiency (used for manual efficiency inputs, ignored if remainder of line is valid).
- Activity in Bq or ì Ci at the date and time specified in column 7.
- Gammas/sec for this energy, at the specified date and time.
- 1-Sigma Uncertainty for this nuclide.
- Calibration date and time for the gammas/sec calibration. The gammas/sec are automatically decay corrected from the date/time in column 5 to the date/time of the spectrum acquisition.
- Half-life of this nuclide in days.
- Branching ratio as gammas/100 disintegrations.

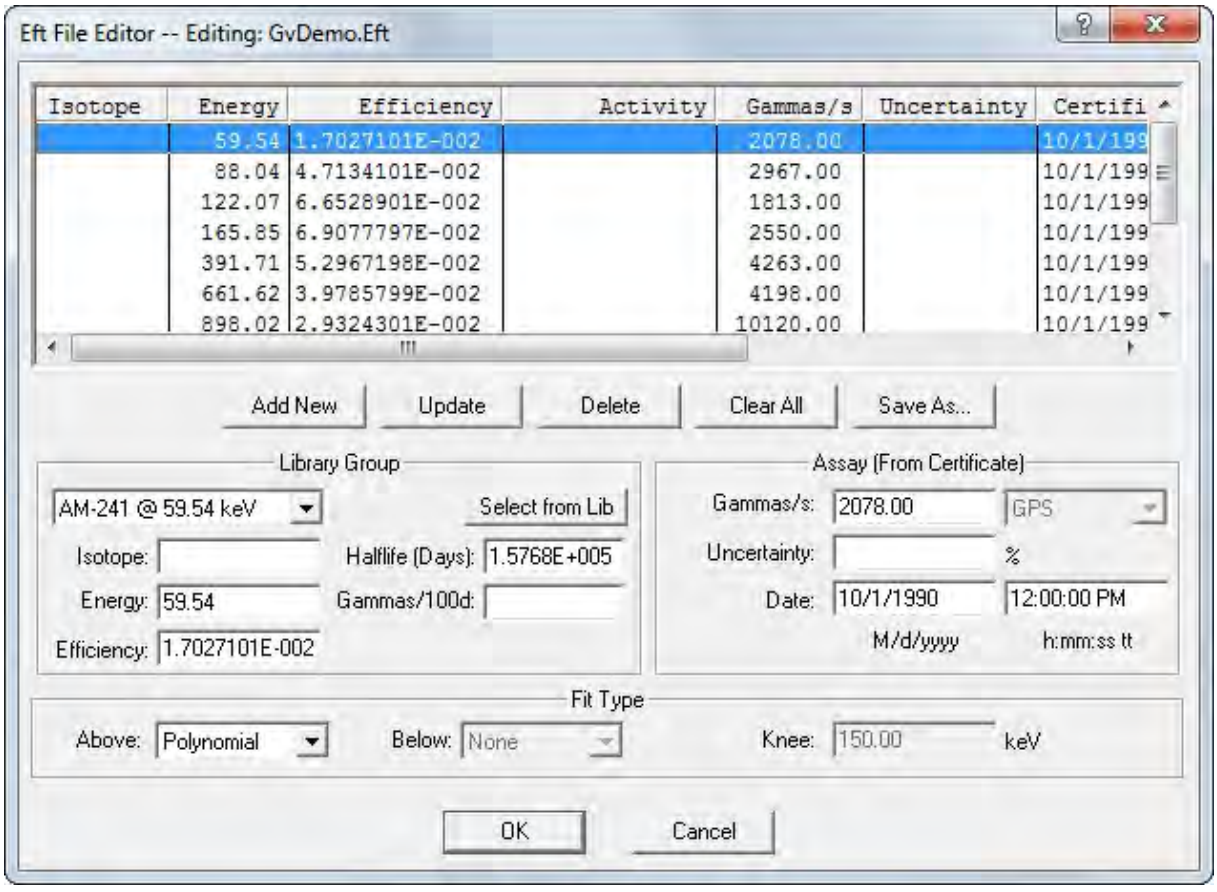


Figure 111. Edit Efficiency Table.

The Gammas per second and activity fields are shown based on the activity units as described below:

- If the units are GPS, then the Activity in the table is displayed as: Activity in edit control divided by (Gammas per 100d divided by 100) and GPS is displayed as the Activity in the edit control.

- If the units are Bq, then the Activity in the table is displayed as the activity in the edit control and the GPS in the table is calculated as the Activity in the edit control multiplied by (Gammas per 100d divided by 100).

- If the units are ì Ci, then the Activity in the table is displayed as the Activity in the edit control and the GPS in the table is calculated as the Activity in the edit control mulitplied by (Gammas per 100d divided by 100) multiplied by 37000.0.

The fields to validate are the Activity and GPS fields in the table. They are calculated from the (1) Activity edit control, (2) Activity unit's combo box, and (3) Gammas/100d field in the library group. Based on units:

- Activity Units set to GPS:
  Activity in table = Activity in edit control / (Gammas/100d * 0.01)
  GPS in table = Activity in edit control

- Activity Units set to Bq:
  Activity in table = Activity in edit control
  GPS in table = Activity in edit control * (Gammas/100d * 0.01)

- Activity Units set to ì Ci:
  Activity in table = Activity in edit control
  GPS in table = Activity in edit control * (Gammas/100d * 0.01) * 37000.0

After the energy list in the .EFT files is the following line:

FitType = <iAbove> <iBelow> <Knee>

where:

<iAbove> = The fit type above the knee (0–3 or 6).
<iBelow> = The fit type below the knee (0–3).
<Knee> = Knee energy for fit types 1–3.

The fit types are:

0	no fit and no efficiency
1	interpolative fit
2	linear fit
3	quadratic fit
6	polynomial fit
8	TCC polynomial fit

This line is used on recall of the efficiency table to select the fit type to be used.

After the fit type comes the total calculated source uncertainty, the number of nuclides in the source uncertainty calculation, and the list of nuclides used in the uncertainty calculation. The total is the individual uncertainties added in quadrature.

To add an energy to the table, enter the values directly or click **Select from Lib**, then click **Add New**. To delete an energy, select the energy and click **Delete**.

To change the values for an energy, select the energy, enter the new values directly or click **Select from Lib**, then click **Update** to record the changes (you must click **Update** or the changes will not be made).

When finished, click **Save As...** to rewrite the new file to disk. To discard the changes you have just made, click **Cancel**; a dialog will verify that you want to discard.

5.3.3.13. The Efficiency Graph Control Menu

Figure 112 shows the control menu for the graph of efficiency vs. energy. It contains selections to turn a **Grid** on/off and to switch from **Log/Log** to **Linear** axes. The graph can also be **Closed** (removed). If closed, it can be redisplayed with the **Graph** command from the Efficiency Calibration Sidebar's control menu.

5.3.3.14. The Efficiency Table Control Menu

Figure 113 shows the control menu for the table of efficiency vs. energy. It contains commands to **Print** and **Close** the table. If closed, it can be redisplayed with the **Table** selection from the Efficiency Calibration Sidebar's control menu.

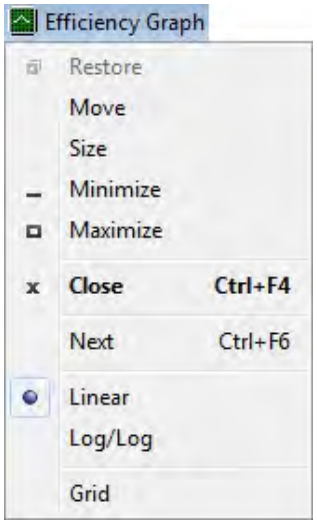


Figure 112. Efficiency Graph Control Menu.

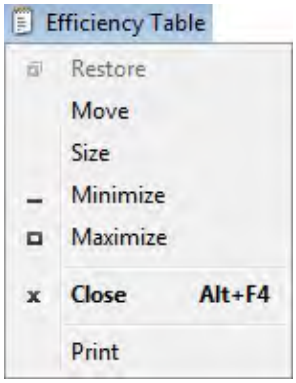


Figure 113. Efficiency Table Control Menu.

5.3.4. Description...

This command opens the dialog shown in Fig. 114, which allows you to create a description of the calibration for the currently displayed spectrum. This description is printed in the standard GammaVision report. It is also displayed each time you use the **Save Calibration...** command. You can modify the description at any time by re-saving the calibration.

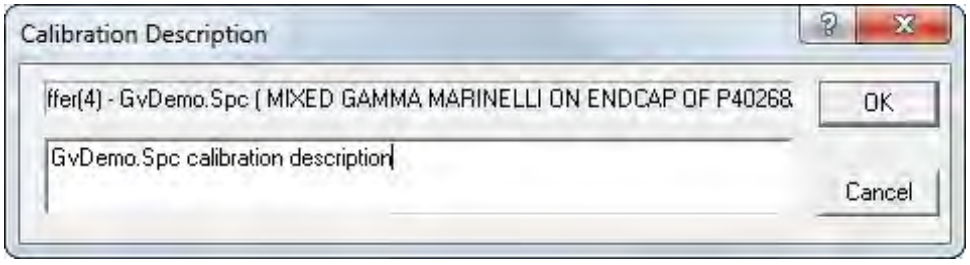


Figure 114. Calibration Description.

5.3.5. Recall Calibration...

This command (see Fig. 115) recalls the calibration fields from the specified file to the working calibration for the currently selected Detector. The current working calibration is lost. The calibration data can be read from any file containing the correct records. This includes .CLB, .SPC, and analy-sis (.UFO) files.

The complete calibration or just the energy or efficiency calibration can be recalled. The **Recall Energy Calibration** and **Recall Efficiency Calibration** checkboxes at the bottom of the dialog

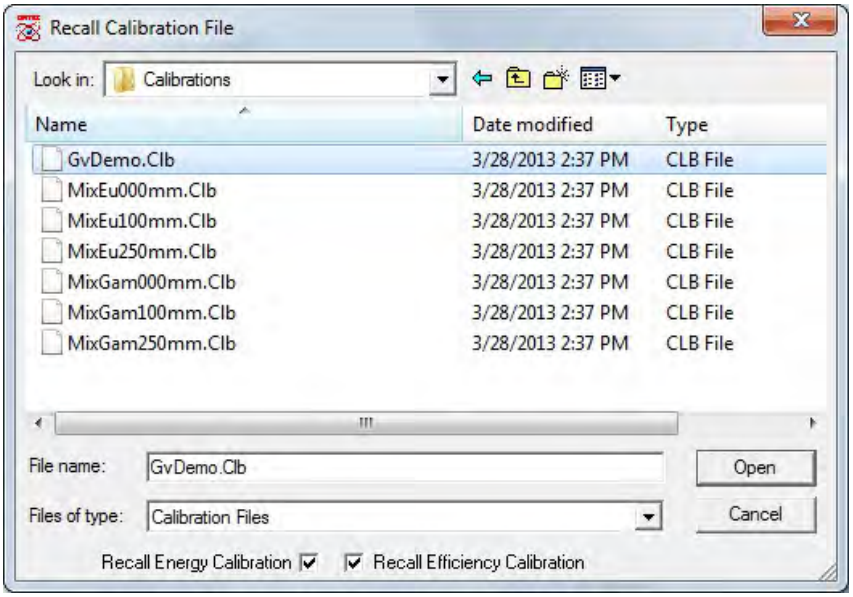


Figure 115. Recall Calibration.

indicate which part(s) of the calibration will be retrieved. Note that an efficiency calibration, by itself, cannot be recalled unless the currently selected Detector is energy calibrated. The original calibration is retained for the parts not retrieved. If one or both calibration segments is retrieved, the calibration file's calibration description is also loaded.

To change the calibration stored in a spectrum file, recall the spectrum file (its calibration is automatically loaded), recall the desired calibration, and then save the spectrum back to disk.

5.3.6. Save Calibration...

Save Calibration saves the current working calibration to disk in the .CLB format. Both the energy and efficiency data are saved.

5.3.7. Print Calibration...

This sends all the calibration data for the working calibration to the display, a printer, or a disk file. The data include the dates the calibrations were performed; the calibration tables (if they exist), the fit types, coefficients, and uncertainties; and for TCC calibrations, the peak-to-total calibration table and LS energy table. Figure 116 shows all available features in this report.

Calibration Data from file: TestCase18.Spc
Energy Calibration Date: 8/29/2013 Time: 6:54:12 AM
Efficiency Calibration Date: 8/29/2013 Time: 6:54:12 AM
Peak-To-Total Calibration Date: 8/29/2013 Time: 6:54:12 AM

Calibration Description:
DET#1 EFF CAL FOR 3.5L MARINELLI - TEN3500.CLB

Energy Calibration Fit
Energy = 0.1626 +0.249971*Channel +4.96664e-009*Channel**2
FWHM (ch) = 4.1178 +0.000981*Channel -5.65412e-008*Channel**2

Energy/FWHM Table

Channel	Energy(kev)	Fit(kev)	Delta	FWHM(kev)	Fit(kev)	Delta
237.48	59.54	59.53	0.02%	1.06	1.09	-2.69%
351.59	88.04	88.05	-0.01%	1.09	1.11	-2.28%
487.68	122.07	122.07	0.00%	1.11	1.15	-3.35%
545.31	136.43	136.48	-0.03%	1.14	1.16	-1.89%
662.84	165.85	165.86	-0.00%	1.14	1.19	-4.15%
1116.18	279.17	279.18	-0.00%	1.20	1.29	-7.51%
1566.22	391.71	391.68	0.01%	1.30	1.38	-5.89%
1900.23	475.35	475.18	0.04%	1.45	1.44	0.07%
2043.55	511.00	511.01	-0.00%	2.51	1.47	41.49%
2252.55	563.26	563.26	0.00%	1.37	1.51	-9.89%
2276.80	569.29	569.32	-0.01%	1.47	1.51	-2.99%
2418.30	604.66	604.70	-0.01%	1.43	1.54	-8.03%
2646.12	661.62	661.65	-0.00%	1.43	1.58	-10.19%
3182.71	795.76	795.80	-0.00%	1.58	1.67	-5.58%
3207.01	801.84	801.87	-0.00%	1.66	1.67	-0.64%
3338.71	834.81	834.80	0.00%	1.56	1.69	-8.38%
3591.48	898.02	897.99	0.00%	1.66	1.73	-3.98%
4461.37	1115.52	1115.47	0.00%	1.74	1.84	-6.01%
4671.07	1167.86	1167.90	-0.00%	1.90	1.87	1.55%
5459.95	1365.13	1365.14	-0.00%	2.01	1.95	3.36%
7343.14	1836.01	1836.00	0.00%	2.09	2.07	1.17%

Efficiency Calibration Fit
Tcc Polynomial Uncertainty = 5.2160 %
Coefficients:
-0.553755 -5.297142 -0.753698 6.686565 0.000000 0.000000

Efficiency Table

Energy	Efficiency	Fit	Delta
59.54	1.5947E-002	1.6159E-002	-1.33%
88.04	1.9047E-002	1.9465E-002	-2.19%
122.07	2.0323E-002	1.9970E-002	1.74%
165.85	1.7593E-002	1.8371E-002	-4.42%
279.17	1.3293E-002	1.3138E-002	1.16%
391.71	1.0246E-002	1.0179E-002	0.64%
604.66	6.9096E-003	7.3110E-003	-5.81%
661.62	6.6841E-003	6.8298E-003	-2.18%
795.76	5.6330E-003	5.9437E-003	-5.52%
834.81	5.7561E-003	5.7336E-003	0.39%
898.02	5.3226E-003	5.4278E-003	-1.98%
1115.52	4.6690E-003	4.6088E-003	1.29%
1836.01	3.0615E-003	3.1136E-003	-1.70%

Calibration Certificate Table

Isotope	Energy	Pct	Halflife	Activity	GPS	Error	Date & Time
Am-241	59.54	36.30	1.58E+005	3600.60	1307.00	3.56%	8/1/2007 11:00:00 AM
Cd-109	88.04	3.79	4.53E+002	36332.00	1377.00	3.59%	8/1/2007 11:00:00 AM
Co-57	122.07	85.60	2.70E+002	891.36	763.00	2.69%	8/1/2007 11:00:00 AM
Ce-139	165.85	80.00	1.38E+002	1223.80	979.00	2.31%	8/1/2007 11:00:00 AM
Hg-203	279.17	81.50	4.66E+001	2963.20	2415.00	2.34%	8/1/2007 11:00:00 AM
Sn-113	391.71	64.17	1.15E+002	2108.50	1353.00	2.35%	8/1/2007 11:00:00 AM
Cs-134	604.66	97.60	7.53E+002	4273.60	4171.00	2.78%	8/1/2007 11:00:00 AM
Cs-137	661.62	84.62	1.10E+004	1058.90	896.00	2.78%	8/1/2007 11:00:00 AM
Cs-134	795.76	85.40	7.53E+002	4281.00	3656.00	2.78%	8/1/2007 11:00:00 AM
Mn-54	834.81	99.98	3.12E+002	2527.50	2527.00	2.78%	8/1/2007 11:00:00 AM
Y-88	898.02	94.00	1.07E+002	4637.20	4359.00	2.42%	8/1/2007 11:00:00 AM
Zn-65	1115.52	50.75	2.44E+002	6894.60	3499.00	2.51%	8/1/2007 11:00:00 AM
Y-88	1836.01	99.36	1.07E+002	4646.70	4617.00	2.84%	8/1/2007 11:00:00 AM

Peak-To-Total Calibration Table

Ptt = Exp(8.7694E-001 - 4.1138E-001 * Ln(Energy))

LS Energy Table

Intercept: 1.0003E+000 Slope: 4.4486E-004 Quad: 5.0000E-001

Figure 116. Print Calibration Report.

5.3.8. Calibration Wizard...

NOTE The Calibration Wizard should not be used with Low Resolution systems (i.e., NaI, LaBr, CZT, etc.) to Create New Energy or TCC Calibrations.

The GammaVision calibration wizard automates the complete calibration process, including spectrum acquisition. The calibration can be done from an MCB or from stored spectra. At the end of the calibration, the complete results are presented for review. During the review, you can repeat any or all of the calibration steps with any changes necessary to improve the calibration.

Figure 117 shows the first calibration wizard screen. The options for each type of calibration are to **Keep Current, Create New**, or **Recall From File**.

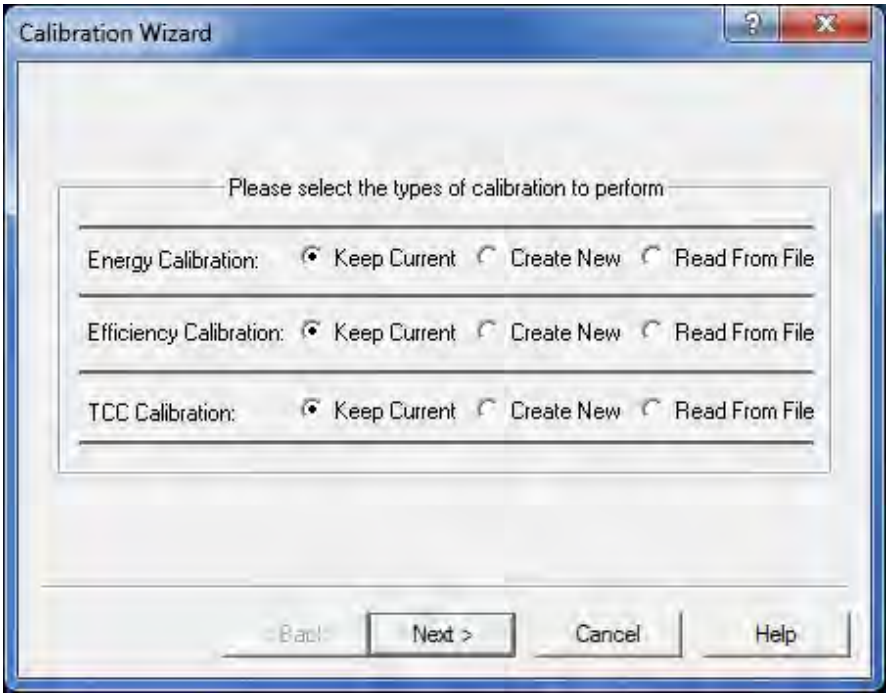


Figure 117. Calibration Wizard Opening Screen.

Keep Current

This means to continue using the calibration stored in the MCB or in the spectrum (the current working calibration). The wizard will skip this calibration step. However, if review of the calibration shows a problem, you can change this selection and repeat the process.

Create New

This choice means that the calibration selected (energy, efficiency, or TCC) will be replaced by the results of the subsequent steps. The TCC calibration is closely linked to the efficiency calibration, so when you select **TCC Calibration**, **Efficiency Calibration** is also selected automatically.

All of the peak calculations use the **Analyze/Settings/Sample Type...** values; see Section 5.5.1.1. This is to ensure that the calibration and analysis calculations are the same. Be sure to check the settings before starting the wizard; several of these settings are important. If spectrum has high dead time, there will also be a significant amount of random summing. The correction for random summing is applied in the calibration calculations. The **Random Summing** factor is discussed in Section 6.11 and entered on the Sample tab under **Analyze/Settings/Sample Type...**. The starting channel of the **Analysis Region** should be set above the low-level cutoff. The peak-cutoff sensitivity used in the calibration is the smaller of the following: 10% or the value entered on the Analysis tab. Note also that the net peak area calculation can be affected by the library match width, as specified on the System tab. *Before calibrating, make sure the **Match Width** parameter is set to the same value you will be using during analysis. Per the note in Section 5.3.1.1, we recommend a value between 0.4 and 0.75.* Lastly, the peak-search sensitivity setting will be the greater of the following: 4 or the value selected on the System tab.

Read From File

This means that the calibration will be read from a .CLB file. The later dialogs will ask for the filename for each calibration separately. Each calibration can be from a different .CLB file.

When the selections have been made, click **Next** to go to the next step in the wizard. The next step will depend on the selections made on this first screen.

5.3.8.1. Energy Calibration — Setting Up a New Calibration or Recalling from File

Create New

If you chose to create a new energy calibration, the dialog shown in Fig. 118 opens. Enter the **Library** filename and select a **Source Label**.

When performing this calibration on new data in the MCB, you must enter the live-time preset (**Count Time**) in seconds, and mark the **Clear Data Before Start** check-box. The counting time must be long enough to accumulate well-formed peaks with low counting uncertainty.

To use the spectrum currently in the MCB, unmark the **Clear Data Before Start** box.

The **Source Label** entered here is used in a later step that tells you which source to put on the detector.

Click **Browse** to find the correct library file. To view or change the contents of the library, click **Edit**. This opens the GammaVision library editor, which is discussed in Section 5.6.3, page 208. When finished, click **Next**.

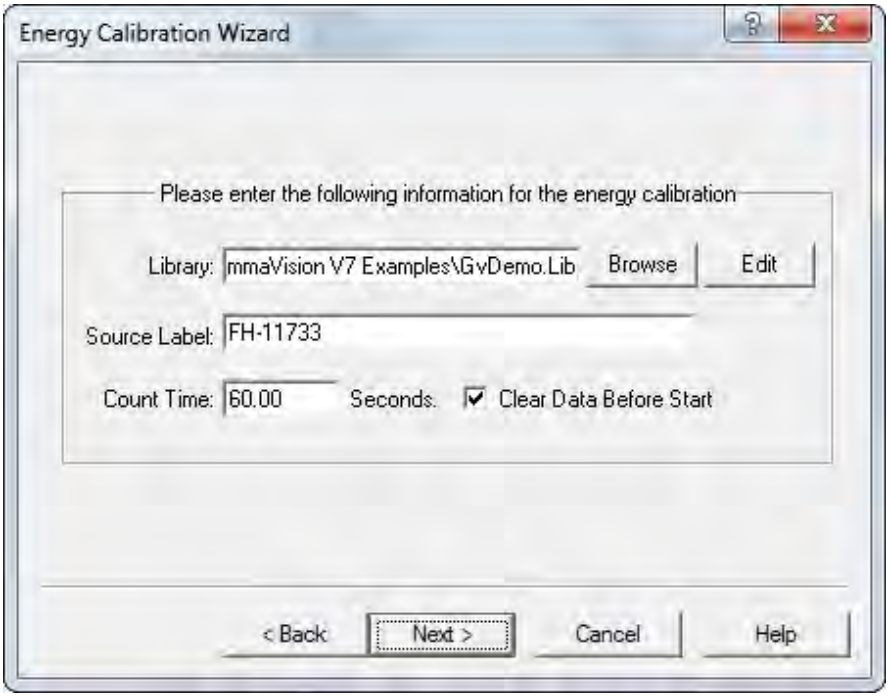


Figure 118. Choose Library and Source Name for Energy Calibration.

If the FWHM calibration fails one of the internal validity tests, a message is displayed. Click **OK** to acknowledge the message and the calibration process will continue. Remember to check the FWHM at the end of the process by clicking on **Edit Energy** on the review page (see Fig. 126).

Read From File

If you selected **Read From File**, the dialog shown in Fig. 119 opens. Enter the name of the file in which the desired energy calibration is stored. The calibration **Description** stored in the file is displayed (read-only) so you can more easily choose the correct file and reduce errors. Any type of file that stores calibration records can be used. This function operates the same as **Calibrate/Recall Calibration** (recalling the energy calibration only). Since this is a complete calibration, no checking (e.g., FWHM) is performed.

When finished, click **Next**.

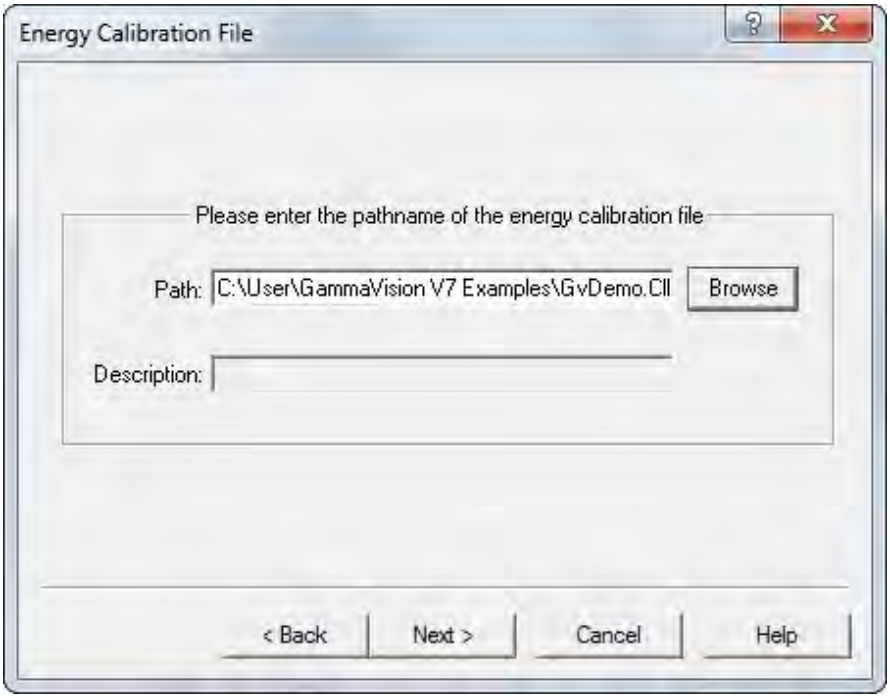


Figure 119. Select the File that Contains the Desired Energy Calibration.

5.3.8.2. Efficiency and Efficiency-plus-TCC Calibrations — Setting Up a New Calibration or Recalling from File

Create New

If you chose to create a new efficiency or efficiency-plus-TCC calibration, the dialog shown in Fig. 120 opens. Use this dialog to enter the source **Certificate File**, **Library** file, **Source Label**, and **TCC Calibration Method** settings.

When performing this calibration on the MCB, you must enter the live-time preset (**Count Time**) in seconds. In addition, you might also wish to mark the **Clear Data Before Start** check-box. The counting time must be long enough to accumulate well-formed peaks with low counting uncertainty. This is especially important for TCC calibration, which uses the summed peaks in the calculations.

Also note that your library and TCC table should include only peaks that exist in the spectrum.

To use the spectrum currently in the MCB, unmark the **Clear Data Before Start** box. This is useful if the same source is used for both energy and efficiency calibration.

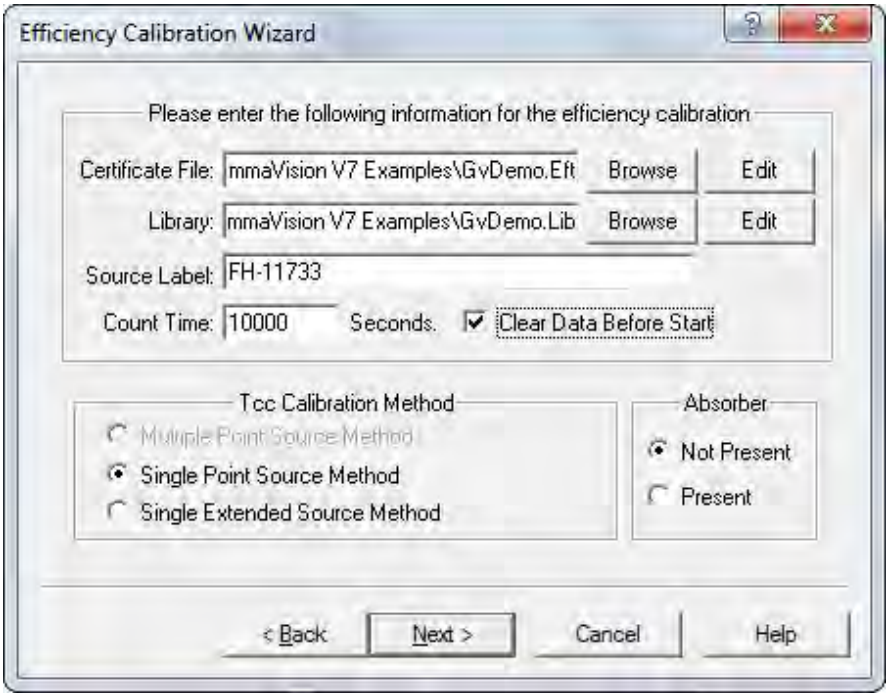


Figure 120. Create a New Efficiency Calibration.

The **Source Label** entered here is used in a later step that tells you which source to put on the detector.

Certificate File

Use the **Browse** button to find the correct certificate. To make changes to the certificate, click **Edit**. This opens the wizard's Certificate File Editor dialog, shown in Fig. 121.

The certificate file is the same as the efficiency standard file, except that the contents of the efficiency field are not used here and all fields must have valid contents. The certificate file also has the EFT extension. Tables with all fields entered can be used for both the calibration wizard and the efficiency calibration (**Calibrate/ Efficiency...**). Any energy in the .EFT file that is not completely filled in will be ignored by the wizard. The file contains all the data needed to perform an efficiency or efficiency-plus-TCC calibration using this standard source. This file can be created here, with the **Efficiency** calibration sidebar (see Section 5.3.3.12) or with an ASCII text editor.

The table contains the following columns:

1) Isotope name (same as library).
2) Gamma-ray energy (keV).
3) Activity in Bq or ì Ci at the date and time specified in column 6.
4) Gammas/sec for this energy at the specified date and time.
5) 1-Sigma Uncertainty for this nuclide.

6) Calibration date and time for the gammas/sec calibration. The gammas/sec are automatically decay corrected from the date/time in column 4 to the date/time of the spectrum acquisition.
7) Half-life of this nuclide in days.
8) Branching ratio (yield) as gammas/100 disintegrations.

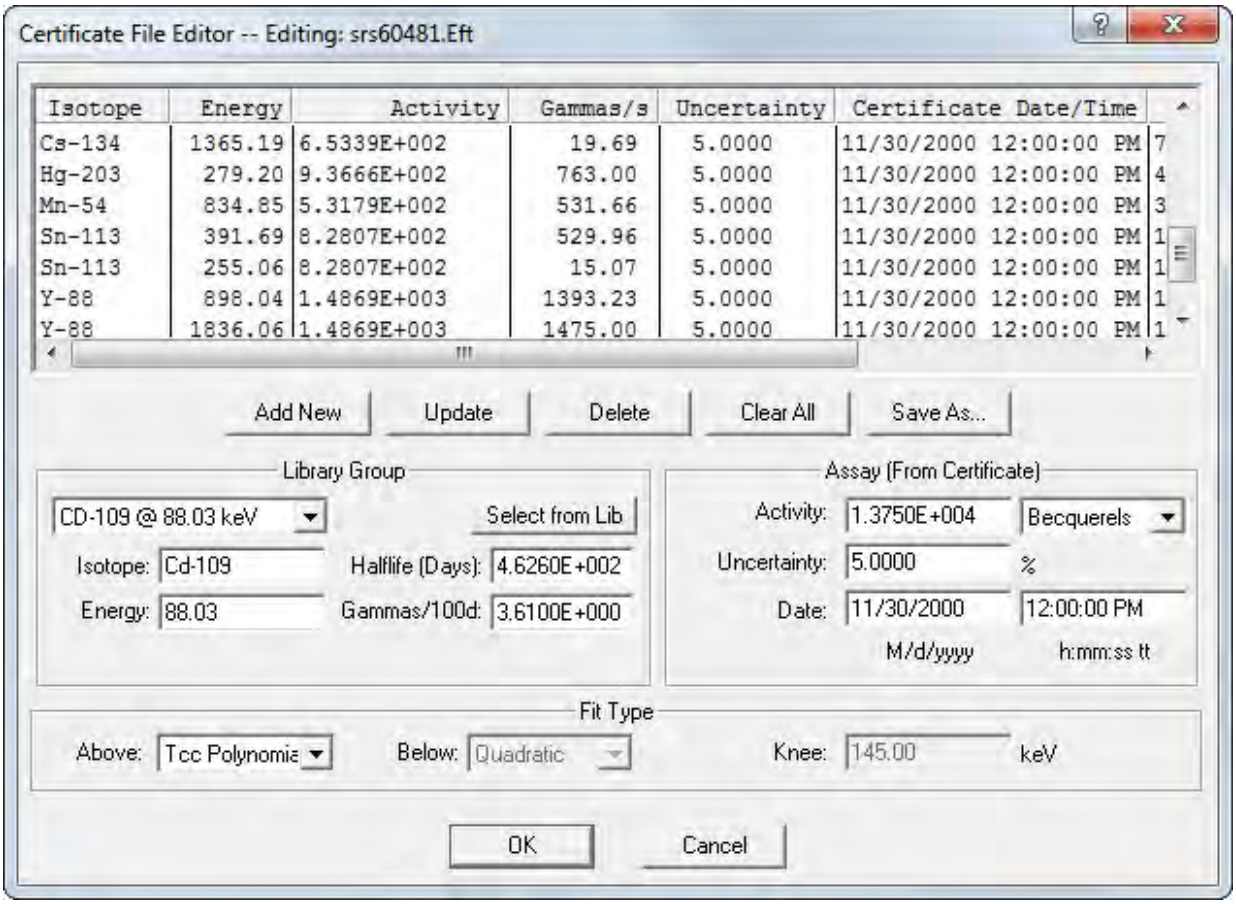


Figure 121. Edit Wizard Certificate File.

To add an energy to the table, enter the values directly or click **Select from Lib**, then click **Add New**.

To delete an energy, select the energy and click **Delete**.

To change the values for an energy, select the energy, enter the new values directly or click **Select from Lib**, then click **Update** to record the changes (you must click **Update** or the changes will not be made).

When finished, click **Save As...** to rewrite the new file to disk. To discard the changes you have just made, click **Cancel**; a dialog will verify that you want to discard.

Library

Click **Browse** to find the correct library file. For TCC calibrations, the library (.LIB or .MDB) file and TCC table should include only the nuclides present in the spectrum.

To view or change the contents of the library, click **Edit**. This opens the GammaVision library editor, which is discussed in Section 5.6.3, page 208.

When finished, click **Next**.

TCC Calibration Method

The **Single Point Source Method** uses a point source with all the nuclides needed in one source. The point source is normally a small area (1 mm–2 mm diameter). Larger sources can be used if they are more than a few centimeters from the detector. An example of the nuclide mixture is given below.

The **Single Extended Source Method** uses bulk or large-volume sources such as Marinelli beakers or bottles with all the nuclides needed in one source.

The source must be a mixture of nuclides with gamma rays that do not have true coincidence summing and nuclides with gamma rays that do have summing. The energies of the gamma rays must extend over the range of interest for the unknown samples. A mixture of ^{109}Cd, ^{113}Sn, ^{139}Ce, ^{203}Hg, ^{134}Cs, ^{137}Cs, ^{88}Y, and ^{54}Mn will be sufficient for most situations. ^{241}Am can be added for lower energies.

NOTE ^{60}Co should not be added because of the interference with gamma rays from ^{134}Cs.

The **absorber present/not present** selection determines the low-energy fitting function. The efficiency for low-energy gamma rays depends on the absorbing material between the detector and the source. The absorbing material and thickness are not important. GammaVision will automatically account for the loss in the fitting process if the absorber is present. The low-energy coefficients are listed as the last 2 (of 6) of the TCC polynomial coefficients and are zero for absorber **Not Present**.

The selection of point or extended source and absorber present or not may depend on the specific detector type and container material. Use the **Next** and **Back** buttons on the Calibration Wizard to view the calibration results and return to this page to change the settings until the best calibration fit is achieved.

When finished, click **Next**.

Read From File — Efficiency

If you selected **Read From File** for the efficiency calibration, the dialog shown in Fig. 122

opens. Enter the name of the file in which the desired efficiency calibration is stored. The calibration **Description** stored in the file is displayed (read-only) so you can more easily choose the correct file and reduce errors. Any type of file that stores calibration records can be used.

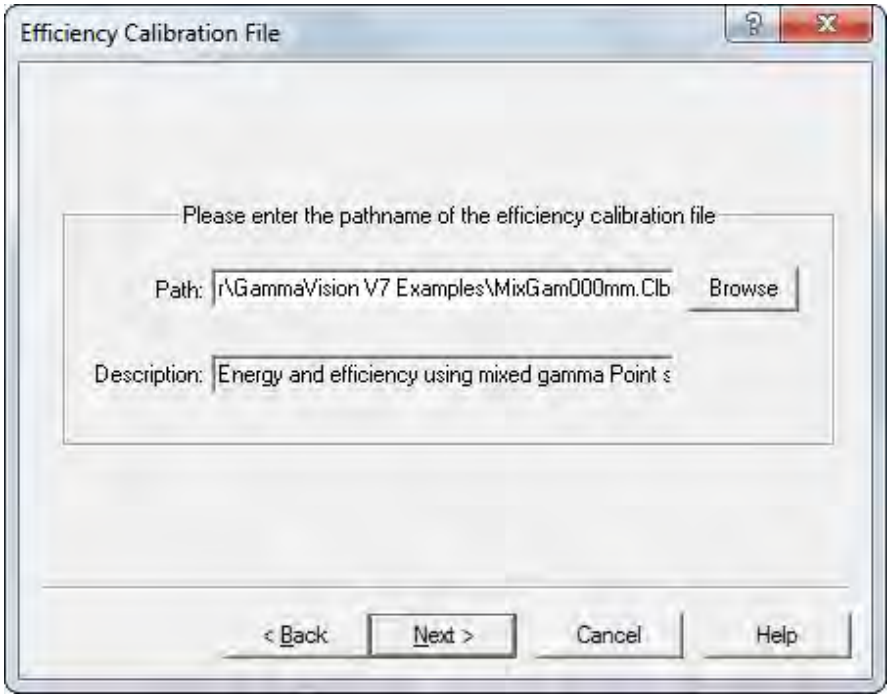


Figure 122. Select the File Containing the Desired Efficiency Calibration.

This function operates the same as **Calibrate/Recall Calibration** (recalling the efficiency calibration only).

When finished, click **Next**.

Read from File — TCC

If you selected **Read From File** for the TCC calibration, the dialog shown in Fig. 123 opens. Enter the name of the file in which the desired TCC calibration is stored. Since the TCC is linked to the efficiency, this will load both the efficiency and the TCC calibration parameters. Be sure to use the same file for the efficiency calibration (**Read From File — Efficiency**) and TCC calibration; otherwise, the TCC calibration loaded may not be complete and will not produce accurate results.

The calibration **Description** stored in the file is displayed (read-only) so you can more easily choose the correct file and reduce errors. Any file that stores calibration records can be used.

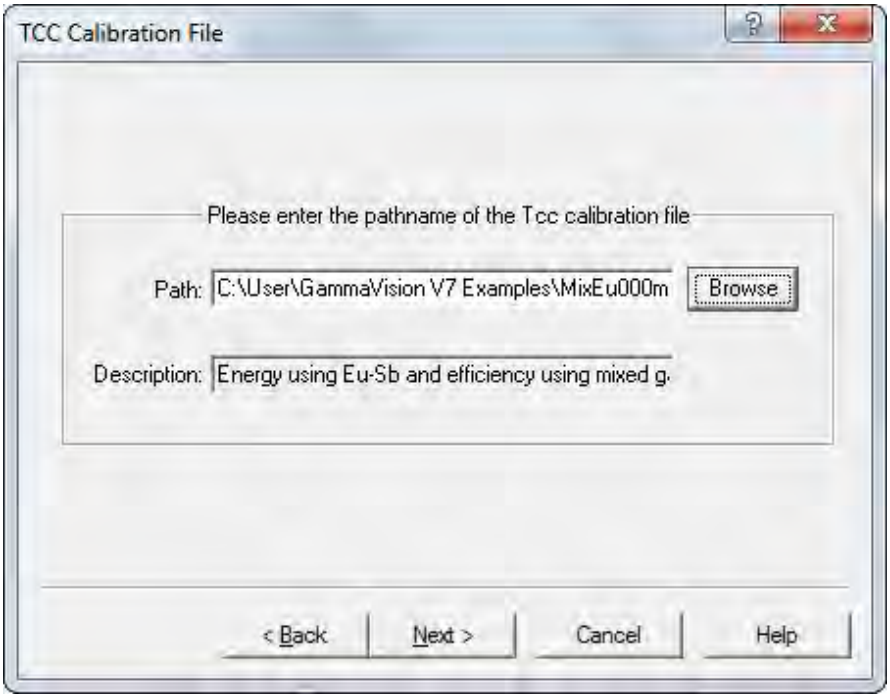


Figure 123. Select the File that Contains the Desired TCC Calibration.

When finished, click **Next**.

5.3.8.3. Performing the New Energy Calibration

If you chose to create a new energy calibration, the dialog shown in Fig. 124 opens. Position the source and click **OK** to begin spectrum acquisition. If the buffer is selected, the current spectrum in the buffer is used.

When spectrum collection is complete (or the buffer is used), the energy and FWHM calibration is performed. If successful, the wizard goes on to the next step.

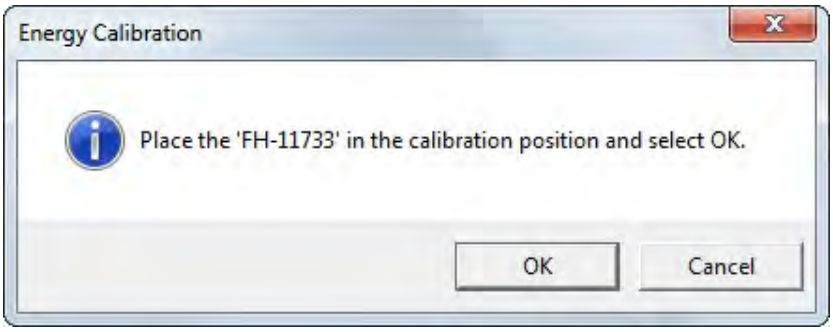


Figure 124. Position the Source for Energy Calibration.

If the energy calibration process detects a severe error, an error message is displayed. Click **OK** to acknowledge the error. The calibration process will stop at this point.

If the energy calibration process detects a minor error, a warning message is shown. Click **OK** to acknowledge the warning and remember that this warning was given. The calibration process will continue as normal. When the final review screen is displayed (Fig. 126), click **Edit Energy** to review the cause of the error and correct it if needed (see Section 5.3.8.5).

5.3.8.4. Performing the New Efficiency or Efficiency-plus-TCC Calibration

If you chose to create a new efficiency or efficiency-plus-TCC calibration, the wizard asks for the next source to be positioned (see Fig. 125). Click **OK** to begin spectrum acquisition. If the buffer is selected, the current spectrum in the buffer is used.

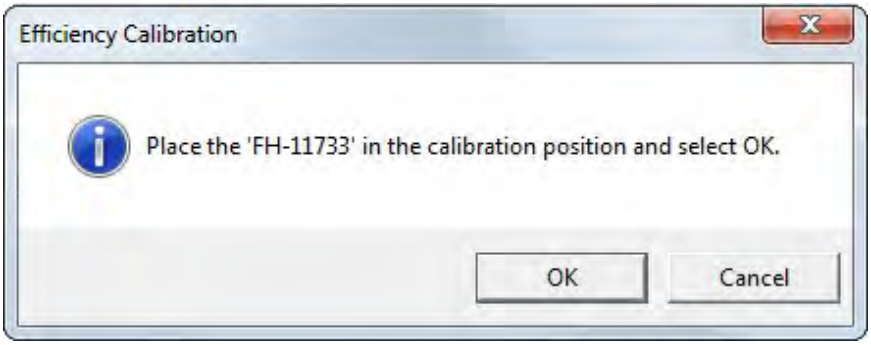


Figure 125. Position the Source for the Efficiency or Efficiency-plus-TCC Calibration.

If the efficiency calibration process detects a severe error, an error message is displayed. Click **OK** to acknowledge the error. The calibration process will stop at this point.

5.3.8.5. Reviewing the Calibration Wizard Results

The final screen in the calibration wizard is the review screen shown in Fig. 126. This shows the plots of the results of all the calibration steps. The TCC functions are not plotted, but indicated as Tcc Calibrated or Uncalibrated.

When the TCC calibration is performed, it includes recalculating the efficiency function, therefore, the efficiency curve (upper right) might not appear to be a good fit to the experimental points. This is because the total efficiency function is the combination of all the different functions.

To review or change the energy or FWHM calibration, click **Edit Energy**. This opens the complete energy calibration dialog as explained in Section 5.3.2, page 105. If any changes are made, the efficiency (and TCC) calibration should be repeated. If you did not select TCC, the efficiency calibration can be redone by clicking on **Edit Efficiency**. This will open up the complete efficiency calibration dialog as explained in Section 5.3.3, page 114. *This does not redo the TCC calibration*.

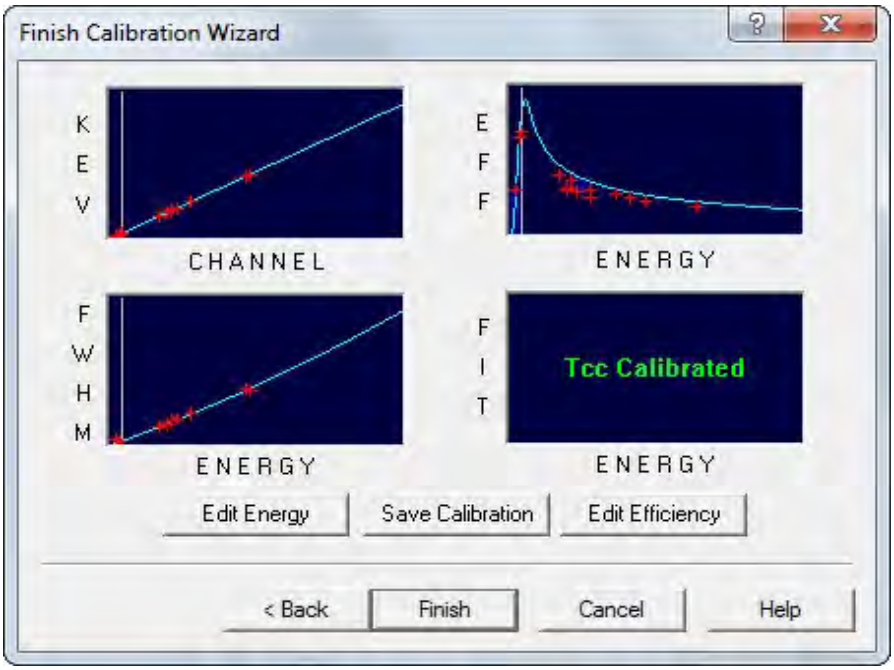


Figure 126. Review the Calibration Results.

Alternatively, you can change a calibration by clicking on **Back** to return to previous wizard screens. Click **Back** to return to the efficiency dialog, then **Back** again to return to the energy dialog.

NOTE If the spectrum currently in the MCB is the right spectrum, be sure to *unmark* the **Clear Data Before Start** checkbox.

Once you have reset the starting parameters as needed, the process will continue on as before with the spectrum collection or file recall.

The calibration is now stored with the MCB or buffer, *but not on disk*. Use the **Save Calibration** button to save the calibration to a file. This should always be done to preserve the calibration for later use.

To complete the calibration wizard and close the dialog, click **Finish**. (**Cancel** operates the same as **Finish**.)

To validate the TCC Calibration, analyze the calibration spectrum with the new Efficiency/TCC calibration and the TCC option enabled in the analysis settings. The calculated nuclide activity should be very close to the source certificate values. The TCC calibration correction can be assessed by comparing the Peak Branching Ratios from the library to the corrected Branching Ratios displayed in the Library usage section of the GammaVision report.

5.4. Calculate

The **Calculate** menu (Fig. 127) provides useful analytical tools for spectrum manipulation. **Smooth** and **Strip...** are only available in buffer windows.

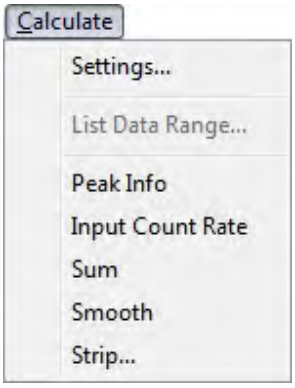


Figure 127. Calculate Menu.

5.4.1. Settings...

This dialog (Fig. 128) allows you to set the "x" factor in the **Peak Info** calculation of full width at 1/x maximum (FW[1/x]M) for the ROI marked by the cursor (see Section 5.4.3). In addition, you can set the number of background channels used on each side of the peak. The background is subtracted before starting the calculation. Enter the factor **x**, an integer from 2 to 99. This number will be retained and used until changed. (**Peak Info** always displays the FWHM, so an x of 2 is not useful.) The number of **Background Points** ranges from 1 to 5, and the default value is 3.

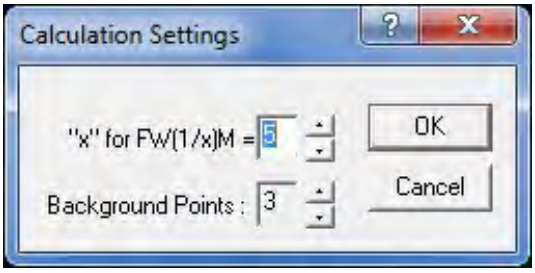


Figure 128.

5.4.2. List Data Range...

Use this dialog (Fig. 129) to retrieve a specified time slice of data from a List Mode (.LIS) file that has been recalled into a buffer window. GammaVision samples the list mode data stream every 250 milliseconds of real time, and can display the data with a granularity of 1 second (see the List Mode discussion in Section 1.6).

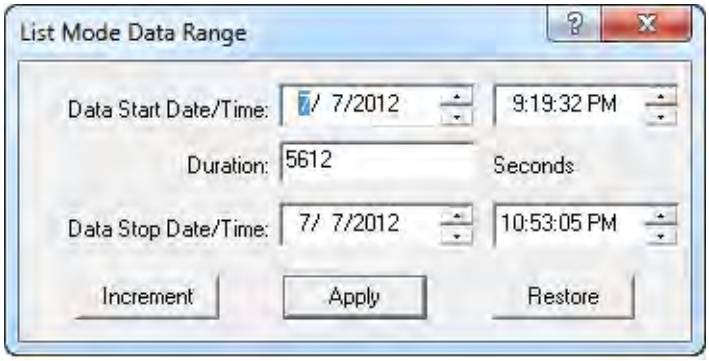


Figure 129. Select a Time Slice of List Mode Data.

Click to highlight the desired start and end **Date/Time** values, then adjust them by clicking the up/down buttons; or set the desired **Data Start Date/Time** and enter the time slice **Duration** in whole seconds.[24] To retrieve the data, click **Apply**. Click **Increment** to add the next more data to the currently displayed time slice; set the **Duration**, then click **Increment**. To save a time slice in any GammaVision file format (i.e., as list files and/or spectrum files), use the **Save** commands.

[24]The analogous JOB stream command, SET_RANGE (page 414), can use fractional real times and durations.

To redisplay the complete data set *rounded down to the nearest whole second*, click **Restore**. To redisplay the entire data set without rounding, close and recall the .LIS file.

This command is duplicated by the **List Data Range** button on the toolbar.

5.4.3. Peak Info

This command operates when the marker is positioned in a peak or in an area marked as an ROI. It displays the following information in a pop-up box and on the Supplementary Information Line (Fig. 130):

- If the spectrum is not calibrated, the centroid channel, FWHM, FW1/xM (all in channels), gross area, net area, and net-area uncertainty are displayed for the ROI.

- If the spectrum is calibrated, the centroid channel, FWHM, FW1/xM in channels and calibration units (e.g., energy), library "best match" energy and activity, gross area, net area, and net-area uncertainty are displayed for the ROI.

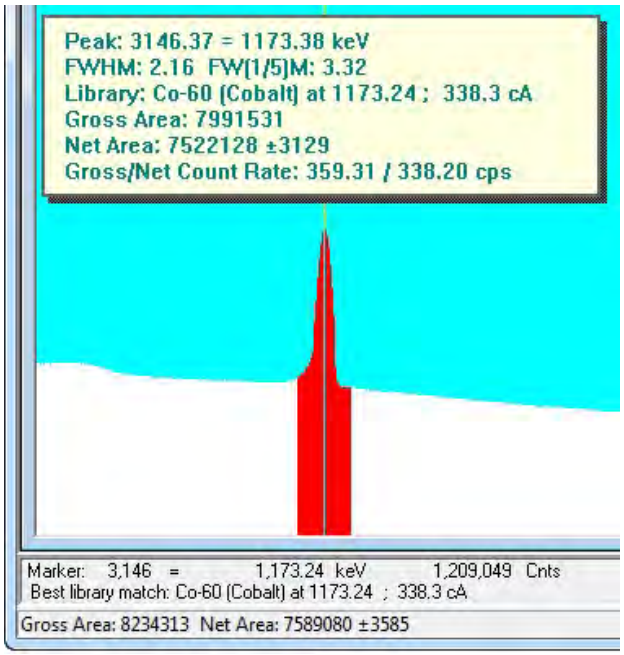


Figure 130. Peak Info Beneath Marker and Above Peak.

If the Detector is acquiring data, the values displayed are continuously updated.

NOTE If the marker is in an ROI, peak information is displayed whether or not the area is a detectable peak. If no ROI is marked, the peak limits are the same as the limits for the ROI Insert button on the Status Sidebar. If a peak is detected, its information is displayed (otherwise a "could not fit peak properly" message is displayed).

To close the pop-up box, click it or press **<Esc>**.

This command is duplicated by the **Peak Info** command on the right-mouse-button menu and by double-clicking the mouse in the ROI.

5.4.3.1. Calculation

The program subtracts the calculated background, channel by channel, and attempts a least-squares fit of a Gaussian function to the remaining data. If unsuccessful, it displays “Could Not Properly Fit Peak.” If successful, the centroid is based on the fitted function. The reported widths are linearly interpolated between the background-subtracted channels. The spectrum components used in the background calculation are illustrated in see Fig. 131.

The background on the low channel side of the peak is the average of the first *n* channels of the ROI, where *n* is the number of background points selected on the dialog under **Calculate/Settings...** (Section 5.4.1). The channel number for this background point is the midpoint fractional channel of the *n* points. The background on the high channel side of the peak is the average of the last *n* channels of the ROI. The channel number for this background point is also the midpoint fractional channel of the *n* points. These *(n−1)* points on each side of the peak form the end points of the straight-line background.

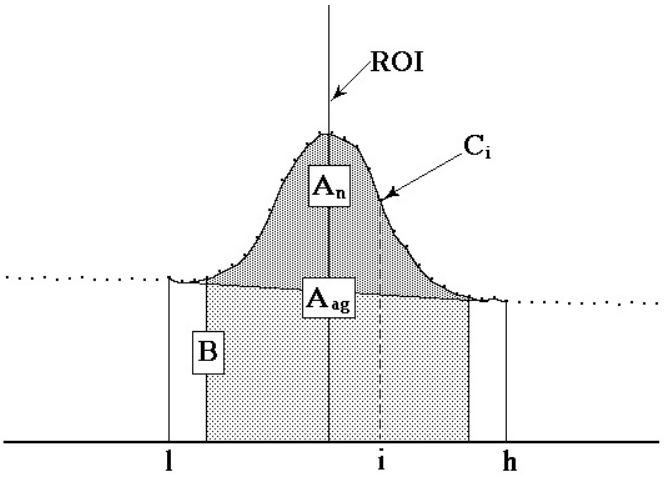


Figure 131. Calculation Details.

The background is given by the following:

$$B = \left(\sum_{i=l}^{l+(n-1)} C_i + \sum_{i=h-(n-1)}^{h} C_i \right) \frac{h - l + 1}{2n} \qquad \textbf{(15)}$$

where:

- B = the background area
- l = the ROI low limit
- h = the ROI high limit
- C_i = the contents of channel i
- n = the number of background points

The gross area is the sum of all the channels marked by the ROI according to the following:

$$A_g = \sum_{i=l}^{h} C_i \qquad \textbf{(16)}$$

where:

A_g = the gross counts in the ROI
l = the ROI low limit
h = the ROI high limit
C_i = the contents of channel i

The adjusted gross area is the sum of all the channels marked by the ROI but not used in the background according to the following:

$$A_{ag} = \sum_{i=l+n}^{h-n} C_i \quad \textbf{(17)}$$

where:

A_{ag} = the adjusted gross counts in the ROI
l = the ROI low limit
h = the ROI high limit
C_i = the contents of channel i
n = the number of background points

The net area is the adjusted gross area minus the adjusted calculated background, as follows:

$$A_n = A_{ag} - \frac{B\,(h-l-(2n-1))}{(h-l+1)} \quad \textbf{(18)}$$

The uncertainty in the net area is the square root of the sum of the squares of the uncertainty in the adjusted gross area and the weighted error of the adjusted background. The background uncertainty is weighted by the ratio of the adjusted peak width to the number of channels used to calculate the adjusted background. Therefore, net peak-area uncertainty is given by:

$$\sigma_{An} = \sqrt{A_{ag} + B\left(\frac{h-l-(2n-1)}{2n}\right)\left(\frac{h-l-(2n-1)}{h-l+1}\right)} \quad \textbf{(19)}$$

where:

A_{ag} = the adjusted gross area
A_n = the net area
B = the background area
l = the ROI low limit
h = the ROI high limit
n = the number of background points

The counting activity, *cA*, is calculated as:

$$cA = \left(\frac{100.0}{Percent}\right) * \left(\frac{Net\ Counts}{Live\ Time}\right) \quad \textbf{(20)}$$

where:

Percent = Gammas per 100 disintegrations (from library list)
Net Counts = Net counts in the peak
Live Time = Live time in seconds

5.4.4. Input Count Rate

This command is supported by most newer ORTEC MCBs and disabled for unsupported units. It displays or hides the input count rate meter (Fig. 132) in the upper left corner of the spectrum window.[25] (This is input count rate used for the dead-time calculation, not the number of processed pulses.) This command is also on the right-mouse-button menu.

Figure 132. Input Count Rate Meter.

Detector windows show the current (live) input count rate, whether or not the MCB is currently acquiring data. Buffer windows show the input count rate when the spectrum was (1) transferred to the buffer from the MCB or (2) saved to disk.

5.4.5. Sum

The **Sum** function performs its calculation as follows, and displays the sum on the Marker Information Line:

1) If the marker is not in an ROI, the counts in all data channels in the buffer (e.g., channel 1 to the maximum channel currently selected) are summed.

2) If the marker is in an ROI, the sum of the data channels in the ROI is shown on the display. This is the same as the gross counts in the **Peak Info** display, but can be used on wider ROIs.

3) You can also sum a region by marking it with a rubber rectangle, then selecting **Sum**. This is illustrated in Fig. 133.

[25]Note that if the full spectrum view is positioned in the same corner, it can obscure the Input Count Rate box.

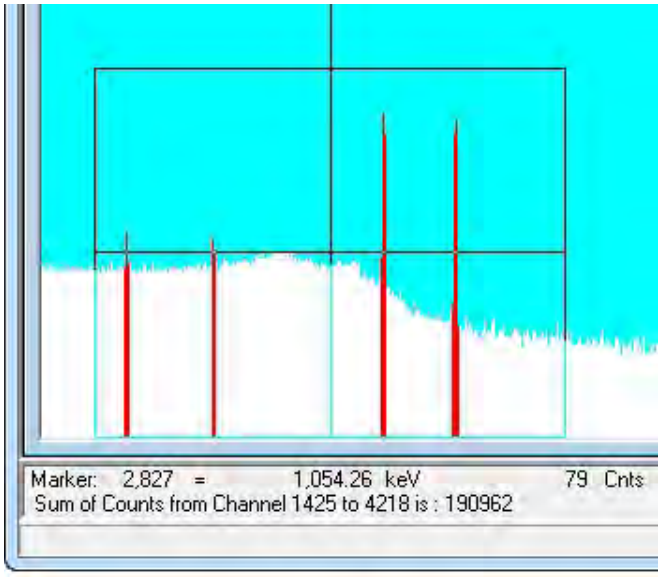


Figure 133. Summing the Channels Within a Rubber Rectangle.

5.4.6. Smooth

The **Smooth** command is available in buffer windows only. It transforms the data in the buffer spectrum according to a five-point, area-preserving, binomial smoothing algorithm. That is, the existing data is replaced, channel-by-channel, with the averaged or smoothed data as follows:

$$S_i = (O_{i-2} + 4O_{i-1} + 6O_i + 4O_{i+1} + O_{i+2})/16 \quad \textbf{(21)}$$

where:

S_i = the smoothed data in channel i
O_i = the original data in channel i

5.4.7. Strip...

This command (Fig. 134) strips the specified disk spectrum from the spectrum in the buffer and stores the result in the buffer. Select a **File name** and **Stripping Factor**, and click on **OK**.

NOTE Any valid spectral data file can be selected, but it must contain the same number of channels as the buffer.

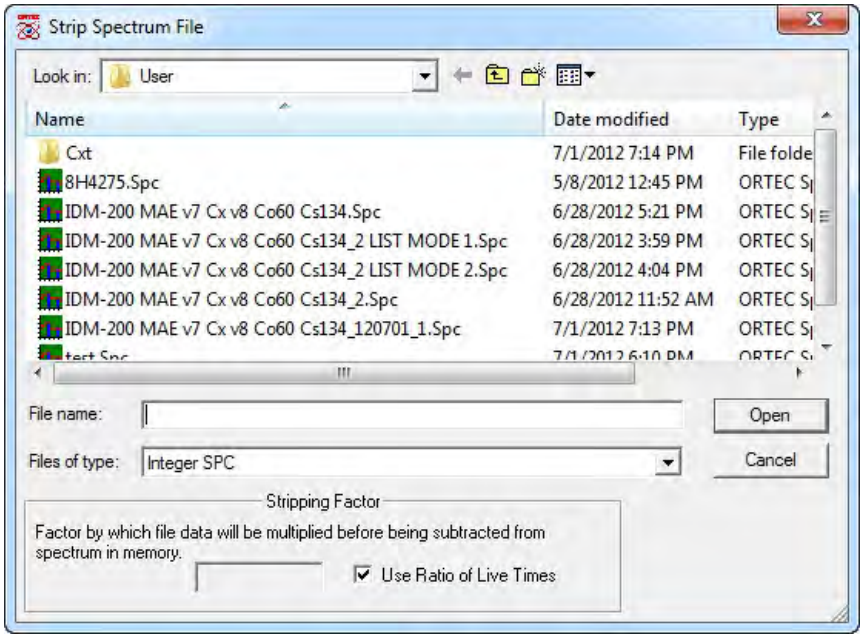


Figure 134. Choose Strip Spectrum.

The strip factor is a real number that is multiplied, channel by channel, by the disk spectrum before being subtracted from the buffer. If the **Use Ratio of Live Times** box is marked, the strip factor is calculated as the ratio of the live time of the buffer spectrum divided by the live time of the disk spectrum. Unmarking the **Use Ratio** box allows you to enter a factor, which can be negative, in which case the spectra are added.

NOTE The live time and real time are not changed by any strip operation. Also, the peak uncertainty (see Section 6.3.4) does not include the stripped areas and might not represent the true uncertainty.

5.5. Analyze

The **Analyze** menu (Fig. 135) contains commands that allow you to analyze all or part of a spectrum on the screen or on disk. The results can be displayed in both graphic and text forms. In the interactive analysis mode, peaks can be added, deleted, or shifted in energy. You can perform these commands on data in a buffer window or in a Detector if the Detector is not acquiring data. If a command is not available, it is disabled (gray). **Interactive in viewed area...** is active only when the Expanded Spectrum View displays ≤4096 channels (zoom in on a portion of the spectrum to activate this command).

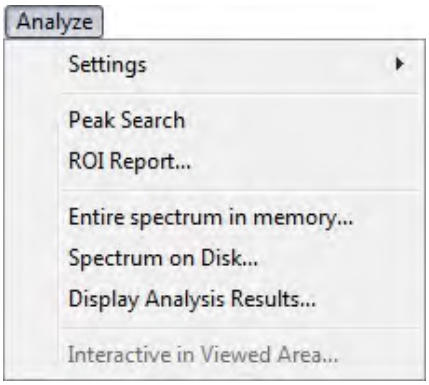


Figure 135. Analyze Menu.

5.5.1. Settings

This opens the submenu shown in Fig. 136. The user-controlled factors in the analysis are defined in these dialogs, and the analysis results can be captured in the analysis report discussed in Chapter 7.

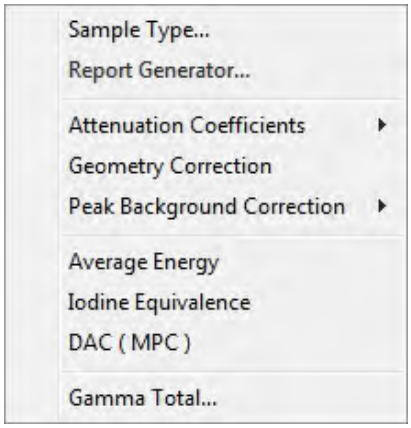


Figure 136. Settings Submenu.

NOTE Version 7 and 8 analysis settings (.SDF) files are not compatible with earlier versions of GammaVision.

5.5.1.1. Sample Type...

This opens the multi-tab Sample Type Settings dialog discussed in the following sections. The fields on this set of screens define a complete set of GammaVision analysis settings. Once defined, they can be saved to a Sample Description (.SDF) file. This .SDF file can then be used in .JOB files, in the QA analysis, as the acquisition preset default in **Ask on Start**, as the current defaults, and in other places within GammaVision.

To create an .SDF file, complete all screens of the dialog, then return to the **Sample** tab. Click the **Save As...** button in the upper right of the dialog; this will open a standard file-save dialog. Enter the path (if necessary) and new filename, then click **OK** to return to the **Sample** tab. Click again on **OK** to close the Sample Type Settings dialog.

NOTE Although this dialog has multiple tabs, any changes to the current set of "working" parameters for the selected Detector will not take effect until you click **OK**. To retain the current working parameters, click on **Cancel**.

Sample Tab

Sample settings (Fig. 137) are those whose values are generally different for each sample type. When an .SDF file is recalled, the date of **Creation** and last date the file was updated (**Edition**) are displayed. Whenever the file is changed, the edition date is updated.

The **Description** is used to identify the sample-type file, and can be 64 characters long.

Clicking on the **Presets** button opens a Presets dialog corresponding to the available presets for this MCB, as discussed in **Acquire/MCB Properties...**.(Remember that these default presets can be used automatically if the appropriate **Ask on Start** box in checked under **Acquire/ Acquisition Settings...**; see Section 5.2.1 for more information.)

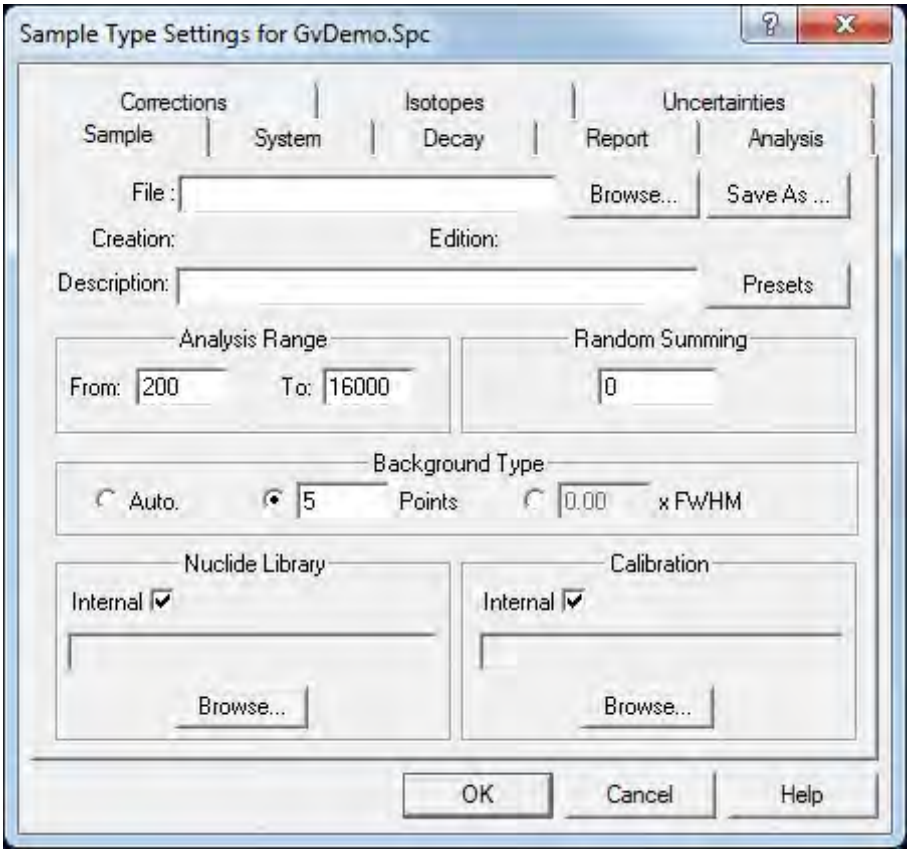


Figure 137. Sample Tab.

The **Calibration** data to be saved with the spectrum or used for online analysis can be the currently loaded **Internal** (working) calibration or a calibration stored on disk. The working calibration is the calibration just created with the **Calibrate** menu commands (see Section 5.3.1) or the calibration most recently recalled from disk. When the .SPC file for this spectrum is saved to disk, the current calibration will be saved with it for later analysis. The interactive analysis (performed with **Analyze/Interactive in viewed area**), uses the internal calibration.

Note that each Detector and buffer can have separate calibrations.[26] This is useful if different types of calibrations (e.g., point source and Marinelli beaker calibrations) are used for different types of samples.

[26]Note to legacy GammaVision users: The Detectors are calibrated directly, therefore it is not necessary to move the spectrum to the buffer in order to do a calibration. If the spectrum is moved to the buffer and the buffer is used for calibration, then the calibration is not associated with the Detector unless the calibration is moved to the Detector by using the **Calibrate/Save Calibration...** and **Calibrate/Recall Calibration...** commands.

The filename of the **Nuclide Library** to be used in the spectrum analysis can be the **Internal** (working) library or a library on disk. The working library is the library from **Library/Select File...**, and will include *any modifications made during the interactive analysis mode*.

The **Background Type** can be set to **Auto**, **X-Points, or X * FWHM.** These are explained in more detail in Section 6.3.1.

Random Summing is the random summing correction factor discussed in Section 6.11. Entering zero turns this correction off.

The **Analysis Range**, in channels, can be entered. This is usually used to eliminate analysis of the ends of the spectrum that do not contain useful data. The **Analysis Range** should be as wide as possible because the automatic energy recalibration feature (see Section 6.3.6) requires separated library peaks to work properly. Also, the correlation of lines from a single nuclide done by the analysis is defeated if the energy range analyzed does not include all the lines.

System Tab

System settings are those settings that are generally the same from sample to sample. However, all of these entries except the **Laboratory** and **Operator** names can be different for each sample type. The dialog is shown in Fig. 138.

The **Laboratory name**, composed of any 64 characters, is printed as the second line on each page of the report. The spectrum name is printed on the next line.

The **Operator name** is the name of the person operating the system. This name will appear on the analysis reports. This field defaults to the user name entered during Windows installation.

MDA Type — This allows the selection of the type of MDA calculation to be used as the method of calculating the MDA to be on the report. The MDA is a measure of how small an activity could be present and not be detected by the analysis. Many factors affect the MDA, which is reported in units of activity, such as becquerels. The calibration geometry, backgrounds (system and source-induced), detector resolution, and particular nuclide all seriously affect the MDA reported. Section 6.9 provides explanations of the different MDA formulas used by GammaVision.

In the **Library** section, **Match Width** sets the maximum amount by which a peak centroid can deviate from the nearest library peak energy and still be associated with that library peak. The value entered is multiplied by the FWHM at the peak energy to get the width used.

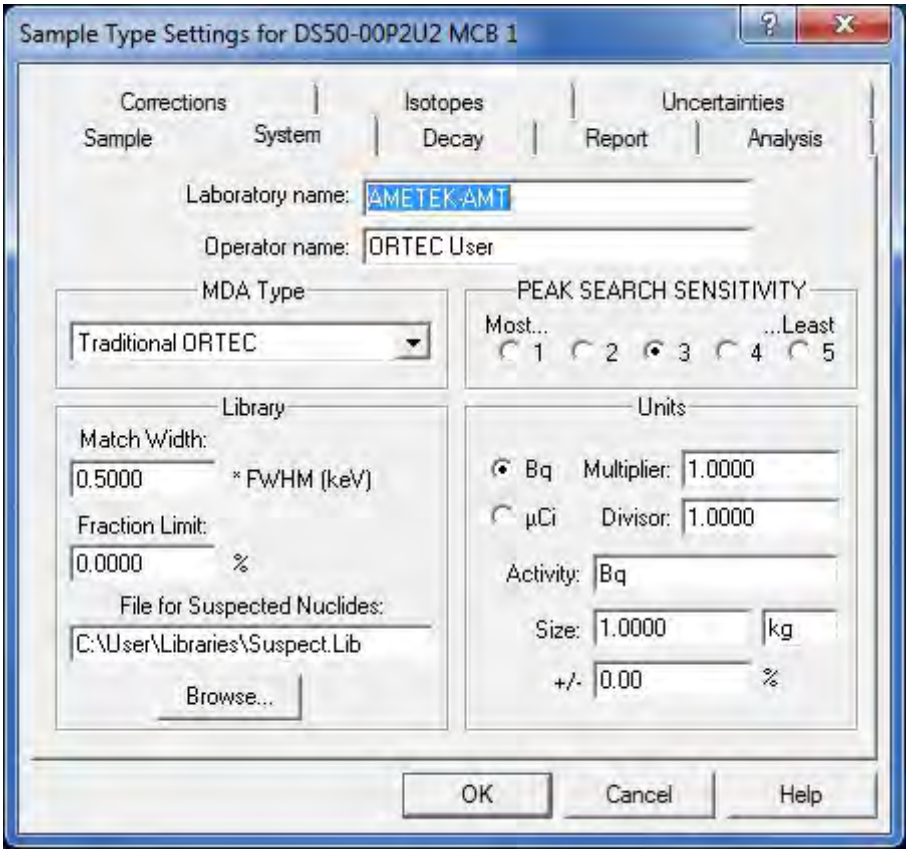


Figure 138. System Tab.

NOTES If the value is too small, some spectrum peaks will be misidentified due to statistical variation in the centroid; if it is too large, some library peaks will be incorrectly identified.

During efficiency calibration, the net peak area calculation can be affected by the library **Match Width** setting in effect at the time the calibration is performed. Before starting an efficiency calibration, make sure the **Match Width** is set to the same value you will be using during analysis. Most users will keep the default setting, 0.5. If using a different setting, we recommend a value between 0.4 and 0.75.

If the **Match Width** is set to a value other than 0.5, the value will be printed on the report.

The **Fraction Limit** is one of the parameters used to determine the presence or absence of a nuclide. The sum of the emission probabilities of the peaks in the spectrum identified with the nuclide is divided by the sum of the emission probabilities of all peaks of the nuclide in the energy range being analyzed. If the result is greater than the fraction limit, the nuclide is marked as being present. To turn off this test, set the limit to zero.

File for Suspected Nuclides — In the list of unknown peaks, there is a column for suspected nuclides. This is the closest energy in the library file to the unknown peak's energy. Suspected nuclides are identified in GammaVision using a suspected-nuclide library. This file is a library file (see Section 5.6). Typically, it is a much larger file than the analysis library file. The identification window is also much larger for this list than for the analysis library. This list might contain common lines (such as 511 keV or ^{40}K) that are present in the spectrum, but not desired in the analysis.

If the suspected-nuclide library contains the same lines as the analysis library, a nuclide whose energy is shifted just out of range for the analysis (the default is 0.5 × FWHM) will be marked as suspected on the unknown list.

The **File for Suspected Nuclides** must not have the same name as the analysis library file. If necessary, make a copy of the analysis library file with a new name.

The **Units** section allows the selection of either becquerels (**Bq**) or microcuries (**µCi**) as the base units, a **Multiplier** and **Divisor** to scale the numbers up or down.

The units label is printed at the top of the activity columns on the report and should reflect the values chosen; that is, if **µCi** is chosen with a multiplier of 1000, then "nanocuries" should be entered in the **Activity** field. If the sample quantity is entered later (see **Acquire/Acquisition Settings...** or **File/Settings...**), the units for quantity (weight or volume) are entered in the **Size** field. The combined label (activity/quantity) is limited to 14 characters. Optionally enter a 1-sigma sample **Size** uncertainty (**+/-**) between 0% and 1000%.

The **Multiplier**, **Divisor**, and sample **Size** values are used to generate the *Activity scaling factor* listed in the Analysis Parameters section of the report, and used by the NPP32 and ENV32 analysis engines to calculate the report's Summary of Library Peak Usage table.

The **PEAK SEARCH SENSITIVITY** sets the sensitivity for the peak search used in the **Peak Search** (Section 5.5.2), **Interactive in viewed area** (Section 5.5.7), and the full-spectrum analysis (Section 5.5.4). Before a suspected peak is accepted, the magnitude of the second difference must be greater than the weighted error of the channel counts. The **PEAK SEARCH SENSITIVITY** is a multiplicative factor used in error weighting.

The sensitivity can be set at any integer value from 1 to 5, with 1 the most sensitive (that is, "1" finds the most peaks). A value of 1 will find small peaks, but will also "find" many false peaks. A value of 5 will locate all the large peaks, but might miss some of the smaller peaks. If too large, some small peaks will be missed. In the interactive mode, many regions will be deconvoluted unnecessarily if the value is too sensitive. The parabolic background method is disabled for energies above 200 keV if the sensitivity is set to 1.

Decay Tab

The **Decay** tab is shown in Fig. 139. This dialog shows all the decay options and date/time entry fields.

Mark the checkboxes in the **Decay Correction** section to enable or disable decay correction **During Acquisition** and decay correction to a given **date** and **time**. Both of these affect the report of the analysis of the total spectrum.

The **Collection date** and **time** can also be entered under **Acquire/Acquisition Settings...**.

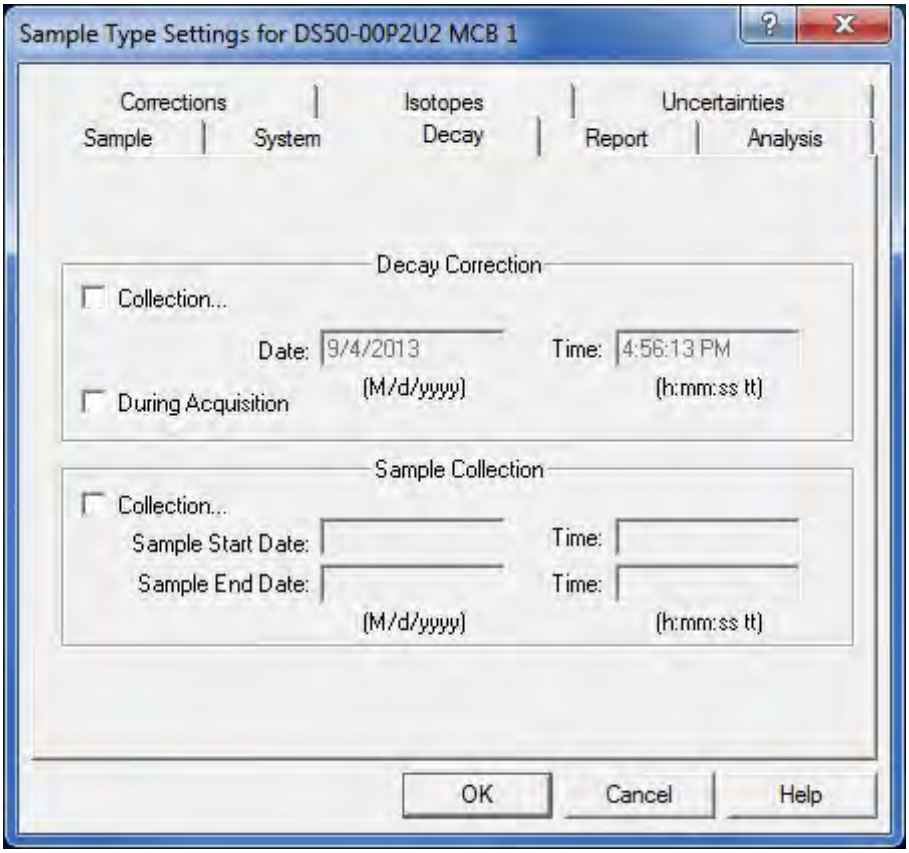


Figure 139. Decay Tab.

Mark the checkbox in the **Sample Collection** section and enter the times for sample collection. These dates/times are the start time of the sample collection and the stop time of the sample collection. For example, for air filters, the start time is the time when the air flow is started and the stop time is when the air flow is stopped. These times are used to calculate the buildup of the activity in the sample. It is assumed that the spectrum is not collected during the build-up time.

The correction for the build-up is given in Section 6.10.5.

Report Tab

This screen (Fig. 140) controls the contents, destination, and some details of the output report discussed in Chapter 7.

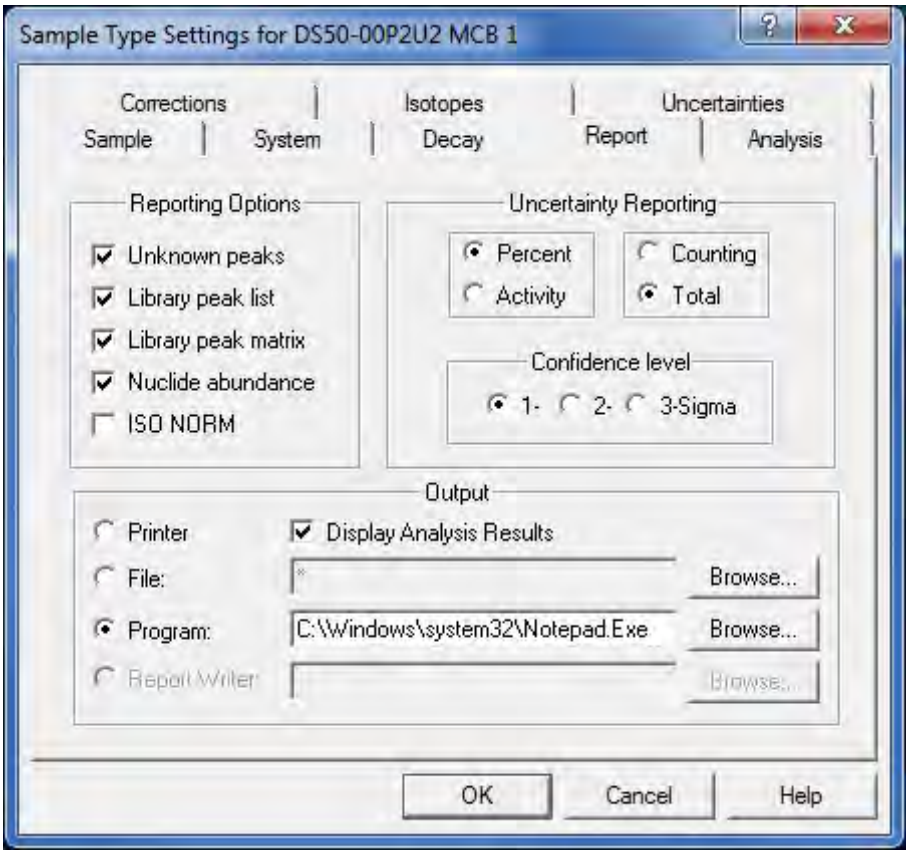


Figure 140. Report Tab.

Reporting Options

Select one or more **Reporting Options** by marking the checkboxes. If there is not enough information for GammaVision to generate one or more of the requested options, the software can print another option if there is enough information for it. For example, suppose a nuclide activity report is the only report option selected. If the spectrum has not been efficiency calibrated, the activities cannot be calculated. In this case, GammaVision will instead print the peak list because there is sufficient information to do that.

Output examples for all the reporting options are discussed in Chapter 7.

The ISO NORM Report

Note that analysis flags in the library editor and in the analysis parameters file, b30winds.ini (n30winds.ini for NAI32), are treated differently between GammaVision's standard analysis and its ISO NORM implementation. The ISO NORM report contents are discussed and illustrated in Section 7.7.12.

Library

No-MDA flag

Note that the "No MDA" flag functions differently for ISO NORM than for the standard GammaVision analysis. If an isotope flagged as "No MDA" is not detected in the sample, it is not reported in the standard GammaVision report sections unless the **Directed Fit** flag is turned on. However, the isotope is always reported in the ISO NORM table.

b30winds.ini (n30winds.ini for NAI32)

The b30winds.ini and n30winds.ini files include settings for the ISO NORM report (Section A.2.2), e.g., settings for the three probability factors, á, â, and ä, plus a flag to report MDA if the activity is less than the CL (In ISO NORM Table, print MDA if y < y*). The probabilities for these factors are set by default to 0.05 for 5% error, with a range of 1.0E−6 to 1. If the input values are outside this range, 0.05 is used. Changing the default parameters requires editing the probability alpha, probability beta, and probability gamma flags in the b30winds.ini or n30winds.ini files (see Section A.2.2). By default, if the CL is greater than the activity, the MDA is reported. However, the In ISO NORM Table, print MDA if y < y* flag can be set to false so that the activity and associated uncertainty are always reported.

Following are additional b30winds.ini/n30winds.ini flags that operate differently for the ISO NORM calculations than for other parts of the GammaVision report:

Print MDA in Nuclide Summary

When the ISO NORM reporting option is selected, this flag (page 447) is ignored so the format of the ISO NORM table remains fixed.

Nuclide Summary MDA Text

This flag (page 448) is ignored; the "MDA" title cannot be changed to read "CL" in the ISO NORM section of the report.

Background Width for MDA

This flag (page 447) is not used in ISO NORM calculations.

Second MDA Type

This flag (page 447) is ignored because there is no second MDA in the ISO NORM table. A second MDA can still be calculated through the regular GammaVision analysis.

Allow MDA Type Change

This flag (page 443) is ignored in the ISO NORM table because there is no other MDA type.

Uncertainty Reporting

The **Confidence level** multiplier shown here is used *on the report only*. All internal checks on peak uncertainty are done at the 1-sigma level. See Section 6 for details on the total uncertainty calculation. The uncertainty can be in **Activity** (e.g., 200 Bq ± 10 Bq) or **Percent** (e.g., 200 Bq ± 5%). If **Counting** is selected, counting uncertainty will be printed. If **Total** is selected, both the counting and total uncertainty will be printed.

Output

When GammaVision performs an analysis, a spectrum files is automatically created with the extension of .AN1. In addition, the results are written to a .UFO file and an ASCII-format .RPT file that use the same base filename as the spectrum file. Use the **Output** section of the Report tab to send the appropriate results file to any Windows-supported **Printer** available to the computer, a disk **File**, a **Program**, or the optional GammaVision **Report Writer**. You can also choose to display the analysis results graphically onscreen, in the same form as for **Analyze/ Display analysis results** (Section 5.5.6).

When **File** is selected, you can specify a new or existing filename; click **Browse...** and select an existing file to overwrite with the new output data; or leave the default asterisk (*) in the filename field. In this case, the report filename will remain the spectrum filename with the extension .RPT.

When **Program** is selected, you can choose any Windows program to be run with the report filename as an argument on the command line. The report filename sent to the program is the spectrum filename with the extension .RPT. The default program is Windows Notepad, Notepad.exe. In this case, when the analysis finishes, Notepad automatically starts, and opens the .RPT file. (You can also use Notepad to save the .RPT file to a different filename if desired or print the report.) The analysis is not complete until you close the selected program.

Instead of Notepad.exe, any user-written program (actually, any program that can read ORTEC .RPT files) can be selected here. In this case, the .RPT filename is used as an argument on the command line of the specified program.

The name of the .UFO file corresponds to the spectrum file from which it derives. A user-written program can read the report filename from the command line, change the extension to .UFO, and read the analysis results from the .UFO file.

The **Report Writer** check box is only active if the GammaVision Report Writer (A44-BW) is installed. This option uses an Access database and SAP® BusinessObjects Crystal Reports™ to produce the desired report. Click **Browse...** to select the report template to be used (see the GammaVision Report Writer's user manual for a complete discussion of templates).

Analysis Tab

Use this screen (Fig. 141) to select the **Analysis Method**, **Additional Error**, **Analysis**, and **Peak Stripping** options to be used. The actual analysis is done by a separate program referred to as an *analysis engine*.

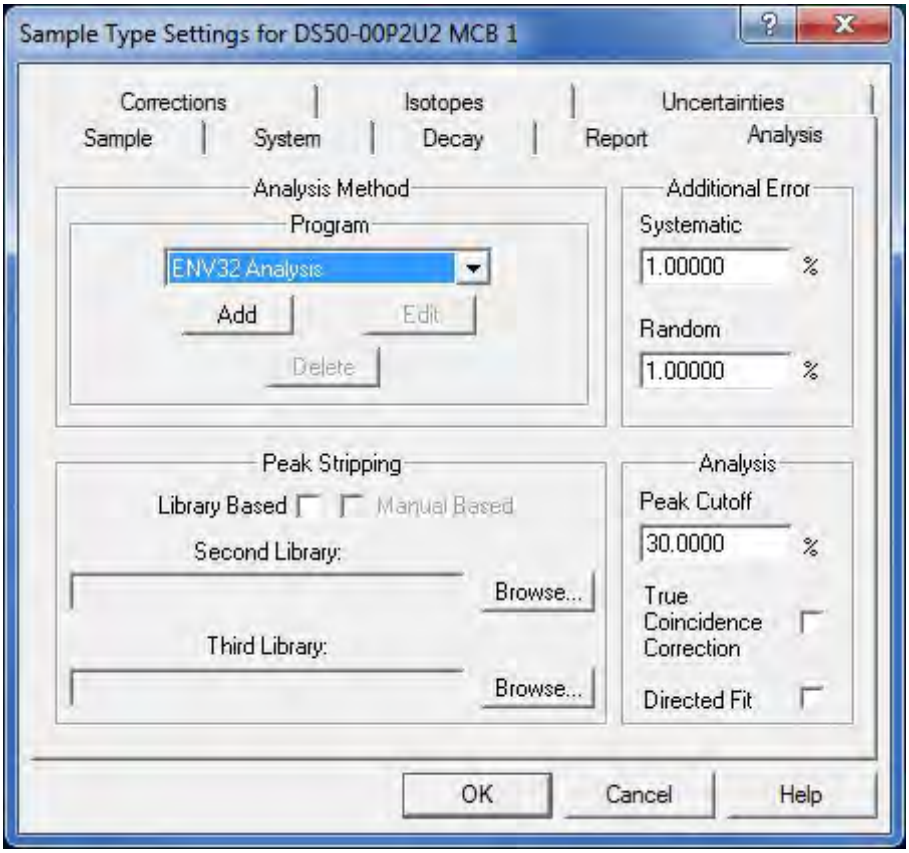


Figure 141. Analysis Tab.

Analysis Method(γ)

The analysis engine for the normal analysis is named WAN32; GammaVision also offers the ROI32, GAM32, NPP32, and ENV32 engines. In Maestro-PRO these are shown as reserved.

See Chapter 6 for more information on the analysis programs.

GammaVision also accommodates user-supplied analysis programs. The program must be able to read the spectrum name from the command line. There are no other restrictions, but if the program does not produce a results file in the .UFO format, the display results functions and the GammaVision Report Writer database will not work. All the analysis options can be taken from the .SPC file. The analysis program should also produce an ASCII report file so the report can be printed by the Windows print spooler.

Additional Error

The parameters in the **Additional Error** section are used in the calculation of the total uncertainty. Total uncertainty is composed of error estimates that follow a normal distribution and error estimates that follow a uniform distribution over a range. Most errors in gamma spectroscopy, whether systematic or random, follow a normal distribution. Error estimates are included for counting, random summing, absorption, nuclide uncertainty, efficiency, and geometry. Enter additional errors (%) related to the measurement that follow a normal distribution at the 1-sigma level. Enter uniform distribution errors (%) at the complete range of the uniform error limit. That is, if the likelihood of an uncertainty is uniform over 3% of the reported results, enter 3.0 in this field. The error estimates from all corrections are explained in Section 6.12.

Peak Stripping

When **Peak Stripping** is enabled, the analysis will perform the library-based peak deconvolution or “peak interference correction” described in Section 6.5.5. Briefly, this will separate peak areas that are too close together to be accurately separated by mathematical deconvolution. GammaVision supports two types of peak stripping: **Library Based** and **Manual Based**. In **Library Based** peak stripping, the program automatically detects overlapped peaks and the associated peaks needed. The program then performs the peak stripping using these peaks. In **Manual Based** peak stripping, you determine the overlapping peaks and the associated peaks. The associated peaks are given in the **Second Library** and the analysis peaks are given in the **Third Library**.

The availability of peak-stripping options depends on the analysis engine you choose. See Section 6.2 for a discussion of the analysis engines, a decision matrix, and selection guidelines.

WAN32 offers both the **Library Based** and **Manual Based** options, however, you can only choose one option at a time (or leave the boxes unmarked to perform no stripping).

When **GAM32** or **ROI32** is selected, the **Library Based Peak Stripping** and **Directed Fit** methods are turned off and the selections disabled.

When **NPP32, ENV32, or NAI32** is selected, the **Library Based Peak Stripping** option is turned on and cannot be disabled. If analysis without library-based peak stripping is desired, then either WAN32, GAM32, or ROI32 analysis engines must be used.

Analysis

Only peaks with 1-sigma counting uncertainty less than the **Peak Cutoff** are used to calculate nuclide activity or report as unidentified. Library peaks with uncertainty higher than the Peak Cutoff may still be reported in different sections of the analysis report for different analysis engines based on parameter settings in the b30winds.ini (n30winds.ini for NAI32) file; see Section A.2.2.

Click **True Coincidence Correction** to enable TCC.

- If the Detector has not been calibrated for TCC, the correction is automatically turned off in the analysis.

- If preparing to analyze a saved spectrum, *be sure it contains a TCC calibration; otherwise the analysis results may be incorrect*. To check a spectrum file for TCC calibration, recall it, step through the Calibration Wizard , and on the final screen (Fig. 126, page 142) confirm that the lower-right window says TCC Calibrated.

Click **Directed Fit** to allow for negative peak areas in low-level spectra. The following rules should normally be followed when using directed fit:

- Preferentially use the ENV32 analysis engine (NAI32 for sodium iodide) unless a feature of one of the other engines is required. ENV32 is required when analyzing complicated spectra with overlapping peaks or large libraries.

- Use NPP32 or WAN32 only for relatively simple spectra that contain only singlet peaks.

- The **Peak Cutoff** is typically set to accept good quality peaks. However, a high value (i.e., 1000) may be used in some cases to preferentially retain peaks found using the normal peak search method rather than resorting to **Directed Fit** so that peak stripping is applied using the library configuration.

For more information, see the Directed Fit discussion in Section 6.3.2.2.

Corrections Tab

The Corrections tab is shown in Fig. 142.

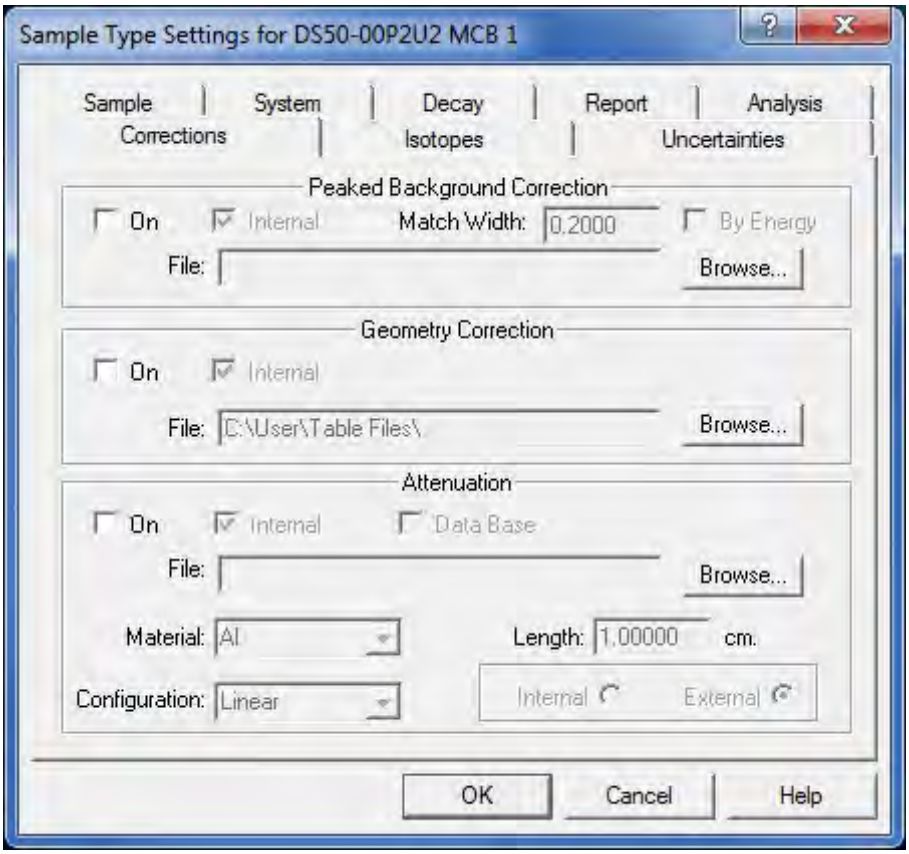


Figure 142. Corrections Tab.

The **Peaked Background Correction** (Section 6.10.4) can be turned **On** or off, and the correction file specified. The filename of the .PBC file to be used for the correction in the spectrum analysis can be the **Internal** (working) file or a **File** on disk. If the **Internal** box is not marked, a filename must be entered. The working file is the one most recently loaded with **Analyze/Settings/ Peak Background Correction(γ)/Select PBC...** (which is discussed beginning on page 175).

Adjust the **Match Width** as desired, but normally no lower than the Library Match Width on the System Tab. For the **By Energy** option, when not using a library you may wish to use a greater PBC match width. It may be useful to perform test acquisitions based on your application.

- If the **By Energy** checkbox is marked, PBC subtraction is also applied to all peaks in the spectrum, and peaks shown in the report's Summary of Peaks in Range table will reflect the background corrected peak areas.

- If **By Energy** is not marked, then background correction is only applied to the Identified Nuclide Peaks and peaks shown in the report's Summary of Peaks in Range table are NOT corrected for background.

The **Geometry Correction**$^{(\gamma)}$ (Section 6.10.5) can be turned **On** or off, and the correction (.GEO) **File** can be specified. The filename of the .GEO file to be used for the correction in the spectrum analysis can be the **Internal** (working) file or a file on disk. If the **Internal** box is not checked, a filename must be entered. The working file is the file most recently loaded with **Analyze/Settings/Geometry Correction**$^{(\gamma)}$ (see Section 5.5.1.4).

The **Linear Attenuation** can be turned **On** or off, **Internal** or **External** can be selected, and the source of the correction parameters (**Internal** or **DataBase**) can be specified. The correction function can be:

- The **Internal** (working) correction loaded in the Absorption Correction dialogs discussed in Section 5.5.1.3.
- A specific .SOR file calculated from two spectra.
- Selected from GammaVision's built-in database of stored coefficients.

The filename of the .SOR file to be used for the correction in the spectrum analysis can be the internal (working) file or a file on disk. If the **Internal** box is checked, the internal file is used, otherwise a filename or database must be entered. The working correction is the correction most recently viewed or calculated per Section 5.5.1.3.

If **Data Base** is selected, the **Material**, **Length**, **Configuration**, and **Internal** or **External** type must also be selected. The material is selected from the list in the database. The **Configuration** is also selected from the database. The database values are based on an absorber **Length** of 1 cm. For larger or smaller lengths (external) and thicker or thinner materials (internal), enter the actual length or thickness. Either **Internal** or **External** absorption can be selected. **Internal** absorption is for cases where the radioactive material is distributed throughout the absorber (matrix) and **External** is where the absorber is between the radioactive material and the detector.

The attenuation correction is explained in detail in Section 6.10.6.

Isotopes Tab

The isotope-specific corrections or calculations are specified on this tab (Fig. 143).

NOTE Be sure the isotope identifiers (e.g., “Xe-133", “I-133") in the average energy, iodine equivalence, and DAC/MPC tables match the identifiers in the analysis library; otherwise, GammaVision will be unable to perform these calculations correctly.

The **Average Energy** calculation (Section 6.13) can be turned **On** or off and can use either the **Internal** correction table most recently created or loaded according to Section 5.5.1.6, or a specific EBAR table (.EBR) file. When enabled, this calculation will produce an addition to the report with the average gamma energy for the spectrum.

The **Iodine Equivalence** calculation (Section 6.14) can be turned **On** or off and can use either the **Internal** correction table or a specific table file. When enabled, this will produce an addition to the report with the iodine equivalence for the spectrum. The working table is the one most recently created or loaded according to Section 5.5.1.7.

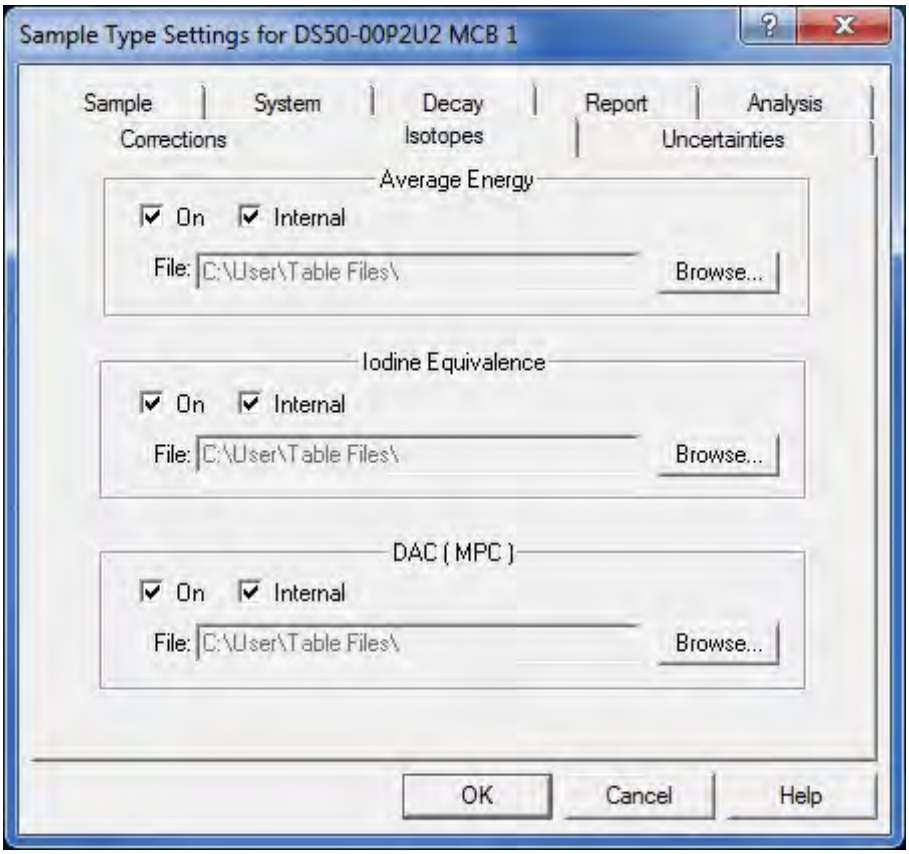


Figure 143. Isotopes Tab.

The Derived Activity Calculation, **DAC**, (also called Maximum Permitted Concentration, **MPC**), can be turned **On** or off, and can use either the **Internal** (working) correction table or a specific table **File**. When enabled, it will produce an addition to the report with the DAC calculation for each isotope in the table that is also in the spectrum and analysis library. See Section 6.15 for details on this calculation. The working table is the table created or loaded in Section 5.5.1.8.

Uncertainties Tab

This tab (Fig. 144) allows you to optionally define up to nine uncertainty values that will be summed and used in the analysis. Both the **Description** and a non-zero **Value** must be defined for an uncertainty entry or it will not be used in the analysis or report. These values are stored in the .SDF file as well as .SPC spectrum files, and are reported in the Analysis Parameters table (Section 7.5).

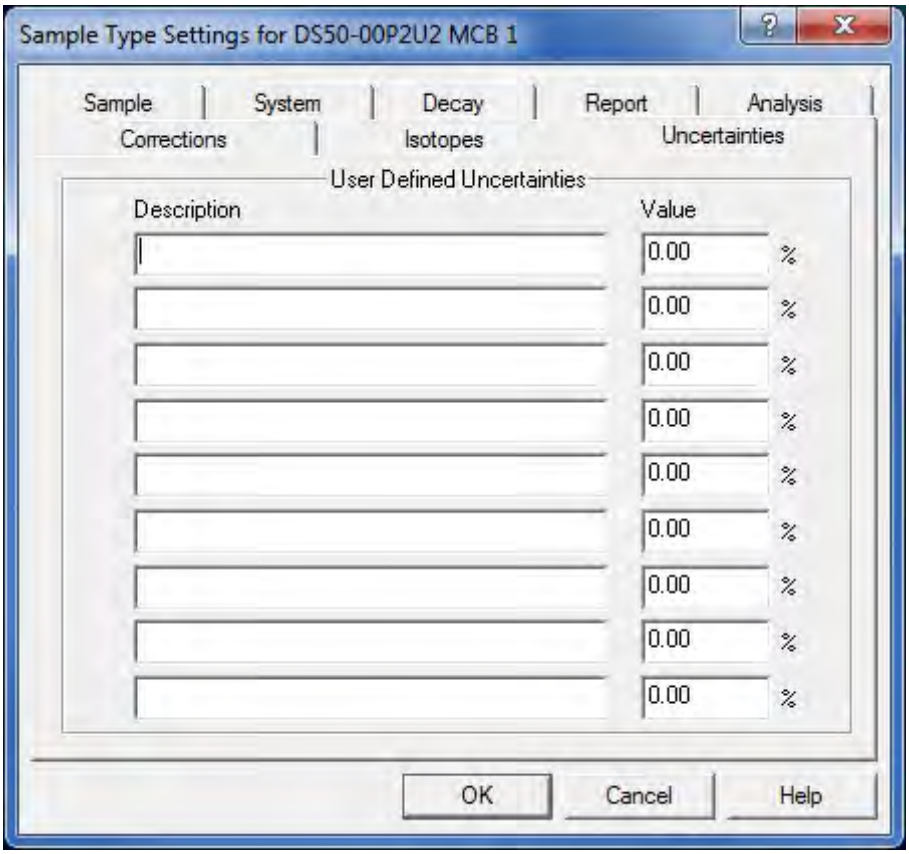


Figure 144. Uncertainties Tab.

5.5.1.2. Report Generator(γ)

If the customizable GammaVision Report Writer (A44-BW) is installed, the **Report Generator Settings** dialog (Fig. 145) will open. There are several report options to choose from.

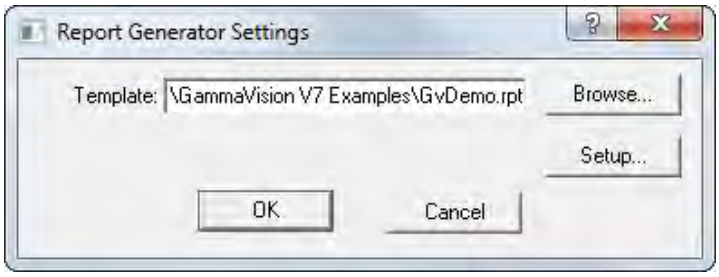


Figure 145. Report Generator.

See the Report Writer user manual for more details on these options. The standard GammaVision analysis report is described in Chapter 7.

5.5.1.3. Attenuation Coefficients(γ)

This command opens the submenu shown in Fig. 146. These commands allow you to create, modify, or view the absorption correction files or database.

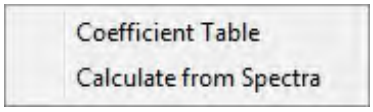


Figure 146. Attenuation Coefficients Submenu.

Coefficient Table

This command lets you add to, modify, and view the absorption correction database. The attenuation database supplied with GammaVision has many common materials already defined.

There are two ways to add new materials to this database:

- Define a new material that is composed of two or more materials already in the database. GammaVision will then calculate the new attenuation curve from the existing attenuation data.

- Define a completely new material, that is, one not composed of materials in the database. In this case, you will enter the attenuation data in the Attenuation Worksheet sidebar, and save the new material and its attenuation data it to the database.

Selecting **Coefficient Table** opens the Attenuation Worksheet Sidebar, Attenuation Table, and Attenuation graph window, as illustrated in Fig. 147.

To select an absorber from the Attenuation Worksheet, click the down-arrow button in the **Absorber** section to display the list of materials in the database, and click the desired entry. Selecting a material loads the attenuation values and redisplays the Attenuation Table and graph. Clicking the mouse on a the table values moves the marker to that energy in both the Attenuation graph window and spectrum windows. Clicking the mouse in either spectrum window or the

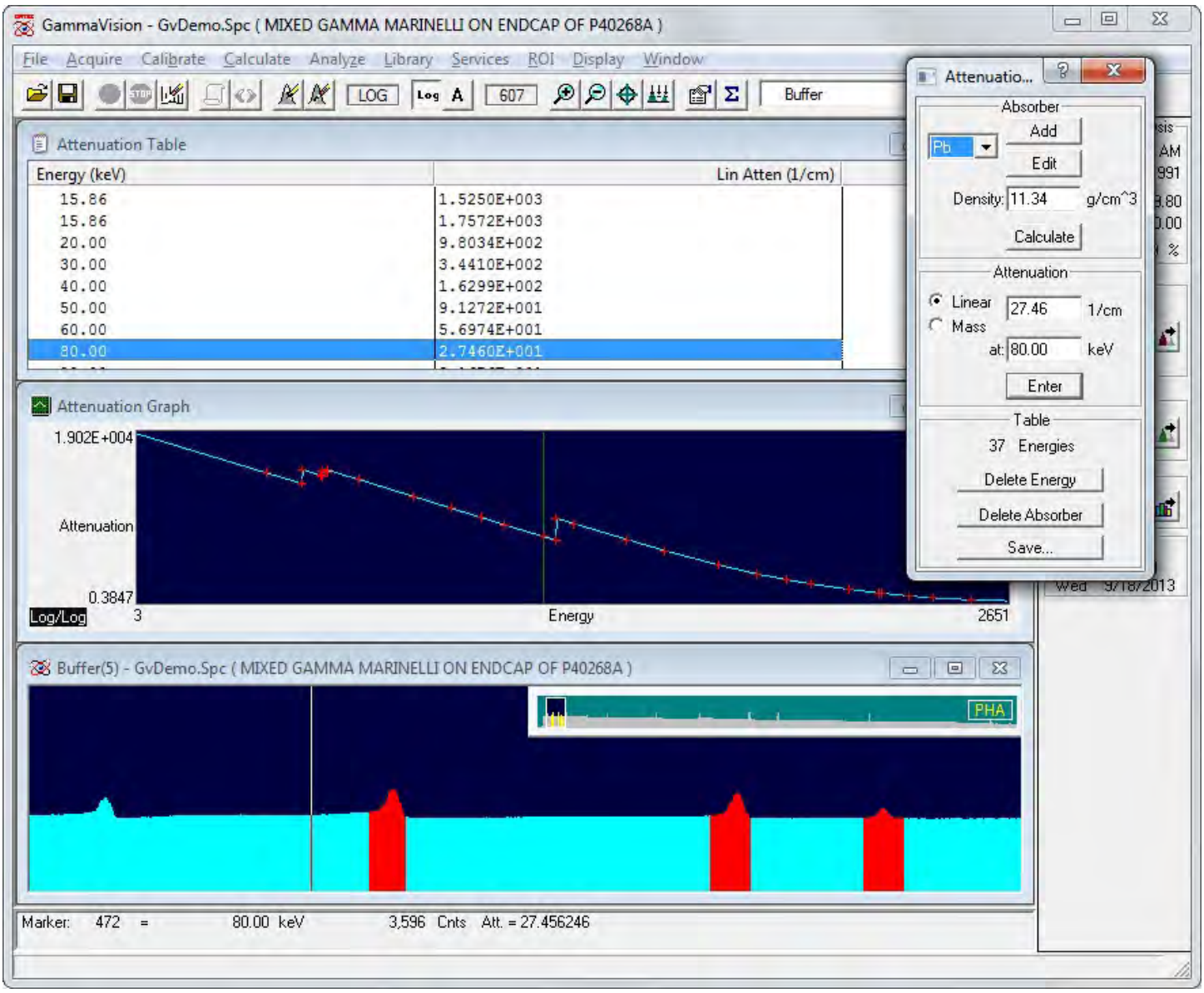


Figure 147. Attenuation Worksheet Table for Absorber Coefficient Table.

Attenuation graph window moves the marker to that energy in the other plots. The attenuation value is displayed on the Marker Information Line.

Adding a Material Composed of Substances Already in the Database

GammaVision makes it easy to add a new absorber made of substances already in the absorber database. The new absorber can be a chemical compound such as sodium iodide (NaI), or a more complex mixture, such as sand and lead.

1) In the **Attenuation** section of the sidebar, click either the **Mass** or **Linear** radio button.

2) Click **Add**. This will open the Absorber Definition dialog (Fig. 148).

3) Enter the **Name** of the new material. As an example, we will use **NaI**.

4) Next, decide whether to describe the ratio of components in the material as *a percentage* or a *mass ratio*; this will determine which radio button should be marked in the **Units** section of the Absorber Definition dialog.

   - If you know the relative number of atoms (or molecules) of each constituent in the absorber — for example, NaI — click on **%**. Amounts entered are multiplied by the atomic weight of the constituent and normalized to 100%.

   - Click **Mass Ratio** if you know the relative amounts of constituents by weight — for example, 90% sand, 10% lead.

5) NaI contains sodium and iodine in a 1-to-1 ratio. Therefore, it should be entered in the Absorber Definition dialog as two separate **Constituent**s, Na and I, each in the relative **Amount** of 1. (Similarly, Al_20_3 would be entered as aluminum in the amount of 2, and oxygen in the amount of 3.)

   - In the **Constituent** section, enter Na and an amount of 1, then click **Add**. The **Constituent** droplist in the upper part of the dialog will now list Na as a component of NaI (Fig. 148).

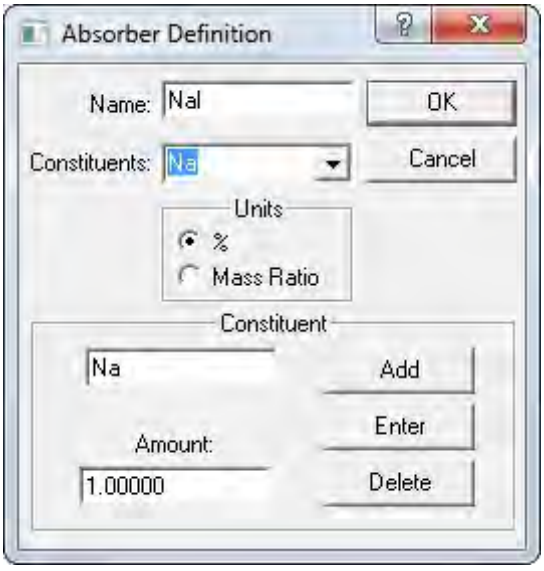


Figure 148. Defining a New Absorber.

   - Return to the **Constituent** section, enter I and an amount of 1, then click **Add**. The droplist at the top of the dialog will now show both components.

   - Click **OK** to close the Absorber Definition dialog.

The new material's name will now be displayed in gray on the sidebar **Absorber** droplist.

NOTE If you choose **Mass Ratio** instead of **%**, the ratios of the masses must be entered and must total 1.00. For example, the atomic mass of NaI is 149.89, so the Na mass ratio is **0.153** (= 22.989/149.89) and the I mass ratio is **0.847** (= 126.90/ 149.89). If an absorber has only one constituent, the mass ratio is **1.00**.

6) If you clicked on **Mass** in step (2), the **Absorber** section of the sidebar will contain a field labeled **Mass**; enter the atomic mass units for the total compound or element. (The atomic mass for NaI is 149.89 [= 22.9897+126.904].) If you clicked on **Linear** in step (2), this field will instead be labeled **Density**; density values can be found in various reference books. (For example, the density of NaI is 3.67 g/cm^3.). Enter the **Mass** or **Density**.

7) Click **Calculate**. If the database contains attenuation data for all of the components in the new material, the Attenuation Table of coefficients will be displayed. Otherwise, a "**Check the mass attenuation data list for missing elements**" message will be displayed.

8) Click the **Constituents** droplist and check spelling and spacing against the Worksheet's droplist. To correct an entry, click it to load it into the bottom section of the Absorber Definition dialog, make the corrections, click **Enter**, then click **OK** to close the dialog. Return to the Attenuation Worksheet and click again on **Calculate**.

9) Once the new absorber's attenuation coefficients have been calculated, the final step is to either save the new absorber to the database (click **Save...** at the bottom of the sidebar) or delete the new entry (**Delete Absorber**). If you save it, the absorber list at the top of the Worksheet will become active, and will now list your new material.

10) To close the **Attenuation Coefficient** feature, including Worksheet, table, and graph, click the Worksheet's × box.

NOTE The **Linear** and **Mass** attenuations are stored separately in the database. If you wish to use both, *each must be added, calculated, and saved*.

Editing or Deleting the Constituents in an Absorber

Suppose that in our example we used an incorrect chemical formula for sodium iodide, Na_2I instead of NaI, and now wish to correct the error. To do this:

1) On the Attenuation Worksheet sidebar, select **NaI(Tl)** from the **Absorber** drop list, then click **Edit**. This will open the **Absorber Definition** dialog.

2) Click the **Constituents** drop list at the top of the dialog, and select **Na**. The fields at the bottom of the dialog will now display **Na** as the **Constituent**, in the **Amount** of **2**. Change the amount to **1** and click **Enter**.

3) To delete a component from an absorber, select it from the **Constituent** drop list and click **Delete**. (This **Delete** button does not remove an absorber from the database, just changes the absorber's composition. To completely remove an absorber, close this dialog, go to the bottom of the sidebar, and click **Delete Absorber**.)

4) Click **OK** to close the Absorber Definition dialog.

5) Next, enter the mass or density as shown in the **Absorber** section at the top of the sidebar and click **Calculate**.

6) Click **Save** to store the complete record in the database.

Adding a New Element or Single-Constituent Material to the Database

Adding a new material involves (1) defining the absorber name, then (2) using the Attenuation Worksheet sidebar to create the corresponding table of attenuation coefficients. To do this you will need enough energy/attenuation pairs to generate a good attenuation function. These values can be found in reference books.

1) If the attenuation values are in g/cm^2, click the **Mass** radio button in the **Attenuation** section of the sidebar. If the attenuation values are in units of 1/cm, click **Linear**. Either method can be used in simple cases, however, if you expect to use the materials entered here in creating absorber files for compounds, **Mass** must be used.

2) On the sidebar, click **Add** to open the Absorber Definition dialog.

3) In the **Name** field, enter the chemical symbol for the element (or substance name) — for example, **Co**.

4) In the **Constituent** section, enter **Co** and an **Amount** of 1.0, then click **OK** to close the dialog and return to the sidebar.

5) Now, in the **Attenuation** section of the sidebar (Fig. 149), enter the energy/attenuation pairs for as many energies as necessary to obtain a good attenuation function. When entering the X-ray edge, use energy values that are close but not equal, e.g., 13.420 and 13.421 keV.

6) Click the **Save** button at the bottom of the sidebar to store the table.

7) Next, enter the mass or density as shown in the **Absorber** section at the top of the sidebar (Fig. 147), and click **Calculate**.

8) Click **Save** again to store the complete record in the database.

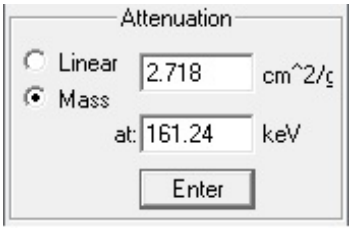


Figure 149. Adding a New Constituent to the Database.

Calculate from Spectra

Selecting this command opens the External Attenuation Sidebar, shown in Fig. 150. External attenuation tables can be built automatically using analysis results (.UFO) files, or manually by entering the peak net area rates for specific energies.

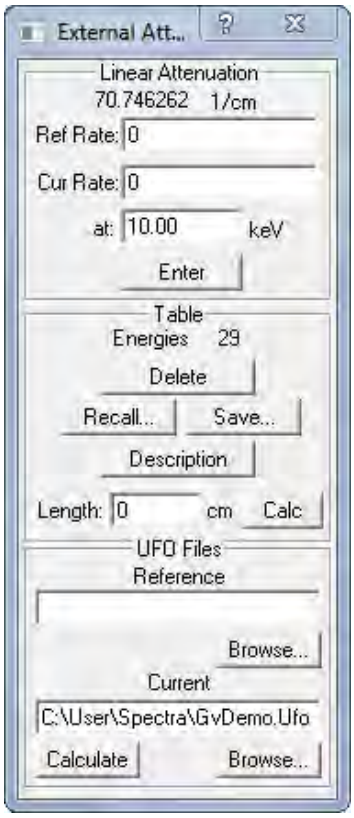


Figure 150. External Attenuation Sidebar.

Automatic Calculation

In the automatic mode, select the **UFO Files** for the analysis of two spectra (**Reference** and **Current**) and click **Calculate**. ***These two spectra must be the spectrum without the absorber and the spectrum with the absorber.*** The two samples should be otherwise as similar as possible. This will produce a table that is the ratio of the net peak areas for all the peaks that are in both spectra. The matching is done by using the identified (library) peak list in both .UFO files. The calculated table is now displayed as shown in Fig. 147.

Enter the thickness of the absorber in the **Length** field at the bottom of the **Table** section of the sidebar. This is important because the attenuation in the database is normalized to 1 cm, and the thickness of the actual sample is entered in the attenuation dialog.

Click the **Description** button to add a description to the file (see Fig. 151). This is used to label the files and is copied into the spectrum file for added verification of results.

Manual Calculation

In the manual mode, you enter the values. In the **Linear Attenuation** section at the top of the sidebar, enter the **Ref Rate** (no absorber), the **Cur Rate** (with absorber), and the energy, then

click **Enter**. The **Ratio** (correction factor) will be displayed above the **Ref Rate** field and in the Attenuation Table.

NOTE The **Ref Rate** must always be greater than the **Cur Rate**.

Enter the thickness of the absorber in the **Length** field at the bottom of the **Table** section of the sidebar. This is important because the attenuation in the database is normalized to 1 cm, and the thickness of the actual sample is entered in the attenuation dialog.

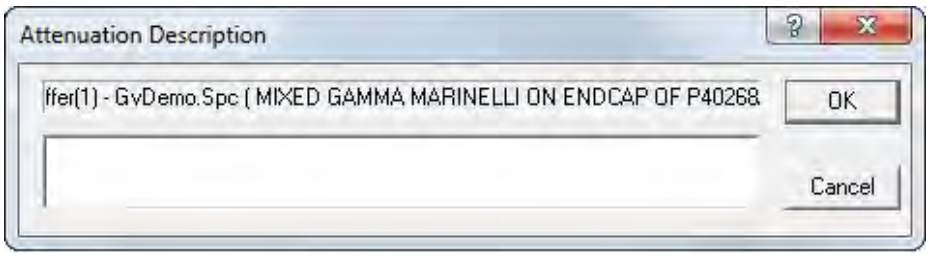


Figure 151. Attenuation Description.

Click the **Description** button to add a description to the file. This is used to label the files and is copied into the spectrum file for added verification of results.

Editing the External Attenuation Table

To remove an energy from the Attenuation Table window, select it with the mouse and click the sidebar's **Delete** button. To change an energy, select it from the table with the mouse, go to the **Linear Attenuation** section of the sidebar, change the values, and click **Enter**.

To save the current table, click the **Save...** button in the sidebar. Click **Recall...** to open a standard file-open to recall an existing table (which has the default extension .ATT).

The External Attenuation Sidebar's Control Menu

Figure 152 shows the External Attenuation Sidebar's control menu (which opens when you click the title bar icon). To edit an existing file in a Notepad-like editor, click **Edit File...**. This opens a standard file-open dialog to select the file, then an ASCII editor screen showing the file contents. Any changes made will be saved to the file. The formatting does not have to be exactly as shown.

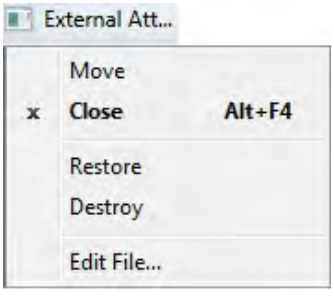


Figure 152.

The **Destroy** selection erases all the values and energies in the currently displayed table. It does not alter the disk file (if any) unless the current table is then saved with the same filename. **Restore** will undo any changes made to the current table, including **Destroy**, *as long as it is used before the External Attenuation Sidebar is closed.*

Close ends the **Calculate from Spectra** session, closing the sidebar, Attenuation Table, and graph windows. The currently selected table becomes the internal or working external attenuation table.

5.5.1.4. Geometry Correction(γ)

This command opens the Geo Correction Sidebar (Fig. 153) for building geometry correction (.GEO) files. These tables can be built automatically using analysis results (.UFO) files, or manually by entering the peak net area rates for specific energies. The correction can be greater or less than 1.0 to allow for corrections between any two geometries.

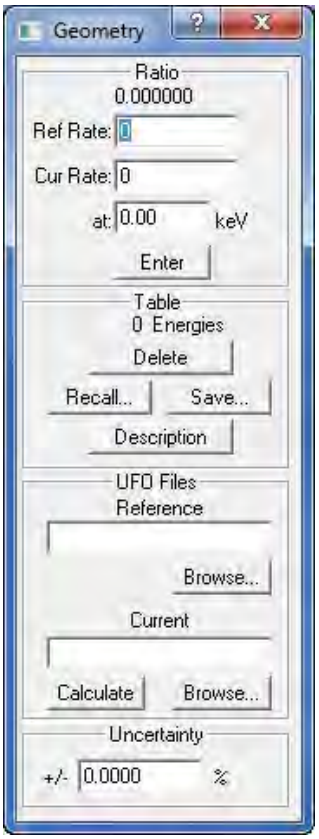


Figure 153. Geometry Correction Sidebar.

NOTE Version 7 geometry correction (.GEO) files are not compatible with earlier versions of GammaVision.

Automatic Calculation

In automatic mode, select the analysis results (.UFO) files for the analysis of the spectra for the two geometries, and click **Calculate**. This will display a table window showing the ratio of the net peak areas for all the peaks common to both spectra. The matching is done by using the identified (library) peak list in both .UFO files.

Click the **Description** button to add a description to the file. This is used to label the files and is copied into the spectrum file for added verification of results.

Manual Calculation

In the manual mode, you enter the values. In the **Ratio** section at the top of the sidebar, enter the **Ref Rate** (Geometry 1), the **Cur Rate** (Geometry 2), and the energy, then click **Enter**. The **Ratio** (correction factor) will be displayed above the **Ref Rate** field in the sidebar, as well as in the table window.

Click the **Description** button to add a description to the file. This is used to label the files and is copied into the spectrum file for added verification of results.

At the bottom of the sidebar, you may optionally enter a 1-sigma **Uncertainty** for this correction, ranging from 0% to 1000%.

Editing the Geometry Correction Table

To remove an energy from the Geometry Correction Table window, select it with the mouse and click the sidebar's **Delete** button. To change an energy, select it from the table with the mouse, go to the **Ratio** section of the sidebar, change the values, and click **Enter**.

To save the current table, click the **Save...** button in the sidebar. Click **Recall...** to open a standard file-open to recall an existing .GEO file.

The Geometry Correction Sidebar's Control Menu

This sidebar's control menu contains the same commands as shown in Fig. 152. To edit an existing file in a Notepad-like editor, click **Edit File...**. This opens a standard file-open dialog to select the file, then an ASCII editor screen showing the file contents. Any changes made will be saved to the file. The formatting does not have to be exactly as shown.

The **Destroy** selection erases all the values and energies in the currently displayed table. It does not alter the disk file (if any) unless the current table is then saved with the same filename. **Restore** will undo any changes made to the current table, including **Destroy**, *as long as it is used before the Geometry Correction Sidebar is closed.*

Close ends the **Calculate from Spectra** session, closing the sidebar and the Attenuation Table and graph windows. The currently selected table becomes the internal or working geometry table.

5.5.1.5. Peak Background Correction(γ)

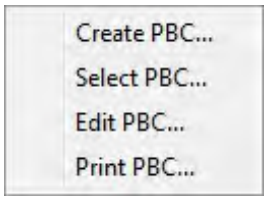


Figure 154. PBC Menu.

The **Peak Background Correction** submenu is shown in Fig. 154. Use these commands to load a new working .PBC file, to create or edit .PBC files, and print PBC tables. The PBC file is used with the Peak Background Correction in the spectrum analysis. Note that the PBC correction is related to the detector and the shield, but not to the geometry of the sample. The .PBC files are organized by nuclide, then by peaks, for each nuclide. Any of the correction table nuclide data include the nuclide name, which can be any combination of eight characters, but must be consistent throughout all files.

At startup, GammaVision automatically attempts to load the PBC table last loaded. Thereafter, it can be replaced at any time using **Select PBC...**. It stays resident in memory after it have been loaded.

Create PBC...

This feature analyzes an existing .UFO file and creates a corresponding .PBC file. It operates in both buffer and Detector windows.

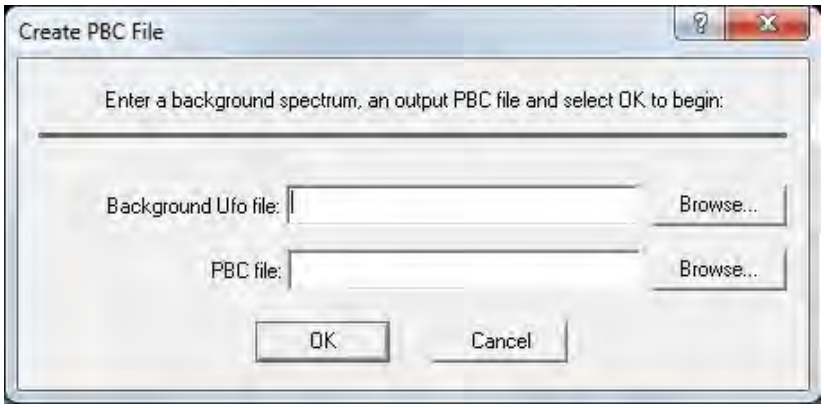


Figure 155. PBC Wizard.

Browse for the **Background Ufo file** to be used (Fig. 155). Then, either enter a new filename for the .PBC file or select an existing .PBC file (the current contents of the file will be overwritten). Note that at startup GammaVision automatically attempts to load the PBC table last used. It stays resident in memory as the *working* or *internal* PBC file once loaded. You can replace this file at any time using **Select PBC...**.

As of v7, **Create PBC...** now adds the unknown peaks to the PBC table. A new nuclide, Un-0, has been added to the library, and its peak list is assigned all of the unknown peaks with uncertainty values less than the **Peak Cutoff** value set on the Analysis tab under **Analyze/Settings/Sample Type...**. These peaks are used in the PBC calculation if the PBC correction's **Match Width by Energy** checkbox is marked on the Corrections tab. Figure 156 shows a PBC table file with all unknown peaks attributed to nuclide Un-0.

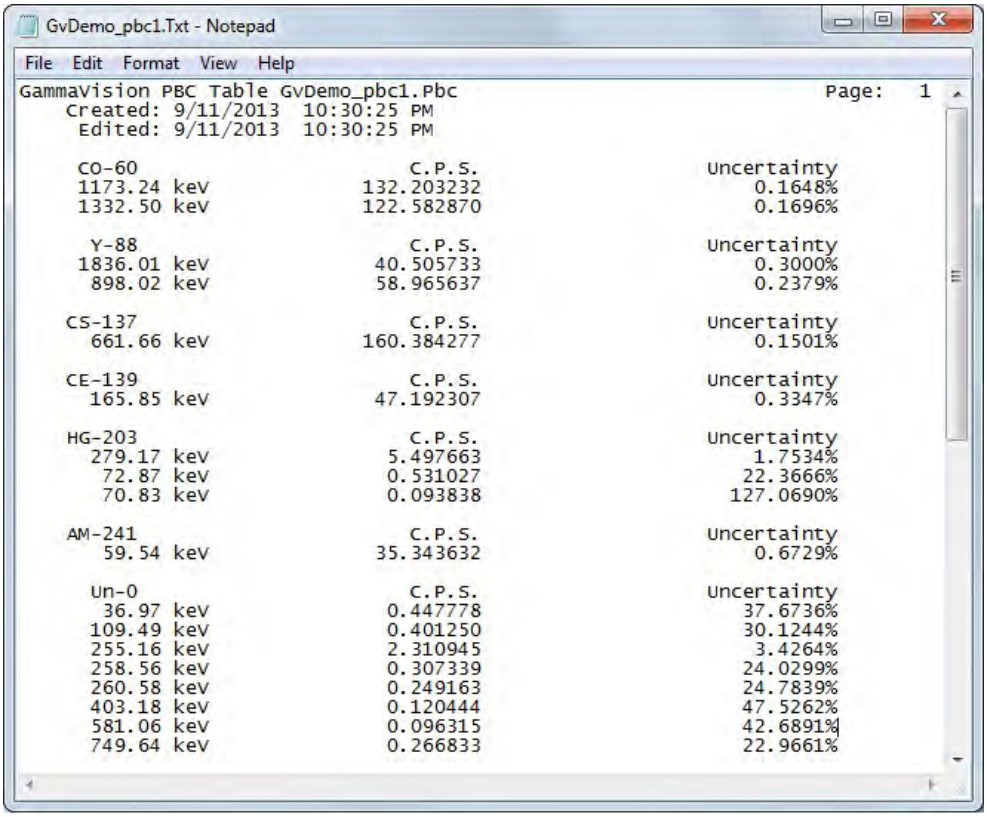
Select PBC...

Use this command to open a standard file-open dialog and select a new working .PBC file. If a .PBC file is already loaded, its name will be displayed in the **File name** field; otherwise, the default, *.PBC, will be shown. Select the desired file and click **Open**. The .PBC files are organized by nuclide, then by peaks, for each nuclide.

Edit PBC...

This function is used to create a new .PBC file or to change the contents of an existing .PBC file. To create a .PBC file, click **Edit PBC...** to open the **Editing** dialog shown in Fig. 157.

Figure 158 shows this dialog's control menu (click the title bar icon to open it). It contains several of the commands necessary to create and edit .PBC files.



GvDemo_pbc1.Txt - Notepad

File Edit Format View Help

```
GammaVision PBC Table GvDemo_pbc1.Pbc                          Page:   1
    Created: 9/11/2013  10:30:25 PM
     Edited: 9/11/2013  10:30:25 PM

     CO-60                    C.P.S.              Uncertainty
     1173.24 keV          132.203232                0.1648%
     1332.50 keV          122.582870                0.1696%

      Y-88                    C.P.S.              Uncertainty
     1836.01 keV           40.505733                0.3000%
      898.02 keV           58.965637                0.2379%

    CS-137                   C.P.S.              Uncertainty
      661.66 keV          160.384277                0.1501%

    CE-139                   C.P.S.              Uncertainty
      165.85 keV           47.192307                0.3347%

    HG-203                   C.P.S.              Uncertainty
      279.17 keV            5.497663                1.7534%
       72.87 keV            0.531027               22.3666%
       70.83 keV            0.093838              127.0690%

    AM-241                   C.P.S.              Uncertainty
       59.54 keV           35.343632                0.6729%

      Un-0                   C.P.S.              Uncertainty
       36.97 keV            0.447778               37.6736%
      109.49 keV            0.401250               30.1244%
      255.16 keV            2.310945                3.4264%
      258.56 keV            0.307339               24.0299%
      260.58 keV            0.249163               24.7839%
      403.18 keV            0.120444               47.5262%
      581.06 keV            0.096315               42.6891%
      749.64 keV            0.266833               22.9661%
```

Figure 156. PBC Table File Displaying Peaks for Nuclide "Un-0."

Manually Creating a New PBC Table

Open the control menu and click **New**. This will clear the **Edit** window so nuclides can be entered manually. Click on the **Insert...** button to open the dialog shown in Fig. 159. *Enter the nuclide name exactly as it appears in the library if Background Correction By Nuclide will be used. If Background Correction by Energy will be used, then a single nuclide named Un-0 can be used.*

In the peak section of the dialog (right side), click **Insert...** to open the dialog shown in Fig. 160. Enter the energy of the gamma ray, the peak activity in cps, and an optional 1-sigma uncertainty between 0% and 1000%.

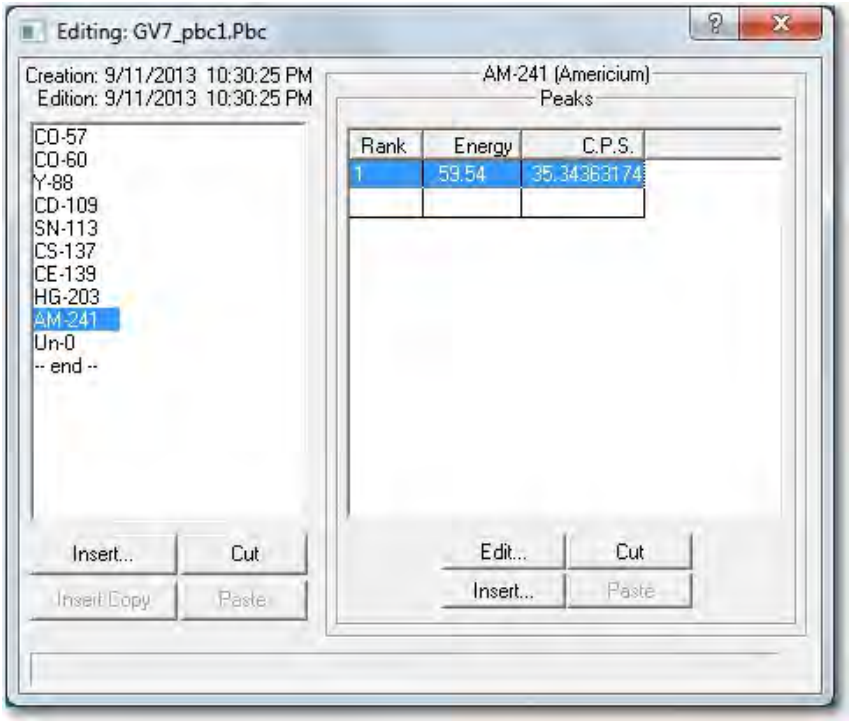


Figure 157. PBC Table Editing Dialog.

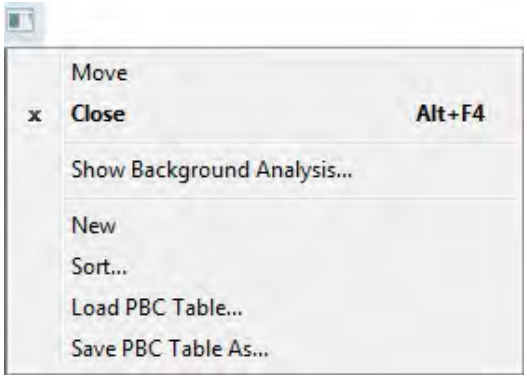


Figure 158. Edit PBC Dialog Control Menu.

Figure 159. Edit or Manually Add Nuclide Name.

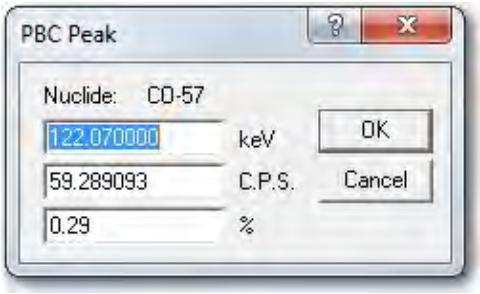


Figure 160. Edit PBC Peak Values.

Automatically Creating a PBC Table

To make a .PBC file from the background spectrum analysis results (.UFO) file, the background count rates are extracted from the analysis results file and inserted in a .PBC file. To do this, open the control menu and click on **Show Background Analysis...**. This will open a standard file-open dialog. Select the correct .UFO file and click **Open**. The list of nuclides in the analysis will be displayed to the left of the PBC Table (see Fig. 161). If no peaks are shown, none were in the analysis file.

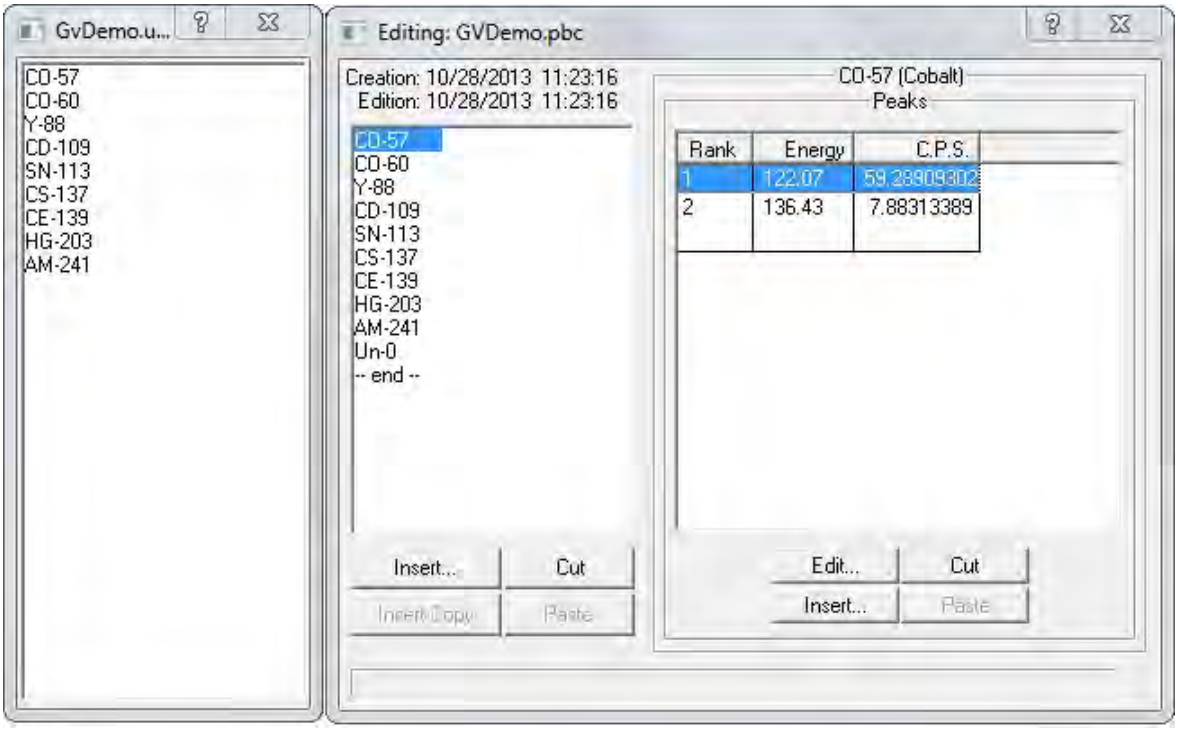


Figure 161. The List of Analysis Nuclides (left) and the PBC Table (right).

Adding Nuclides

There are two **Insert** buttons at the bottom of the PBC nuclide list: **Insert...**, which is for manually specifying the nuclide; and the button below it, which will be labeled with the name of the nuclide selected in the analysis results list (when no nuclide is selected, this button is labeled **Insert Copy**).

To automatically add an analysis nuclide to the PBC list: Go to the analysis results list and click once on the nuclide of interest. This will activate the gray **Insert Copy** button at the bottom of the PBC list, and change its label to **Insert** plus the name of the nuclide. Now, in the PBC list, locate the nuclide immediately *below* the desired insertion position, then click **Insert [nuclide name]**. This will insert the nuclide, and display the energies and backgrounds for its peaks in the analysis.

Double-clicking on a nuclide in the analysis results list will insert it into the PBC list immediately above the highlighted PBC-list nuclide.

To manually add a nuclide to the PBC list, locate the nuclide immediately *below* the desired insertion position, and click once to highlight it. Next, click the manual **Insert...** button to open the dialog shown in Fig. 159, then follow the manual nuclide and peak insertion instructions.

The entire analysis nuclide list can be copied to the PBC list by opening the analysis list's control menu (Fig. 162) and selecting **Copy All to PBC**.

To change the name of a nuclide on the PBC list, double-click it to open the PBC Nuclide dialog (Fig. 159).

To remove a nuclide from the PBC list, click the nuclide, then on **Cut**. This will remove the nuclide from the list. In addition, it will activate the gray **Paste** button at the bottom of the PBC list, and change its label to include the name of the cut nuclide. This is illustrated for ^{152}Eu in Fig. 163.

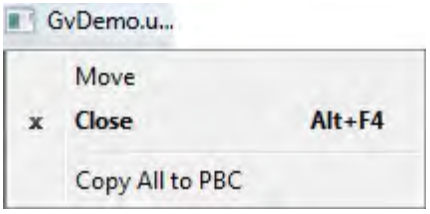


Figure 162. Control Menu.

Figure 163. Cut Nuclide Ready to Paste.

Rearranging a PBC List (Optional)

The order in which nuclides appear in the .PBC file does not matter. However, if you wish to rearrange the list for ease of reading, you can do so by cutting and pasting.

Peak Editing

When a nuclide is selected in the working .PBC file, the right half of the Edit PBC dialog shows the peak list. Note the column headers, **Rank**, **Energy**, and **C.P.S.**. To sort the peak list by a particular parameter in the list, click the appropriate header.

To edit a peak, either double-click the peak in the right-hand list, or click it once then click the **Edit** button. This will open the PBC Peak dialog (Fig. 160).

Use the same PBC Peak dialog to add a peak: click the peak *just below* the desired insertion point in the peak list, then click **Insert...**. This will open the PBC Peak dialog. Enter the energy and counts for the peak and click **OK**.

Peaks can be deleted with **Cut** and, for easier readability, moved with **Cut**/**Paste**. The order of the peaks is not important and has no effect on the correction.

Several peaks can be cut at one time from the list, then pasted back into the list into a different order. Cut peaks remain queued up for pasting, last one first. Each relocated peak will be

assigned a **Rank** number according to its new position. Click the peak *just below* the desired insertion point in the peak list, then click **Paste**.

Saving or Canceling Changes and Closing the Edit Session

To save this modified .PBC file and use it as the working file, click the control menu, then **Save PBC Table As...**. Either use the current filename (which will overwrite the previous values) or assign a new filename, then click **Save**. (GammaVision will assign the default .PBC extension.) To exit the edit session, click the control menu, then **Close**.

To abandon any changes and restore the .PBC file to its condition before editing, click the control menu, then **Close**. A dialog will open asking if you want to save the changes; select **No**.

Print PBC...

Use this command to open a .PBC file and print the PBC table or save it as an ASCII text file, ordered either **by Nuclide** or **Energy**. A standard file-open dialog allows you to select the desired .PBC file, then a printer dialog opens so you may choose a printer or the file-save option.

Figure 164 shows a PBC table saved in both orientations.

5.5.1.6. Average Energy(γ)

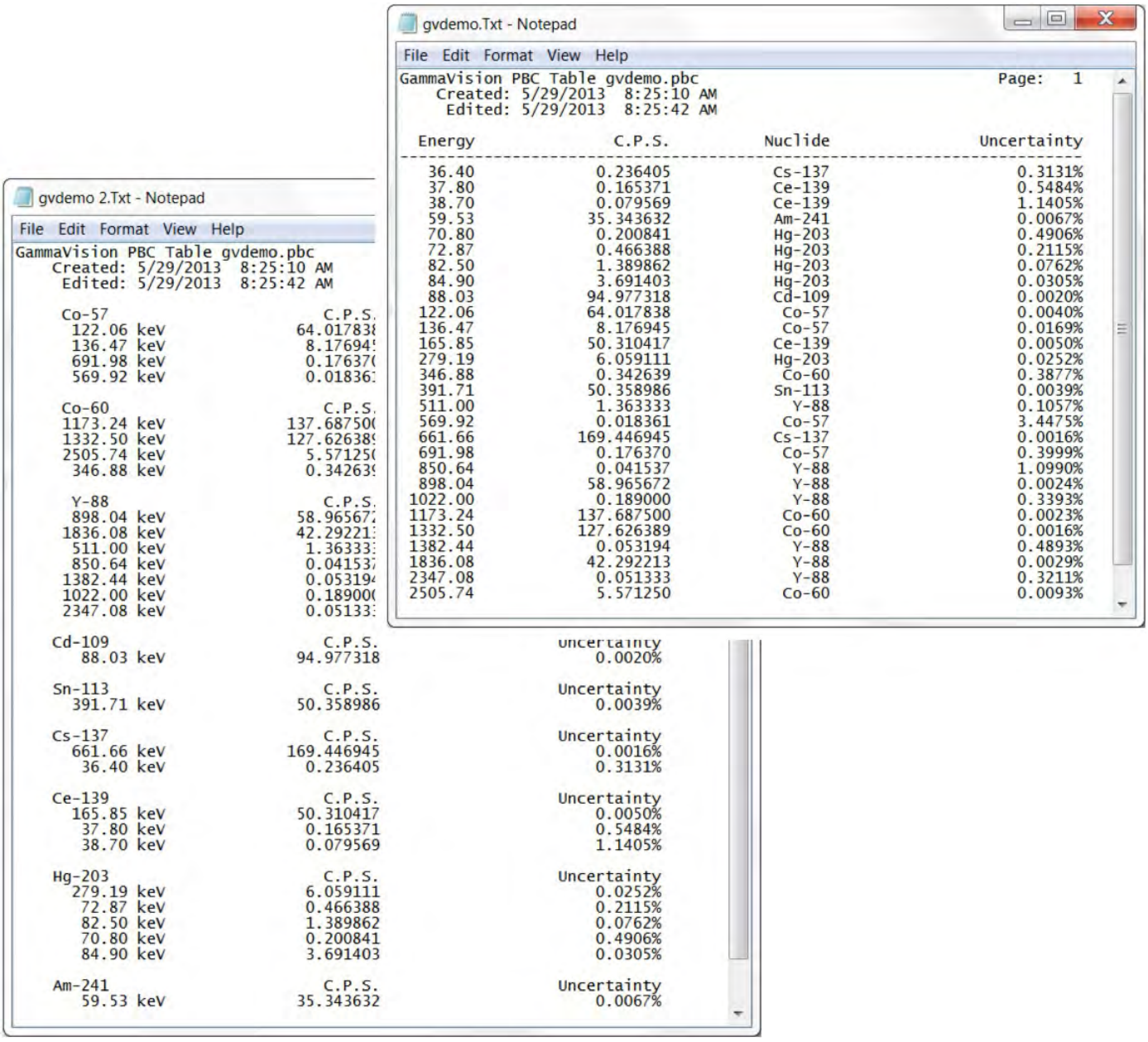
The Average Energy table is built using the sidebar shown in Fig. 165. The calculation is described in Chapter 6. To make the table, enter the energy per disintegration (**keV**) and the **Isotope** name for each isotope to be included in the report. *The isotope name must be exactly as given in the analysis library.*

Now click **Enter** to create and display the table (see Fig. 166). Each time another isotope is added, the table updates.

To remove an isotope from the table, click it to select it, then click **Delete Isotope** on the side-bar. To edit an isotope name or energy, select it with the mouse, make the necessary changes on the sidebar, and click **Enter**. The table will update.

To save the current table, click **Save...**. This opens a file-save dialog. Enter a filename and click **Save**; GammaVision will append the default .EBR file extension.

To display an existing table, click **Recall...**, select the desired file, and click **Open**.



gvdemo 2.Txt - Notepad

File Edit Format View Help

```
GammaVision PBC Table gvdemo.pbc
    Created: 5/29/2013  8:25:10 AM
     Edited: 5/29/2013  8:25:42 AM

     Co-57                          C.P.S.
      122.06 keV                 64.017838
      136.47 keV                  8.17694
      691.98 keV                  0.17637(
      569.92 keV                  0.01836

     Co-60                          C.P.S.
      1173.24 keV               137.68750(
      1332.50 keV               127.62638
      2505.74 keV                 5.57125(
       346.88 keV                 0.34263

      Y-88                           C.P.S.
       898.04 keV                 58.96567
      1836.08 keV                 42.29221
       511.00 keV                  1.36333
       850.64 keV                  0.04153
      1382.44 keV                  0.05319
      1022.00 keV                  0.18900(
      2347.08 keV                  0.05133

    Cd-109                          C.P.S.
       88.03 keV                 94.977318

    Sn-113                          C.P.S.
      391.71 keV                 50.358986

    Cs-137                          C.P.S.
      661.66 keV                169.446945
       36.40 keV                  0.236405

    Ce-139                          C.P.S.
      165.85 keV                 50.310417
       37.80 keV                  0.165371
       38.70 keV                  0.079569

    Hg-203                          C.P.S.
      279.19 keV                  6.059111
       72.87 keV                  0.466388
       82.50 keV                  1.389862
       70.80 keV                  0.200841
       84.90 keV                  3.691403

    Am-241                          C.P.S.
       59.53 keV                 35.343632
```

gvdemo.Txt - Notepad

File Edit Format View Help

```
GammaVision PBC Table gvdemo.pbc                          Page:   1
    Created: 5/29/2013  8:25:10 AM
     Edited: 5/29/2013  8:25:42 AM

  Energy              C.P.S.          Nuclide              Uncertainty
-------------------------------------------------------------------------
   36.40            0.236405          Cs-137                0.3131%
   37.80            0.165371          Ce-139                0.5484%
   38.70            0.079569          Ce-139                1.1405%
   59.53           35.343632          Am-241                0.0067%
   70.80            0.200841          Hg-203                0.4906%
   72.87            0.466388          Hg-203                0.2115%
   82.50            1.389862          Hg-203                0.0762%
   84.90            3.691403          Hg-203                0.0305%
   88.03           94.977318          Cd-109                0.0020%
  122.06           64.017838           Co-57                0.0040%
  136.47            8.176945           Co-57                0.0169%
  165.85           50.310417          Ce-139                0.0050%
  279.19            6.059111          Hg-203                0.0252%
  346.88            0.342639           Co-60                0.3877%
  391.71           50.358986          Sn-113                0.0039%
  511.00            1.363333           Y-88                 0.1057%
  569.92            0.018361           Co-57                3.4475%
  661.66          169.446945          Cs-137                0.0016%
  691.98            0.176370           Co-57                0.3999%
  850.64            0.041537           Y-88                 1.0990%
  898.04           58.965672           Y-88                 0.0024%
 1022.00            0.189000           Y-88                 0.3393%
 1173.24          137.687500           Co-60                0.0023%
 1332.50          127.626389           Co-60                0.0016%
 1382.44            0.053194           Y-88                 0.4893%
 1836.08           42.292213           Y-88                 0.0029%
 2347.08            0.051333           Y-88                 0.3211%
 2505.74            5.571250           Co-60                0.0093%
```

Figure 164. PBC Table Ordered by Nuclide (left) and by Energy (right).

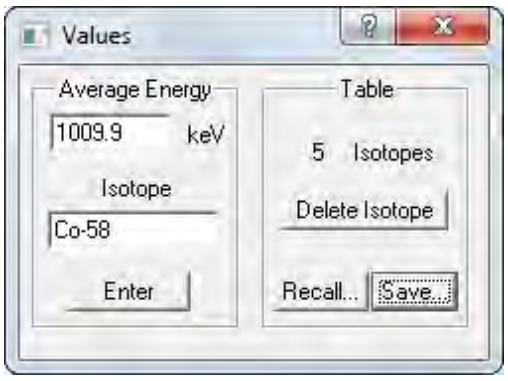


Figure 165.

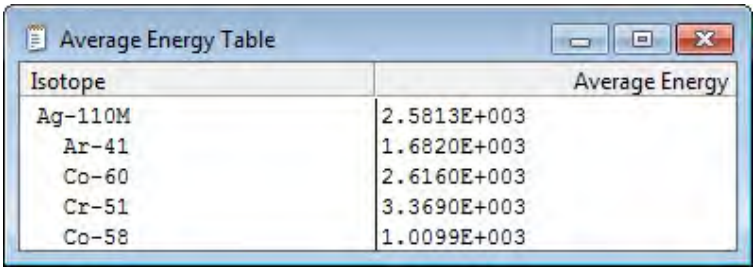


Figure 166. Average Energy Table.

Average Energy Sidebar Control Menu

Figure 167 shows the Average Energy Sidebar's control menu. To edit an existing file, click **Edit File...** and select a file. It will open in a Notepad-like ASCII editor screen (Fig. 168). The formatting does not have to be exactly as shown. Clicking on **Save** will save any changes to the file (in other words, this is not a **Save As...**).

Destroy clears all values from the current table. **Restore** abandons any changes and returns the table to its condition before editing (even after using **Destroy**), *as long as the **Restore** is executed before the Average Energy Sidebar is closed.* **Close** closes the sidebar and table, and makes the currently selected table the internal or working Average Energy table.

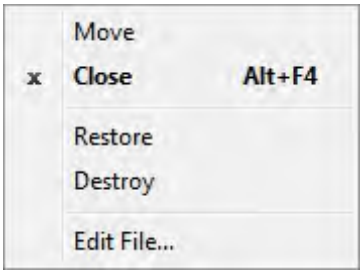


Figure 167. Average Energy Sidebar Control Menu.

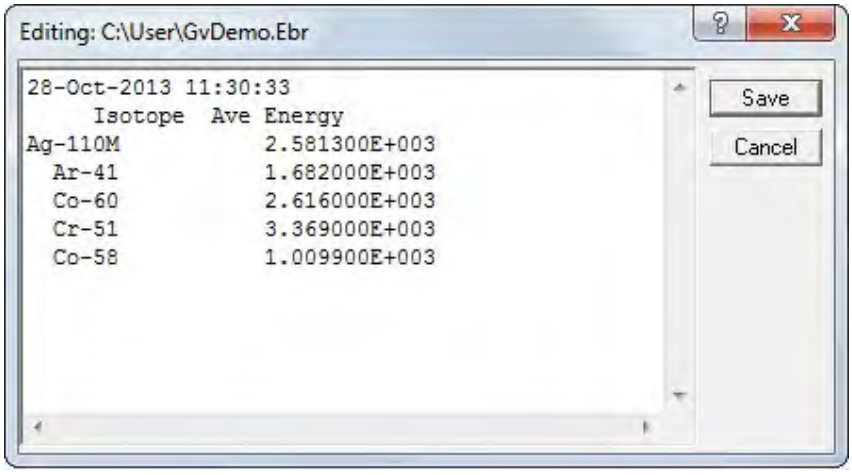


Figure 168. Editor Screen for Average Energy Table.

Average Energy Table Control Menu

Figure 169 shows the Average Energy Table control menu. It contains commands to **Print** the table and to **Close** the table.

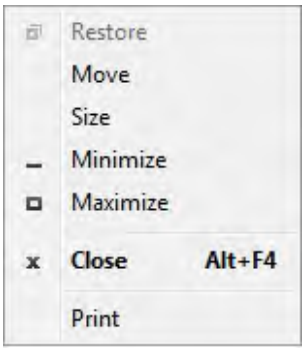


Figure 169. Average Energy Table Control Menu.

5.5.1.7. Iodine Equivalence$^{(\gamma)}$

The Iodine Equivalence table is built using the sidebar shown in Fig. 170. The calculation is described in Section 6.13. To make the table, enter the **Iodine Equivalence** and **Isotope** name for each isotope to be included in the report. *The isotope name must be exactly as given in the analysis library.*

Now click **Enter** to create and display the table (see Fig. 171). Each time another isotope is added, the table updates.

To remove an isotope from the table, click it to select it, then click **Delete Isotope** on the sidebar. To edit an isotope name or energy, select it with the mouse, make the necessary changes on the sidebar, and click **Enter**. The table will update.

To save the current table, click **Save...**. This opens a file-save dialog. Enter a filename and click **Save**; GammaVision will append the default .IEQ file extension.

To display an existing table, click **Recall...**, select the desired file, and click on **Open**.

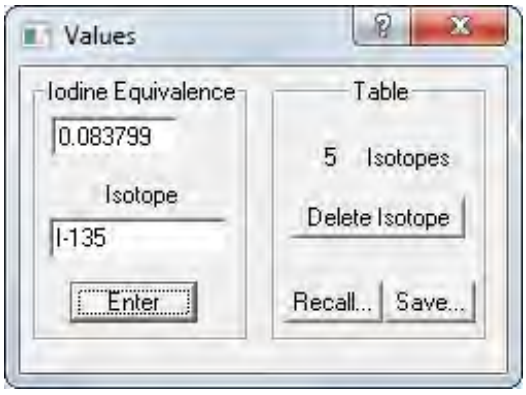


Figure 170. Iodine Equivalence Sidebar.

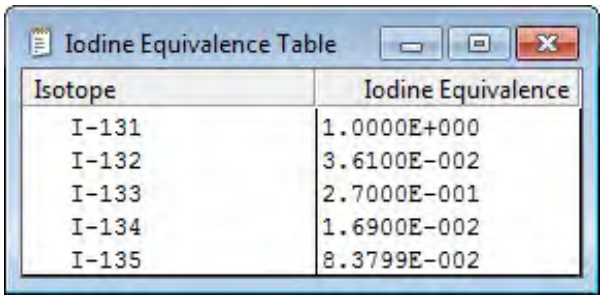


Figure 171. Iodine Equivalence Table.

Iodine Equivalence Sidebar Control Menu

Figure 172 shows the Iodine Equivalence Sidebar's control menu. To edit an existing file, click **Edit File...** and select a file. It will open in a Notepad-like ASCII editor screen (Fig. 173). The formatting does not have to be exactly as shown. Clicking on **Save** will save any changes to the file (in other words, this is not a **Save As...**).

Figure 172.

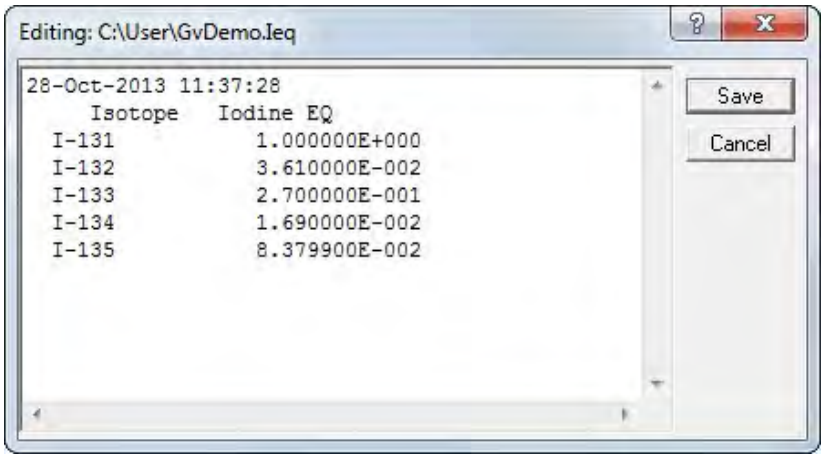


Figure 173. Editor Screen for Iodine Equivalence Table.

Destroy clears all values from the current table. **Restore** abandons any changes and returns the table to its condition before editing (even after using **Destroy**), *as long as the **Restore** is executed before the Iodine Equivalence Sidebar is closed.* **Close** closes the sidebar and table, and makes the currently selected table the internal or working Iodine Equivalence table.

Iodine Equivalence Table Control Menu

The Iodine Equivalence Table's control menu has the same commands as shown in Fig. 169, including the **Print** command.

5.5.1.8. DAC (MPC)$^{(\gamma)}$

The DAC (MPC) table is built using the sidebar shown in Fig. 174; the calculation is described in Section 6.15. To make the table, enter the DAC value (**Bq/Kg**) and the **Isotope** name for each isotope to be included in the report. *The isotope name must be exactly as given in the analysis library.* Now click **Enter** to create and display the table (see Fig. 175). Each time another isotope is added, the table updates.

To remove an isotope from the table, click it to select it, then click **Delete Isotope** on the sidebar. To edit an isotope name or energy, select it with the mouse, make the necessary changes on the sidebar, and click **Enter**. The table will update.

The DAC units displayed at the top of the sidebar are the currently defined analysis units on the Systems tab under **Analyze/Settings/Sample Type...**. If a .DAC file using different units is recalled, the dialog in Fig. 176 opens, warning of this difference. Click **Yes** to open the dialog for the conversion factor (Fig. 177). Enter the factor and click **OK** to scale the table values and put the table in the analysis units. If **No** is selected, the analysis and table will be in different units and the DAC/MPC calculation will produce unknown results.

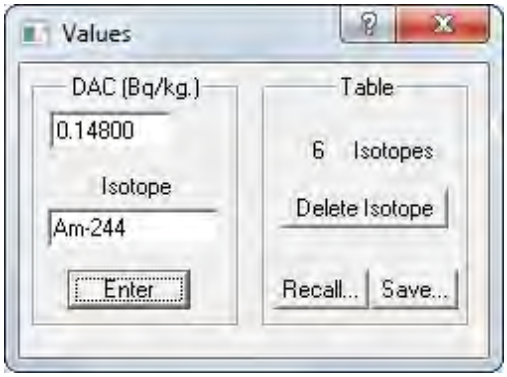


Figure 174. DAC (MPC) Sidebar.

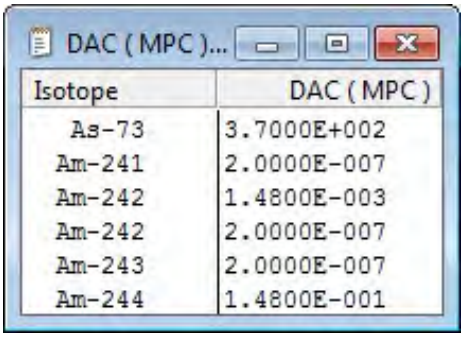


Figure 175. DAC (MPC) Table.

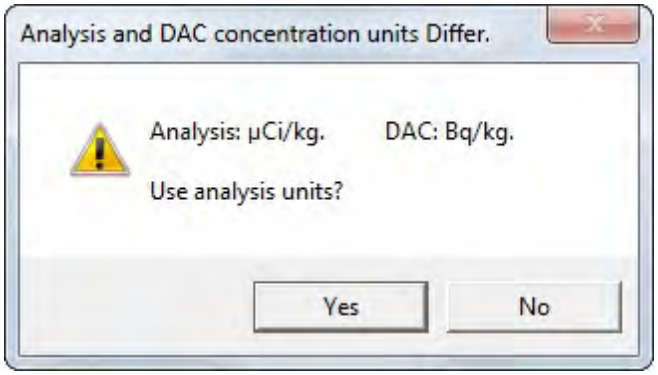


Figure 176. Warning Message.

To save the current table, click **Save...**. This opens a file-save dialog. Enter a filename and click **Save**; GammaVision will append the default .DAC file extension.

To display an existing table, click **Recall...**, select the desired file, and click on **Open**.

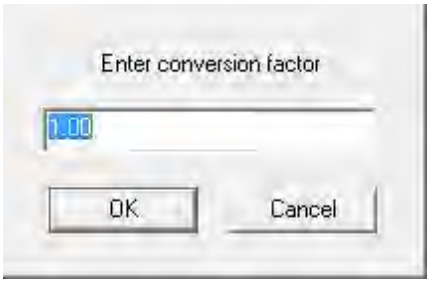


Figure 177. Conversion Factor.

DAC (MPC) Sidebar Control Menu

The DAC (MPC) Sidebar contains the same commands as the menu in Figure 172. To edit an existing file, click **Edit File...** and select a file. It will open in a Notepad-like ASCII editor (Fig. 178). If you make any changes, click **Save** before closing the editor window.

Destroy clears all values from the current table. **Restore** abandons any changes and returns the table to its condition before editing (even after using **Destroy**), *as long as the **Restore** is executed before the DAC (MPC) Sidebar is closed.* **Close** closes the sidebar and table, and makes the currently selected table the internal or working DAC (MPC) table.

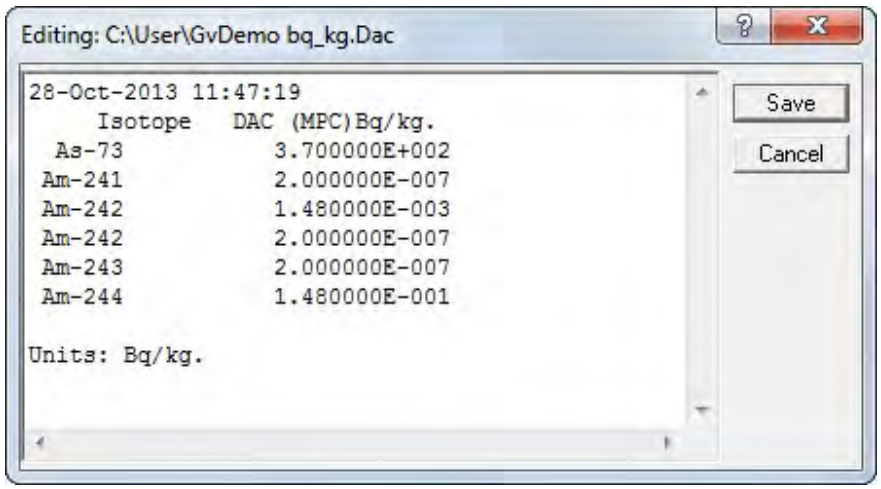


Figure 178. Editor Screen for DAC (MPC) Table.

DAC (MPC) Table Control Menu

The DAC (MPC) Table's control menu has the same commands as shown in Fig. 169, including the **Print** command.

5.5.1.9. Gamma Total...(γ)

As of v6.08, GammaVision supports the EDF's Gamma Total calculations and report file output.[2] Figure 179 shows the Gamma Total/EDF Reports Setting dialog. The filenaming conventions for the four EDF output file types are discussed on page 188. In addition to these output files you will also be creating .SPC format spectrum files, as discussed below. These will be stored in the location specified for spectra in **File/Settings...** (Section 5.1.1.4).

> **NOTE** Gamma Total report filenames are keyed to the MCB **ID** number assigned during MCB configuration. Before performing these analyses, see the discussion on the assignment of MCB **ID** numbers on page 11 in Section 2.3.2. If you have more than 10 MCBs, or MCBs with the same final digit in their instrument ID, be sure it is possible to identify which results files correspond to each particular MCB.

Gamma Total analyses can be performed on live spectra or on stored .SPC spectrum files. The Gamma Total setup is saved with the .SPC file. When you recall a spectrum file previously used for Gamma Total analysis, the Gamma Total dialog will display the analysis settings in effect when the spectrum was saved. These settings can be changed as desired for reanalysis (however, the new settings will not be saved with the spectrum unless you re-save the .SPC file).

Figure 179. Gamma Total Setup Dialog Configured for Gamma Total Reporting.

Each analysis produces one or more characteristic output files, as discussed in the following section. In addition, an EDF Special Applications Report section is added to the end of the standard GammaVision report (see Section 7.8). This table lists the Gamma Total settings used in the analysis, and the quantitative results. *If the **EDF Table Only** box is marked, the standard report contains only the header information and the EDF Special Applications Report table.* Otherwise, the EDF table is included on the standard report, along with the other report options specified on the Report tab under **Analyze/Settings/Sample Type...** (page 156).

To turn off the EDF table in the GammaVision report, unmark all reporting options before the next analysis.

Gamma Total analyses are typically predicated on an energy range of 100 keV to 2 MeV. If you use a different energy range, you might wish to adjust the **Integration Range** on the Gamma Total dialog accordingly.

Output File Naming Convention

Background Report File

The background report file is named according to:

B#ddmmyy.XXX

where # is the last digit of the instrument **ID** number as assigned by the MCB Configuration program; and ddmmyy is the analysis date as two-digit date, two-digit month, and the last two digits of the year.

Analysis Report File

Analysis report files, for gamma total and germanium reporting, are named according to:

#_ddmmyy.Seq

where # is the last digit of the instrument **ID** number as assigned by the MCB Configuration program; ddmmyy is the analysis date as two-digit date, two-digit month, and the last two digits of the year; and Seq is the spectrum sequence number, as determined by the entry in the **Gamma Total Sequence** and **Germanium Sequence** fields on the Gamma Total dialog.

Germanium Results File

The germanium reporting file is named according to:

DETAIL.Seq

where Seq is the spectrum sequence number, as determined by the entry in the **Germanium Sequence** field on the Gamma Total dialog.

Maintenance Report File

These files, for cesium reporting, are named according to:

RDTCS_#.XXX

where # is the last digit of the instrument **ID** number.

Hardware and Analysis Configuration

Before acquiring data for a Gamma Total analysis, prepare the system as follows:

- The detector must be energy and efficiency calibrated.

- Select **Analyze/Settings/Sample Type...** and configure the analysis settings according to your site procedures.

- Use **Acquire/MCB Properties...** to set the presets and other hardware properties.

Configuring and Generating the Gamma Total Reports

Background Counting Procedure

On the Gamma Total dialog, mark *only* the **Count Background** checkbox (unmark any Gamma Total options in the left column, if they are marked). This procedure auto-generates a background report, so there is no need to mark the **Write Background Report** checkbox.

Select the location for the **Gamma Total Report Dir**. The background file will be written to this folder.

Remove any entries from the **Background Spectrum**, **Cesium Spectrum**, and **Geometry File** fields, and click **OK**.

Count, analyze with **Analyze/Entire spectrum in memory...**(γ), and save the resulting background spectrum for use in other Gamma Total analyses. This will generate a Gamma Total background file, B#ddmmyy.XXX, in addition to the background .SPC file.

Cesium Counting Procedure

On the Gamma Total dialog, mark *only* the **Count Cs-137** checkbox (unmark any Gamma Total or background options, if they are marked). This selection auto-generates a maintenance report so there is no need to mark the **Write Maintenance Report** checkbox.

Select the location for the **Gamma Total Report Dir**. The maintenance file will be written to this folder.

Browse for a **Background Spectrum**; then select the **Geometry File** location and enter a new or existing geometry filename. Click **OK**.

Count, analyze with **Analyze/Entire spectrum in memory...**(γ), and save the resulting cesium spectrum for use in Gamma Total Reporting analyses. This will generate a Gamma Total maintenance file, RDTCS_#.XXX, and a geometry file with a user-assigned filename and a .TXT extension, in addition to the cesium .SPC file.

Gamma Total Counting Procedure

On the Gamma Total dialog, mark the **Enable Gamma Total Reporting** checkbox (make sure **Count Background** and **Count Cs-137** are unmarked). This will automatically mark the **Enable Gamma Total Calculation** and **EDF Table Only** boxes.

Select the location for the **Gamma Total Report Dir**.

Browse for a **Background Spectrum**; then select the **Geometry File** location and enter an existing geometry filename. Click **OK**.

If **Write Background Report** is checked, a background report will be generated. If you also specify a cesium spectrum, the K-factor to be used in the Gamma Total activity calculation will be calculated from the cesium and background spectra. If the geometry file is specified as well, then the K-factor calculated on-the-fly will be saved to the geometry file (instead of reading the K-factor from the geometry file). In addition, if the cesium spectrum is specified and **Write Maintenance File** is marked, a maintenance file will be generated.

Count, analyze with **Analyze/Entire spectrum in memory...**$^{(\gamma)}$, and save the resulting spectrum. This will generate a Gamma Total analysis file `#_ddmmyy.Seq`, in addition to the Gamma Total `.SPC` file.

To count only the background within the **Integration Range** when performing background QA measurements (Section 8.2.2), mark the **Use Range for Background QA** checkbox in the bottom section of the dialog.

Germanium Counting Procedure

On the Gamma Total dialog, mark *only* the **Enable Germanium Reporting** checkbox (unmark any other reporting selections except, optionally, **Report ISO NORM MDA On Reports**, as described below.).

Select the location for the **Gamma Total Report Dir** and the **Germanium Report Dir**.

No entries are required in the **Background Spectrum**, **Cesium Spectrum**, and **Geometry File** fields. However if you want a background report generated, mark the **Write Background Report** field and recall a **Background Spectrum**. If you also specify a cesium spectrum, the K-factor to be used in the Gamma Total activity calculation will be calculated from the cesium and background spectra. If a geometry file is specified as well, then the K-factor calculated on-the-fly will be saved to the geometry file (instead of reading the K-factor from the geometry file). If you want a maintenance file generated, mark **Write Maintenance File** and include a cesium spectrum.

To save the ISO NORM MDA values, instead of the regular MDA values, to the germanium results file, mark the **Report ISO NORM MDA On Reports** checkbox.

NOTE To enable this checkbox, you must first mark the ISO NORM checkbox on the Report tab under **Analyze/Settings/Sample Type...**.

Count, analyze with **Analyze/Entire spectrum in memory...**(γ), and save the resulting spectrum. This will generate a Gamma Total analysis file #_ddmmyy.Seq, and a germanium results file DETAIL.Seq, in addition to the germanium .SPC file.

To count only the background within the **Integration Range** when performing background QA measurements (Section 8.2.2), mark the **Use Range for Background QA** checkbox in the bottom section of the dialog.

5.5.2. Peak Search

This command initiates a Mariscotti[27]-type peak search on the spectrum. The peak-search sensitivity is selected on the Systems tab of the Sample Type Settings dialog (see the discussion beginning on page 152). Each peak found is marked with an ROI. If the system is calibrated, the width of the ROI is three times the calculated FWHM of the peak. If not calibrated, the width of the ROI is based on the width of the peak as determined by the peak search. Overlapping or close peaks might have contiguous ROIs. Existing ROIs are not cleared.

The report function can be used with **Peak Search** to produce a semi-quantitative nuclide list for the spectrum.

5.5.3. ROI Report...

The **ROI Report...** function creates a report describing acquisition conditions and contents of all ROIs, and sends it to a disk file, the display, or the printer. The dialog shown in Fig. 180 can direct the report output to a disk file (name chosen by user), a printer, or the screen.

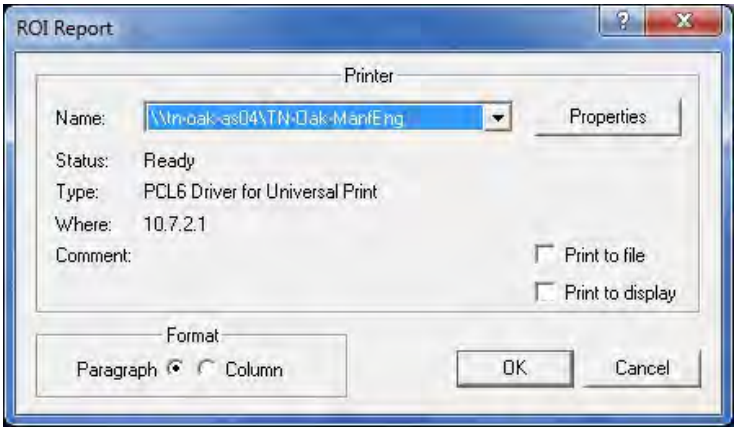


Figure 180. Generate an ROI Report.

[27]M.A. Mariscotti, "A Method for Automatic Identification of Peaks in the Presence of Background and its Application to Spectrum Analysis," *Nuclear Instruments and Methods* **50**, 309–320 (1967).

Only the ROIs in the expanded view are shown on the display. You can also select from two report formats, **Paragraph** and **Column**.

Examples of the **Paragraph** and **Column** format are illustrated in Figs. 181 and 182, respectively. The information supplied is the same in both formats.

If the spectrum is not calibrated, the following are reported for each ROI:

- ROI number
- Start channel of the ROI
- Stop channel of the ROI
- Gross area of the peak
- Net area of the peak, as calculated in **Calculate/Peak Info**
- Error in net area, as calculated in **Calculate/Peak Info**
- Centroid channel of peak, as calculated in **Calculate/Peak Info**
- FWHM
- FW(1/x)M

```
Detector # 1  ACQ 30-Sep-91 at 14:47:00   RT = 250057.0   LT = 250000.0

           No detector description was entered
           Background in shield with copper liner

ROI # 1    RANGE: 297 = 63.26keV  to  323 = 67.86keV
           AREA : Gross =  4231    Net = 490    +/-116
           CENTROID: 309.50  = 65.47keV
           SHAPE: FWHM = 0.96     FW(1/10)M = 2.11
           No close library match.

ROI # 2    RANGE: 708 = 135.95keV  to  736 = 140.91keV
           AREA : Gross =  5898    Net = 482    +/-145
           CENTROID: 724.08  = 138.80keV
           SHAPE: FWHM = 0.66     FW(1/10)M = 1.40
           ID: Hf181 at 136.28keV
           Corrected Rate = 0.76 +/- 0.23 Bq

Detector # 1    ACQ 30-Sep-91 at 14:47:00   RT = 250057.0   LT = 250000.0
            No detector description was entered
            Background in shield with copper liner
```

Figure 181. Example of Paragraph-Format Report.

If the spectrum is calibrated, both energy and channel values are given for 1–9 above, and in addition the following is included:

- The best match, if any, from the library

And, if a match is found in the library:

- The activity, calculated using the net area, the live time, and the efficiency

ROI#	RANGE	(keV)	GROSS	NET	+/-	CENTROID	FWHM	FW(1/10)	LIBRARY (keV)	Bq	+/-
1	63.26	67.86	4231	490	116	65.47	0.96	2.11	No close library match.		
2	135.95	140.91	5898	482	145	138.80	0.66	1.40	Hf181 136.28	0.76	0.23
3	507.40	513.06	8632	5445	140	510.22	2.73	4.56	Sr85 514.00	0.74	0.02
4	1455.81	1463.59	2088	1588	69	1460.68	2.07	3.97	Br82 1474.90	2.72	0.12
5	2610.29	2620.19	818	609	48	2614.98	2.83	4.55	No close library match.		

Figure 182. Example of Column-Format Report.

5.5.4. Entire Spectrum in Memory...(Y)

This selection initiates an analysis of the entire spectrum in the active buffer or Detector window (if the Detector is not acquiring data), generating .RPT, .UFO, and .AN1 files. The analysis is performed in the background and the display is available for continued interactive use. The spectrum is moved to disk for the analysis so the spectrum in the Detector or buffer can be changed if needed. When the analysis is completed, you are notified and the report is generated. If any errors occur, the error number is displayed along with the spectrum name. The errors corresponding to the error numbers are explained in Appendix C.

If the **Program** radio button on the Report tab of **Analyze/Settings/Sample Type...** has been selected, with Notepad.exe designated as the output program, GammaVision will open Windows Notepad and display the analysis report. The software will not accept inputs while the report display is shown. When you exit Notepad, control returns to GammaVision. At this point, if you select **Analyze/Display Analysis Results**, the .UFO file for the spectrum just analyzed will automatically be displayed.

5.5.5. Spectrum on Disk...(Y)

This command analyzes a spectrum stored on disk, using the analysis parameters stored in the spectrum file. A standard file-open dialog is displayed. A background analysis is performed as soon as you open the spectrum filename, and a .UFO and .RPT file are generated. When the analysis is complete a message is displayed on the information line. If any errors occur, the error number is displayed along with the spectrum name. The numbers are explained in

Appendix C.

If the **Program** radio button on the **Report** tab of **Analyze/Settings/Sample Type...** has been selected, with Notepad.exe designated as the output program, GammaVision will open Windows Notepad and display the analysis report. Close Notepad to end the analysis session and return to GammaVision.

5.5.6. Display Analysis Results...

This command displays the results of an analysis of the complete spectrum by reading the results stored in a .UFO file(Fig. 183).[28]

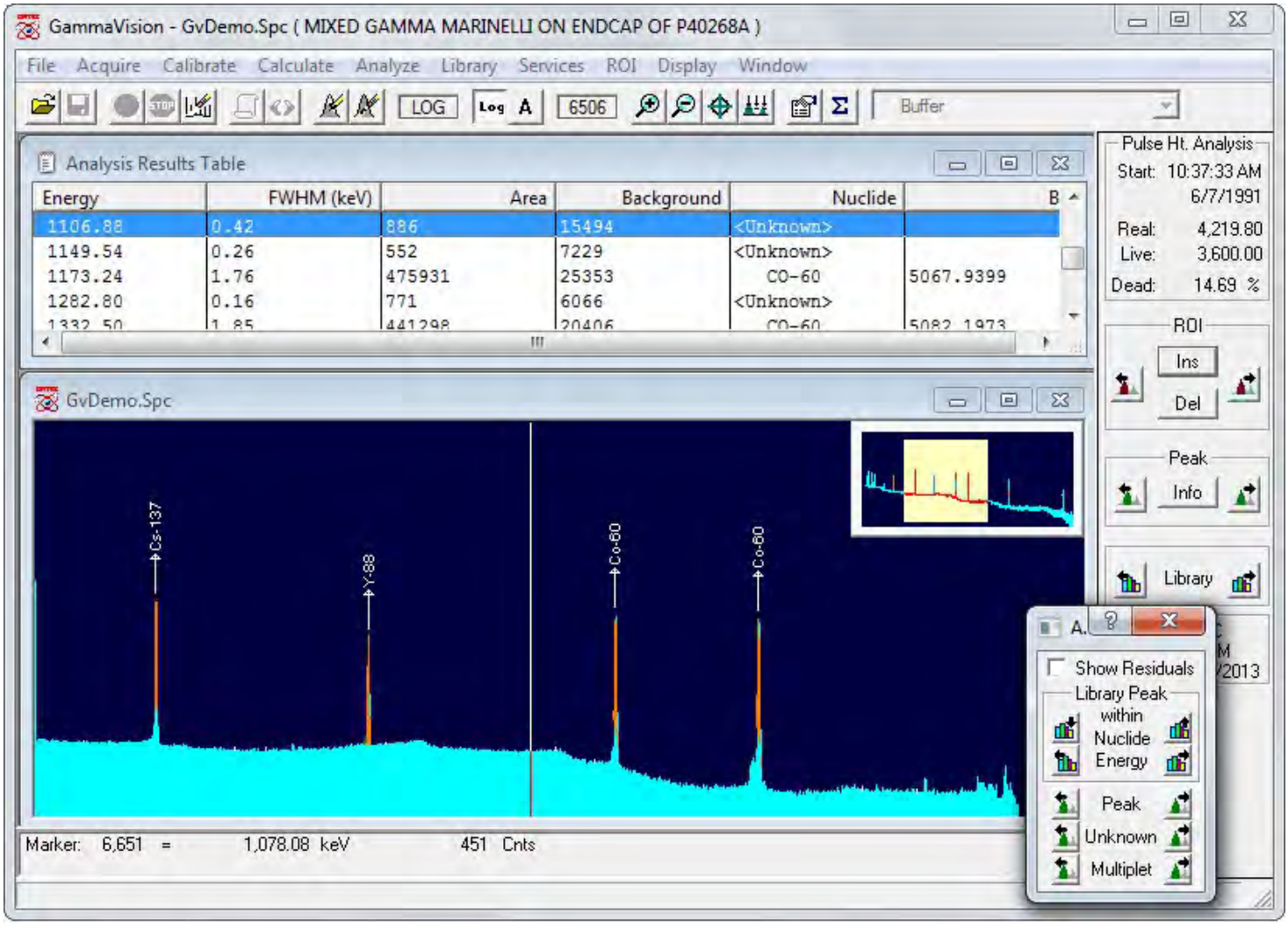


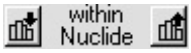
Figure 183. Display from .UFO File.

[28].UFO files are created by any analysis command, including **Entire spectrum in memory**(γ) and **Spectrum from disk** on the **Analyze** menu, and **Start/Save/Report**(ā) on the **Acquire** menu.

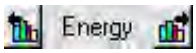
This analysis considers all of the spectrum and all library entries, thus differing from the interactive analysis results. When you select **Display analysis results**, the .UFO file matching the active spectrum's filename will be highlighted and ready to open; just click **OK**. To compare the analysis results to the corresponding spectrum, the spectrum analyzed should first be recalled into a buffer window.

5.5.6.1. Analysis Sidebar

Figure 184 shows the Analysis Sidebar. The buttons move the marker up and down through the results list, library, and spectrum simultaneously.



The **within Nuclide** buttons move up and down the library list for the selected nuclide, in the order the energies are stored in the library. Since the library energies are not usually stored in increasing energy order, this will cause the marker to jump about the spectrum. This is useful in deciding if a nuclide is present or not, by looking for all the lines associated with the nuclide. If the selected peak has a zero area, it is not displayed.



The **Energy** buttons move the cursor up and down through the library peak list in energy order. Only non-zero-area peaks are shown. Since the library used for the analysis might not be the same as the working library, this might be a different set of peaks than found with the **Library** buttons on the Status Sidebar.

The **Peak** buttons move the marker up and down through all the peaks in the spectrum. This includes non-zero-area library peaks and unknown peaks above the peak-search sensitivity cutoff.

Figure 184. Analysis Results Sidebar.

The **Unknown** buttons move the marker up and down through the unknown peaks that satisfy the sensitivity cutoff, in energy order, skipping over any library peaks.

The **Multiplet** buttons move up and down through the multiplet or deconvoluted regions in the spectrum. The multiplet up button goes to the first (lowest-energy) peak of the next higher multiplet. Similarly, the multiplet down button goes to the last (highest-energy) peak of the next lower multiplet. To look at individual peaks in the multiplet, use the **Peak**, **Energy**, or **Unknown** buttons.

The **ROI**, **Peak**, and **Library** buttons on the Status Sidebar are also active.

Marking the **Show Residuals** check box adds a line beneath the spectrum that displays the difference between the actual spectrum and the calculated spectrum based on the analysis and the calibration peak shape. An example is shown in Fig. 185.

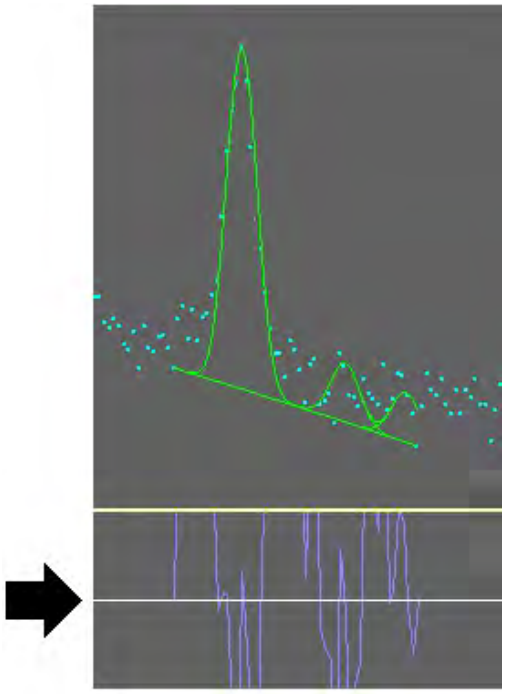


Figure 185. Spectrum Residuals Display (arrow).

5.5.6.2. Analysis Results Spectrum Window

This release of GammaVision features an improved Analysis Results Spectrum Window that gives you more flexibility in displaying and printing your analysis results. Right-clicking in the spectrum window opens the right-mouse-button menu shown in Fig. 186.

Plot Absolute Residuals/Plot Relative Residuals

These commands are active if the **Show Residuals** check box is marked on the analysis sidebar. The residuals are a comparison of the counts in each channel (*Actual*) to the calculated counts for that channel as determined by the peak-fitting algorithm (*Fitted*). **Plot Absolute Residuals** displays the difference in each channel, in counts, between *Actual* and *Fitted* counts. **Plot Relative Residuals** displays the difference in each channel, in standard deviations (abbreviated **STD** on the screen), between *Actual* and *Fitted* counts divided by the square root of the *Actual* counts; that is, $(Actual - Fitted) / \sqrt{Actual}$.

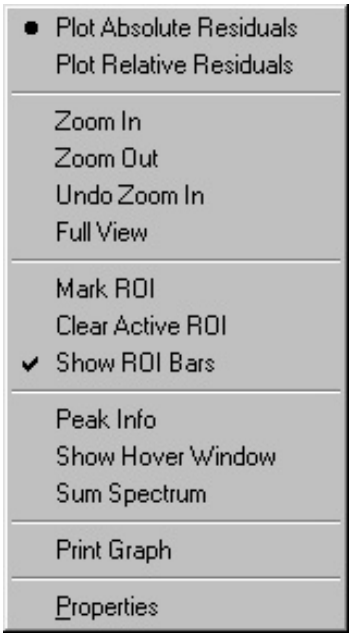


Figure 186. Analysis Results Spectrum Window Menu (right-click to open).

The **Properties** command allows you to modify the screen colors and y-axis scaling for the residuals histogram.

Zoom In

Zoom In adjusts the horizontal and vertical scales in the Expanded Spectrum Window to view a smaller portion of the spectrum. This command is duplicated by the **Zoom In** button on the toolbar.

Zoom Out

Zoom Out adjusts the horizontal and vertical scales in the Expanded Spectrum Window to view a larger portion of the spectrum. This command is duplicated by the **Zoom Out** button on the toolbar.

Undo Zoom In

This will undo or reverse the last **Zoom In** operation done with the rubber rectangle. It restores the display to the horizontal and vertical expansion before the **Zoom In**. It is not the same as **Zoom Out**.

Full View

Full View adjusts the horizontal and vertical scaling to display the entire spectrum in the Expanded Spectrum View.

Mark ROI

This allows you to mark a peak as an ROI by clicking and dragging the rubber rectangle across a portion of the spectrum, then selecting **Mark ROI**. If **Show ROI Bars** is on, the new ROI will be marked with the active ROI Bars until you either move to or create another ROI.

Clear Active ROI

This clears the ROI bits in all ROI channels that adjoin the channel containing the marker.

Show ROI Bars

These are vertical markers that indicate the lower and upper boundaries of each ROI in the spectrum. The ROI bars for an inactive/unselected ROI have solid fill; when you click an ROI to activate it (only one is active at a time), the bars for the active ROI change to a diagonal fill (see Fig. 187). To display the ROI bars, right-click in the expanded window to open the right-mouse-button menu, then click **ROI Bars** to checkmark it. To hide the ROI bars, click the command again to clear the checkmark.

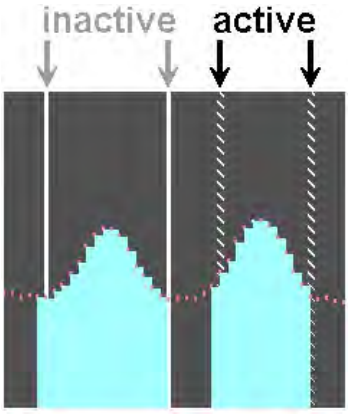


Figure 187. Inactive (solid) and Active (diagonal fill) ROI Bars.

When you activate an ROI by clicking on it, the low (start) and high (end) positions marked by the ROI bars are displayed on the Marker Information Line.

You can shift the start and end channels of an ROI by clicking and dragging the ROI bars (allow a moment for the display to update).

The ROI bar color is controlled by the **Markers** droplist in the Graph Properties dialog.

Peak Info

This command opens a **Peak Info** box (Fig. 188) for the selected peak and leaves the box open until you click inside it. This command works for peaks loaded from a .UFO file, and ROIs created within GVPlot or loaded from an .ROI file. The contents of the **Peak Info** box are described in Section 5.4.3. You can simultaneously display multiple Peak Info boxes as long as they do not overlap. A new Peak Info box will close any existing boxes that it overlaps. For very narrow peaks, you might find it useful to position the marker with the left/right arrow keys before calling the **Peak Info** command. When the marker is on a peak, the right side of the Marker Information Line will display a **Peak Area** readout.

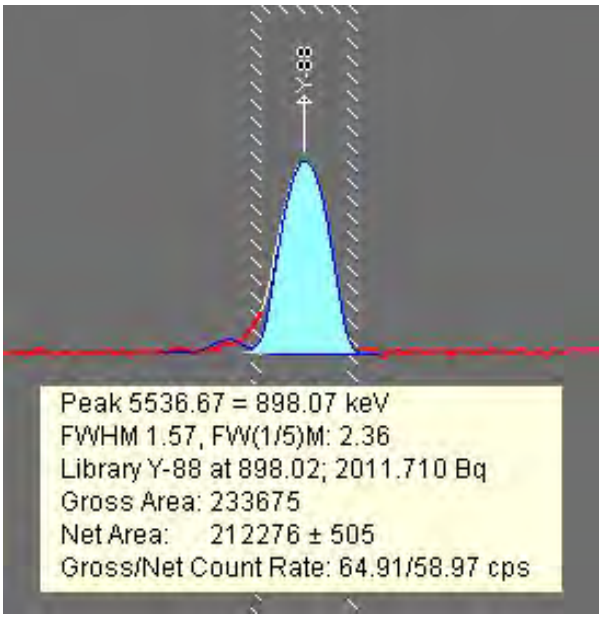


Figure 188. The Peak Info Window for an ROI.

Show Hover Window

When you select this command, a checkmark is displayed by this menu item to indicate that it is in hover-window mode. In this mode, the Peak Info window opens when the mouse pointer is paused over a peak for approximately 1 second, and closes when the pointer is moved away from the peak. To turn off hover mode, select **Show Hover Window** again to remove the checkmark. This mode can be used together with **Peak Info**.

Sum Spectrum

This sums the gross counts in the area selected with the rubber rectangle or, if you have not selected an area, the gross counts in the entire spectrum. The results are displayed on the status line, and indicate the span of channels summed.

Print Graph

This command prints the Analysis Results Spectrum Window. It duplicates **File/Save Plot**.

Properties

This opens the Graph Properties dialog (Fig. 189), which lets you set the graph colors, symbol type, and axis scaling factors. All settings are reset when you exit GammaVision.

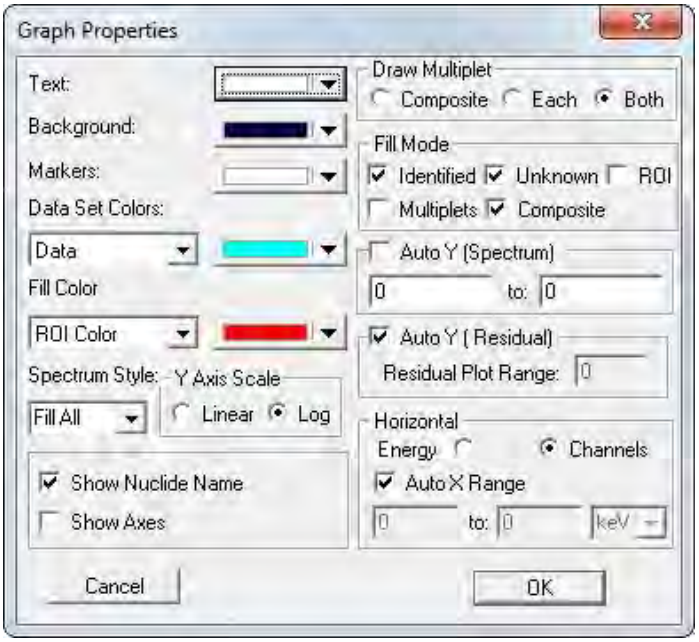


Figure 189. Customize Graph Styling.

The **Text** color affects the color of the axes, axis labels, and spectrum title. **Background** controls the color of the spectrum background. **Markers** applies to the ROI bars, and nuclide labels and pointers.

Data Set Colors allows you to choose separate colors for spectrum **Data**, **Fit**ted peaks, and **Residual**s; select a data type from the left-hand droplist, then choose a color from the list on the right. Similarly, use **Fill Color** to control the colors of **ROI**s, **Nuclide Peak**s, **Unknown Peak**s, **Multiplet**s, and **Composite**s. **Spectrum Style** determines how the histogram data are represented (**Points**, **Line**, or **Fill All**).

The **Show Nuclide Name** checkbox allows you to hide or display the nuclide markers for an analyzed spectrum. Clearing the **Show Axes** checkbox removes the axes so the histogram occupies the entire window without an inside border.

Set the **Y Axis Scale** of the spectrum window to **Linear** or **Log**arithmic. You can also do this with the **LOG** button on the toolbar except as noted in the bullet list below.

The **Draw Multiplet** radio buttons determine whether multiplets are drawn as a **Composite** curve, shown individually (**Each**), or displayed as individual peaks superimposed with the composite curve (**Both**). These modes are compared in Fig. 190. This display is most easily seen with all **Fill Mode**s turned off (checkboxes unmarked).

The **Fill Mode** checkboxes allow you to determine which peak types, if any, will be displayed in fill mode rather than data-point mode.

The toolbar's **Auto** button is interlocked with the **Auto Y (Spectrum)** checkbox. Therefore, clicking the toolbar's **Auto** button on and off respectively turns on and off the **Auto Y (Spectrum)** feature in the analysis results Graph Properties dialog, and vice versa.

Similarly, the **LOG** button on the toolbar is interlocked with the **Linear** and **Log** radio buttons in the **Y Axis Scale** section of the Graph Properties dialog.

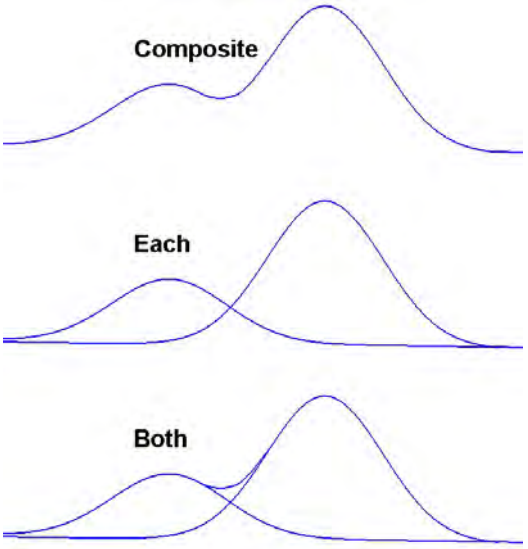


Figure 190. Draw Multiplet Modes.

The y-axis in the Display Analysis Results window is referred to as being in *auto mode* when (1) the **Auto Y (Spectrum)** checkbox is marked or (2) the **Auto Y (Spectrum)** box is unmarked and the range is set from 0 to 0. In auto mode, the **LOG** and **Auto** toolbar buttons behave as they do in the regular Detector and buffer windows.

When the **Auto Y (Spectrum)** checkbox is unmarked and the range is other than 0 to 0, the y-axis is referred to as being in *manual range mode*. When the y-axis is in manual range mode, the **LOG** and **Auto** buttons behave as follows:

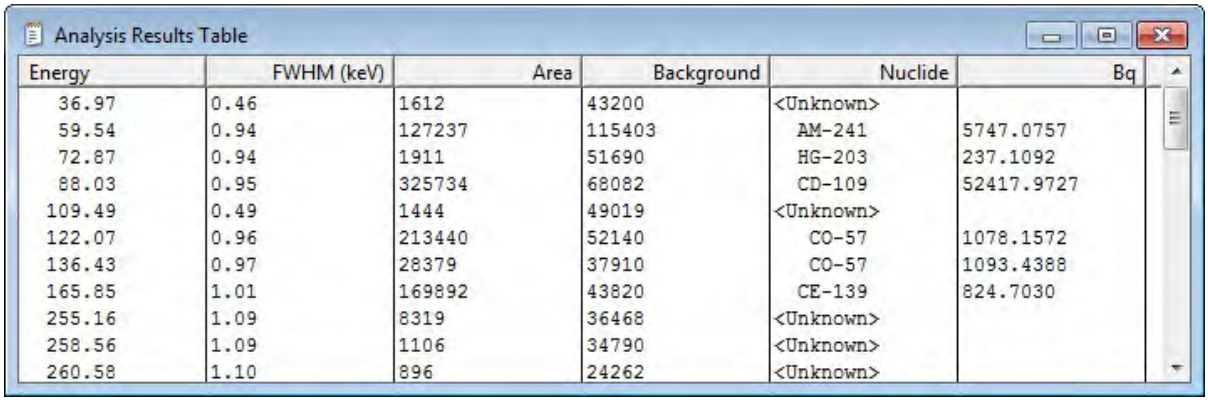
- The **LOG** button toggles the y-axis between logarithmic (on) and linear (off) scaling.
- The **Auto** button toggles the y-axis between the auto (on) and manual (off) ranges.
- The **LOG** and **Auto** buttons work independently. They can both be turned on at the same time to achieve an Auto range with a logarithmic scale.

NOTE Manually setting the range for one axis disables zooming for that axis only. If both axis ranges are manually fixed, all zooming is disabled.

5.5.6.3. Analysis Results Table

Figure 191 shows the Analysis Results Table window. The table records can be sorted by any parameter (e.g., energy, area, nuclide, FWHM) by clicking on the desired column header.

The Analysis Sidebar's control menu is shown in Fig. 192 (click the title bar icon to open the menu). Mark or unmark **Table** to show or hide the Analysis Results Table; use **Print** on the Analysis Results Table control menu to print the table as displayed (note that this is not the same as the complete report described in Chapter 7).



Energy	FWHM (keV)	Area	Background	Nuclide	Bq
36.97	0.46	1612	43200	<Unknown>	
59.54	0.94	127237	115403	AM-241	5747.0757
72.87	0.94	1911	51690	HG-203	237.1092
88.03	0.95	325734	68082	CD-109	52417.9727
109.49	0.49	1444	49019	<Unknown>	
122.07	0.96	213440	52140	CO-57	1078.1572
136.43	0.97	28379	37910	CO-57	1093.4388
165.85	1.01	169892	43820	CE-139	824.7030
255.16	1.09	8319	36468	<Unknown>	
258.56	1.09	1106	34790	<Unknown>	
260.58	1.10	896	24262	<Unknown>	

Figure 191. Analysis Results Table.

When the Analysis Results Table is displayed and GammaVision is in interactive-analysis mode, you can see more details about any peak by double-clicking on that peak in the table. This opens a **Details** window, as shown in Fig. 193. Use the **Peak** buttons to step to the next-highest-energy and next-lowest-energy peaks. Click **Close** or press **<Esc>** to exit.

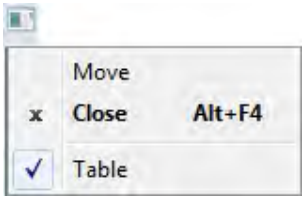
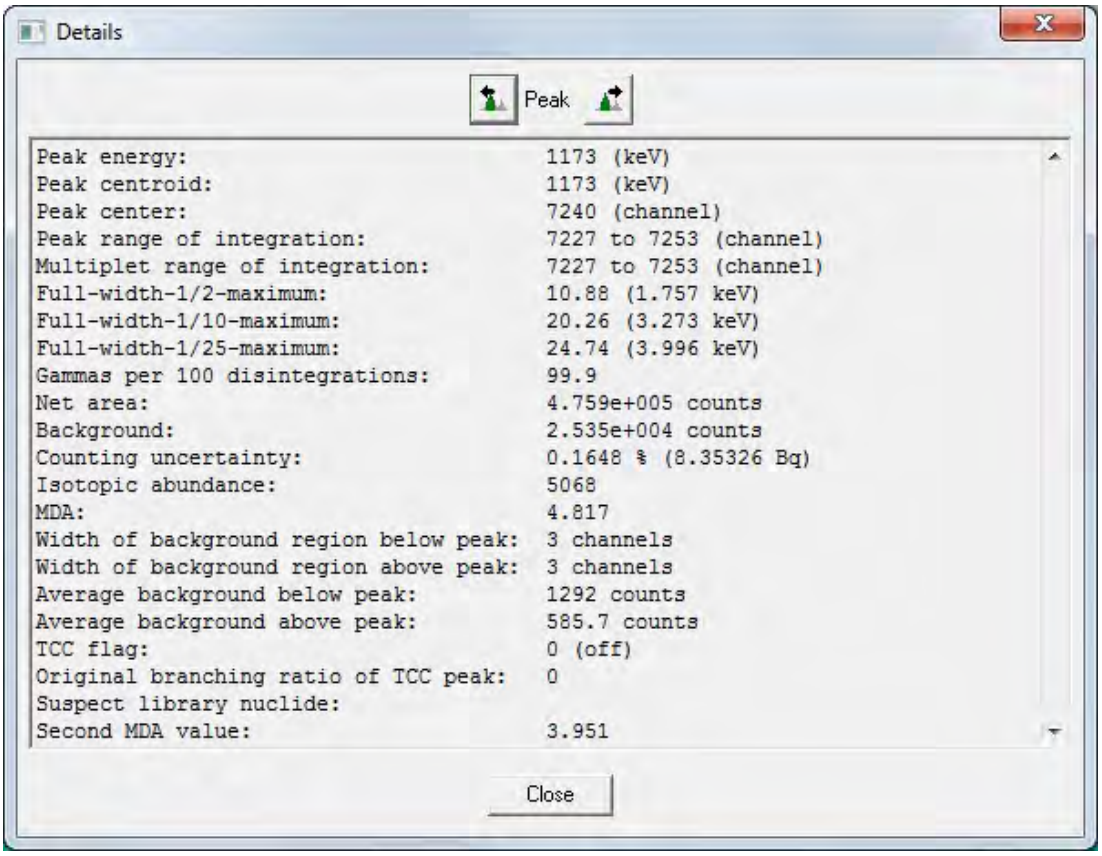


Figure 192.



Peak energy:	1173 (keV)
Peak centroid:	1173 (keV)
Peak center:	7240 (channel)
Peak range of integration:	7227 to 7253 (channel)
Multiplet range of integration:	7227 to 7253 (channel)
Full-width-1/2-maximum:	10.88 (1.757 keV)
Full-width-1/10-maximum:	20.26 (3.273 keV)
Full-width-1/25-maximum:	24.74 (3.996 keV)
Gammas per 100 disintegrations:	99.9
Net area:	4.759e+005 counts
Background:	2.535e+004 counts
Counting uncertainty:	0.1648 % (8.35326 Bq)
Isotopic abundance:	5068
MDA:	4.817
Width of background region below peak:	3 channels
Width of background region above peak:	3 channels
Average background below peak:	1292 counts
Average background above peak:	585.7 counts
TCC flag:	0 (off)
Original branching ratio of TCC peak:	0
Suspect library nuclide:	
Second MDA value:	3.951

Figure 193. Details of Analyzed Peak Derived from the .UFO File.

The **Details** window shows the following peak information, derived from the .UFO file structure (which is described in detail in the *File Structure Manual*):

Peak energy
The library peak energy in keV, or the centroid energy for unknown peaks.

Peak centroid
The peak centroid energy from the spectrum.

Peak center
The peak centroid channel from the spectrum.

Peak range of integration
The low and high channel numbers for the peak region. These are the beginning and end channel numbers for the background region around a single peak. See also **Multiplet range of integration**.

Multiplet range of integration
The low and high channel numbers for the multiplet region. These are the beginning and end channel numbers for the background region around the entire multiplet. All peaks in the multiplet will have the same low-/high-channel values.

Full-width-1/2-maximum
The full width at half maximum of the peak. It is a measured value for single peaks and a calculated value for peaks in a multiplet region.

Full-width-1/10-maximum
The full width at tenth maximum of the peak. It is a measured value for single peaks and a calculated value for peaks in a multiplet region.

Full-width-1/25-maximum
The full width at twenty-fifth maximum of the peak. It is a measured value for single peaks and a calculated value for peaks in a multiplet region.

Gammas per 100 disintegrations
Branching ratio from library, if peak was identified.

Net area
The corrected net area of the peak. For example, the PBC correction could be applied to this number.

Background
The corrected peak background calculated by the program.

Counting uncertainty
The 1-sigma counting uncertainty in the peak net area, as a fraction.

Isotopic abundance
The activity for this nuclide based on this peak only. It is zero for unknown peaks or if there is no efficiency calibration.

MDA
The minimum detectable activity for this nuclide based on this peak only. It is zero for unknown peaks or if there is no efficiency calibration.

Width of background region below peak
Width of background region above peak
The number of channels used in the calculation of the background below and above the peak (as selected on the Sample tab under **Analyze/Settings/Sample Type...**). If the background selection is set to a given number, then these will both be the same. For the **Auto** background setting, these can be different.

Average background below peak
Average background above peak

TCC flag
Was TCC enabled?

Original branching ratio of TCC peak
Original branching ratio if TCC was enabled

Suspect library nuclide
Suspect library nuclide name, if peak was not identified.

Second MDA value
If a second MDA calculation is specified in the b30winds.ini (n30winds.ini for NAI32) file, this is the second MDA value. Otherwise, the value is zero.

5.5.7. Interactive in Viewed Area...

Interactive in viewed area... starts an interactive analysis session by analyzing the spectrum now displayed. This command is active only when the Expanded Spectrum View displays ≤4096 channels (zoom in on a portion of the spectrum to activate this command). The working library

selected with **Library/Select File...** is used. The analysis parameters have been set in the **Analyze/Settings/Sample Type...** dialogs. When the analysis is complete, the graphical results and peak area table are displayed as illustrated in Fig. 194. The table records can be sorted by such parameters as energy, area, FWHM, and background by clicking on the desired column header.

NOTE This interactive method uses a different analysis engine than the one specified in the Sample Defaults (**Analyze/Settings/Sample Type...**), therefore, results from the two engines might differ somewhat. To see the analysis results generated by the Sample Defaults, use **Display Analysis Results...** instead of the interactive function.

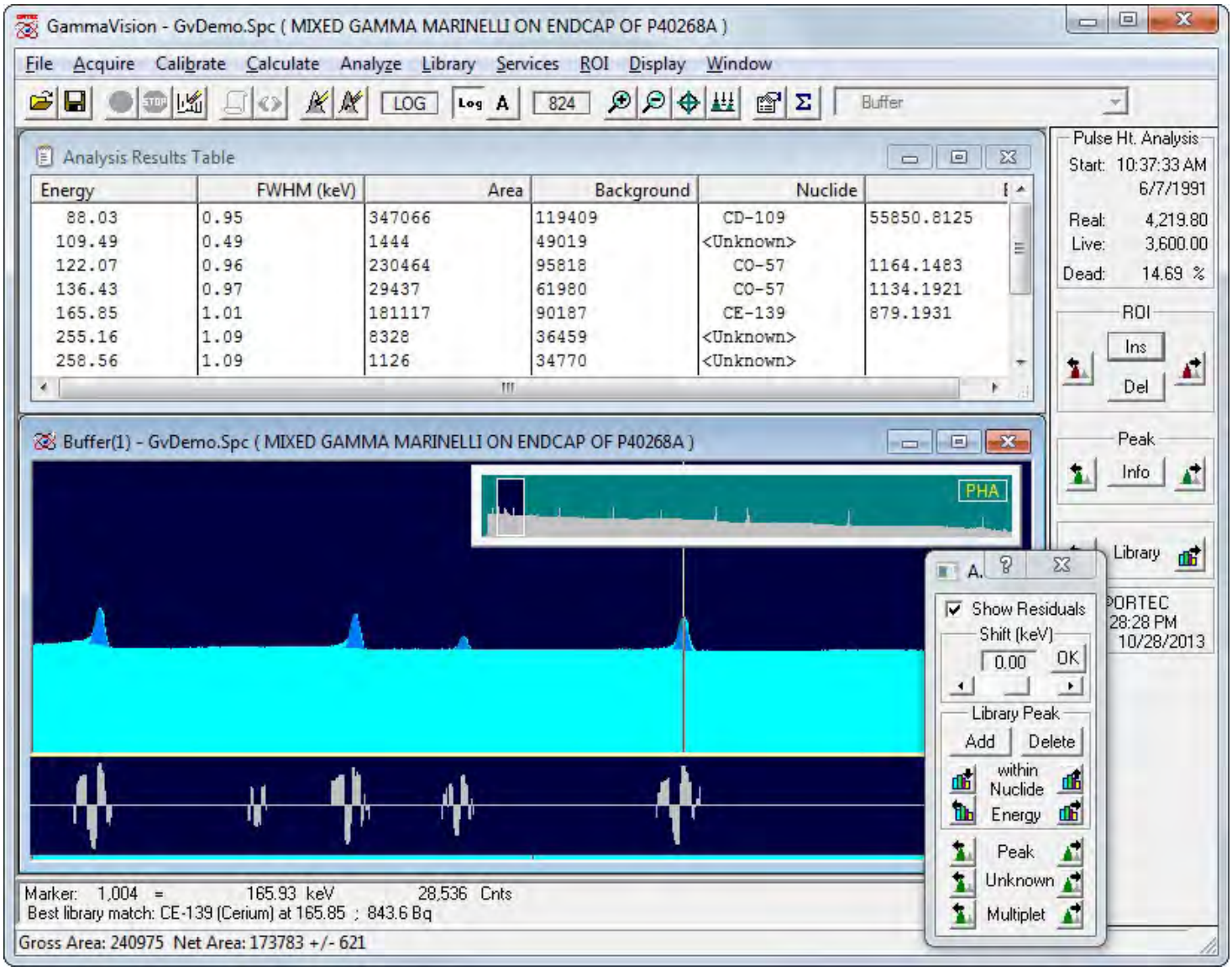
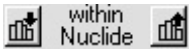


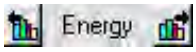
Figure 194. Results Interactive in Viewed Area.

Figure 195 shows the interactive Analysis Sidebar. The buttons move the marker up and down through the results lists, library, and spectrum simultaneously.

The buttons in the **Library Peak** section pertain to the results from the analysis; the other buttons pertain to the spectrum. The peak-found buttons move to the next higher or lower peak in the analysis results list. This includes non-zero-area library and unknown peaks above the cutoff. See **Peak** button below.



The **within Nuclide** buttons move up and down the library list for the selected nuclide, in the order the energies are stored in the library. Since the library energies are not usually stored in increasing energy order, this will jump the marker around in the spectrum. This is useful in deciding if a nuclide is present or not, by looking for all the lines associated with the nuclide. Only non-zero-area peaks are displayed.



The **Energy** buttons move the marker up and down through the library peak list in energy order. Only nonzero-area peaks are shown. Since the library used for the analysis might not be the same as the working library, this might be a different set of peaks than found with the **Peak** buttons.

Figure 195. Analysis Display Controls.

The **Peak** buttons move up and down through the peaks found by the online peak search. (The sensitivity is set in the system settings.) This might select more peaks than the analysis peaks above because of the difference in the cut-off. If the sensitivity for analysis is low, e.g., 5%, many peaks will not be reported because their uncertainty is too high. They will have been found by the analysis, but not reported.

The **Unknown** buttons move the marker up and down through the unknown peaks in energy order, skipping over any library peaks. Only peaks that satisfy the sensitivity cutoff are shown. Note that the **Library Peak** and **Unknown** buttons select different groups of peaks.

The **Multiplet** buttons move up and down through the multiplet or deconvoluted regions in the spectrum. The next time the multiplet up button is clicked, the marker goes to the first (lowest-energy) peak of the next-higher multiplet. The next down button goes to the last (highest-energy) peak of the

next-lower multiplet. To look at individual peaks in the multiplet, use the **Peak**, **Energy**, or **Unknown** buttons.

To add a peak to the analysis library, position the marker at the desired location and click **Add**. This adds a temporary nuclide to the library (assigned the name "**Analyze**" in the results table) with a peak at this energy. A new analysis is performed and the new results are displayed. More peaks can be added as needed.

To delete a peak, click the peak energy in the Analysis Results List. The marker will jump to this channel in the spectrum. Click **Delete**. A new analysis is performed and the new results are displayed.

The energy calibration for all the peaks in the spectrum can be shifted with the **Shift (keV)** field and slide bar (Fig. 196). Select the amount of shift and click **OK**. The shift increments in energy equivalent to 0.1 channel. GammaVision will perform the new analysis and display the results.

Figure 196. Shift keV.

The residuals are the differences between the calculated spectrum (based on peak shape, peak area, and background) and the actual raw data. These can be displayed in the spectrum window by marking the **Show Residuals** check box (refer to Fig. 185). The scaling factor for the residual display is the same as for the data display. In log mode, the scale of the residuals display is somewhat exaggerated and the residuals might appear more significant than they actually are.

The results of this analysis are stored in memory and can be stored as a .UFO file on disk by selecting **Store Results As...** from the Analysis Sidebar's control menu. Mark/unmark the **Table** item to show/hide the Analysis Results Table. Use the **Print** command in the results window's control menu to print the results table.

5.6. Library

The **Library** menu commands (Fig. 197) allow you to select, display, create, edit, or print the library files used in the **Analyze** and **Calibrate** sections, using either the GammaVision library editor discussed here or the NuclideNavigator III library editor. Library files are organized by nuclide, then by the nuclide's peaks. Both .LIB and .MDB libraries are supported.

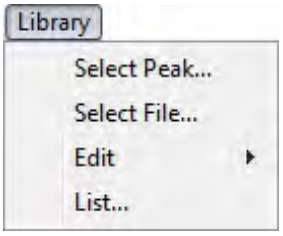


Figure 197. Library Menu.

The nuclide library is used with reference to the peak-search or report functions for quantitative identification of and activity calculations for spectral components

according to calibrated peak energy. The nuclide library data include the nuclide name, half-life, and half-life uncertainty. The nuclide names can be any combination of eight characters, but must be consistent throughout all files. The library peak data include the energies and branching ratio or gammas/disintegration for each energy.

At startup, GammaVision automatically attempts to load the library last loaded (the first time you run GammaVision, the library DEFAULT.LIB is used). Thereafter, this *working library* can be replaced at any time with **Library/Select File...**. The library stays resident in memory after it has been loaded.

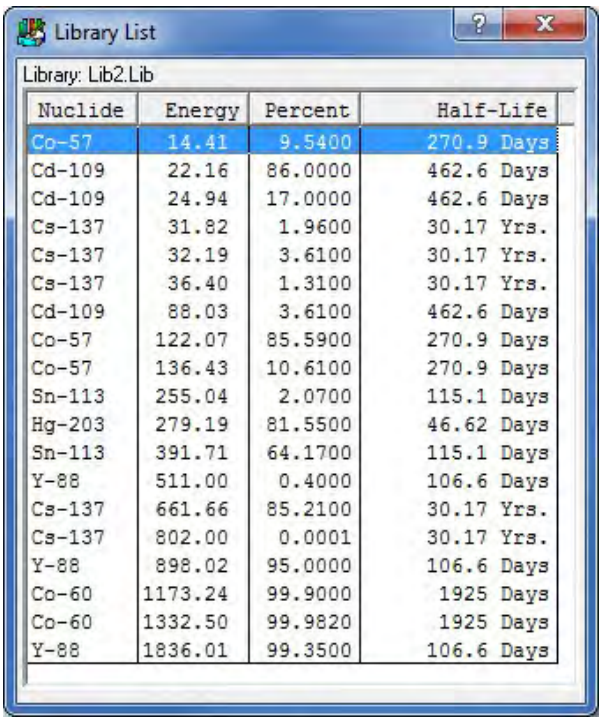
In the analysis report, the nuclides are listed in the order they are in the library. The size of a working library is limited to 65,000 bytes for any combination of nuclides and peaks (e.g., about 100 nuclides with 1900 peaks or 200 nuclides with 1600 peaks). Master or reference libraries (e.g., MASTER.LIB from A53-BI or MASTER.MDB from NuclideNavigator), from which the working libraries are built, can be any size. To analyze using larger libraries, such as those created by NuclideNavigator III, the library for the analysis is specified in **Analyze/Settings/Sample Type...** as the library from disk.

NOTE Some old libraries might need to be rebuilt by copying the complete library to a new library with the **Library/Edit...** feature (Section 5.6.3). The "**Can't read library**" error means this should be done.

5.6.1. Select Peak...

This opens a window containing a list of the library peaks in energy order (Fig. 198). This list shows the nuclide name, energy, gammas/100 disintegrations, and half life. Clicking on any field moves the marker line to that energy in the spectrum.

The Library List can be sorted by nuclide, energy, percent, or half life by clicking on the desired column header.



Nuclide	Energy	Percent	Half-Life
Co-57	14.41	9.5400	270.9 Days
Cd-109	22.16	86.0000	462.6 Days
Cd-109	24.94	17.0000	462.6 Days
Cs-137	31.82	1.9600	30.17 Yrs.
Cs-137	32.19	3.6100	30.17 Yrs.
Cs-137	36.40	1.3100	30.17 Yrs.
Cd-109	88.03	3.6100	462.6 Days
Co-57	122.07	85.5900	270.9 Days
Co-57	136.43	10.6100	270.9 Days
Sn-113	255.04	2.0700	115.1 Days
Hg-203	279.19	81.5500	46.62 Days
Sn-113	391.71	64.1700	115.1 Days
Y-88	511.00	0.4000	106.6 Days
Cs-137	661.66	85.2100	30.17 Yrs.
Cs-137	802.00	0.0001	30.17 Yrs.
Y-88	898.02	95.0000	106.6 Days
Co-60	1173.24	99.9000	1925 Days
Co-60	1332.50	99.9820	1925 Days
Y-88	1836.01	99.3500	106.6 Days

Figure 198. Peak List Dialog Box.

5.6.2. Select File...

This opens the **Load Library File** dialog (Fig. 199). If a library has already been selected, it is shown in the **File name** field. If **File name** contains a generic entry of *.LIB or *.MDB, no library is currently selected. Select the desired

disk and filename and click **Open**. This library becomes the working library.

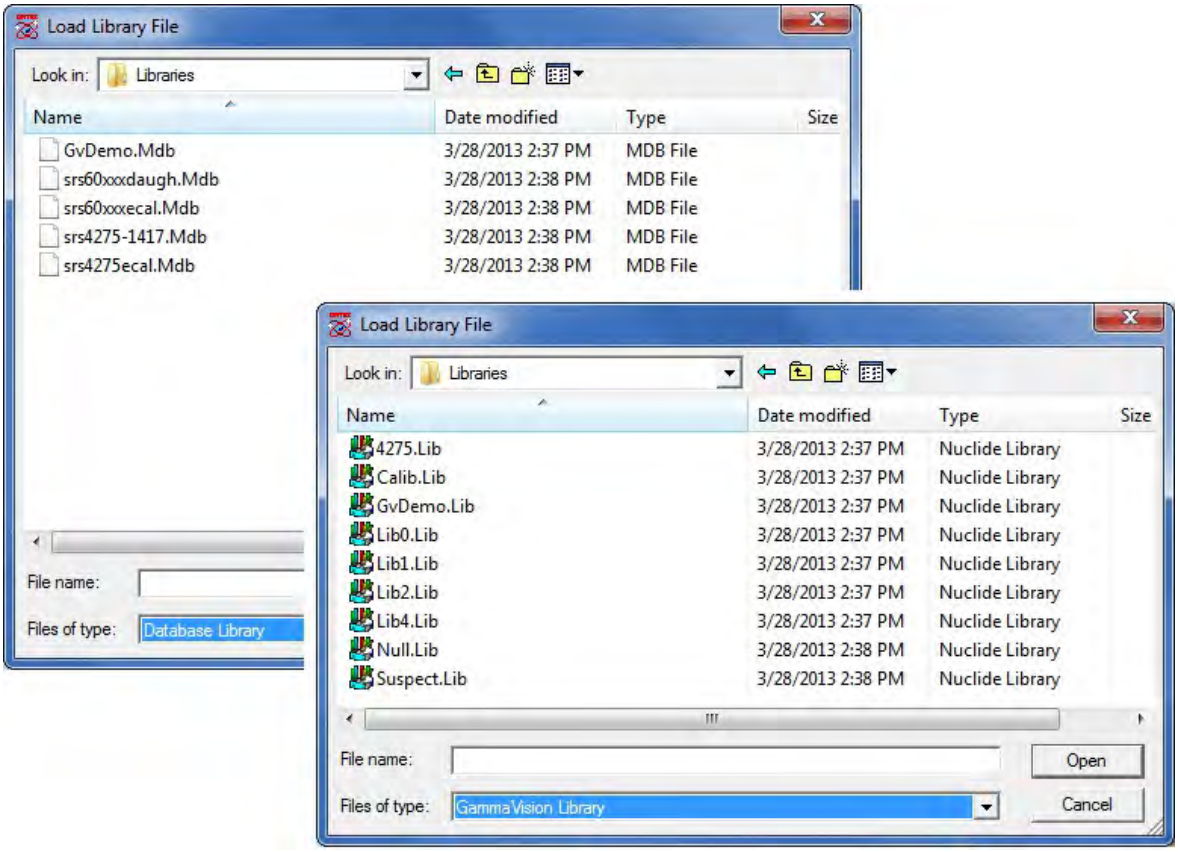


Figure 199. Select an .LIB- or .MDB-Format Library File.

5.6.3. Edit...

Use this command to create a new library file or change the contents of an existing library file. It allows you to select the **GammaVision Editor...** or **Nuclide Navigator...** (if NuclideNavigator III is installed). The GammaVision library editor is discussed here. The NuclideNavigator editor is described in the NuclideNavigator III user manual.

Figure 200 shows the GammaVision library Editing dialog.

The control menu (click the title bar icon to open it) is shown in Fig. 201. It contains several of the commands necessary to create, edit, and print the .LIB files.

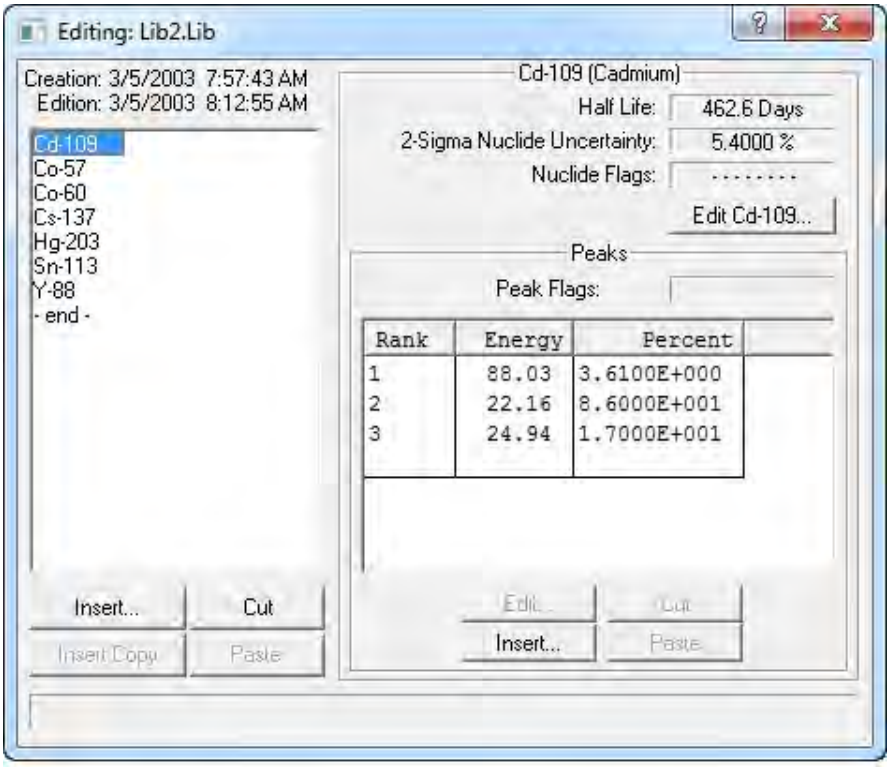


Figure 200. Editing Library Dialog.

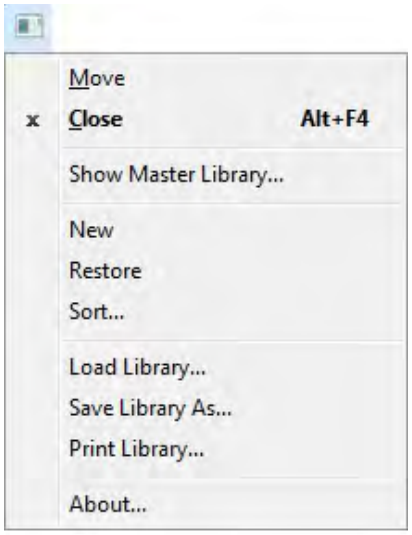


Figure 201. Library Edit Dialog Control Menu.

5.6.3.1. Copying Nuclides From Library to Library

To copy nuclides from one library to another library — for example, to make a working library from a master library — click on the **Edit** window's control menu and select **Show Master Library**. This will open a file selection dialog. Choose the desired disk and file and click **Open**. Both libraries will be displayed side by side, as illustrated in Fig. 202.

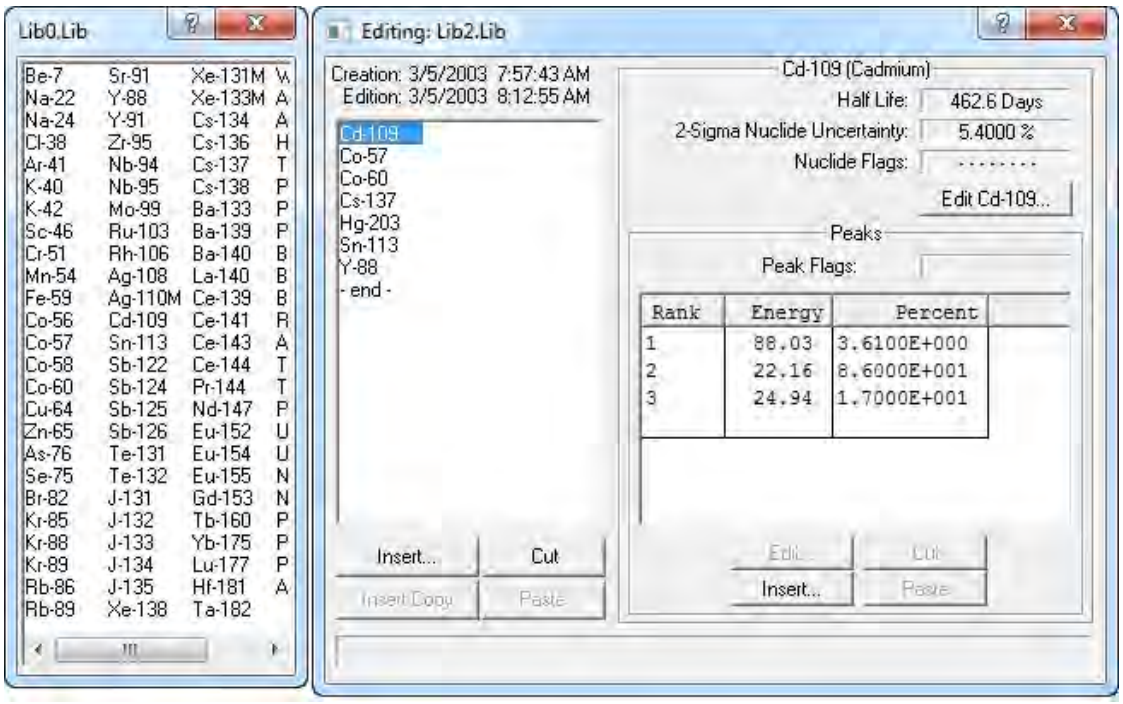


Figure 202. The Master Library (left) and Library Editing Dialog (right).

To copy a nuclide from the master library to the working library: Go to the master library list and click once on the nuclide of interest. This will activate the gray **Insert Copy** button at the bottom of the Editing dialog's nuclide list, and change its label to **Insert** plus the name of the nuclide. Now, in the Editing dialog, locate the nuclide immediately *below* the desired insertion position, click it once, then click **Insert [nuclide name]**. This will insert the nuclide and display its peak list on the right.

Double-clicking on a nuclide in the master library will add it to the working library, inserting it immediately above the currently highlighted nuclide in the list.

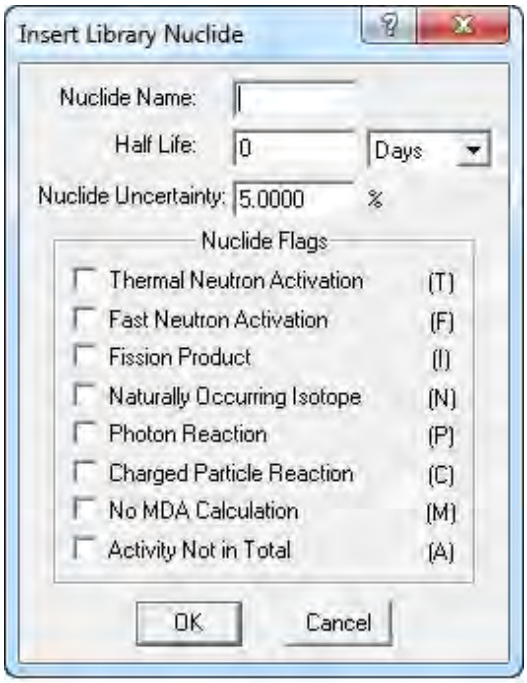


Figure 203. Add a Nuclide.

5.6.3.2. Creating a New Library Manually

Open the control menu and click **New**. This will clear the Editing dialog so nuclides can be entered manually. Click the **Insert...** button to open the Insert Library Nuclide dialog, shown in Fig. 203. Enter the **Nuclide Name** and **Half Life** and click **OK**.

NOTE We recommend that you enter the standard name for the nuclide so that Nuclide Navigator will be able to recognize it. If you use a non-standard name, the TCC calculations could fail due to an inability to compute the parent daughter relationships.

Click the desired row under the **Rank/Energy/Percent** heading to highlight that row. Now, at the bottom of the (right-hand) peak list, click **Insert...** to open the Edit Library Peak dialog (Fig. 207). Enter the energy of the gamma ray and the branching ratio of the peak.

5.6.3.3. Editing Library List Nuclides

To edit the information about a nuclide in the working library:

Click the nuclide to highlight it. The **Edit...** button (in the upper right of Fig. 200) will change to **Edit** plus the name of the nuclide, as shown in Figure 204.

Figure 204. Ready to Edit this Nuclide.

Click **Edit [nuclide]...**. This will open the Edit Library Nuclide dialog (Fig. 205). The **Nuclide Name**, **Half Life**, **Uncertainty**, and **Nuclide Flags** will already be listed.

The **Uncertainty** is a single number that represents the overall uncertainty (2 sigma or 95% confidence level) in the branching ratios entered for this nuclide. The 1-sigma uncertainty is added in quadrature to form the total uncertainty on the final report. The **Uncertainty** value should be taken from the nuclear data sheet for this nuclide. The default is 5%, but 2% is a realistic number.

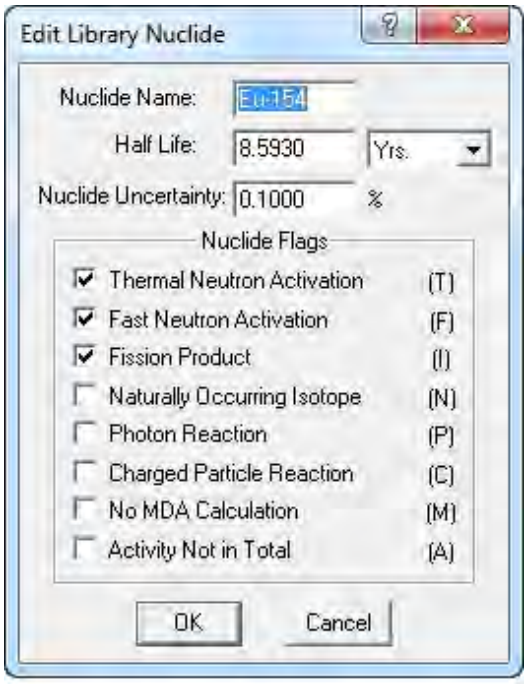


Figure 205. Edit or Manually Add Nuclide Name.

The first six **Nuclide Flags** are used to show how the nuclide was produced. For example, **Thermal Neutron Activation (T)** indicates that this nuclide is produced when the parent nuclide absorbs a slow neutron. This can be helpful in organizing reports by nuclide category. More than one flag can be checked. Libraries produced with Nuclide Navigator II or later versions will already have these flags set. For other libraries, it will be necessary to consult a reference for the proper settings.

The **No MDA Calculation** flag indicates that the nuclide will not be reported unless present in the spectrum. If this is not marked, the MDA value will be printed if the nuclide is not present in the spectrum.

This flag is handled differently for the ISO NORM calculations than for the regular Gamma-Vision report. If an isotope flagged as NO MDA is not detected in the sample, it is not reported in the standard GammaVision report sections unless the Directed Fit flag is turned on. However, the isotope is always reported in the ISO NORM table.

The **Activity Not in Total** flag indicates that the activity for this nuclide will not be included in the total activity for this sample.

These flags are listed on the report and saved in the .UFO file.

Manually Adding Nuclides

To manually add a nuclide to the library list, locate the nuclide immediately *below* the desired insertion position, and click once to highlight it. Next, click the manual **Insert...** button to open the Edit Library Nuclide dialog. The dialog will be blank. Fill in the name and half life as well as any other inputs and click **OK**.

Deleting Nuclides from the Library

To remove a nuclide from the library, click the nuclide, then **Cut**. This will remove the nuclide from the list. In addition, it will activate the gray **Paste** button at the bottom of the nuclide list, and change its label to include the name of the cut nuclide. This is illustrated for ^{152}Eu in Fig. 206.

Figure 206. Cut Nuclide is Ready to Paste.

Rearranging the Library List

The order of the nuclides in the library is the order in which they are listed on the report. Nuclides can be rearranged in the .LIB file list by cutting and pasting them into a different location. To move a nuclide to a new position in the list, highlight the nuclide to be moved; **Cut** it from the list; locate the nuclide immediately *below* the desired new position and click once on that nuclide to highlight it; then click the **Paste** button (which will be labeled with the name of the **Cut** nuclide). The **Cut** nuclide will be inserted in the space above the highlighted nuclide.

Several nuclides can be cut at one time from the list, then pasted back into the list into a different order. Cut nuclides remain queued up for pasting, last one first, according to the nuclide name on the **Paste** button.

To move a nuclide to the end of the library list, **Cut** the nuclide from the list, highlight the **--end--** entry, and click the **Paste** button**.**

Editing Nuclide Peaks

When a nuclide is selected in the working .LIB file, the right half of the Editing dialog shows the peak list. Note the column headers, **Rank**, **Energy**, and **Percent**. To sort the peak list by a particular parameter in the list, click the appropriate header. Be sure to check the flag settings in old libraries and edit if necessary.

To edit a peak, either double-click the peak in the right-hand list, or highlight it and click the **Edit** button. This will open the Edit Library Peak dialog (Fig. 207). The **Energy (keV)**, **Gammas per 100 Disintegrations**, **Photon Flags**, and **Peak Flags** will already be listed.

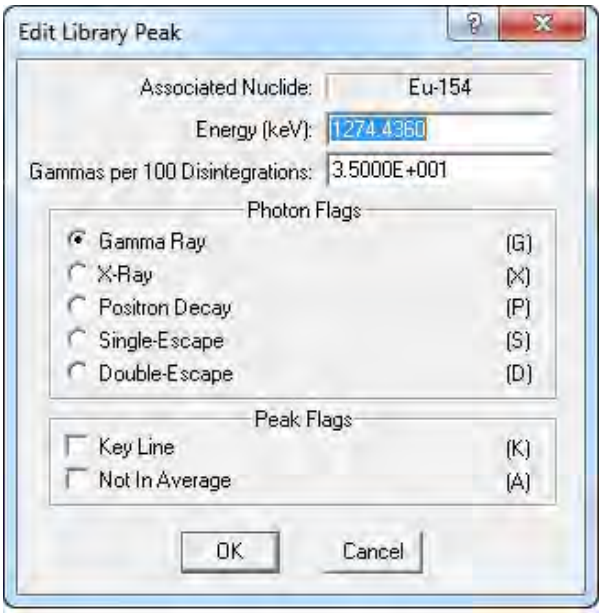


Figure 207. Edit or Manually Add Library Peak Values.

The **Photon Flags** are used to show the peak origin. **Gamma Ray (G)** and **X-Ray (X)** mean the peak energy is due to a nuclear or atomic transition, respectively. **Positron Decay (P)** is used for the 511 keV peak. **Single-Escape (S)** peaks are peaks for which a single 511 keV photon has escaped the detector. This can only occur for full-energy peaks above 1.022 MeV. A **Double-Escape (D)** peak is one for which two 511 keV photons have escaped the detector. Both single- and double-escape peaks are broader than gamma-ray peaks. Neither can be used for activity calculations because the activity of the peak is not related directly to the activity of the full-energy peak. Nonetheless, these can be included in the library to account for the peak in the spectrum.

The **Not In Average (A)** flag in the **Peak Flags** section of the dialog should be set for these peaks. All the peaks marked as **Key Line (K)** must be present before the nuclide will be listed as present on the report. If no lines are marked as key lines, the nuclide will be listed as present if the first line is in the spectrum.[29]

Adding Nuclide Peaks

To add a peak: Click the peak *just below* the desired insertion point in the peak list, then click **Insert...**. This will open the Edit Library Peak dialog; all the fields will be blank. Enter the necessary information for the peak and click **OK**.

[29]To duplicate the operation of older versions of GammaVision, mark either no lines or only the first line as a key line.

Rearranging the Peak List

The entries in the peak list can be rearranged with the **Cut** and **Paste** buttons. Several peaks can be cut at one time from the list, then pasted back into the list into a different order. Cut peaks remain queued up for pasting, last one first. Each relocated nuclide will retain its energy and counts/sec values, but will be assigned a **Rank** number according to its new position. Click the peak *just below* the desired insertion point in the peak list, then click **Paste**.

5.6.3.4. Saving or Canceling Changes and Closing

To save this modified .LIB file and use it as the working file, click the control menu, then **Save Library As...**. Either use the current filename (which will overwrite the previous values) or assign a new filename, then click **Save**. (GammaVision will assign the default .LIB extension.) To exit the edit session, click the control menu, then **Close**.

To abandon any changes and restore the .LIB file to its condition before editing, click the control menu, then **Close**. A dialog will open asking if the changes should be saved; select **No**.

5.6.4. List...

The **List...** function (Fig. 208) will print a list of the library, ordered either by **Nuclide** or **Energy**, to either the printer or a disk file.

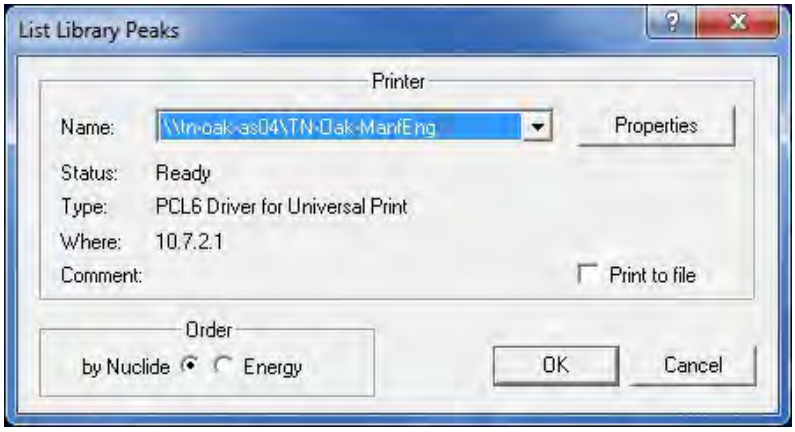


Figure 208. Print Library to Printer or File.

5.7. Services

The **Services** menu (Fig. 209) contains several functions and utilities.

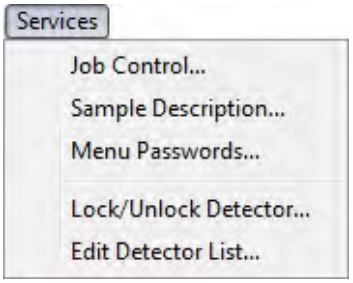


Figure 209. Services Menu.

5.7.1. JOB Control...

Most of the functions under the various GammaVision menus can be automated by writing a *JOB*, which consists of one or more commands written in ASCII text (see Chapter 10 for an in-depth discussion). JOBs allow you to easily perform repetitive tasks and/or define initial conditions at Detector startup. These files are given a filename extension of .JOB. To start a JOB or edit a .JOB file, select **Services/ Job Control...** to display the dialog shown in Fig. 210.

To see the list of commands in a particular .JOB file, mark the **Show Contents** checkbox, then click to highlight the desired filename.

To run a JOB, select it and click on **Open**.

Once a JOB is started, most menu functions will be disabled (gray) to prevent interference with JOB as it runs. The .JOB filename will be displayed on the Title Bar.

If a JOB is running and you try to start another one, the dialog shown in Fig. 211 will show the name of the current JOB and ask if you wish to **Terminate** or continue running the JOB (click on **Close** or press **<Esc>**).

5.7.1.1. Editing a .JOB File

You can edit a .JOB file from the Run JOB File dialog or by opening the file in Notepad. To edit in the Run JOB File dialog:

- Select a file from the list and click on the **Edit File** button. This will open the .JOB file in a Windows Notepad window.
- Edit as desired, then use the Notepad **Save** or **Save As** command to save the changes (or close Notepad without saving to cancel the changes).
- Close Notepad. The newly edited file will be shown in the Run JOB File dialog's **Show Contents** list box.

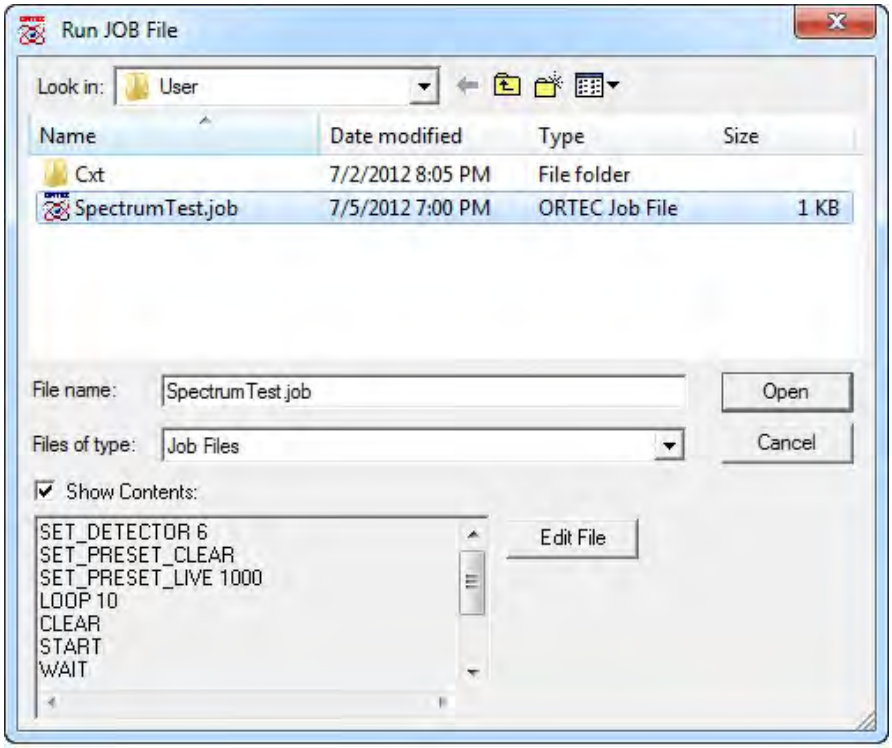


Figure 210. Select and/or Edit .JOB File.

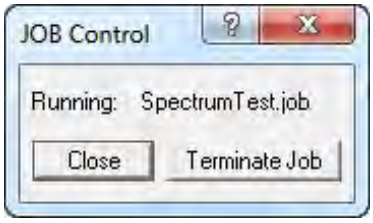


Figure 211. Terminate Current JOB?

If a JOB is terminated prematurely because of some error condition, a message box briefly explaining the cause of the error will be displayed. More details on the error can be found by cross-referencing with the error message directory in Appendix C.

5.7.2. Sample Description...

This command opens the dialog shown in Fig. 212 for reading, editing, or entering the Sample Description of the displayed spectrum. This description can be up to 128 characters in length, and automatically accompanies the spectrum when it is subsequently copied or saved to a file. This description also appears in the title bar at the top of the window while the spectrum is displayed. For files in the .CHN format, only the first 63 characters are saved in the spectrum file.

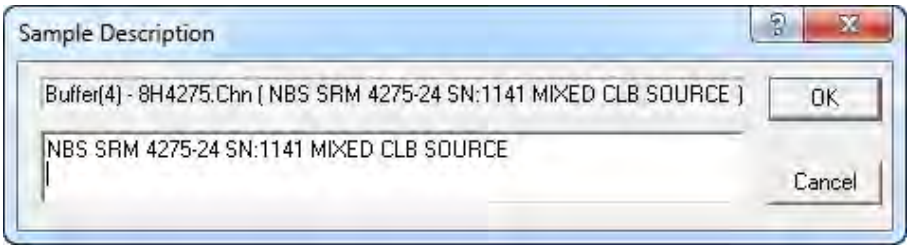


Figure 212. Sample Description Entry.

5.7.3. Menu Passwords...

This feature of GammaVision (Fig. 213) allows you to protect each of the commands on the menu-bar menus by a password. When a menu item is password protected, that function cannot be used unless the password is entered. Each menu item can have a different password or the passwords can all be the same.

NOTE ***There is no master password, and passwords cannot be determined from the system***. If the password is lost, contact ORTEC Customer Service for assistance.

The passwords are not case-sensitive, that is, uppercase and lowercase letters are treated the same. This protection is valid for all instances of GammaVision running on this computer. To prevent the use of passwords, password-protect the **Set Password** menu item itself.

If a menu item already has a password, there will be an asterisk (*****) to the left its item name. To set, change, or clear the password, click the menu item name to highlight it, then click **Password...** to open the next dialog.

If there is no password for this item, the Password for dialog (Fig. 213) will open. Enter the desired **Password** and re-enter in the **Verification** field, then click **OK**. To leave this dialog without setting or changing a password, click **Cancel**.

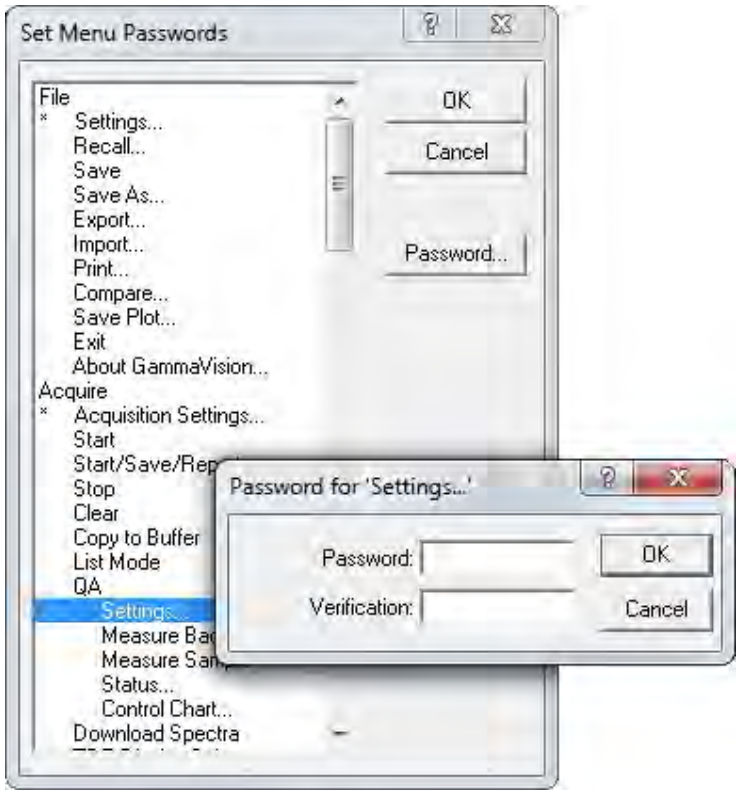


Figure 213. Menu Passwords.

If there is a password for the menu item, the Verify Old Password dialog (Fig. 214) will open. ***You cannot change a password without knowing the old password.*** Enter the old password and click **OK**. If the password just entered is not correct, an error message (Fig. 215) will be displayed. If you do not know the old password, click **Cancel** to exit without changing the password. If you enter an incorrect password, the Enter New Password dialog (which will be similar to Fig. 213) will open for entry of the new password.

Enter a new password, as described above. To remove the password, leave the box in Fig. 213 ***blank (not spaces)*** and click **OK**.

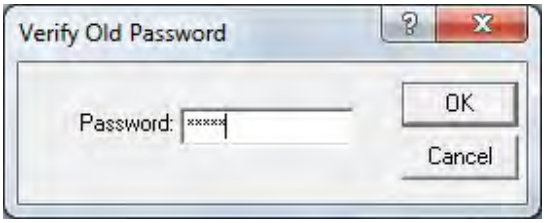


Figure 214. Verify Old Password.

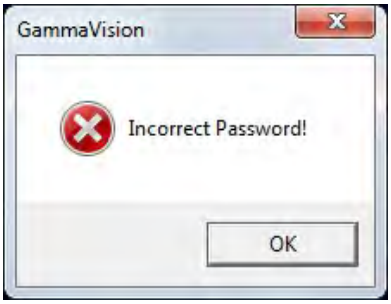


Figure 215. Wrong Password.

When finished editing all of the desired passwords, click **OK** on the **Set Passwords** dialog to keep the changes. Clicking on **Cancel** will restore all password states to their previous condition.

5.7.4. Lock/Unlock Detectors...

This facility enables you to protect a Detector from destructive access (e.g., **Start**, **Stop**, **Clear**) by any program on the computer or network. While any program can *view* the data and read the contents on any Detector in the system — locked or unlocked — the contents of a locked Detector cannot be changed without knowing the password.

NOTE ***There is no master password***. If the password is lost, contact ORTEC Customer Service for assistance in unlocking the detector.

- **Locking** — Select the **Lock/Unlock** command to display the dialog shown in Fig. 216. Enter the **Owner** name. Then enter a password in the **Password** field, and re-enter it in the **Verify** field (the two entries must agree). Click on **OK**. The password is not case-sensitive (that is, uppercase and lowercase letters are treated the same).

- **Accessing a locked detector** — If a Detector is currently locked, selecting **Lock/Unlock** will display the Unlock Detector dialog shown in (Fig. 217) and will display the name of the Owner on the Supplemental Information Line, as shown in Fig. 218. You must enter the correct password to unlock the Detector.

  If a JOB file or network user attempts to change any Detector settings on the Properties dialog will display the Locked Detector dialog shown in Fig. 219.

- If you enter the incorrect password in either the Unlock or Locked Detector dialog, the dialog will reopen and wait for the correct password. If you do not know the password, click on **Cancel** to close the dialog (you will still have read-only access to the Detector).

- **Removing the password** — To remove the password lock, issue the **Lock/Unlock** command, enter the password to unlock it, then reissue **Lock/Unlock**, *completely delete* the

Owner entry, click on **OK** (which will display an "Owner name must be supplied!"), then click on **Cancel**.

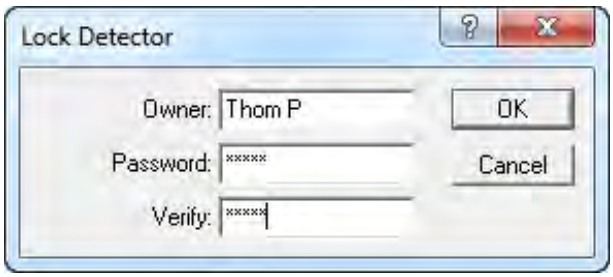


Figure 216. Enter Owner and Password to Lock a Detector.

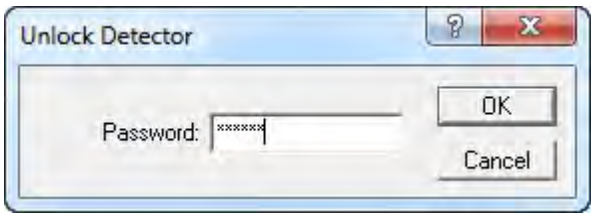


Figure 217. Unlocking a Detector.

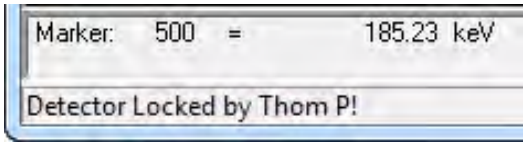


Figure 218. Name of Detector Owner.

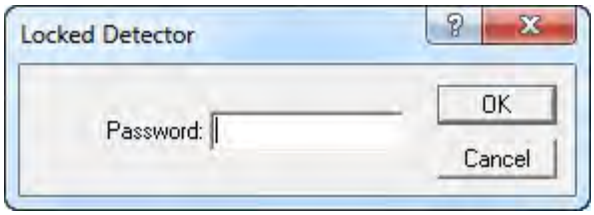


Figure 219. Password Required To Unlock Detector.

5.7.5. Edit Detector List...

This function allows you to select the Detectors that will be available to GammaVision on this computer. Other CONNECTIONS applications (e.g., ScintiVision™, AlphaVision®, MAESTRO) on the same computer can have their own lists. In this way, the different Detectors on the network can be segregated by function or type.

NOTE When you invoke this command, all Detector windows close without warning, all buffer windows close with a warning, and a buffer window opens, followed by the Detector List Editor dialog! The buffer window remains open after you have closed the editor dialog.

Figure 220 shows the Detector List Editor dialog. On the left is the **Master Detector List** of all Detectors on the system. This master list is created by the MCB Configuration program (see Section 2.3) and is the same for all ORTEC programs running on all computers connected to the workgroup. The default description for each instrument is derived from the hardware and can be changed within the configuration program.

Figure 220. Detector List Editor Dialog.

The GammaVision **MCA Pick List** initially contains all of the instruments in the master list.

- **Add** — To add a Detector to the GammaVision **Pick List** for this computer, click on the name in the Master list, then click on **Add**. To add all the Detectors on the **Master Detector List**, click on **All**.

- **Remove** — To remove a Detector from this local pick list, click on the name in the **Pick List** and click on **Remove**. To remove all the Detectors, click on **New**.

When Detector selection is complete, click on **OK**. These selections will be saved to disk and used by GammaVision until changed on this screen or until the entire network is reconfigured. CONNECTIONS programs such as GammaVision can have more than one Detector pick list on the computer. For more information on creating and using alternate pick lists, see the -P listname discussion on page 437.

5.8. ROI

An ROI — *region of interest* — is a way to denote channels or groups of channels in the spectrum as having special meaning. An ROI can be used to mark peak areas for the printout or to mark a peak to stop acquisition when that peak reaches a preset value. Channels marked as ROI channels are displayed in a different color than the unmarked channels.

The **ROI** menu is shown in Fig. 221. Its functions are available in both buffer and Detector windows. See Section 4.4.3 for ROI operations performed with the mouse.

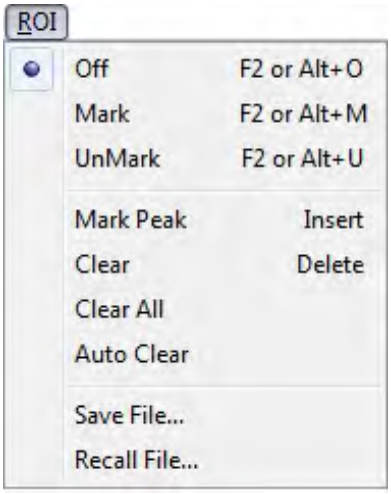


Figure 221. ROI Menu.

5.8.1. Off

This sets the ROI status to Off. In this state, the ROI bit for the channels does not change as the cursor moves. This function is duplicated by **<Alt + O>** and by **<F2>** (which toggles between **Off**, **Mark**, and **UnMark**).

The usual ROI status is Off so the marker can be moved on the display without changing any of the ROI bits.

5.8.2. Mark

This sets the ROI status to the Mark (set) condition. In this state, the cursor channels are marked as the cursor is moved with <→> or <←> into the channel. Moving the marker with the mouse does not change the ROI in this mode. This function is duplicated **<Alt + M>** and by **<F2>** (which toggles between **Off**, **Mark**, and **UnMark**).

ROIs can also be marked with the rubber rectangle and right-mouse-button menu (see Sections 4.4.3 and 5.11.8), and as described in Section 5.8.4.

5.8.3. UnMark

This sets the ROI status to the Unmark (reset) condition. In this state, the channels are unmarked as the cursor is moved with <→> or <←> into the channel. Moving the marker with the mouse does not alter the ROI in this mode. This function is duplicated by **<Alt + U>** and by **<F2>** (which toggles between **Off**, **Mark**, and **UnMark**).

5.8.4. Mark Peak

This function marks an ROI in the spectrum, at the marker position, in one of two ways.

- If the spectrum is calibrated, the region is centered on the marker with a width of three times the calibrated FWHM. There does not need to be a peak at the marker position.

- If the spectrum is not calibrated, the region is centered on the peak located within two channels of the marker and as wide as the peak. If the peak search fails, or if the peak is not well-formed, no ROI is marked. There is no limit on the size of a peak or ROI; therefore, in some uncalibrated spectra, large ROIs might be marked.

ROIs can also be marked this way with the **ROI Ins** button on the Status Sidebar, the **Mark ROI** button on the toolbar, **Keypad<Ins>**, and **<Insert>**. See also **Mark ROI** on the right-mouse-button menu, Section 5.11.8.

5.8.5. Clear

This clears the ROI bits of all ROI channels contiguous to the channel containing the marker. This is duplicated by the **ROI Del** button on the Status Sidebar, **Keypad<Del>**, the **<Delete>** key, and the **Clear ROI** toolbar button. See also **Clear ROI** on the right-mouse-button menu., Section 5.11.9.

5.8.6. Clear All

This resets all the ROI bits in the displayed spectrum (i.e., removes all ROI markings from the spectrum). However, it does not affect the ROI status of **Mark**/**Unmark**/**Off**.

5.8.7. Auto Clear

When this option is active (click to display a checkmark beside it) and you perform a peak search (see Section 5.5.2), all existing ROIs are cleared from the spectrum before the search is performed.

5.8.8. Save File...

This allows you to save to disk a table of the channel numbers, for the current spectrum, that have the ROI set. The contents of the spectrum are not changed.

Selecting **Save File...** opens a standard file-open dialog. Enter the **File name**. The default file extension is .ROI. If the file already exists, the system ask if you want to overwrite the data in the existing file or cancel the save. Click on **OK** to overwrite the file.

5.8.9. Recall File...

Recall File... sets the ROIs in the buffer or active Detector to the table in the disk file created by **ROI/Save File...** (Section 5.8.8), or from the table stored in an .SPC file. This command opens a standard file-open dialog. Enter the **File name**. The ROIs in the buffer or active Detector will be set according to the table of values in the file. The previous ROIs will be cleared. The data contents of the buffer or Detector are not altered by this operation, only the ROI bits in the buffer or Detector are set.

Note that in .ROI and spectrum files the ROIs are saved by channel number. Therefore, if the spectrum peaks have shifted in position, the ROIs in the file will not correspond exactly to the spectrum data.

5.9. Display

Two of the most important functions of GammaVision are to display the spectrum data and to provide an easy and straightforward way to manipulate the data. This is accomplished using the **Display** menu functions, shown in Fig. 222, and their associated accelerators. The **Display** functions are available in both the Detector and buffer modes.

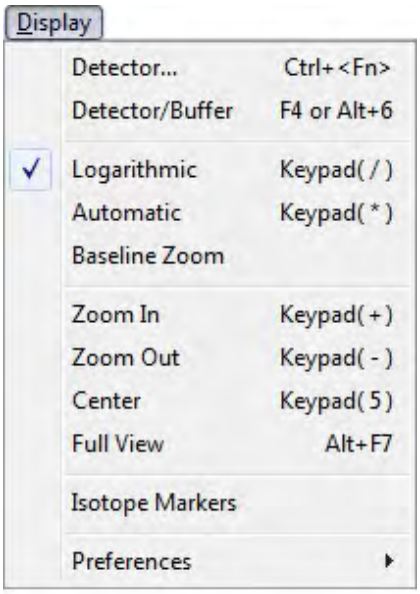


Figure 222. Display Menu.

5.9.1. Detector...

Selecting this function opens the **Pick Detector** list shown in Fig. 223. Click on a Detector on this list to display its memory in the Full and Expanded Spectrum Views. The **Pick Detector** list shows the available Detectors, listed by Detector number, and a brief description. To close the dialog, press **<Esc>**.

This is duplicated by the Detector droplist on the toolbar (see page 49). In addition, the first 12 Detectors on the list can be selected by pressing **<Ctrl + F1>** for the first Detector in the pick list, **<Ctrl + F2>** for the second Detector, and so on, through **<Ctrl + F12>** (see Section 9.4.8).

The current pick list is selected from the Master Detector List using **Services/Edit Detector List...**, as discussed in Section 5.7.5.

5.9.2. Detector/Buffer

This command switches the active window spectrum and Status Sidebar displays between the last active Detector and the last active buffer. The Full and Expanded Spectrum Views display the data in histogram form. This command is duplicated by the accelerators **<F4>** and **<Alt + 6>**. You can also use the toolbar's Detector droplist.

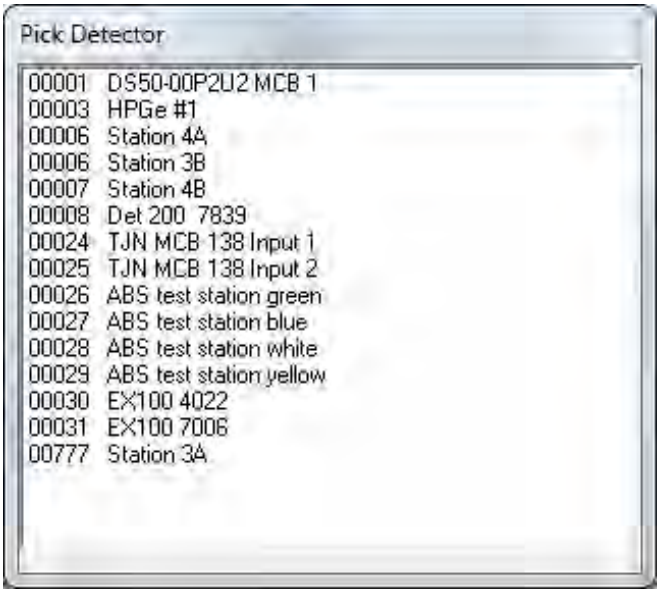


Figure 223. Detector Selection List.

5.9.3. Select Spectrum

This menu displays a floating dialog box that mimics the behavior of the Spectrum navigation controls on the sidebar when the active buffer contains an N42 file. (Section 4.5) Unlike the sidebar controls, the floating dialog can be controlled using keyboard commands.

5.9.4. Logarithmic

Logarithmic toggles the vertical scale of the Spectrum display between the logarithmic and linear modes. This function is duplicated by **Keypad</>** and the **Log/Linear Display** button on the toolbar.

5.9.5. Automatic

Automatic switches the Expanded Spectrum View to a linear scale that is automatically adjusted until the largest peak shown is at its maximum height without overflowing the display. It also toggles the vertical scale of the spectrum display between the automatic and manual modes. If the logarithmic scale was enabled, the display is switched to linear. This function is duplicated by **Keypad<*>** and the **Vertical Auto Scale** toolbar button.

5.9.6. Baseline Zoom

When you select **Baseline Zoom**, the baseline of the spectrum displayed in the expanded view is always zero counts. In this mode, a checkmark is displayed beside the item name on the menu. When Baseline Zoom is off (no checkmark beside the item name), the baseline can be offset to a higher value. This is useful to show small peaks on a high background. When the baseline is offset, the box in the Full Spectrum View is raised above the baseline to show the offset. This is duplicated on the toolbar.

5.9.7. Zoom In

Figure 224. Vertical and Horizontal Full-Scale Setting on the Toolbar.

Zoom In adjusts the horizontal and vertical scales in the Expanded Spectrum View to view a smaller portion of the spectrum. The vertical scale is divided by two and the horizontal scale is reduced by about 6% of the full horizontal scale. The current horizontal and vertical full-scale values are shown on the toolbar (see Fig. 224). This command is duplicated by **Keypad<+>**, the toolbar's **Zoom In** button, and **Zoom In** on the right-mouse-button menu.

5.9.8. Zoom Out

Zoom Out adjusts the horizontal and vertical scales in the Expanded Spectrum View to view a larger portion of the spectrum. The vertical scale is doubled and the horizontal scale is increased by about 6% of the full horizontal scale. This command is duplicated by **Keypad<–>**, the toolbar's **Zoom Out** button, and **Zoom Out** on the right-mouse-button menu.

5.9.9. Center

This function forces the marker to the center of the screen by shifting the spectrum without moving the marker from its current channel. This function is only required when moving the marker with the mouse; the keyboard functions for moving the marker automatically shift the spectrum to center the marker when the marker travels past the end of the current expanded display. **Center** is duplicated by **Keypad<5>** and the **Center** button on the toolbar.

5.9.10. Full View

This function sets the Expanded Spectrum View to the maximum number of channels in the spectrum (the ADC conversion gain).

5.9.11. Isotope Markers

The isotope markers can be used in energy calibrated spectra to locate other gamma rays of the same nuclide (from the library) when any one of the gamma rays from that nuclide is selected. In this way, you can easily see if the selected nuclide is present by comparing the spectrum peaks with the displayed markers. The marker is a solid color rectangle placed at the energy of the gamma ray, with the nuclide name shown above the top of the

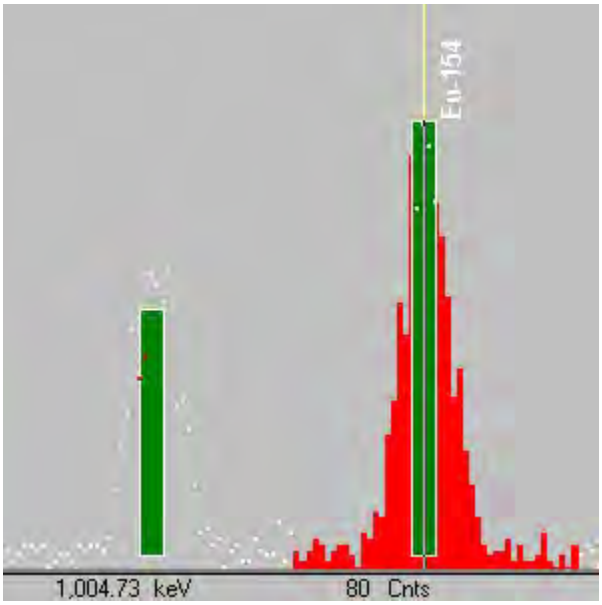


Figure 225. Isotope Markers.

rectangle (Fig. 225). The markers are shown in both the full and expanded views (Fig. 226). The base of the rectangle is positioned at the level of the background for the peak.

The amplitude of the marker for the selected peak is normally proportional to the peak area. However, the amplitude can be changed by placing the mouse in the rectangle, where it will become a double-sided arrow. While the double arrow is displayed, click and hold the left mouse button and move the pointer higher or lower on the y-axis to make the rectangle larger or smaller. The amplitude of the marker for the other peaks is proportional to the amplitude of the first peak and the yield (branching ratio). As the amplitude of the peak is changed with the mouse, all the other rectangles will change proportionally.

The markers are shown in one of two colors. If the peak area, calculated in the same manner as for **Peak Info**, is positive (indicating the peak was found), then the rectangle is one color (normally green). If the peak area is negative or zero (indicating the peak was not found), then the rectangle is another color (normally blue).

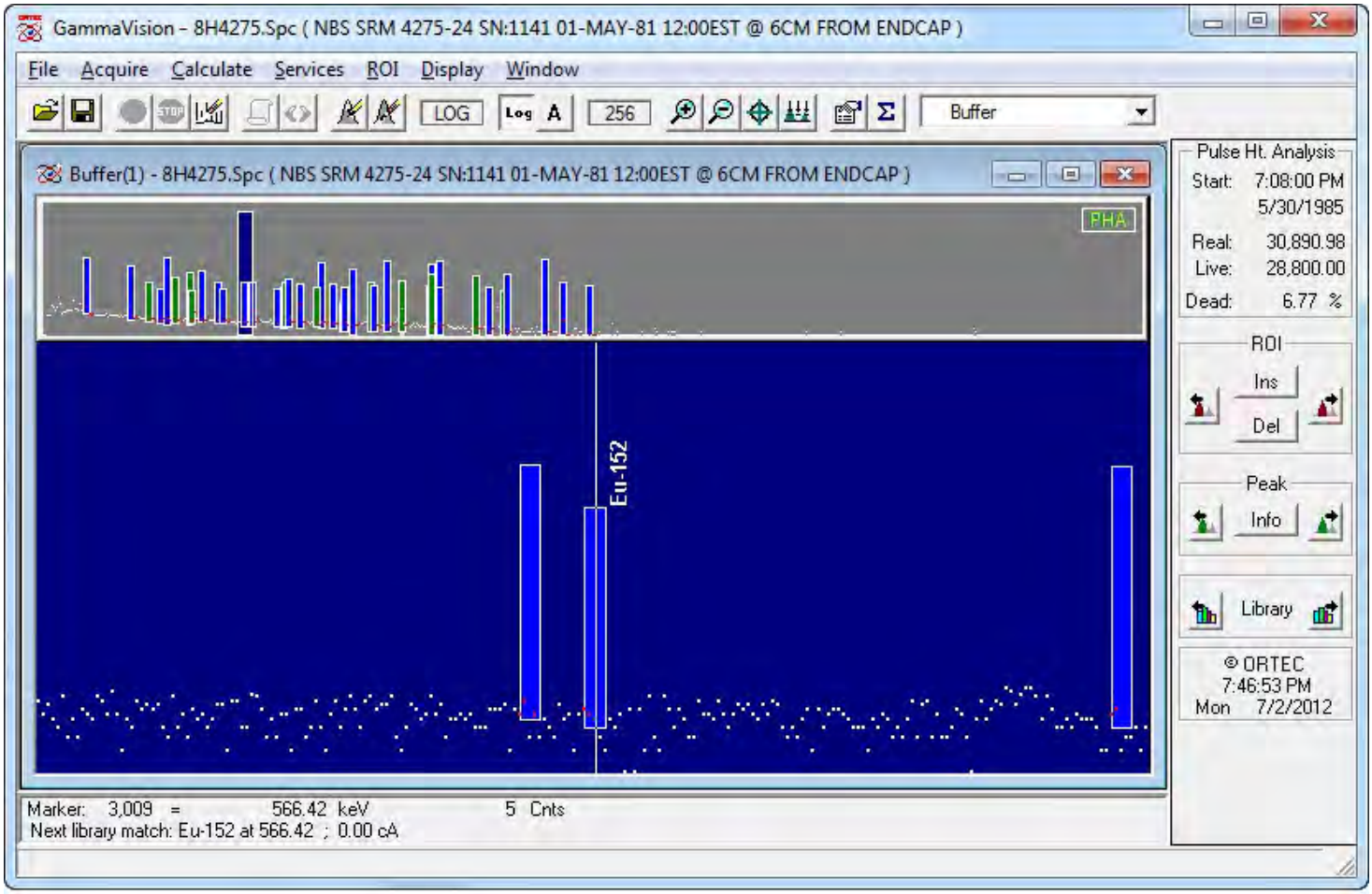


Figure 226. Isotope Markers, Expanded View.

5.9.12. Preferences...

This displays the options available for selecting the screen colors and spectrum display options. The submenu is shown in Fig. 227.

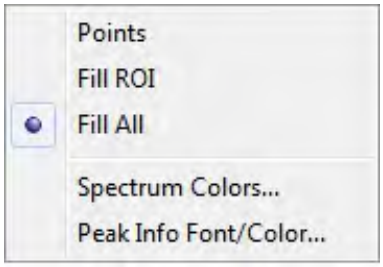


Figure 227. Display Preferences Submenu.

5.9.12.1. Points/Fill ROI/Fill All

Use these functions to select the histogram display mode for both spectrum windows.

In **Points** mode, the data are displayed as points or pixels on the screen, in the colors chosen for **Foreground** and **ROI** under **Display**/**Preferences**/**Spectrum Colors...** (see Section 5.9.12.2).

In **Fill ROI** mode, the unmarked regions of the spectrum are displayed as points, while the ROIs are filled from the baseline to the data point with the **ROI** spectrum color.

In **Fill All** mode, all the data points are filled from the baseline to the data point with the **Foreground** and **ROI** spectrum colors.

Figure 228 shows a comparison of the three display modes. Note that the point/pixel size in the **Point**- and **Fill ROI**-mode illustrations has been exaggerated to make them easier to see.

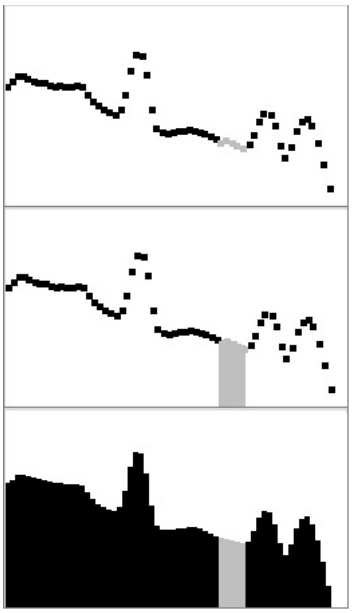


Figure 228. Comparison of the Points, Fill ROI, and Fill All Display Modes.

5.9.12.2. Spectrum Colors...

Use this dialog (see Fig. 229) to select colors for various features in the two spectrum windows. Each scroll bar controls the color of a different feature. The vertical colored stripes behind the scroll bars show the available colors.

The **Background** scroll bar controls the background color of the spectrum window, **Foreground** determines the color of the spectrum points or fill, **ROI** governs the color of the ROI points or fill. The points/fill of a compared spectrum (**File**/**Compare...**) use the **Compare** color, unless they overlap with the original spectrum, in which case the **Composite** color is used.

Click each list and select the desired color. Changes take effect immediately. To reset to the default colors, click on **Defaults**. To accept the color changes, click **OK**. To exit without saving your changes, click **Cancel**.

NOTE These color settings affect only the GammaVision spectrum windows.

5.9.12.3. Peak Info Font/Color

This function opens the **Font** dialog (Fig. 230). It allows you to select the font type, size, and color used to display **Peak Info** data in the text box in the spectrum windows (see Section 5.4.3, Fig. 130).

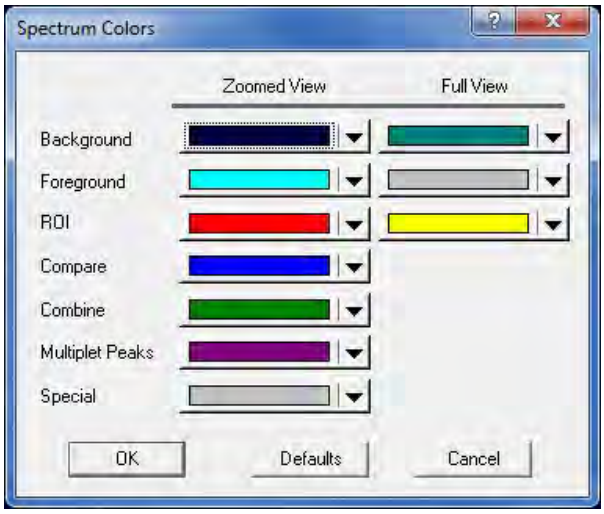


Figure 229. Display Color Selections.

Figure 230. Peak Info Font/Color Dialog.

5.10. Window

This menu contains standard Windows commands for controlling the display of the spectrum windows (Fig. 231). In addition to the spectrum window display mode (**Cascade**, **Tile Horizontal**, **Tile Vertical**, etc.), the list of open buffer and Detector windows is shown. The currently active spectrum is checkmarked.

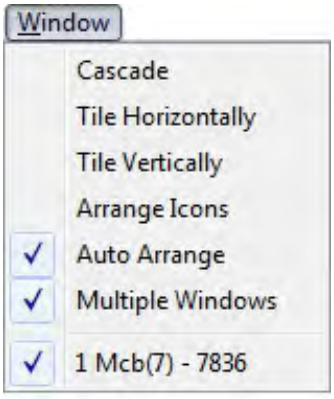


Figure 231. Window Menu.

The **Multiple Windows** command lets you choose between the newer multiple-detector-window mode and the original single-detector-window mode. In single-window mode (no checkmark beside **Multiple Windows**), to bring another window forward as the active window, click on its entry in the list. This is especially useful if one window has been resized and has obscured other windows.

5.11. Right-Mouse-Button (Context) Menu

Figure 232 shows the right-mouse-button (context) menu for the spectrum windows. For Detector windows only, the **Start**, **Stop**, and **Clear** commands are affected by the **Group Acquisitions** setting in the Acquisition Settings dialog, which determines whether these commands will be executed for all currently displayed Detectors or for the active Detector only; or directs the program to ask each time if you wish to execute the command for one or all displayed Detectors. See Sections 5.2.2, 5.2.4, and 5.2.5 for more information.

Figure 232. Right-Mouse-Button Menu.

5.11.1. Start

Duplicates the **<Alt + 1>** accelerator, the **Start Acquisition** toolbar button, and the **Start** command on the **Acquire** menu.

5.11.2. Stop

Duplicates the **<Alt+ 2>** accelerator, the **Stop Acquisition** toolbar button, and the **Stop** command on the **Acquire** menu.

5.11.3. Clear

Duplicates **<Alt+ 3>**, the **Clear Spectrum** toolbar button, and the **Clear** command on the **Acquire** menu.

5.11.4. Copy to Buffer

Duplicates **<Alt + 5>** or the **Copy to Buffer** command on the **Acquire** menu.

5.11.5. Zoom In

Zoom In duplicates **Keypad<+>**, the toolbar's **Zoom In** button, and **Zoom In** on the **Display** menu; and zooms in on the area marked with a rubber rectangle.

5.11.6. Zoom Out

Zoom Out duplicates **Keypad<->**, the toolbar's **Zoom Out** button, and **Zoom Out** on the **Display** menu; and zooms out on the area marked with a rubber rectangle.

5.11.7. Undo Zoom In

This will undo or reverse the last **Zoom In** operation done with the rubber rectangle. It restores the display to the horizontal and vertical expansion before the **Zoom In**. It is not the same as **Zoom Out**.

5.11.8. Mark ROI

See Sections 4.4.3 and 5.8.4.

5.11.9. Clear ROI

See Section 5.8.5.

5.11.10. Peak Info

See Section 5.4.3.

5.11.11. Input Count Rate

See Section 5.4.4.

5.11.12. Sum

See Section 5.4.5.

5.11.13. MCB Properties...

See Section 5.2.11.

6. ANALYSIS METHODS(V)

6.1. General

The GammaVision program analyzes spectrum files and produces a list of the background, net area, counting uncertainty, FWHM, and net count rate for all peaks in the spectrum. If possible, it also gives a list of the average activity of the nuclides in the sample, the activity of each nuclide based on each gamma-ray energy in the library, the MDA for each peak energy of all nuclides in the library, and the reasons the unacceptable peaks were not used for the activity calculation. Peaks that are not the correct shape (according to the calibration) are marked as such; peak areas that are the result of deconvolution of overlapping energies are also marked; gamma-ray energies not in the analysis library are reported as suspected nuclides if a suitable candidate is found in the suspected nuclide library.

The result is a report containing all the descriptions stored with the spectrum file, the analysis parameters, user inputs, and the list of peaks and nuclides found in the spectrum. The standard GammaVision report is discussed in Chapter 7.

6.2. The Analysis Engines

6.2.1. Analysis Engine Options

GammaVision includes six analysis engines, which are discussed in general terms below. The traditional HPGe engines were WAN32 and GAM32. NPP32 and ENV32 were created in more recent years to address applications for which WAN32 and GAM32 were not optimized. ROI32 allows you to choose which spectral regions are to be analyzed, after which the unmarked parts of the spectrum are evaluated with a simplified WAN32 analysis. The NAI32 engine is designed specifically for low resolution spectrum analysis (i.e., sodium iodide). All six engines produce a report file (.RPT) and a binary output (.UFO) file. The following is a basic summary of processes used by each analysis engine. Section 6.2.2 contains a decision matrix to assist you in choosing an analysis routine.

6.2.1.1. WAN32

WAN32 does a preliminary library-based peak search of the spectrum. The analysis assumes that all gamma-ray listed in the library exist in the spectrum so it tries to fit a peak at every energy listed in the library. The **Peak Cutoff** value specified in the Sample Defaults File (SDF) is compared to the 1 sigma counting uncertainty for each peak to determine if that energy will be used for further analysis. With a large **Peak Cutoff** value (> 200), this engine can “find” false peaks. A Mariscotti peak search is then implemented on the remainder of the spectrum. For nuclides with no clean (well resolved) gamma rays WAN32 offers **Manual-Based** peak stripping.

6.2.1.2. GAM32

GAM32 does a preliminary Mariscotti peak search of the spectrum and removes library nuclides for which sufficient energy peaks were not found based on **Fraction limit**. A library-based peak search is then performed using the reduced library. This analysis engine is used for specialized applications and generally should not be selected. GAM32 overcomes the false-positive weakness of "library-directed" analysis when the sample is completely unknown, and the activity-accuracy weakness of the traditional "matrix" method.

In most cases, the MDA for a nuclide will not be reported because all nuclides without gamma rays in the spectrum will have been removed from the library. In a few cases, the nuclide will be eliminated in the deconvolution step and the MDA will be reported for this case. To remove these possibilities, go to the System tab under **Analyze/Settings/Sample Type...** and select **Suppress Output** from the **MDA Type** droplist.

For information on library reduction during GAM32 analysis, see Section 6.2.3.

6.2.1.3. NPP32

NPP32 does a preliminary library-based peak search like WAN32. Gain shift corrections can be applied for an accurate determination of peak energy and associated nuclide activity. After the Library-based analysis is complete, a Mariscotti peak search is used to find any peaks that were not included in the library or did not pass the library peak search criteria. A **Directed Fit** can also be used to generate negative peak areas to meet environmental reporting requirements for singlet peaks. Standard reports have a "Summary of Peaks in Range" section that displays potential library matches and associated activity concentration for each peak found during analysis. NPP32 and ENV32 do especially well with **Library-Based** peak stripping.

For the deconvolution of multiplets in the re-analysis phase, the peaks are allowed to shift in energy, up to two channels. The entire multiplet moves as a group. This gives more accurate peak areas when the energy shifts between the calibration and the sample spectrum. (Note that this is in addition to the recalibration for energy for the entire spectrum.)

6.2.1.4. ENV32 and NAI32

ENV32 and **NAI32** are very similar in operation, but designed for different spectrum types - ENV32 for HPGe, and NAI32 for Sodium Iodide and other lower resolution detector types. These engines optionally perform a preliminary Mariscotti peak search of the spectrum and remove library nuclides for which sufficient energy peaks were not found. A library-based peak search is then performed using the reduced library. Gain shift corrections can be applied for an accurate determination of peak energy and associated nuclide activity. **Directed Fit** can also be used to generate negative peak areas to meet environmental reporting requirements for singlet

and multiplet peaks. Standard reports have a “Summary of Peaks in Range” section that displays potential library matches and associated activity concentration for each peak found during analysis.

See Section 6.2.3 for more information on the library reduction process.

6.2.1.5. ROI32

The ROI32 analysis engine operates on the entire spectrum, performing an ROI analysis on user-marked ROIs and a modified WAN32 analysis (no peak stripping or directed fit) on unmarked regions. You can either mark ROIs on a live or retrieved spectrum, then use the **Analyze/Entire Spectrum in Memory**(ã) command; or use the **Analyze/Spectrum on Disk**(γ) command on a spectrum file in which ROIs have already been marked and saved.

ROI Analysis

1) The ROI center is used to calculate the ROI peak energy using the existing energy calibration. If the ROI peak energy is within the match width of a library peak, then the ROI will be used. *Otherwise, the ROI will be ignored*. In other words, ***do not mark an ROI around unknown peaks***.

2) To calculate the ROI peak background, you can set the number of background points to be used at 1, 3 or 5 on the Sample tab under **Analyze/Settings/Sample Type....** *If **Auto** background is selected, **then 5 points will be used always**.* The background points to be used for the background calculation are within the selected ROI region, not adjacent and outside the ROI region.

3) The background of the ROI peak is calculated as:

$$B = \left(\frac{B_1 + B_2}{2 * N} \right) * (H - L + 1) \qquad \textbf{(22)}$$

where:

L = the lowest-energy channel of the ROI
H = the highest-energy channel of the ROI
N = 1, 3, or 5, depending on the background method chosen, as discussed above.

and the sum of background counts on the low and high end of the ROI, B_1 and B_2, respectively, are given by:

$$B_1 = \sum_{1}^{N} C_{LB}$$
$$B_2 = \sum_{1}^{N} C_{HB} \quad \textbf{(23)}$$

where

C_{LB} = counts per background channel at the low end of the ROI
C_{HB} = counts per background channel at the high end of the ROI

4) The gross counts within the ROI are calculated as:

$$G = \sum_{L}^{H} Counts\ in\ ROI \quad \textbf{(24)}$$

5) The net peak area is the adjusted gross counts minus the adjusted calculated background, as follows:

$$A_{ag} = G - (B_1 + B_2) \quad \textbf{(25)}$$

thus:

$$A = A_{ag} - B\left(\frac{H - L + 1 - 2N}{H - L + 1}\right) \quad \textbf{(26)}$$

where all parameters have been defined above. If the 3-point background method is chosen on the Sample tab (page 150), all three parameters calculated above — *B*, *G*, and *A* — should be the same as calculated with the **Peak Info** method (Section 5.4.3).

6) This simplifies to:

$$A = B - G \quad \textbf{(27)}$$

Additional Considerations

- If there are multiple ROIs defined for a nuclide, then only the first ROI peak is used to calculate the nuclide activity.

- In ROI32 engine, if a nuclide has multiple peaks and only one peak is marked with a ROI, then the nuclide activity displayed is the activity of only the marked ROI peak.

- In the WAN32 analysis results section of the report, the nuclide activity is the same as the activity reported in the ROI Peak Summary section of the report.

6.2.2. Selecting an Analysis Engine — Decision Matrix

A library-based peak search looks for potential peaks for all gamma rays listed in the library.

Sensitivity is set by the **Peak-Cutoff** settings. A Mariscotti peak search uses a second differential method to identify peaks. Sensitivity is set by the **Peak-Search Sensitivity** setting. Mariscotti peak searches do a better job of identifying peaks within multiplets; library-based peak searches will do a better job of finding a weak or misshapen peak listed in the library.

Feature	ENV32	WAN32	NPP32	GAM32	ROI32	NAI32
Uses an optional initial Mariscotti peak search	√			√		√
Uses an initial library-based peak search		√	√		√	
ROI peak search on user-marked peaks					√	
Library based peak stripping	√	√	√			√
Manual based peak stripping		√				
Removes nuclides from library not found in a preliminary peak search	√		√	√		√
Reports MDA for removed nuclides	√		√			√
Utilizes gain shift corrections	√	√	√	√		√
Directed fit (negative or misshapen peak areas) option available	√[a]	√[b]	√[b]			√[a]
More sensitive in finding misshapen peaks		√	√		√	
Displays all possible library nuclide matches and calculates activity for all peaks found.	√		√		√	√
Peak Search designed for High Resolution (**H**) (i.e., HPGe) or Low Resolution (**L**) (i.e., Sodium Iodide) spectra	H	H	H	H	H	L

[a] Singlets and multiplets.
[b] Singlets only.

6.2.2.1. Guidelines for Selecting an Analysis Engine

1) Decide which peak search method is best for your application.

2) Establish the sensitivity for the peak search (**Peak Cutoff** for library directed; **Sensitivity** for Mariscotti).

3) Decide if an accurate analysis of the multiplets is important. If so, select NPP32 or the ENV32 analysis engine.

4) Notice if there are false negatives in your answers. That is nuclides have been initially detected and later dropped. If so, revert to the WAN32 analysis engine.

6.2.3. Library Reduction Based on Nuclide Rejection (ENV32, GAM32 and NAI32 Analysis Engines Only)

The Library Reduction step is optionally enabled or disabled with the "Library Reduction Flag" in the b30winds.ini (or n30winds.ini for NAI32) file (Section A.2.2.1). By default, this setting is enabled for HPGe analysis (b30winds.ini) and disabled for Sodium Iodide analysis (n30winds.ini). If enabled, a raw peak search is performed on the spectrum. The list of peaks found is compared to the peaks in the library, and the nuclides not likely to be present are removed from the library. After the library is reduced, a search is performed for the remaining library peaks, and the raw data (Mariscotti) peak search is run again to pick up any peaks not accounted for in the library-directed search. If **Directed Fit** is turned on, then peaks from nuclides that were previously rejected are fit using the **Directed Fit** method (Section 6.3.2.2) and the activity is calculated.

6.2.3.1. Library Reduction based on Peak Order

The following process is used for the library reduction when the "ENV factor" in the b30winds.ini (n30winds.ini for NAI32) (Section A.2.2.1) is not set to zero:

1) If the first peak for a nuclide in the library is not found meeting the peak cutoff, then that nuclide is removed from the analysis.

2) If the first peak for a nuclide in the library is found meeting the peak cutoff limit then each subsequent peak for that nuclide (to a maximum of three peaks per nuclide) is evaluated to determine if the nuclide should be removed from the analysis as follows:

3) For each subsequent peak *i* (to the maximum of three per nuclide), evaluate as follows:

If $(E_i * Br_i) \leq ENV * (E_1 * Br_1)$, then

Go to the next peak,

Else,

a) Calculate the expected peak area for the i^{th} peak as:

$$A_i = A_1 \left(\frac{E_i * Br_i}{E_1 * Br_1} \right)$$

b) Calculate the critical level L_c for the i^{th} peak as:

$$L_c = 2.33 * \sqrt{(B_i * W/M)}$$

If $A_i > L_c$ and the i^{th} peak is not a valid peak (that is, the peak is not found or the peak uncertainty is greater than the peak cutoff), then the nuclide is removed from the library.

Next peak *i*.

where:

E_1 = efficiency for the first valid peak
Br_1 = branching ratio for the first valid peak
E_i = efficiency for subsequent library peaks
Br_i = branching ratio for subsequent library peaks
A_1 = activity calculated for the first nuclide peak
A_i = activity calculated for subsequent library peaks
B_i = peak background for subsequent library peaks
W = peak width for subsequent library peaks
M = number of total points outside the peak used to calculate background
ENV = user-adjustable **ENV factor** from the b30winds.ini (n30winds.ini for NAI32) file located in C:\Program Files\GammaVision (Section A.2.2.1). A setting of zero disables this reduction process, but the reduction based on the Key Line and Fraction Limit test in the next step still occurs.

6.2.3.2. Library Reduction Based on Key Line and Fraction Limit Tests

In this library reduction algorithm, the key line and fraction limit tests are carried out to determine if nuclides will be removed.

For the key line test, the first in-range peak for a nuclide is always considered as a key line, even if it is not marked as a key line. All key lines for a nuclide must be found in the spectrum, even if the key line has overlap with another library peak. If any of the qualifying key lines are not

found, the key line test fails and the nuclide is rejected.

If the fraction limit is not zero then the fraction of the branching ratios is calculated by summing the branching ratios of all identified peaks and dividing by the sum of all peak branching ratios whether identified or not. If the calculated fraction is less than the Fraction Limit set on the Analysis tab, the nuclide is rejected.

If the "Fraction Limit Test flag" in b30winds.ini (n30winds.ini for NAI32) is False and **Directed Fit** is enabled on the System tab, the library peak flags are checked to determine if a peak is "qualified" for its branching ratio to be summed (in the total sum and the identified peak sum). Peaks with the "Not In Average" flag set in the library are excluded along with peaks outside the analysis range.

6.3. Calculation Details for Peaks

For all library peaks in the analysis energy range, the program attempts to calculate the net peak area and centroid of a peak at that channel. At this step in the analysis, each peak is considered to be a singlet. A singlet is a single, isolated peak; that is, it is far enough away from other peaks in the spectrum so that the spectrum is background on both sides of the peak (does not overlap another peak).

6.3.1. Background Calculation Methods

You can select the method from among these types: automatic, X-point average, and X * FWHM (see Section 5.5.1.1).

6.3.1.1. Automatic

For the first pass, the peak centroid is the library energy (Fig. 233).

To calculate the first pass background on the low-energy side of the peak, the 5-point average of the channel contents is calculated for the region from the peak-centroid channel to the channel which is 6 times the library match width (normally 0.5) times the calculated FWHM (from the calibration) below the centroid. The 5-point average data at a given point is the sum of the data from two channels below the point to two channels above the point divided by 5. This is the same as smoothing the data with a smoothing width of 5 and coefficients of 0.2 for all points. The background value is the minimum value of the moving 5-point average and the background channel number is the center channel of the 5. If the minimum average value is within one sigma (counting statistics) of the actual channel value at the assigned channel point, this 5-point average is the low energy background value for this peak. If the average value is not within one sigma of the actual data, a 3-point average is used instead of the 5-point average to calculate a new minimum value. This 3-point average minimum value is compared with the actual data at

the assigned channel and is accepted if it is within 1 sigma of the actual data. If the 3-point average also fails this test, the data value at the assigned channel is used for the background.

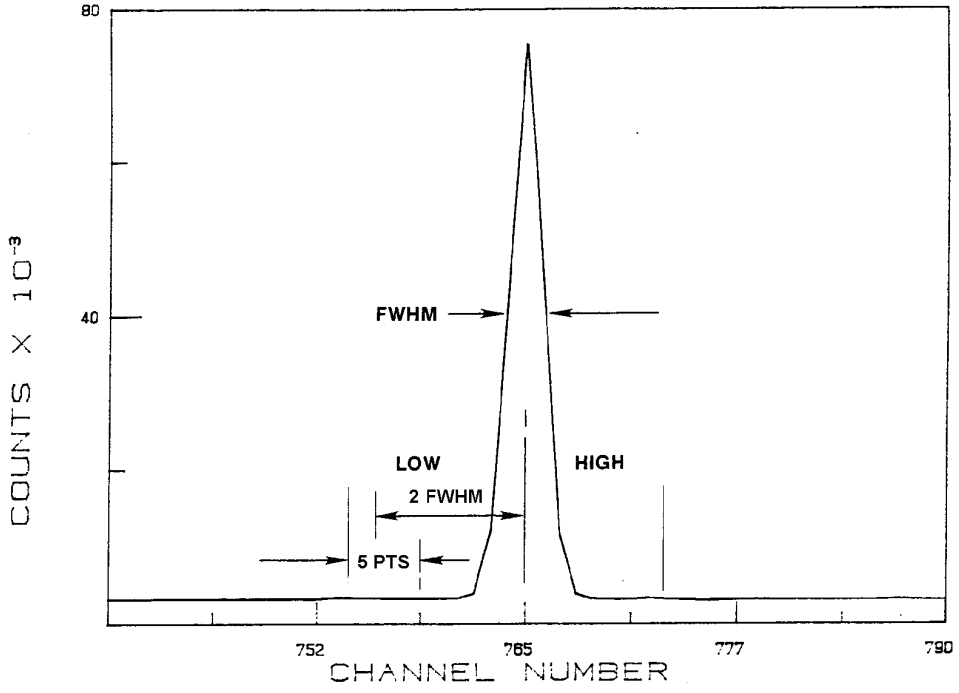


Figure 233. Background Calculation.

The same process is repeated for the high-energy side of the peak to calculate the background value above the peak. The background under the peak is the straight line between these two values.

The net peak area and background are calculated from this first pass. Next, the width is reduced or increased depending on the peak-area-to-background ratio and the library match width. This adjustment makes two improvements: (1) it reduces the number of channels in the peak for small peaks (decreasing the uncertainty), and (2) it improves the area calculation for peaks moved from the library energy.

This background calculation method (that is, automatically selecting 5-, 3-, or 1-point averaging, depending on which method best approximates the spectrum data) has advantages, when there are closely spaced peaks, over other methods. For example, because the 1-point method will be used when a small peak is very near a large peak, a more accurate measure of the background may be obtained as compared to using more points in the average (Fig. 234).

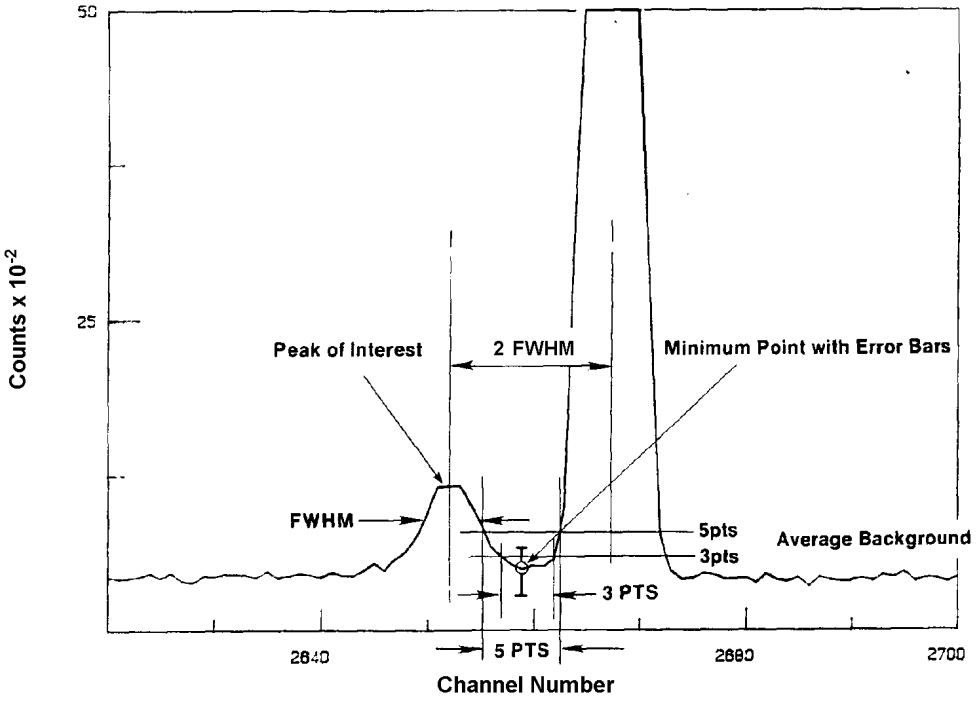


Figure 234. Background of a Small Peak Near Large Peak.

The background of the small peak is less affected by the other peak because the automatic method will tend toward the smaller values.

Even in the case of peaks that are further apart than those shown in Fig. 234, the background is less dependent on the scatter in the data when the X-point method is used.

6.3.1.2. X-Point Average

If the X-point method is chosen, then the number of points specified by "X" will be used in average background determination on each side of the peak centroid. The minimum value of X is 1 point. In general, more points provide a better approximation of peak background when there high scatter in the channel-by-channel data. However, a very large number of background points could result in the deconvolution of nearby peaks that may be fit more accurately as singlets.

6.3.1.3. X.X * FWHM

This option calculates the number of background points by multiplying the calibration FWHM (in channels) at the specified energy by the X.X factor and rounding up to the next highest integer value. This methodology can provide a more robust peak background determination than the static X-Point averaging by scaling the number of background points to the expected peak width at low or high energies and across varying ADC Conversion gains.

6.3.1.4. Example Background

An example is shown in Fig. 235, with the spectrum printout in Table 5. The report section for this peak is shown in Fig. 236.

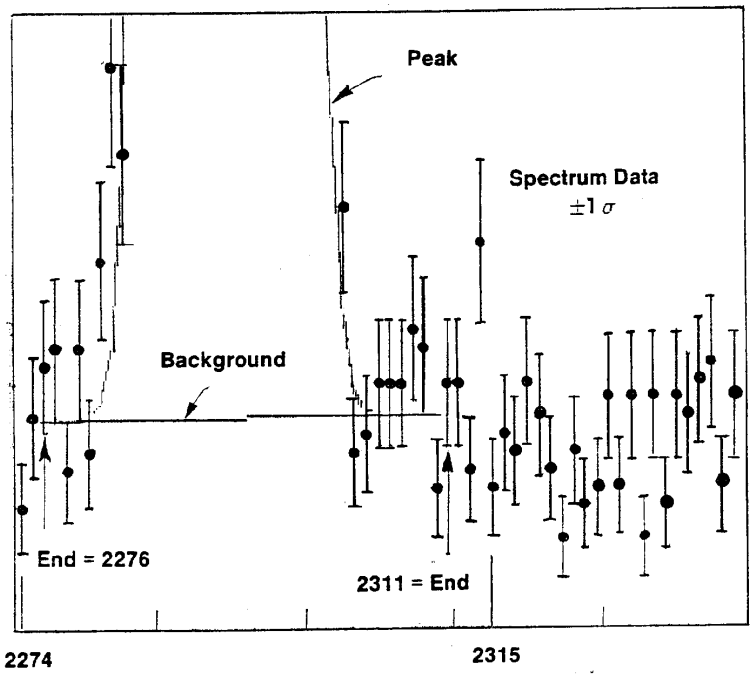


Figure 235. Example Peak Background Calculation.

The FWHM for this peak is 6.85 channels. The centroid is at channel 2292.16. The background search width is from channel 2271 to 2313. The 5-point averages are shown in Table 5, and the minima are 11.8 at channel 2276 and 12.2 at channel 2311. The background slope is +0.0114 and the offset is −14.4.

UNIDENTIFIED PEAK SUMMARY

PEAK CHANNEL	CENTROID ENERGY	BACKGROUND COUNTS	NET AREA COUNTS	INTENSITY CTS/SEC	UNCERT 1 SIGMA %	FWHM keV	SUSPECTED NUCLIDE
2292.16	569.78	432.	17711.	59.04	.81	1.734	Bi-207

s Peak fails shape tests.

Figure 236. Peak Results for Previous Peak.

Table 5. Spectrum and Five-Point Smooth.

Channel	Spectrum	5-pt smooth
2270	17	13.8
2271	14	14.6
2272	14	13.2
2273	14	12.2
2274	7	12.4
2275	12	12.8
2276	15	11.8
2277	16	13.6
2278	9	13.2
2279	16	14.4
2280	10	17.6
2281	21	21.2
2282	32	29.8
2283	27	54.2
2284	59	97.4
2285	132	185.6
2286	237	349.6
2287	473	614.0
2288	847	967.4
2289	1381	1386.6
2290	1899	1772.6
2291	2333	2084.2
2292	2403	2204.8
2293	2405	2128.0
2294	1984	1850.6
2295	1515	1497.0
2296	946	1077.6
2297	635	718.4
2298	308	429.2
2299	188	248.2
2300	69	126.0
2301	41	66.4
2302	24	31.0
2303	10	20.0
2304	11	14.6
2305	14	12.6
2306	14	14.0
2307	14	15.0
2308	17	13.8
2309	16	13.8
2310	8	13.8
2311	14	12.2
2312	14	13.4
2313	9	13.4
2314	22	12.8
2315	8	12.0
2316	11	13.0
2317	10	11.0
2318	14	11.2
2319	12	10.0

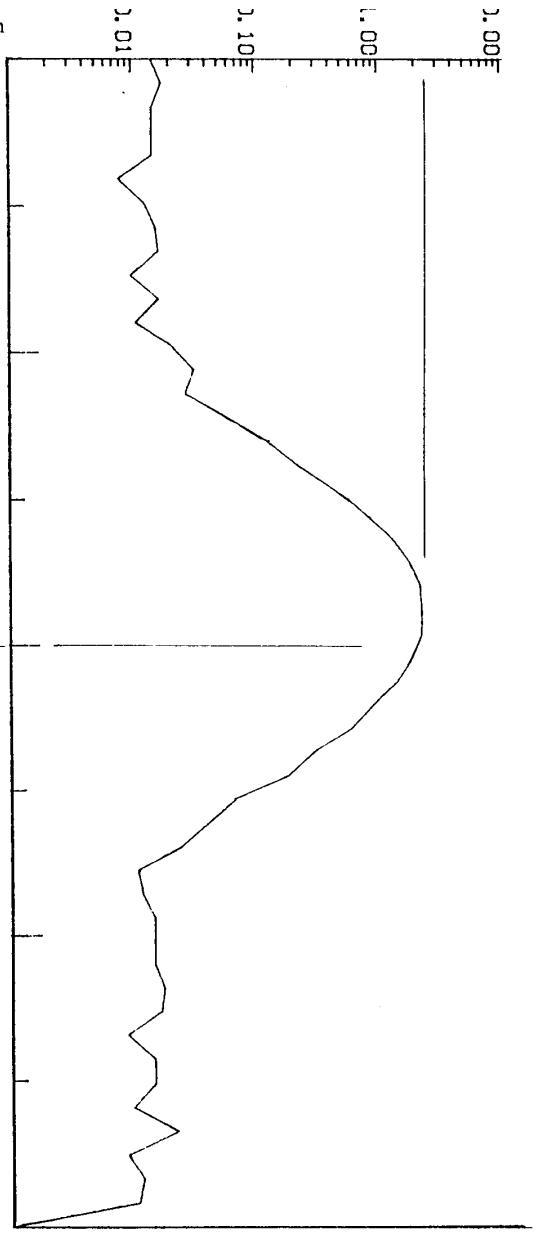


Fig. 237 shows an example of the differences among the four methods for determining the background.

```
 PEAK      CENTROID     BACKGROUND  NET AREA    INTENSITY   UNCERT      FWHM
 CHANNEL   ENERGY       COUNTS      COUNTS      CTS/SEC     1 SIGMA %   keV
+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+-+
     Background width: best method (based on spectrum).
 2939.64   718.00       1514.       79.         .009        70.82       1.517

     Background width: average of five points.
 2939.64   718.00       1372.       12.         .001        422.37      1.517

     Background width: average of three points.
 2939.64   718.00       1299.       43.         .005        119.77      1.517

     Background width: minimum data point.
 2939.64   718.00       1214.       72.         .008        69.70       1.517
```

Figure 237. Example of Different Background Method Results.

6.3.2. Peak Area — Singlets

6.3.2.1. Total Summation Method

The gross area of the peak is the sum of the contents of each channel between the background channels (including the two background channels) as follows:

$$A_g = \sum_{i=l}^{h} C_i \qquad \textbf{(30)}$$

where:

A_g = the gross area
C_i = the data value of channel i
l = the center channel of the background calculation width at the low energy side of the spectrum
h = the center channel of the background calculation width at the high energy side of the spectrum

This peak area calculation method (referred to as total summation) maintains precision as the peak gets smaller, is less sensitive to random fluctuations in the data, and is less sensitive to the differences between the spectrum peak shape and the calibrated peak shape.

Refer to Fig. 235, Fig. 236, and Table 5 to calculate the gross area for the example peak. The integral from channel 2276 to 2311 is 18143 counts.

The net area is the gross area minus the background in those channels (Fig. 238).

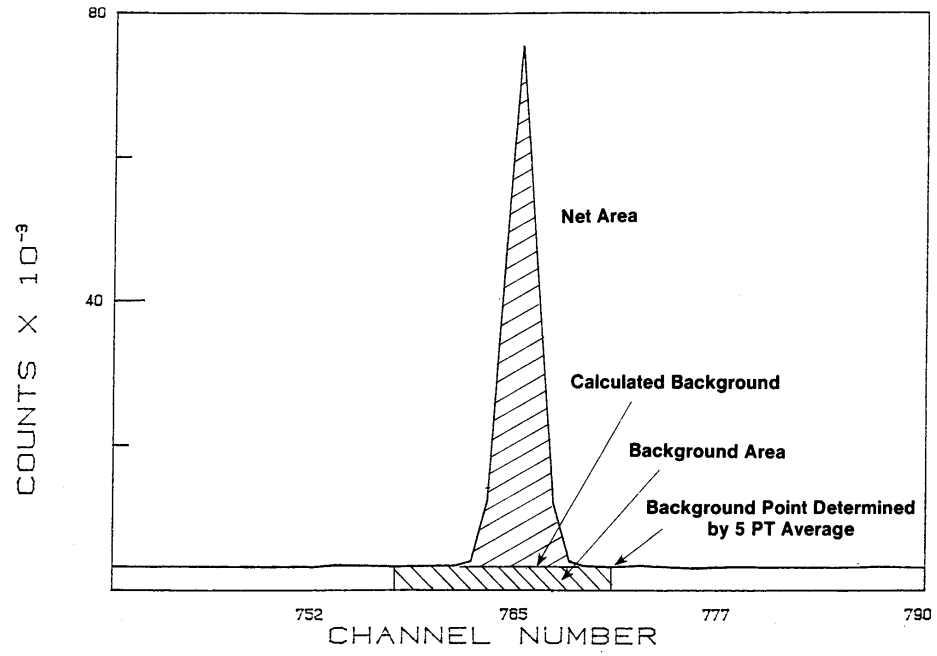


Figure 238. Gross and Net Peak Area.

$$A_b = \frac{B_l + B_h}{2} \times W \qquad (31)$$

where:

A_b = the background area
B_l = the background on low side of peak
B_h = the background on high side of peak
W = the peak width

If the PBC correction is enabled, the calculation is performed as discussed in Section 6.10.4.

6.3.2.2. Directed Fit Method

In some cases the total summation method does not produce the desired answer for the peak area and does not produce negative peak areas. Another method of obtaining the peak area for a particular energy is to fit the spectrum region with a background plus peak shape function. This so-called “directed fit” — enabled on the Analysis tab — can be applied to peaks and has the ability to produce negative peak areas, and therefore, activity results less than zero.

The directed fit to the library peak area is performed if the following are true:

1) The option is enabled.

2) The spectrum is energy calibrated.
3) The peak was rejected for any test by the total summation method.

Directed Peak Fit for singlet peaks is determined using a range of 4.84 times the calibration FWHM times the Analysis Settings Match Width times the **Directed Fit Peak Region Width Factor** (Section A.2.2.1) centered on the library peak energy. For multiplets, the range is based on the start channel of the first peak minus the background width and the stop channel of the last peak plus the background width.

Background, Gross Area, and Net Area are then calculated as described in Section 5.4.3. The net area is then corrected for contributions from identified nuclide peaks and peak background by adding these areas to the background. Any remaining area is assigned to the Directed Fit nuclide peak. When multiple nuclides have interferences at approximately the same energy the first nuclide that is dependent on that peak energy for the activity calculation is evaluated first, and nuclides that have peaks that are not interfered are evaluated afterwards.

6.3.2.3. ISO NORM Singlet Peak Method

The guidelines for singlet peak calculations are in Annex C of the ISO 11929:2010 standard, and are similar to the standard GammaVision total summation method discussed in Section 6.3.2.1.

When the peak background does not dominate, the peak width should be ~2.5 FWHM, per ISO 11929 Eq. C.9:

$$t_g \approx 2.5\,h \quad \textbf{(32)}$$

where h is the FWHM of the peak.

In case of a dominant background, the peak region width should be 1.2 FWHM, per Eq. C.10:

$$t_g \approx 1.2\,h \quad \textbf{(33)}$$

When t_g is 2.5, almost the entire peak area is included in the region. However, when t_g is 1.2, the peak region only covers about 84% of the whole peak area. Therefore, a correction factor for the peak area is needed, as discussed in the remainder of this section.

In GammaVision, the percent **Peak Cutoff**, entered on the Analysis tab, is used by default as the criterion for dominant background. Background is considered dominant except when the peak uncertainty is less than the Peak Cutoff, in which case the peak is flagged as “identified.”

Therefore, for all identified singlet peaks, the default region width should be about t_g × FWHM for this method.

If the library peaks are not found, the MDA values are calculated with a width of ~1.2 FWHM. Since the exact criteria for dominant background are not specified in ISO 11929, GammaVision includes a "Dominant Background Peak Cutoff and Override Flag" in the b30winds.ini (n30winds.ini for NAI32) file (Section A.2.2.1) to enable you to define a dominant background cutoff. This entry is formatted as:

```
25.0     T
```

The first parameter is the user-defined dominant background peak uncertainty cutoff. The default value is 25%, and ranges from >0% to <1000%. The second parameter is a Boolean flag. If the flag is set to false (F), the user-defined peak cutoff for dominant background is used. If the flag is true (T), the **Peak Cutoff** value on the Analysis tab is used.

To calculate a correction factor when the peak region does not cover all the peak area, let the peak region width be v (in units of the peak FWHM):

$$t_v = v * h \tag{34}$$

Assume the peak shape is a perfect Gaussian. Let f be the ratio between the net counts in the region and the true total peak area, then f can be calculated as:

$$f = 2\Phi cv - 1.0 \tag{35}$$

where Φ is a Gaussian integral function defined as:

$$\Phi(x) = \frac{1}{\sqrt{2\pi}} \sum_{-\infty}^{x} e^{\left(\frac{x^2}{2}\right)} dx \tag{36}$$

and c is a constant equal to:

$$\sqrt{2\ln(2)} = 1.177410 \tag{37}$$

The correction factor f is used as a divisor in the calculations of the peak area:

$$\begin{aligned} N &= N_0/f \qquad N_0 > 0 \\ N &= N_0 \qquad N_0 \le 0 \end{aligned} \tag{38}$$

where N_0 is calculated with the region width chosen per ISO 11929. The *f* factor is not used when N_0 is zero or negative since no peak is present and a negative peak area is non-physical.

The use of *f* is consistent with Eq. D.5 in ISO 11929:

$$Y = \frac{X_g - Z_0}{T i f M \varepsilon} \quad \textbf{(39)}$$

The definition of the quantities involved in above equation can be found in section D.5.1 of ISO 11929. The factor *f* in the denominator is defined in Eq. 35 above, and *i* is the branching ratio. The *f* factor is not used to scale the peak background. The background does not scale as the peak area (that is, even though 84% of the peak area is covered, it is incorrect to state that only 84% of the background is included).

When *x* is positive, the Gaussian integral $\Phi(x)$ can be calculated as:

$$\Phi(x) = 1 - Erfc\left(\frac{x}{\sqrt{2}}\right) \quad \textbf{(40)}$$

where *Erfc(x)* is the Complimentary Error Function:

$$Erfc(u) = \frac{2}{\sqrt{\pi}} \sum_{u}^{\infty} e^{(-u^2)}\, du \quad \textbf{(41)}$$

The Complimentary Error Function is calculated using the following analytic approximation:[30]

$$Erfc(x) = t\, e^{(\varphi)} \quad \textbf{(42)}$$

where *t* and φ are defined in the following equations:

$$\varphi = \left(-z^2 - a_0 + t(a_1 + t(a_2 + t(a_3 + t(a_4 + t(a_5 + t(a_6 + t(a_7 + t(a_8 + t a_9)))))))\right) \quad \textbf{(43)}$$

[30]Press, W. H., et al., *Numerical Recipes in C: The Art of Scientific Computing*, Cambridge University Press; 2nd ed. (October 30, 1992).

where:

a_0 = 1.26551223

$$z = abs(x) \tag{44}$$

$$t = \frac{1}{1 + 0.5x} \tag{45}$$

a_1 = 1.00002368
a_2 = 0.37409196
a_3 = 0.09678418
a_4 = −0.18628806
a_5 = 0.27886807
a_6 = −1.13520398
a_7 = 1.48851587
a_8 = −0.82215223
a_9 = 0.17087277

The approximation work wells for the range of x values we are concerned with.

To calculate the actual peak region start and stop channels, the half width of the region is calculated first, e.g., 0.5 t_g. This half width is converted by rounding to an integer, in channels, with a lower limit of 1 channel. For best precision, the analysis engine compares the rounded-down and rounded-up values and selects the best match to the desired overall regional width. For high-energy peaks, it may not matter whether the integral width is rounded down or up, however, there may be a big difference for some low-energy peaks. For example, if the energy calibration at low energies is ~0.5 keV per channel and the calibrated peak FWHM is ~1.0 keV, the difference between the two rounding methods could be as great as one FWHM. For a desired peak region width of 1.2 FWHM, the width obtained by rounding up could be about 2.2 FWHM, defeating the intent to use a narrow peak width when the background is dominant.

The ISO peak evaluation method is applied only for peaks that meet the following requirements:

1) The peak is in the library.
2) The peak range, including the designated number of background points, has no overlap with both lower or higher energy peaks.
3) The energy separation between the current peak and the nearest low- and high-energy peaks should be greater than the separation for deconvolution (the latter determined by the “Peak overlap range in units of peak FWHM” parameter in b30winds.ini (n30winds.ini for NAI32).
4) The peak shape is close to Gaussian. Peaks marked with ***** or **@** on the report do not qualify.

5) The peak centroid cannot be too far from the library energy. Peaks marked with } on the report do not qualify.

6.3.3. Example Peak Area

6.3.3.1. Total Summation Method

Again, refer to Fig. 235, Fig. 236, and Table 5 to calculate the background for this peak (PBC correction disabled). Substituting in the above formulas yields:

$$\begin{aligned} Background\ area &= \frac{11.8+12.2}{2} \times (2311-2276+1) \\ &= 432 \end{aligned} \quad \textbf{(46)}$$

and

$$Net\ area = 18143-432 = 17711 \quad \textbf{(47)}$$

6.3.3.2. Directed Fit Method

A section of a spectrum with a negative peak is shown in Fig. 239. The raw data values and the generated fit are shown. In this case the, background at the low energy end of the peak is 1170 counts per channel and on the high end is 1173 counts per channel. This gives a total background of 35145 counts and the net peak of −133 counts.

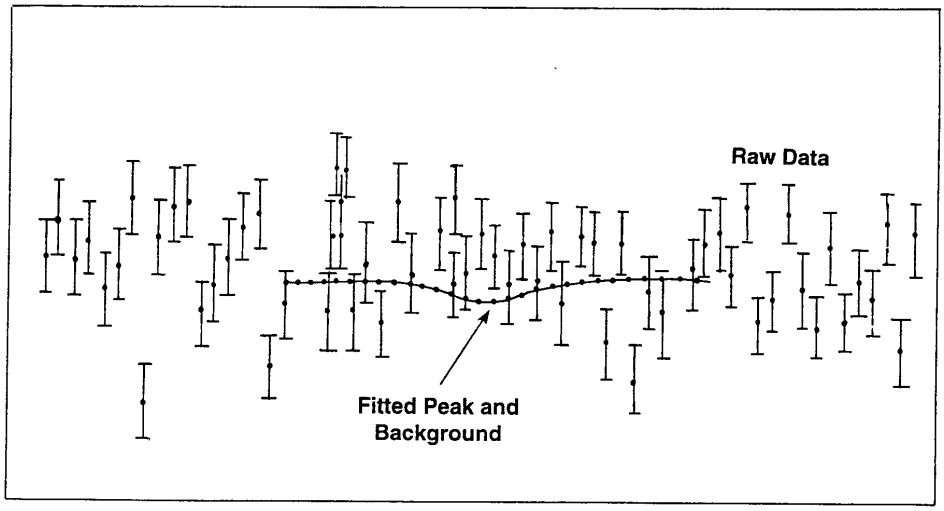


Figure 239. Example of Directed Fit.

Since these values are derived from a fitting process, it is difficult to duplicate the calculations manually.

6.3.4. Peak Uncertainty

The counting statistical uncertainty is the uncertainty in the gross area and the uncertainty in the background added in quadrature. The uncertainty in the gross area is the square root of the area. The uncertainty in the background is not as simple because the background is a calculated number. The background area uncertainty is the uncertainty in the channels used to calculate the end points of the background multiplied by the ratio of the number of channels in the peak to the number of channels used to calculate the background. For wide peaks and low counts per channel, there is high uncertainty in the calculated background.

$$bkg\ error = \left(\frac{(background\ area)\ (peakwidth)}{(width\ of\ low\ average\ +\ width\ of\ high\ average)} \right)^{1/2}$$

$$gross\ area\ error = \sqrt{gross\ area} \qquad (48)$$

$$net\ area\ error = \sqrt{(gross\ area\ error)^2\ +\ (background\ error)^2}$$

If the PBC correction is enabled, the uncertainty calculation is performed as discussed in Section 6.12.12.

PBC correction is disabled for the following example. Referring back to Fig. 235, Fig. 236, and Table 5, the background uncertainty is:

$$Background\ error = \sqrt{\frac{(432)(2311 - 2276 + 1)}{5 + 5}}$$

$$= 39.4 \qquad (49)$$

$$Net\ area\ error = \sqrt{(18143 + 1552.4)}$$

$$= 140.4\ or\ 0.8\%\ of\ net\ peak\ area$$

The peak width is calculated at the half maximum, tenth maximum, and twenty-fifth maximum for the net peak shape. The peak width points are linearly interpolated between the two channels that bracket the respective height value.

6.3.4.1. Peak Uncertainty in ZDT Spectra

This is discussed in Section 5.2.11.4.

6.3.5. Peak Centroid

The peak centroid channel in total summation is the center-of-moment of the peak and is calculated as the weighted channel number of the peak. That is, the peak centroid is the sum of the net channel contents times the channel number divided by the sum of the channel contents. The centroid is calculated as:

$$Peak\ centroid = \frac{\sum_{i=l}^{h} i \cdot C_i}{\sum_{i=l}^{h} C_i} \quad \textbf{(50)}$$

where:

l, h = the peak low and high channels
i = the channel number
C_i = net contents of channel i

For the directed fit method, the centroid can be refined from the fitting process.

From the Table 5 values and the calculated background, the net spectrum is shown in Table 6, continuing the example calculation on this peak.

The FW.04M is 2.2 times the FWHM for a Gaussian peak. The peak integration channels are then 2284 to 2300. The channel numbers are rounded to the nearest integers. The centroid for this example is $4.0366\times10^7 / 1.761\times10^4 = 2292.16$.

6.3.6. Energy Recalibration

The spectrum energy calibration can be redone “on the fly” for the spectrum being analyzed. This improves the analysis results and adjusts for small changes in the hardware gain. Energy recalibration is first performed using singlet peaks only. Then, after deconvolution, the spectrum is recalibrated using all the peaks. If the energy calibration changes, the spectrum is reanalyzed.

For all peaks in the library, the peak centroid energy in the spectrum is compared with the library energy. If the difference between the library energy and the centroid energy is less than 0.5 keV, or the current **Match Width** (the FWHM multiplier entered on the System tab

under **Analyze/Settings/Sample Type...**), or one channel — whichever is greater — that centroid is associated with that library energy. The FWHM multiplier can be changed. If it is within this limit and has counting error less than 10% or the input sensitivity value (whichever is less), it is a qualified recalibration peak.

The energy range is split into two parts and the number of qualified library peaks in each region is counted. It there are more than the user-set number of qualified recalibration peaks in both regions of the spectrum, these spectrum centroids and library energies are used to recalculate the energy calibration for the spectrum. The default energy is 0 keV and the number of peaks is 1000 below and 1000 above. Only this analysis is affected and the calibration in the spectrum file is not changed. If the energy recalibration is performed, a notice is written on the report, even if the recalibration had little or no effect. The new coefficients are printed on the output report.

Since this energy recalibration is dependent on the library and the spectrum, changes in the library can affect the calibration, and hence the peak energies reported. Only the energy factors are changed. The shape coefficient and efficiency coefficients are not altered. While the automatic energy recalibration will correct for small changes in the calibration, it is not intended as a substitute for accurate calibrations or as a correction for systems suffering from stability problems.

For an accurately calibrated spectrum, this recalibration will have little effect. Its effect will be most pronounced on deconvolutions of multiplets; this is discussed in Section 6.5.

Table 6. Example Net Spectrum.

Channel	Background	Net Spectrum
2270	11.7152	5.284
2271	11.7266	2.273
2272	11.7380	2.262
2273	11.7494	2.250
2274	11.7608	-4.760
2275	11.7722	0.227
2276	11.7836	3.216
2277	11.7950	4.205
2278	11.8064	-2.806
2279	11.8178	4.182
2280	11.8292	-1.829
2281	11.8406	9.159
2282	11.8520	20.148
2283	11.8634	15.136
2284	11.8748	47.125
2285	11.8862	120.113
2286	11.8976	225.102
2287	11.9090	461.091
2288	11.9204	835.079
2289	11.9318	1369.068
2290	11.9432	1887.057
2291	11.9546	2321.046
2292	11.9660	2391.034
2293	11.9774	2393.023
2294	11.9888	1972.011
2295	12.0002	1503.000
2296	12.0116	933.988
2297	12.0230	622.977
2298	12.0344	295.965
2299	12.0458	175.954
2300	12.0572	56.942
2301	12.0686	28.931
2302	12.0800	11.920
2303	12.0914	-2.091
2304	12.1028	-1.102
2305	12.1142	1.885
2306	12.1256	1.874
2307	12.1370	1.863
2308	12.1484	4.851
2309	12.1598	3.840
2310	12.1712	-4.171
2311	12.1826	1.817
2312	12.1940	1.806
2313	12.2054	-3.205
2314	12.2168	9.783
2315	12.2282	-4.228
2316	12.2396	-1.239
2317	12.2510	-2.251
2318	12.2624	1.737
2319	12.2738	-0.273

Because of this recalibration feature, the analysis results of spectra can change when a library is changed, or if the peak sensitivity is changed to a value under 10% (see fixed cutoff above). Such changes between analyses can result in the recalibration being enabled in one case and disabled in the other case. This can result in the analyses being different in several different ways. The peak areas and backgrounds can be different because the integration limits for each peak will change slightly. This change is usually very small, but in a spectrum with very few counts it can be a high percentage of the total peak. In a given spectrum, some peak areas might change and others might be constant. Some peaks might move from the identified list to the unknown list (or the reverse) because the uncorrected centroid is too far from the library energy for validation.

In addition, an energy difference for all good library peaks is calculated. This is the sum of the absolute value of the difference between the peak centroid energy (before recalibration) and the library energy, expressed as a fraction of the FWHM, divided by the number of peaks in the sum. This yields a number between 0 and 1 for good 3-point (or more) calibrations, with 0 being the best calibration. For 2-point calibrations, this number can be much larger than 1.0 because the calculated FWHM (which is a linear function) does not fit the spectrum FWHM at the ends of the spectrum. If high values are reported, and the analysis results are unacceptable, a better calibration should be made. The calibration section can be used to produce a multi-point calibration which will reduce the energy difference.

$$QUALITY\ FACTOR = \frac{\sum_{i=1}^{n} \frac{|E_{pi} - E_{Li}|}{FWHM_{Li}}}{n} \quad \textbf{(51)}$$

where:

E_{pi} = the energy of the ith peak in the spectrum
E_{Li} = the energy of the corresponding peak in the library
$FWHM_{Li}$ = the calculated FWHM of the peak at the library
n = the number of peaks in a spectrum with matching library peaks

This “energy-normalized difference” is printed on the report. For a complex spectrum this number will range from 0.1 to 0.3. A large value indicates that a new calibration should be performed or that the library does not match the spectrum well. Smaller values are usually associated with fewer peaks or a better calibration.

If an energy recalibration has occurred, the library peak list is reanalyzed with the new energy calibration. This results in more accurate peak values for centroid and area.

6.3.7. Peak Search

After the library peaks are located, the spectrum is searched for any other peaks. This is needed, even if the list of unknown peak values is not requested, for correct calculation of the peak background near peak multiplets and for determination of the peak centroids for deconvolution of multiplets not in the library. The stepped background test compares the background above the peak area to the background of the peak area (see "Background for Multiplets," Section 6.5.2).

The peak search method is based on the method proposed by Mariscotti. In this method it is assumed that the spectrum, $C(n)$, is continuous and the background is a linear function of the channel number in the vicinity of a peak. This implies that the second derivative is zero for background regions and non-zero in the peak regions. In order to reduce the effect of statistical fluctuations, the smoothed second difference is used (see Fig. 240).

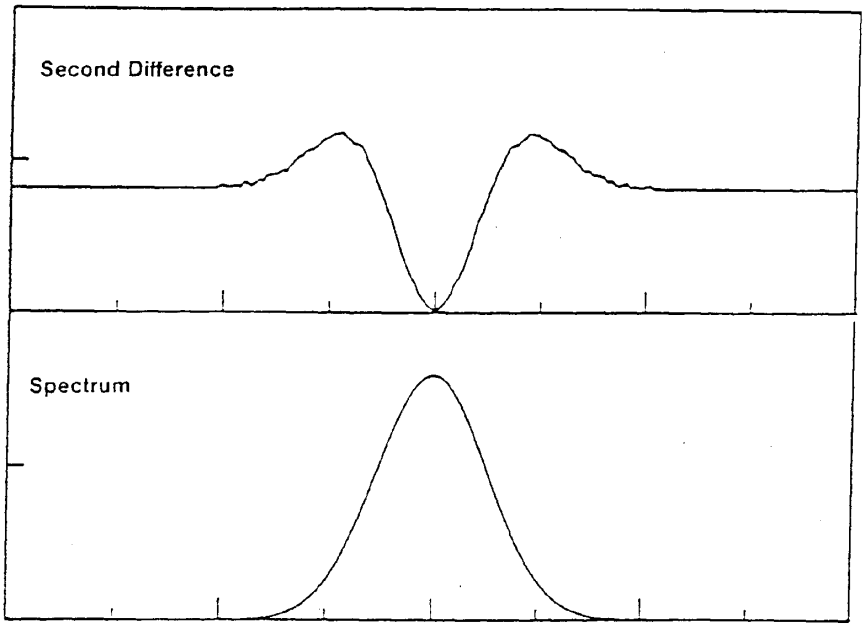


Figure 240. Second Difference.

The second difference can be represented as:

$$C''(n) = \sum_{i=0}^{2j} k_i C(n - j + i) \qquad (52)$$

where:

k_i = the smoothed second difference weighting functions
$2j + 1$ = the smoothing width

For regular peaks, $j = 4$; for wide peaks, $j = 9$. There are nine coefficients for regular peaks and 19 for wide peaks. The criterion for using the wide-peak filter is that the spectrum resolution in keV per channel at the center of the spectrum is <0.15 keV/channel.

The peaks are located where the second derivative varies significantly from zero.

A typical gamma-ray spectrum is shown in Fig. 241. This gamma-ray spectrum is far from the ideal spectrum of a well-formed peak on a smooth background. Shown are seven features that can be distinguished and accounted for in the peak-detection algorithm.

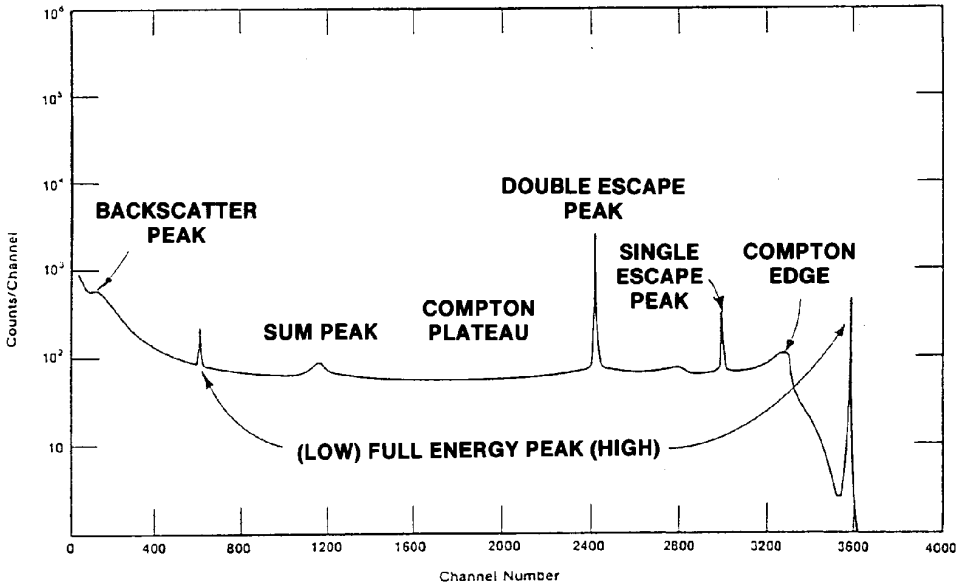


Figure 241. A Typical Gamma-Ray Spectrum.

1) The full-energy photopeak that results from the complete capture of all the photon energy in the detector and is the most well-defined feature
2) The Compton edge for the full-energy peak
3) The Compton plateau
4) The backscatter peak
5) The pulse pileup or sum peaks from the addition of the peak energies in the detector or electronic processing
6) The single-escape peak
7) The double-escape peak

Not all of these will appear in a given spectrum. For example, escape peaks cannot occur for photons less than about 1 MeV.

The shape of the second derivative can be used to reject Compton edges and other non-peak structure in the data (Fig. 242).

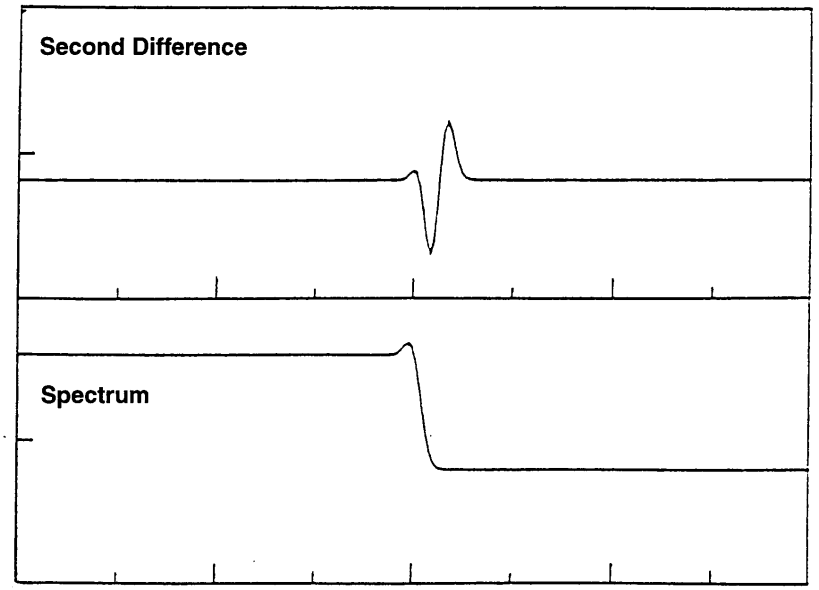


Figure 242. Second Difference for a Compton Edge.

6.3.7.1. Peak Acceptance Tests

The second difference must pass the following tests to be considered a peak.

$$C''(n) < -G\sqrt{C(n)} \quad \textbf{(53)}$$

where G is related to S, the **PEAK SEARCH SENSITIVITY** factor, set on the System tab under **Analyze/ Settings/Sample Type...**, as follows:

$$G = (0.35 * S + 1.45) * 13.03 * F \quad \textbf{(54)}$$

where:

G = a constant proportional to the resolution of the detector
F = 1.35 for the wide-peak filter and 1.0 for the regular-peak filter

In addition, the spectrum data at the channel indicated by the second derivative must pass these tests.

$$C''(n+1) > C''(n)$$
$$C''(n-2) > C''(n-1) \quad \textbf{(55)}$$

where:

$C(n)$ = the channel data of the nth channel
$C''(n)$ = the second difference at the nth channel

If the wide-peak filter is used, the second derivatives must also meet the following criterion:

$$C''(n-1) > C''(n) \quad \textbf{(56)}$$

The peak centroid is calculated using the weighted channel sum method as follows:

$$P = \frac{\sum_{i=l}^{h} i * C_i}{\sum_{i=l}^{h} i} \quad \textbf{(57)}$$

where:

P = peak centroid in channels
C_i = net contents of channel i
i = channel number
l = peak low limit
h = peak high limit

Once a peak is located, it is recorded and the peak search starts again.

After a peak has been located, if it is not in the library, the peak background, net area, and uncertainty are calculated in the same manner as library peaks. If the peak uncertainty is less than the sensitivity threshold level you entered, the peak is added to the list of unknowns. If the peak is within the deconvolution width (approximately 3.3 times the FWHM) of a library peak, then the peak is marked on the output list. The unknown peaks are included in a deconvolution when they are close enough to affect the peak area calculation.

If a peak is located in the spectrum and the library peak is a subsidiary peak, where the major peak has not been found, the peak will be maintained in the unknown list.

6.3.8. Narrow Peaks

The peak width is compared to the calibration width at the half and tenth maximum. If the peak is too wide or too narrow it is marked to show this in the output report. If the peak is too narrow, it is not used in the abundance calculation unless the “accept-low-peaks” or “accept-all-peaks” switch (*T=accept low peaks*, page 444) is turned on. If accept-all-peaks is on, all are accepted. If accept-low-peaks is on, the peak is further tested. If the peak area is less than 200 counts, it is accepted. If the peak area is between 200 and 300 counts and the background is less than half the peak area, the peak is accepted. If the peak area is over 300 it is rejected.

6.4. Suspected Nuclides

The suspected nuclides feature will identify peak energies in the unknown peak list, based on a second gamma-ray library. The unknown peak list is the list of all peaks located in the spectrum that are not in the analysis library. It is intended to help identify unexpected peaks or can be used to note peaks that are always present but for which no analysis is desired (e.g., ^{40}K or 511 keV). The name for the suspected nuclide library is specified on the System tab under **Analyze/ Settings/Sample Type...**.

For each energy listed in the unknown peak list, the nuclide with the closest energy within four times the FWHM is listed. In the event that two energies are found with the same difference, the lowest energy entry in the library is printed. If none is found, a symbol is printed. In addition, the same symbol is printed if the suspected library is not found, a read error occurs, or the spectrum is not calibrated.

The suspected nuclide feature can be used with calibrated spectrum files (and no analysis library) to obtain a quick list of nuclides in the sample and their peak count rates.

6.5. Locating Multiplets

A peak is considered to overlap if its start or end channels are within another peak region. The peak overlap range factor in b30winds.ini (n30winds.ini for NAI32) determines whether two peaks close in energy will be deconvoluted as a multiplet or stripped. The lowest setting for this parameter is 1.0.

If the library energies are less than 10 eV apart, only the lowest energy peak is included in the deconvolution. The peak areas for the other peaks (within 10 eV) are set to zero. The conflicting peaks are marked as energy-conflicting peaks. This message appears on the report and the individual peaks are labeled in the comment field of the nuclide/peak matrix. See the discussion of library-based peak stripping, Section 6.5.5.

All peaks found by the peak search routine and not in the library are included in the deconvolution regardless of the sensitivity setting, unless all the deconvolution candidates are unknown peaks with uncertainty greater than the sensitivity setting, in which case the region is ignored.

6.5.1. Defining a Multiplet Region for Deconvolution

After a list of peaks is determined from the library-directed and Mariscotti peak searches, multiplets are identified. Note that peaks which are found by the Mariscotti peak search but do not pass the sensitivity (peak cutoff) test are flagged for further multiplet consideration. For each located peak, the energy of the next peak is checked to see if it is less than or equal to 3.08 times the FWHM of the peak currently being processed. If so, the two peaks are marked as a multiplet. The energy of successive peaks is checked, using the same criteria, to determine if they belong in the multiplet. After the last peak in the multiplet is identified, the multiplet is flagged for peak deconvolution.

Because a multiplet identified in this way might contain a combination of library peaks and unidentified peaks, the analysis engine processes it as follows:

- If library energies are less than 10 eV apart, the lowest-energy peak is included in the deconvolution and the other peaks within 10 eV are set to zero.

- If all the peaks in the multiplet are unidentified (i.e., not listed in the library) and do not meet the sensitivity criterion, the entire region is ignored.

The width of the multiplet region is from 1.5 times the FWHM below the lowest peak to 1.5 times the FWHM above the highest-energy peak (Fig. 243).

6.5.2. Establishing Multiplet Background

Three background types are used for multiplets: *stepped*, *parabolic*, and *straight-line*. Selection of the background type depends on the shape of the peak background.

1) Stepped background is used if the slope of the peak background across the peak area is less than the slope of the background adjacent to the high-energy side of the peak. That is, if the background under the peak is declining faster than the background above the highest-energy peak in the background, the stepped background is selected; see Fig. 244.

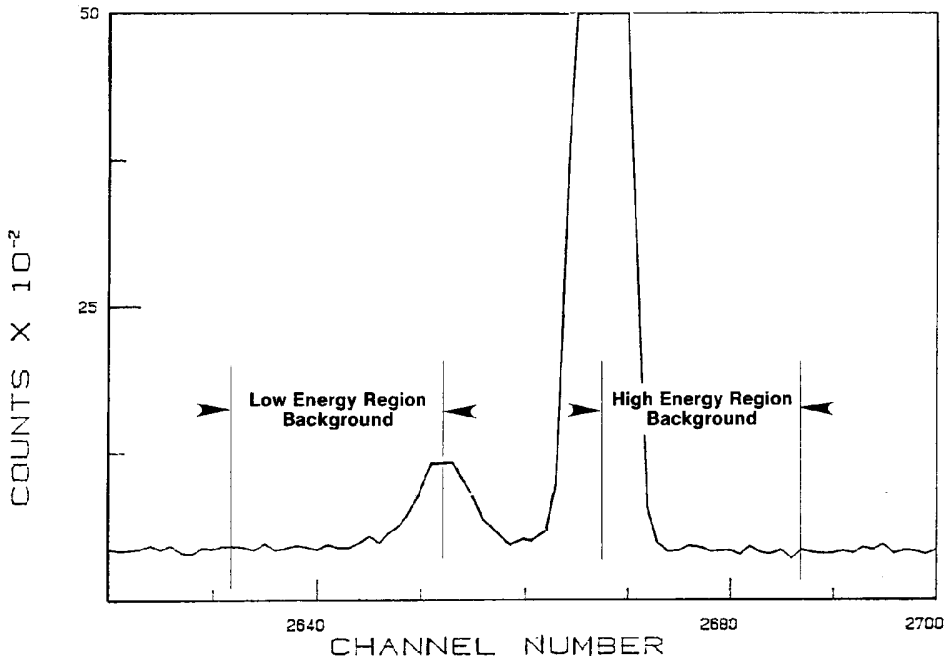


Figure 243. Background for Multiplets.

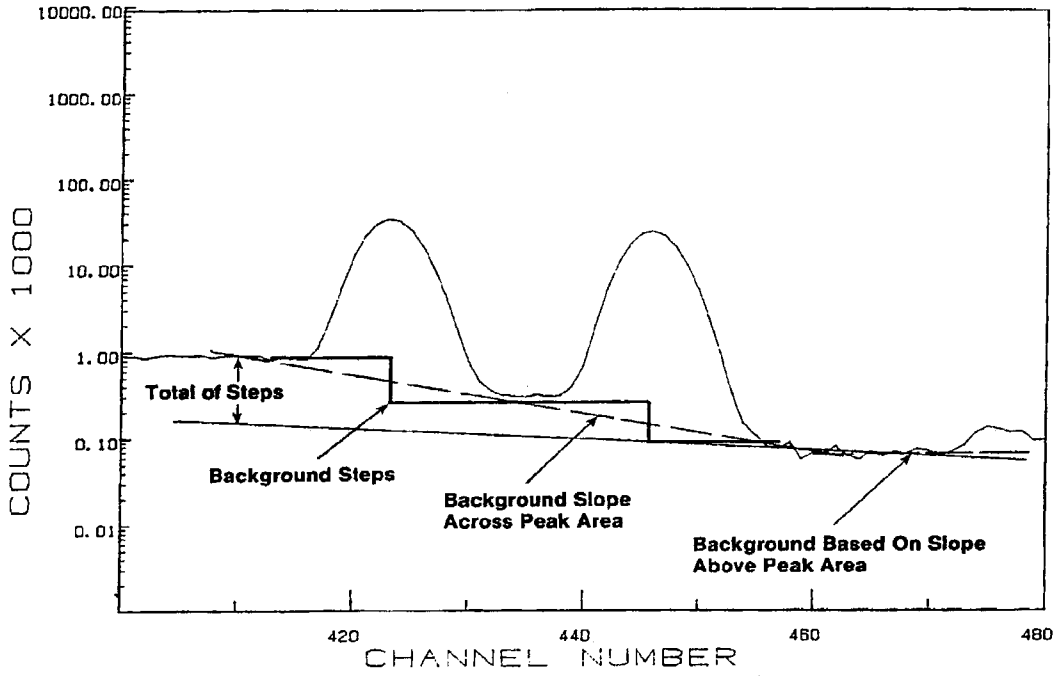


Figure 244. Stepped Background.

2) Parabolic background is selected if:

- The background on the low-energy side of the multiplet is less than the background on the high-energy side.

- At least three contiguous points in the lower 75% of the multiplet region are less than the straight-line background.
- The energies of the peaks are less than 200 keV.
- The peak sensitivity is 2 or higher; see Fig. 246.

3) Straight-line background is selected if the other two background methods do not apply.

6.5.2.1. Stepped Background

The total height of the background steps is the difference between the background below the peak region and the value of the peak background above the peak region projected back to the background point at the low-energy end of the multiplet; see Fig. 244. The size of the step inserted at each peak centroid is proportional to the height of the peak. The result is then smoothed. This background is calculated after the deconvolution, the net spectrum is recalculated, and the deconvolution is repeated.

A real spectrum with stepped background is shown in Fig. 245. The two components of the doublet are of equal size.

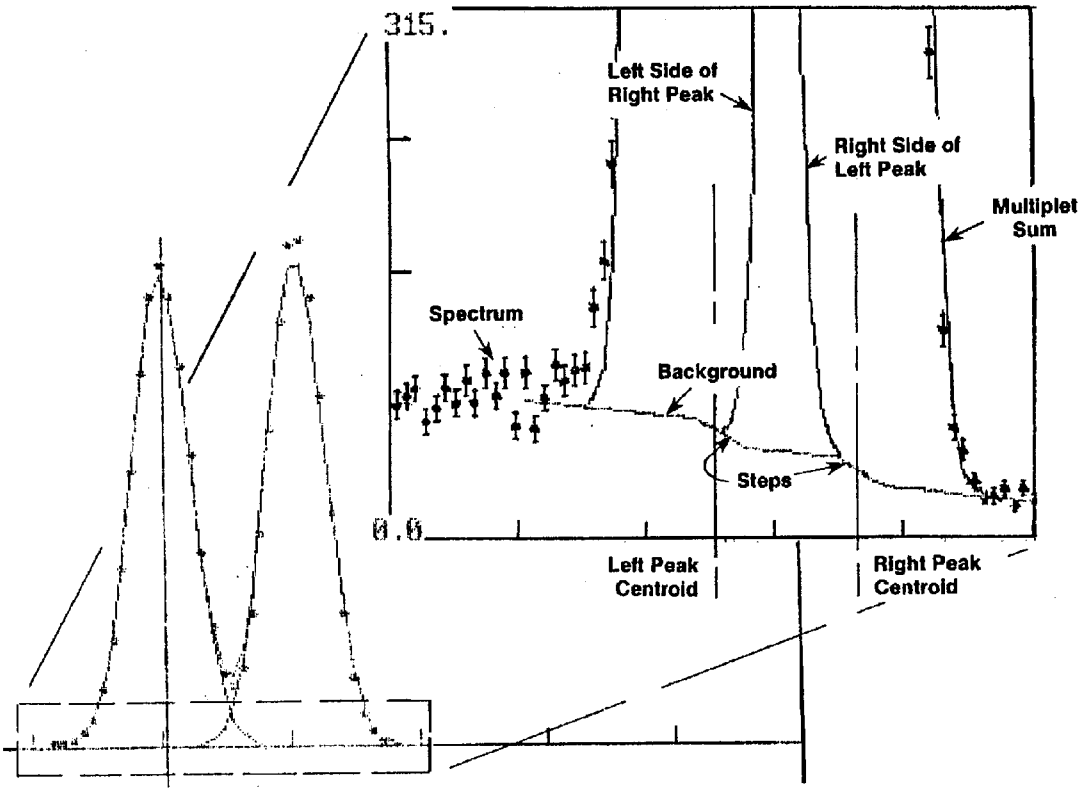


Figure 245. Stepped Background.

6.5.3. Parabolic Background

The parabolic background is calculated as the least squares fit to the actual spectrum data at the low-energy background data point, the spectrum data point at the channel most below the straight-line background and the spectrum data at the high-energy background data point. This parabolic form is calculated channel-by-channel and subtracted from the original spectrum to obtain the net spectrum for the fit.

Figure 246 shows this case for an actual spectrum.

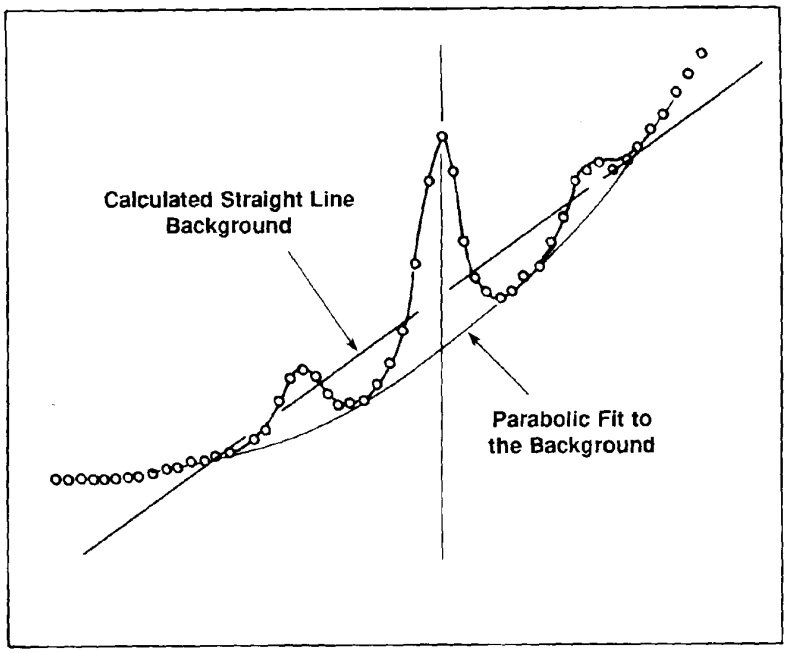


Figure 246. Parabolic Background.

6.5.4. Total Peak Area

The net spectrum, which is the composite of the contributions of the individual peaks, can be represented as a weighted sum of the Gaussian peak shapes. The weighting factors of each component are proportional to the area of that component peak.

The peaks to be included in the deconvolution are each positioned at the library energy or the peak finder energy of the component. The shape is calculated for the peak at the given energy even though the change in shape with energy within the energy range of the multiplet is small. The calibration peak shape is used. The contribution of a unit-height peak is calculated for each channel in the multiplet range for each candidate energy. This matrix of peak amplitudes multiplied by the weighting factors and summed is equal to the net spectrum. For NPP32 and ENV32, the peak centroids are allowed to vary in the fitting. The peak positions for all peaks are allowed

to shift in the fitting process to obtain a reduced chi-square. The library peaks are all shifted the same, while unknown peaks each shift independently. The weighting factors are determined by solving the matrix equation. The final result, that is, the area of the individual components of the multiplet, is the corresponding weighting factors times the unit-height area of the peaks at their respective positions.

If any of the weighting factors (and therefore the peak areas) are negative or zero as a result of the deconvolution, that peak candidate is deleted from the list and the remaining candidates are re-fit. Peak areas for deleted peaks are set to zero. The fitting process is repeated until no peak areas are negative or there is only one peak remaining. If there is only one peak remaining, the peak parameters for this peak are recalculated as if this peak were a singlet. The peak shape parameters and energy are set to the calculated peak parameters.

The background reported for each component peak in a multiplet is the gross area for three times the FWHM centered at the peak centroid minus the component peak area (Fig. 247). This means that for each peak the areas of the other peaks in the multiplet are treated as background. By including all the area not associated with the actual peak in the region of the peak, the uncertainty due to the background is more accurately calculated.

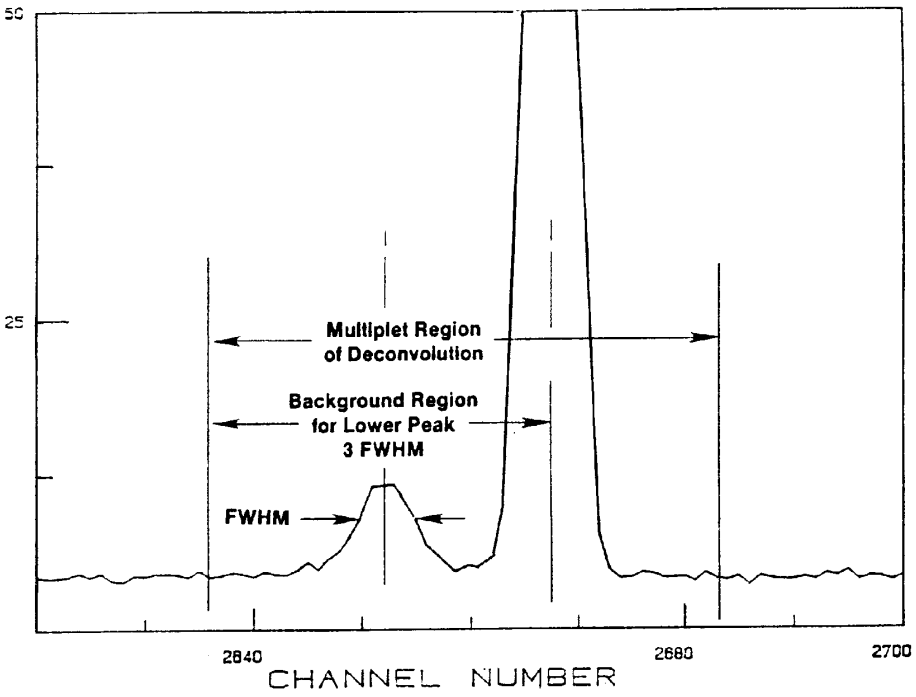


Figure 247. Background for Multiplet Components.

In the case of a multiplet, the sum of the reported backgrounds and net peak areas will be more than the sum of the gross spectrum for the same region because the background and some (if not all) of the net peak counts will be counted more than once.

The energy recalibration affects the multiplets in two ways. For inclusion in the list of deconvolution candidates, the first peak for this nuclide must be present. If the first peak has not been found because it failed the centroid test (see above), then subsequent peaks are not used. The deconvolution will then be performed with fewer candidates. Secondly, the library energies are used to define the location of the multiplet component library peaks. The peak finder energies are derived from the channel number, so although the reported energy might change, the position relative to the actual data does not change. A mismatch of these will result in an inaccurate fit, and a different fit when the peak channels are shifted relative to the spectrum.

6.5.5. Library-Based Peak Stripping

In a few cases, all of the gamma-rays emitted by one isotope are very close in energy to gamma-rays emitted by other isotopes in the sample. The peaks from the two gamma rays cannot be separated correctly using conventional analysis, so the activity for one isotope cannot be correctly determined. This alternative to deconvolution can be used to obtain peak areas of the components of a multiplet. It uses peak areas from other parts of the spectrum to determine the areas of some of the components and calculates the remaining areas. It is also referred to as peak-interference correction.

When enabled on the System tab under **Analyze/Settings/Sample Type...**, the program can operate automatically using only one library, or manually using three user-defined libraries detailing the peak overlaps.

6.5.5.1. Automatic Peak Stripping

In the automatic or library-based method, GammaVision automatically identifies the isotopes in the library that are too close together and calculates their activities indirectly. This method is simpler to use than the manual method.

The first step is to search the library for isotopes with severely overlapping gamma rays. The criterion for severe is that the peaks are within two channels of one another (regardless of the energy per channel). For peaks that are this close, the peak areas will be more accurate if they are found indirectly. Any such peaks are marked in the library as being too close together.

For example, the only useful gamma ray emitted by ^{226}Ra is 185.99 keV. The peak overlaps the 185.72 keV peak of ^{235}U. If these two isotopes are both in the library, ^{226}Ra and the 185.72 keV ^{235}U peak are flagged when the library is read. Table 7 shows some other common examples. These energies are from Erdmann and Soyka. Other references might have different energies, but the overlaps will still occur.

The spectrum is then analyzed as described with one exception: any peaks that are marked as too close are not used in the isotope activity calculations. Instead, the activity of one isotope is based on other gamma rays from that isotope. That activity is then used to calculate the contribution to

the overlapped peak of this isotope. That contribution is subtracted from the total peak area to obtain the peak area due to the other isotope.

Table 7. Gamma Peak Overlap Examples.

Isotope	Energy (keV)	Probability	Isotope with close energy
^{99m}Tc	140.99	89.3	^{99}Mo
^{224}Ra	241.00	3.90	^{92}Sr
^{226}Ra	185.99	3.28	^{235}U
^{241}Am	26.35	2.5	^{237}U
^{241}Am	33.20	0.11	^{144}Ce
^{241}Am	59.54	36.3	^{237}U

In the example above, the activity of ^{235}U is calculated from the area of the peak at the next most probable energy, i.e., 143 keV. Then the area of the 185.72 keV ^{235}U peak is calculated using the branching ratio of that gamma ray, the efficiency, and the activity. The ^{235}U area is subtracted from the area of the peak at 185 keV to give the area due to ^{226}Ra. From this, the activity of ^{226}Ra in the sample is calculated.

A special peak stripping process is discussed below. Assume for an analysis library, there are three library peaks defined for a nuclide, denoted as Peak1, Peak2, and Peak3. Those three peaks could be 143.7, 163.3 and 185.7 keV respectively for the U-235 nuclide. Furthermore, assume both the 163.3 and 185.7 keV peaks have overlap with other library peaks so that peak stripping must be performed at those energies. For example, the 185.7 keV peak has overlap with the Ra-226 peak at 186.20 keV.

As described in the earlier in this section, the (initial) U-235 nuclide activity will be calculated based on the 143.7 keV peak. Then the activity thus calculated is used to deduce the U-235 peak areas for the 163.3 and the 185.7 keV peaks respectively. After subtractions of the U-235 contributions to the 163.3 and 185.7 keV peaks, the remaining peak areas at those energies are assigned to other nuclide peaks, if the remaining areas are large enough (that is, the uncertainty of the remaining peak area is below the peak cutoff). For example, the remaining area for the 185.7 keV peak is assigned to Ra-226.

However, when the uncertainty of the remaining peak area is above the peak cutoff, Ra-226 would be declared as absent. Consequently, the whole peak area at 185.7 keV is given “back” to the U-235 peak. That is, the U-235 peak area at 185.7 keV would be no longer deduced based on the nuclide activity calculated from the 143.7 keV peak. Furthermore, if the U-235 peak activity calculated based on the whole peak area at 185.7 keV could pass the activity-range test, then the final U-35 activity would be re-calculated, based on not only the 143.7 keV U-235 peak, but also

the 185.7 keV U-235 peak.

It is then evident that the re-calculated averaged U-235 activity would be different from the activity based solely on the 143.7 keV peak. Once the U-235 averaged activity has been updated, the U-235 peak at 163.3 keV would be left out of sync., since the area was derived based on the U-235 activity calculated based on the 143.7 keV peak alone.

In principle, the updated averaged activity should be used to derive the 143.7 keV area again. But to simplify the analysis process, this has not been implemented with current version of the analysis engines. The difference in the peak area is expected to be small anyway due to the activity-range test mentioned in above process.

6.5.5.2. Manual Peak Stripping

The manual method of analysis uses three libraries. The first is the working analysis library with the severely overlapped peak multiplets removed. Multiplets that can be deconvoluted by fitting should remain in the first library. The **Second Library** contains the peaks that are to be stripped from the overlapped doublet. The amount to be stripped is based on the analysis from Library 1. The nuclide name for the stripped peak must be the same in both libraries, as this is how the program determines which peak areas to use. The **Third Library** contains the nuclides with the other peak in the overlapped doublets. The computations for the third library are the same as the first library except that deconvolutions are not performed and MDAs are not calculated for the third-library nuclides. You have complete control over the three libraries and can choose which peaks to use in each step. Nuclides that appear in both Libraries 1 and 3 are reported twice on the report.

For example, consider the case in which a spectrum contains nuclides A, B, C, D, E, and F. Nuclide D has energies of 200 keV and 500 keV, and nuclide F has only one peak at 500 keV. Let Library 1 contain five nuclides labeled A, B, C, D, and E. Let Library 2 contain nuclide D, and Library 3 contain nuclide F. In Library 1, nuclide D is listed with only the energy at 200 keV. In Library 2, nuclide D is listed with only the energy at 500 keV.

The analysis of the spectrum using Library 1 will give an activity for nuclide D based on the peak at 200 keV (as well as activities for A, B, C, and E). Using this activity, the peak count rate for the nuclide D peak at 500 keV will be calculated using Library 2 and the calibration and corrections, if any. This peak count rate will be converted to a peak shape function (a Gaussian) based on the calibration peak shape and the counting time. This peak will be subtracted channel by channel from the net spectrum. This new net spectrum will then be analyzed using Library 3.

The results of all the calculations (that is, the equivalent peak areas and gross areas) will be shown on the full report. If Library 1 or 3 does not contain any peaks in the energy range being analyzed, this option is turned off. If Library 2 does not contain any peaks in the energy range or

any peaks in Library 1, the subtraction of peak areas does not take place, but the analysis using Library 3 is still performed. This can be an easy way to obtain a report with MDA for some nuclides (those in Library 1) and without MDA for other nuclides (those in Library 3).

6.6. Fraction Limit

To verify the identification of a particular nuclide in a spectrum, the number of identified peaks is compared to the number of possible peaks, where "identified" peaks are those with a 1-sigma counting uncertainty less than the **Peak Cutoff** value, and the possible peaks include only those within the low-/high-energy analysis range. Peaks with the "Not in Average" flag set as NOT TRUE in the library are excluded. It is expressed as follows:

$$Fraction = \frac{\sum_{l=1}^{n} Br_l}{\sum_{p=1}^{m} Br_p} \quad \textbf{(58)}$$

where *Br* is the branching ratio for the peak for the given nuclide, adjusted for TCC where applicable; *l* is the sum over the located peaks; and *p* is the sum over the possible peaks. This fraction is between 100 for all peaks located and 0 for no peaks located.

This value is compared to a limit value, entered on the System tab under **Analyze/Settings/ Sample Type...** (page 152), to determine whether this nuclide's peaks are present in sufficient measure to say the nuclide is present. The *fraction limit test* is passed if the fraction is above the selected value.

To disable the fraction limit test, enter a limit of zero on the System tab.

6.7. Nuclide Activity

The nuclide activity is calculated for all peaks in the library whose energy is between the energy limits you have selected for the analysis (in-range). There are several methods of determining if a nuclide is present or not, and if MDA should be reported.

A nuclide is reported with an activity value under the following conditions:

1) If more than one peak is listed for the nuclide, the following apply:

- The first in-range peak that is not marked as "Not in Average" and not closely overlap-

ping another library peak, such that peak stripping would be applied, must be identified.[31]
- All peaks marked as key lines must be identified.
- The Fraction Limit Test must be satisfied.
- For GAM32 and ENV32, the Library Reduction requirements must be satisfied (See Section 6.2.3.)

2) If only one peak is listed for the nuclide, the following apply:

   - If the peak does not closely overlap another library peak, it must identified in the analysis range.
   - If the "Not in Average" flag is set for this peak, the nuclide is automatically rejected when using all analysis engines except for WAN32, which ignores the "Not in Average" flag under this condition.
   - If the peak closely overlaps another library peak such that peak stripping would be applied, the uncertainty of the area remaining after peak stripping must be less than the **Peak Cutoff**.

3) **Directed Fit** forces an activity to be reported for nuclides that do not meet the preceding criteria.

If a nuclide is not reported with an activity value, and the "No MDA Calculation" flag is not set in the library, the MDA value will be reported in the Summary of Nuclides in Sample. Otherwise, the nuclide will be omitted from the Summary of Nuclides in Sample.

The nuclide activity, based on the peak at energy *E*, is given by:

$$A_{Ei} = N_{Ei} * \xi \quad \textbf{(59)}$$

where:

$$\xi = \frac{TDC * Mult * RSF * GeoFac * AttCorr}{LT * \varepsilon_E * Br * Div * s} \quad \textbf{(60)}$$

N_{Ei} = net peak area for peak at energy *E*
TDC = decay corrections, incorporating *DDA*, *DC*, and *DDC* as defined in

[31] "Identified" in this discussion indicates the peak counting uncertainty at 1 sigma is less than the **Peak Cutoff** value.

Sections 6.10.1 through 6.10.3.

Mult = multiplier entered on the System tab.
RSF = random summing correction factor (Section 6.11).
LT = live time.
ε_E = detector efficiency at energy *E* (Section 5.3.3); this efficiency factor is stored in the .CLB record of the .SPC spectrum file.
Br = peak branching ratio from library.
GeoFac = geometry correction factor (Section 6.10.5).
AttCorr = attenuation correction (Section 6.10.6).
Div = divisor entered on the System tab.
s = sample quantity entered on the System tab.

This "peak activity" is reported in the nuclide peak matrix (if requested). If there is more than one peak in the energy analysis range for a nuclide, then an attempt to average the peak activities is made. The result of the average is the average nuclide activity.

6.7.1. Average Activity

The average activity for the nuclide is calculated by weighting each acceptable peak activity by its respective branching ratio as follows:

$$A_{avg} = \frac{\sum_{i=1}^{n} A_{Ei}\, Br_E}{\sum_{i=1}^{n} Br_E} \qquad \textbf{(61)}$$

where:

A_{Ei} = the activity of nuclide peak *i* at energy *E* per Eq. 59, 60
Br_i = the gamma/disintegration of the *i*th peak
n = the number of peaks included in the activity

Acceptable peaks for the weighted average calculation must meet the following criteria:
(1) The "Not in Average" flag is not set in the library.
(2) The peak has been positively identified per the criteria in Section 6.7.
(3) If the **Activity Range Test flag** is set to True in the b30winds.ini (n30winds.ini for NAI32) file (Section A.2.2), then the following criteria must be satisfied for peaks after the first non-interfered peak to be included in the weighted average:

$$[A_1 - (F * |A_1|)] \le A_n \le [A_1 + (F * |A_1|)] \quad \textbf{(60a)}$$

Where

A_1 = First Non-Interfered Peak Activity
A_n = nth Subsequent Peak Activity
F = MIN$(r * ó_1, F_{max})$
F_{max} = Maximum Activity Range Multiplier (Section A.2.2 b30winds.ini / n30winds.ini setting)
r = Peak Activity Range Factor (Section A.2.2 b30winds.ini / n30winds.ini settings)

$$ó_1 = \sqrt{\sigma^2_{count_1} + \left(\frac{\sigma_{nuc}}{200}\right)^2 + \sigma^2_{eff_1}}$$

$ó_{count\_1}$ = First Peak Counting Uncertainty
$ó_{nuc}$ = Nuclide Uncertainty from library (2-sigma)
$ó_{eff\_1}$ = First Peak Efficiency Uncertainty (Section 6.12.17)

6.7.2. Nuclide Counting Uncertainty Estimate

Many radioisotopes have more than one peak useful for calculating the measured activity of the isotope. The uncertainty caused by counting statistics can vary widely among those peaks. This variation can be caused by differences in the net counting rates in the peaks or the background levels under the peaks. GammaVision utilizes a relatively simple yet statistically rigorous method for choosing the peaks to achieve optimum precision. When more than one peak is available, the software performs two assessments:

1) It finds the peak with the smallest percent standard deviation.
2) It computes the percent standard deviation for the linear average of all peaks detected according to the criteria in Section 6.7.

The option which yields the lowest percent standard deviation is the method used to calculate the nuclide counting uncertainty for the radioisotope. The mathematical process for this selection is summarized below:

Assume σ_A is the reported nuclide counting uncertainty, σ_{Pi} is the counting uncertainty for the i^{th} peak and n is the total number of peaks used to calculate the nuclide activity. All the uncertainties are relative.

Furthermore, let us define σ_{Pmin} as the minimum counting uncertainty of all the n peaks:

$$\sigma_{Pmin} = MIN(\sigma_{Pi}),\ i = 1, \ldots, n \quad \textbf{(62)}$$

where *MIN* is the minimum function which returns the minimum value from a list of values in the parenthesis (from 1 to n above).

The averaged nuclide counting uncertainty σ_{avg} is calculated from:

$$\sigma_{avg} = \frac{\sqrt{\sum \sigma_{Pi}^{2}}}{n} \quad \textbf{(63)}$$

The reported nuclide counting uncertainty is calculated at 1 sigma and reported at 1, 2, or 3 sigma, depending on the **Confidence level** setting on the Report tab. It is calculated as:

$$\sigma_{A} = MIN(\sigma_{Pmin}, \sigma_{avg}) \quad \textbf{(64)}$$

GammaVision compares the averaged peak counting uncertainty and the minimum peak counting uncertainty and reports the smaller value as the nuclide counting uncertainty.

6.8. Total Activity (ROI32 Analysis Engine Only)

Total activity represents the summed activity calculated for all nuclides found in the sample. It is calculated as follows and printed immediately after the Summary of ROI Nuclides table in the analysis report.

$$A_{tot} = \sum_{n=1}^{Nuclides} A_{avg} \quad \textbf{(65)}$$

where A_{avg} is calculated per Section 6.7.1. Note that if MDA is reported for A_{avg} for a particular nuclide, that nuclide's contribution is not included in A_{tot}.

6.9. MDA

The Minimum Detectable Activity (MDA) is a measure of how small an activity could be present and not be detected by the analysis. There are many factors affecting the MDA, which is reported in activity units such as becquerels. The calibration geometry, the backgrounds (system- and source-induced), the detector resolution and the particular nuclide all substantially affect the MDA reported.

In most instances, the MDA value is calculated based on the background value of the peak. If the peak area was not used in the activity calculation because it failed the sensitivity test, or a shape test, the peak area is added to the background for the MDA calculation unless the MDA defines the background separately. If the background is 0, it is set to 1 for the MDA calculation. The background will still be reported as 0 on the report. By reviewing the individual MDA values (which are printed on the nuclide/peak matrix) you can determine how relevant the selected MDA value is to the physical situation. The MDA reported for the nuclide is the value for the first peak in the library.

6.9.1. Computing MDA Values

MDA values for many methods depend on area and background values. Area and background determination varies from method to method. The information needed to validate the MDA results can be found in the peak analysis Details dialog (Fig. 248; refer also to Section 5.5.6.3); the analysis options (.SDF file) for the spectrum (Section 5.5.1.1); reports (Chapter 7); and manual integration of the spectrum peaks.

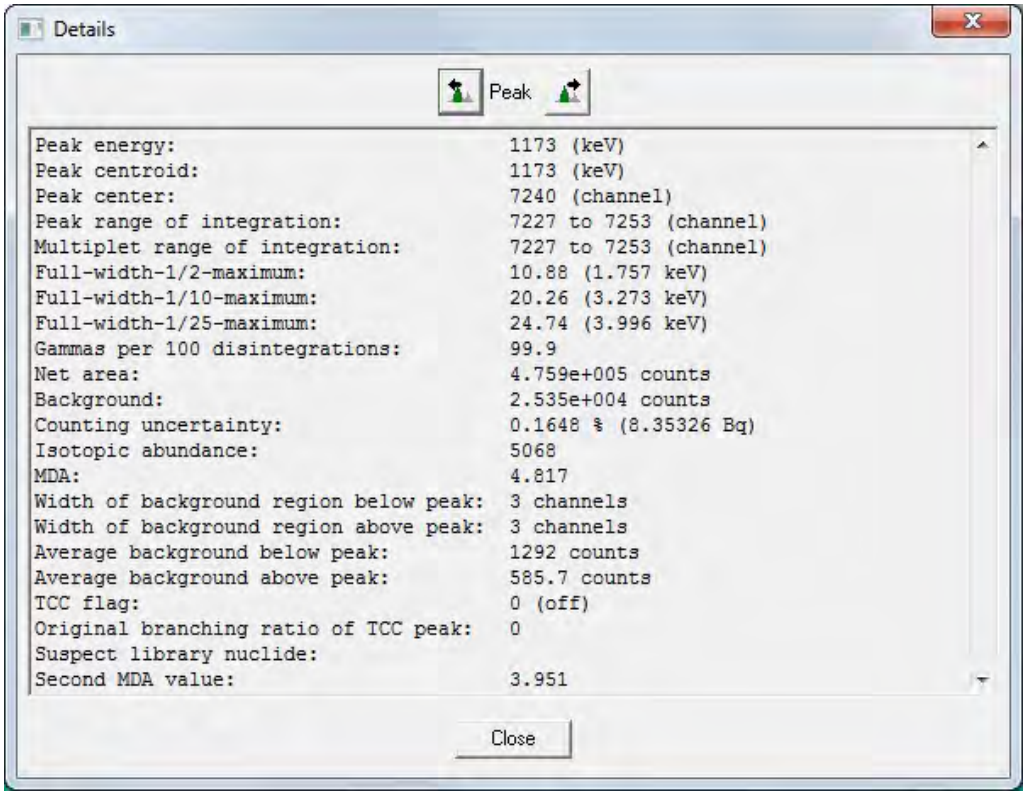


Figure 248. Peak Analysis Details Dialog is One Source of Data for the MDA Calculation.

6.9.1.1. Area Methods

A_1 Gross area under the peak determined by integrating the peak with a width of 2.5 times FWHM (counts). Areas computed in this manner are used in Methods 4, 11, and 14 below.

To determine the area:

1) Determine the (decimal representation) centroid energy of the peak.

2) Determine the (decimal representation) channel of this centroid (based on the energy calibration).

3) Determine the (decimal representation) FWHM of this peak (based on the FWHM calibration at the centroid channel).

4) Determine half of the FWHM range (denoted as I_L), which is calculated as the integer representation of (*1.25 * FWHM + 0.5*). Note that this value is capped at 100.

5) Determine the centroid for integration (denoted as C_I), which is simply the centroid channel determined in step (2) rounded to the closest whole (integer) number.

6) Determine a lower channel of integration (denoted as C_{Low}) as follows. This value has a minimum value of 1.

$$C_{Low} = C_I - I_L$$

7) Determine an upper channel of integration (denoted as C_{High}) as follows:

$$C_{High} = C_I + I_L$$

8) A_1 is then simply the sum of all channels from C_{Low} to C_{High}.

A_2 Net peak area reported on the Identified Peak Summary Report or peak Details dialog (counts). Areas computed in this manner are used in Methods 9 and 10 below.

A_3 Gross area under the peak determined by integrating the peak with a width of 2.5 times FWHM minus one channel on the high- and low-energy side of the peaks. Areas computed in this manner are used in Method 13 below.

To determine the gross area:

1) Determine the (decimal representation) centroid energy of the peak.

2) Determine the (decimal representation) channel of this centroid (based on the energy calibration).

3) Determine the (decimal representation) FWHM of this peak (based on the FWHM calibration at the centroid channel).

4) Determine half of the FWHM range (denoted as I_L), which is calculated as the integer representation of (*1.25 * FWHM + 0.5*). Note that this value is capped at 100.

5) Determine the centroid for integration (denoted as C_I), which is simply the centroid channel determined in step (2) rounded to the closest whole (integer) number.

6) Determine a lower channel of integration (denoted as C_{Low}) as follows. This value has a minimum value of 4.

$$C_{Low} = C_I - I_L + 1$$

7) Determine an upper channel of integration (denoted as C_{High}) as follows:

$$C_{High} = C_I + I_L - 1$$

8) A_3 is then simply the sum of all channels from C_{Low} to C_{High}.

6.9.1.2. Background Methods

B_1 Background reported in the Identified Peak Summary (counts). These backgrounds are used in Methods 1, 2, 5, 6, 7, 8, 12, and 16 below. For some MDA methods, if the peak fails validity tests, $B_1 = B_1 + peak\ area$.

B_2 The average of three high-energy channels and three low-energy channels as part of peak area method A_3 (counts). Backgrounds computed in this manner are used in Method 13 below.

B_3 The sum of the counts on the high-energy portion of the peak and the low-energy portion of the peak. The boundary of the peak is established as described for A_1. Backgrounds computed in this manner are used in Methods 14 and 15 below.

To determine the area:

1) Determine the (decimal representation) centroid energy of the peak.

2) Determine the (decimal representation) channel of this centroid (based on the energy calibration).

3) Determine the (decimal representation) FWHM of this peak (based on the FWHM calibration at the centroid channel).

4) Determine the integer value representation of the centroid channel (denoted as C_{Int}) simply by rounding the centroid channel down to the closest whole (integer) number.

5) Determine the width of 2.5 times the FWHM (denoted as I_B, range 4 to 100), then round to next integer; e.g., round 5.0 to 5, and 5.0001 to 6.0 to 6. This value is calculated as follows:

$$I_B = (Integer)\ 2.5 * FWHM + 0.9999$$

6) Determine half the I_B range (denoted as L) as follows and rounded down to the next closest whole integer:

$$L = (Integer)\ I_B / 2$$

7) Determine the start channel of the main peak region (denoted as Pk_{Start}). This value is set at the minimum value of 1, and is calculated as:

$$Pk_{Start} = C_{Int} - (integer)\ (-0.45 + IB / 2)$$

8) Determine the end channel of the main peak region (denoted as Pk_{End}) as follows:

$$Pk_{Start} = C_{Int} + L$$

9) Determine the starting channel for *N1* integration (denoted as $N1_{Low}$) as follows:

$$N1Low = Pk_{Start} - L$$

10) Determine the ending channel for *N1* integration (denoted as $N1_{High}$) as follows:

$$N1High = Pk_{Start} - 1$$

11) *N1* is then the summation of all counts from channel $N1_{Low}$ to $N1_{High}$.

12) Determine the starting channel for *N2* integration (denoted as $N2_{Low}$) as follows:

$$N2Low = Pk_{Start} + 1$$

13) Determine the ending channel for *N2* integration (denoted as $N2_{High}$) as follows:

$$N2High = Pk_{Start} + L$$

14) *N2* is then the summation of all counts from channel $N2_{Low}$ to $N2_{High}$.

15) The final value B_3 is then simply the sum of *N1* and *N2*.

6.9.1.3. Computing MDA

The MDA methods are computed from count rates, CR_{mda}. To convert CR_{mda} from counts to activity, a conversion factor MDA_{conv} is used that contains detector efficiency, branching ratio, and activity correction factors.

$$MDA_{conv} = \frac{1.0}{\xi * LT} \quad \textbf{(66)}$$

where ξ is defined in Eq. ? and *LT* is the live time.

6.9.2. GammaVision MDA Methods

6.9.2.1. Method 1: Traditional ORTEC

$$CR_{mda} = \frac{\frac{100}{SENS} * \left(\sqrt{2 * B_1 + \frac{2500}{SENS^2}} + \frac{50}{SENS} \right)}{LT} \quad \textbf{(67)}$$

where:

SENS = **Peak Cutoff** value (%) on the Analysis tab or in the .SDF file
LT = live time (sec)

NOTE If the peak is rejected, the peak area is added to the background term B_1.

6.9.2.2. Method 2: Critical Level ORTEC

$$CR_{mda} = 2.33 * \frac{\sqrt{B_1}}{LT} \quad (68)$$

Critical level (CL) is defined as the smallest concentration of radioactive material in a sample that will yield a net count (above background) that will be detected with a 95% probability.

NOTE If B_1 is computed as zero, it is assigned a value of 1 for CL calculations.

6.9.2.3. Method 3: Suppress MDA Output

The MDA is not calculated and is set to zero.

6.9.2.4. Method 4: KTA Rule

$$CR_{mda} = \frac{\sigma * \sqrt{\frac{A_1}{N} * FWHM}}{LT} \quad (69)$$

where:

N	=	number of channels under peak A_1 (channels)
$FWHM$	=	full width at half maximum (in channels, where channels is rounded to the nearest integer); use the Details dialog for the proper value
σ	=	**Confidence Level** on the System tab or in the .SDF file (1, 2, or 3 sigma)

6.9.2.5. Method 5: Japan 2 Sigma Limit

$$CR_{mda} = 2 * \frac{\left(1 + \sqrt{1 + 2B_1}\right)}{LT} \quad (70)$$

6.9.2.6. Method 6: Japan 3 Sigma Limit

$$CR_{mda} = 4.5 * \frac{\left(1 + \sqrt{1 + 0.8888 * B_1}\right)}{LT} \quad (71)$$

6.9.2.7. Method 7: Currie Limit

$$CR_{mda} = 1.645 * \frac{\sqrt{B_1}}{LT} \quad (72)$$

NOTE If B_1 is computed as zero, it is assigned a value of 1 for MDA calculations.

6.9.2.8. Method 8: RISO MDA

$$CR_{mda} = 4.65 * \frac{\sqrt{B_1}}{LT} \quad (73)$$

NOTE If B_1 is computed as zero, it is assigned a value of 1 for MDA calculations.

6.9.2.9. Method 9: LLD ORTEC

$$CR_{mda} = 4.66 * \frac{\left(\frac{\sigma_p}{100} * A_2\right)}{LT} \quad (74)$$

where σ_p is the counting uncertainty (%). This value is found in the peak Details dialog.

6.9.2.10. Method 10: Peak Area

This method is useful if negative peak areas are expected.

$$CR_{mda} = \frac{A_2}{LT} \quad (75)$$

6.9.2.11. Method 11: Air Monitor — GIMRAD (also called DIN 25 482 Method)

$$CR_{mda} = \frac{1.35 * \left(1.0 + \sqrt{1.0 + 2.96 * A_1 * \frac{FWHM}{N}}\right)}{LT} \quad (76)$$

where *FWHM* is in channels, derived from the FWHM calibration. Unlike the KTA Method (Section 6.9.2.4), *FWHM* here is a decimal, not the whole-integer representation.

6.9.2.12. Method 12: Regulatory Guide 4.16

This is a frequently used method in the USA.

$$CR_{mda} = \frac{2.71 + 4.66\sqrt{B_1}}{LT} \quad (77)$$

6.9.2.13. Method 13: Counting Lab — USA

This method is used when a minus MDA is needed in situations when the background is greater than the peak area.

$$CR_{mda} = \frac{A_3 - B_2 N}{LT} \quad (78)$$

where N is the number of channels included in the integration of the peak (channels)

6.9.2.14. Method 14: Erkennungsgrenze (Detection Limit) DIN 25 482.5

This method is described in the German DIN 25 482 teil 5. It is designed to establish a critical value for the spectrum.

$$CR_{mda} = \frac{1.96^2 * N_A * \left(1 + \sqrt{1 + \left(\frac{4 * B_3}{1.96^2}\right)\left(\frac{N_A}{2N_B}\right)\left(1 + \frac{2N_B}{N_A}\right)}\right)}{4 * LT * N_B} \quad (79)$$

where:

N_A = number of channels in the peak rounded up using the A_1 peak method (page 274).

N_B = number of channels in the background regions above and below the peak. Usually, this number is approximately half of the number of peak channels, N_A (channels). It is calculated as follows:

1) Determine the peak centroid channel as a whole (integer) number.
2) Determine the FWHM at this channel, based on the FWHM calibration.

3) Determine the integration channel range (I_B, ranging from 4 to 100) by multiplying 2.5 by the FWHM and rounding up to the next integer (i.e., such that 5.0 is 5 and 5.0001 to 6.0 is 6).
4) N_B is then simply I_B / 2 and rounded up as described in (3).

6.9.2.15. Method 15: Nachweisgrenze DIN 25 482.5

This method represents the lowest true value of activity that can be reliably reported with similiar samples. Its value is approximately twice the value computed for Erkennunggrenze (Section 6.9.2.14), where N_A and N_B are defined.

$$CR_{mda} = \frac{2 * 1.96 * \sqrt{B_3 * \left(1 + \frac{N_A}{2N_B}\right)}}{LT} + \frac{(2 * 1.96)^2 * \left(1 + \frac{N_A}{2N_B}\right)}{4 * LT} \quad \textbf{(80)}$$

6.9.2.16. Method 16: EDF — France

This method is defined for the EDF and CEA in Rapport CEA-R-5506, *Determination du Seuilet de la Limite de Detection en Spectrometrie Gamma*.

$$CR_{mda} = 6.2 * \frac{\sqrt{B_1}}{LT} \quad \textbf{(81)}$$

NOTE If B_1 is computed as zero, it is assigned a value of 1 for MDA calculations.

6.9.2.17. Method 17: NUREG 0472

$$CR_{mda} = 4.66 * \frac{\sqrt{B_1}}{LT} \quad \textbf{(82)}$$

6.9.2.18. Method 18: ISO Decision Threshold (CL)

This is discussed in Section 6.17.2.1.

6.9.2.19. Method 19: ISO Detection Limit (MDA)

This is discussed in Section 6.17.2.2.

6.10. Corrections

If enabled, the following corrections are made on a nuclide-by-nuclide or peak-by-peak basis.

6.10.1. Decay During Acquisition

The decay during acquisition correction is used to correct the activity of nuclides whose half-life is short compared to the spectrum real time.

The correction is:

$$DDA = \frac{ln2 \times \frac{Real\ time}{half-life}}{1 - e^{-\left(ln2 \times \frac{Real\ time}{half-life} \right)}} \quad \textbf{(83)}$$

where:

DDA = the decay correction factor
Real time = the spectrum real time (in seconds)
half-life = the half-life of the nuclide of interest

This can be viewed as scaling up the activity measured to the value of the activity at the start of the measurement. The correction goes to 1 (no change) as acquisition time becomes much smaller than the half-life.

The decay during acquisition technique is superior to making use of a hardware dead-time correction. For example, suppose a sample contains two nuclides, one with a short half-life and one with a long half-life. The count rate of the short half-life nuclide will be higher at the beginning of the count time than at the end of the count. This means more counts per unit time will be accepted at the beginning of the count time than at the end. So even if the count time is extended by the hardware to compensate for the lost counts at the beginning of the counting period, the count rate is so low at the end of the count that not enough counts will be added in. For the long half-life nuclide, the count rate does not change during the count time, so the live-time correction will correctly account for the lost counts during the count time.

6.10.2. Decay Correction

If disabled on the Decay tab or in the .SDF file, the decay correction is set to 1.0. If enabled, this correction projects the activity at the time of count back to the time the sample was collected. This is useful when there is a long time, relative to the half-life, between the sample collection time and the sample count time. The sample collection time is entered on the Decay tab (alterna-

tively, the number of half-lives can be set in b30winds.ini (n30winds.ini for NAI32); see Section A.2.2). If the time is greater than 12 half-lives, the correction is not made and the message is printed out. Twelve half-lives corresponds to a decay factor of about 4000. Both the time of count and decay-corrected values are presented on the report. The total activity is the decay-corrected activity.

Decay correction is determined as follows:

$$DC = e^{\left(\frac{\ln(2)\,\Delta T}{T_1}\right)} \quad \textbf{(84)}$$

where

$\Delta T = T_{Count} - T_{Collection}$

6.10.3. Decay During Collection

If the sample was collected over an extended time (see page 155), this correction will account for the buildup or increase of activity in the sample during the collection time. The correction is given by:

$$DDC = \frac{ln(2) \times \frac{Elapsed\ time}{half-life}}{1 - e^{-\left(ln(2) \times \frac{Elapsed\ time}{half-life}\right)}} \quad \textbf{(85)}$$

6.10.4. Peaked Background Correction

The Peaked Background Correction (PBC) is used to correct for the presence of peaks in the background spectrum that also occurs in the sample. If the peak is not of interest in the analysis results, there is no need to make this correction. The values in the PBC table are the counts per second at each library energy. These count rates are multiplied by the sample live time to calculate background counts, and the resulting background counts are added to the respective peak background. *Note that this background subtraction may raise the peak uncertainty above the peak cutoff such that a peak is no longer considered as identified.*

This section describes how peaks are qualified for PBC correction. The correction and uncertainty calculations are covered in Section 6.12.12.

6.10.4.1. PBC Match Width (By Energy option OFF)

Background correction is applied to Identified Peaks that have matching nuclide names in the Library and PBC file and peak energy within the calculated background match width. The default **PBC Match Width** is 0.5, which is the same as the default Library Match Width. If the Library Match Width on the System tab is increased for a particular measurement type, then the PBC Match Width should be increased to at least the same value. If the **PBC Match Width** is zero (i.e. for backward compatibility with earlier versions of GammaVision) then the default match width will be used. The **PBC Match Width** is applied as follows:

For each peak at energy E_0, the PBC match width in keV is calculated first:

$$\Delta E = f_{PBC} * FWHM \quad \textbf{(86)}$$

where $FWHM$ is the calibrated peak FWHM at that energy and f is the **Match Width** value specified on the Correction tab. Then the energy range from E_1 to E_2 is considered for PBC matching width:

$$E_1 = E_0 - \Delta E, \qquad E_2 = E_0 + \Delta E \quad \textbf{(87)}$$

A PBC peak is considered a matching peak if the PBC peak energy is within this energy range. The PBC uncertainty calculation is discussed in Section 6.12.12.

6.10.4.2. Match by Energy Only (By Energy option ON)

Background correction is applied to spectrum peaks as described above regardless of whether or not the spectrum or background peak is associated with a matching nuclide name. Multiple background peaks, including those associated with different nuclides in the PBC file, can be applied to the same spectrum peak if they are within the specified energy range. If a PBC file peak is within the match width of more than one spectrum peak then it will only be applied to the closest peak. Unlike **PBC By Nuclide** energy, the results of **PBC By Energy** are evident in the Summary of Peaks in Range and Unidentified Peak tables in addition to the Identified Peaks.

For example, if a PBC peak has an energy of 186.00 keV, and there are peaks at 185.70 keV and 186.20 keV found in the spectrum, then the 186.00 keV PBC peak is considered to be associated with the 186.20 keV peak (energy difference 0.2 keV) rather than the 185.70 keV peak (energy difference 0.3 keV) even though the PBC peak is within the acceptance range of both spectrum peaks.

For the above example, if the PBC match width is 0.1 keV, then PBC subtraction will not be applied to either peak. If the PBC match width is 0.5 keV, then PBC subtraction will be applied to the 186.20 keV peak only, but not to the 185.70 keV peak, *even if the latter is within the PBC match width*. In the following table, some scenarios are tabulated.

PBC Peak *E* = 186.00 keV		PBC Total Match Width (*f* * *FWHM*) in keV		
Peak No.	**Peak E (keV)**	**0.1**	**0.2**	**0.5**
Peak #1	185.70	PBC — No	PBC — No	PBC — No
Peak #2	186.20	PBC — No	PBC — Yes	PBC — Yes

If there are multiple PBC peaks associated with a spectral peak, and if all those PBC peaks are within the PBC **Match Width**, then that peak is subject to multiple PBC corrections. For example, if there is another PBC peak at 186.3 keV, that PBC peak would be associated with the 186.20 keV peak, leading to two PBC peaks to subtract from. In addition, if there is another PBC peak at 185.6 keV, then that PBC peak would be associated with the 185.7 keV only. When multiple PBC are applied, the uncertainties of each PBC are propagated accordingly. See the discussion in Section 6.12.12.

6.10.5. Geometry Correction

The geometry correction is used to adjust the activities reported in a sample of a given source/detector geometry when the system was calibrated using a different source/detector geometry. This is useful when many different geometries are used in a laboratory and calibrated sources are not available for all the geometries used. For more information, see Section 5.5.1.4.

The correction factor multiplies the peak activity for each peak in the library as shown in Eq. 88. The factors are stored as a function of energy.

$$A_{Geo} = A * GeoFac \quad \textbf{(88)}$$

where:

A_{Geo} = corrected activity for a given energy
A = uncorrected activity for a given energy
$GeoFac$ = the correction factor for that energy

The correction is not applied to unknown peaks. The peak values in the isotope/peak list in the output report are uncorrected values. The peak uncertainty is maintained as a constant percentage. The factor is linearly interpolated between the points in the table and linearly extrapolated outside the energy range of the table points.

The geometry correction table is stored in the spectrum file (.SPC). The correction can be enabled or disabled for a specific analysis.

6.10.5.1. Example

As an example of this correction, two spectra were taken of the same point source (Fig. 249). In case 1, the source was about 4 cm from the end cap and on-axis of the detector. The second geometry (case 2) is with the source about 7.5 cm from the center of the detector in a position in the plane of the end cap of the detector.

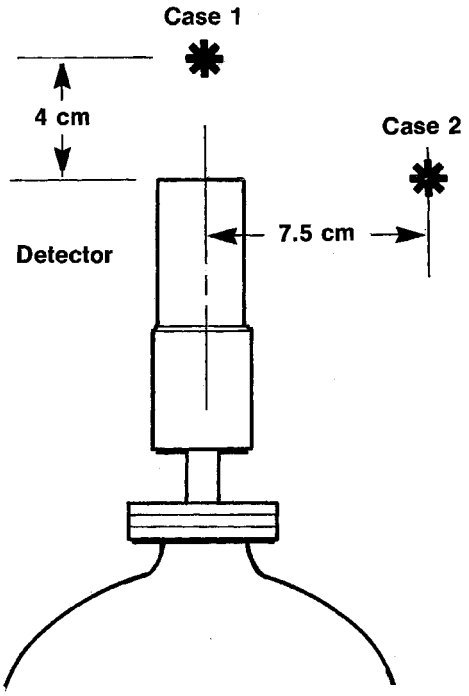


Figure 249. Example Geometries Used.

Table 8 shows the analysis of the two spectra for the peaks due to ^{154}Eu. The ratio of the peak count rates is shown in column 4. These values are entered into the geometry table. The spectrum was re-analyzed with the geometry correction turned on. The comparison of all three analyses is shown in Table 9.

Note that the ^{155}Eu activity is not corrected as much as needed. This is primarily due to all of the ^{155}Eu gamma-ray lines falling below the lowest energy in the correction table. It is in these low energies that the differences in the geometries is most noticeable.

The geometry correction table can be made automatically using analysis results files (.UFO) of the pairs of geometries or manually by entering the correction factor and energy pairs.

Table 8. Geometry Correction Table.

Energy (keV)	Peak Count Rate Case 1	Case 2	ratio
123.14	63.23	51.07	1.238
591.74	3.31	2.19	1.511
723.3	11.50	7.47	1.539
873.20	5.75	3.79	1.517
1004.76	7.71	4.91	1.570
1274.45	10.29	6.07	1.695

Table 9. Geometry Correction Results.

Nuclide	Activity		
	Case 1	Case 2 no correction	Case 2 correction
^{154}Eu	12750	7730	13000
^{155}Eu	8020	5180	6300
^{125}Sb	2900	1956	2840

6.10.6. Absorption

The absorption factor is used to correct for the absorption of gamma-rays by material between the detector and the source. The factors are stored as a function of energy in the *attenuation database*, Atd.mdb, in C:\User. Materials that are always present (such as the detector end cap) will be accounted for in the efficiency calibration. Source containers will not normally be accounted for, nor will an absorbing matrix such as soil. In these cases, the absorption of the gamma-rays will cause low values for the isotopic abundances to be reported unless the absorption correction is made. One of two types of absorption correction (as defined in ASTM E181-82)[32] can be selected. External absorption is for cases where all the source gamma-rays pass through the absorber. Internal absorption is for cases where the radioisotope is mixed with the absorber so that some of the gamma-rays go through a lot of absorber and some only go through a small amount of absorber.

6.10.6.1. External Absorption

The external absorption is used when the source is separate from the absorber, as in a source in a metal can. All of the gamma rays from the source must pass through all of the absorber before reaching the detector.

$$AttCorr = e^{\mu x} \quad \textbf{(89)}$$

where:

μ = the table value at energy E; normally the mass attenuation coefficient

x = the absorption factor; a function of the sample weight, density, or thickness such that it is in inverse units of μ (**Length**, entered on the Corrections tab)

[32]"Standard General Methods for Detector Calibration and Analysis of Radionuclides," ASTM E181-82, also ANSI N42.14-1978, IEEE, NY, NY.

For values between the table values, the μ are linearly interpolated between the table values using the natural logarithms of the μ values and their associated energies when using the coefficient table. If the spectrum is being used to calculate the μ values, linear interpolation is used on the μ values and their associated energeis to obtain μ between energies. The correction value is always 1 or greater.

6.10.6.2. Internal Absorption

The internal absorption is used when the source and the absorber are mixed together, such as soil or sand samples. Some of the gamma rays pass through no part of the absorber and some pass through the entire sample. The following formula for the corrected areas assumes that the absorbing matrix is homogeneous and that the source is uniformly distributed in the matrix.

$$AttCorr = \frac{\mu x}{1 - e^{-\mu x}} \quad \textbf{(90)}$$

where:

μ = the table value at energy E; normally the mass attenuation coefficient

x = the absorption factor; a function of the sample weight, density or thickness such that it is in inverse units of ì (**Length**, entered on the Corrections tab)

Internal Absorption Correction

For other absorbing conditions, these approximations might not apply. The corrections should be checked against a known situation to ensure that these conditions are met for the current analysis situation.

The absorption table values can be constructed from mass attenuation coefficients or by ratioing unattenuated spectrum results with attenuated spectrum results. The ratio method is difficult to apply to the internal absorption correction because of the difficulty in obtaining appropriate spectra.

The mass attenuation coefficients are available from many sources. For mixtures not listed in the table, use the molecular weight fractions to obtain an average attenuation coefficient. For example, for water, multiply the hydrogen coefficient by 2.016, the oxygen coefficient by 16 and divide the sum by 18.016.

The table will contain the attenuation coefficients for the absorber being used. The x-factor, which you enter, is in inverse units of the attenuation coefficient. If the coefficient is entered in cm^2/g, then the factor must be in g/cm^2, which is the density (g/cm^3) times the thickness of the sample.

The linear attenuation coefficients can also be used. In this case the input factor will be the thickness. It might be more convenient to use the linear attenuation coefficients so that the input factor can be directly related to the sample.

To use the ratio of two spectra, take at least two spectra with and without the absorber. It is not necessary that the peaks be listed in the library, only that the peaks be defined in the spectra. The half-life of any nuclide used should be very long compared to the time of measurement of both spectra, so that decay corrections will not have to be made. The program calculates the ratio of the peak areas from the absorber-in and absorber-out analysis output files. This will give a table of energies (peak energies) and multipliers. The program now stores the natural log of the multipliers to obtain a table of energies and coefficients. The coefficients are divided by the thickness of the absorber (**Length**, entered on the Corrections tab, Fig. 142, p. 162), so that the factor you have entered is the sample thickness.

6.10.6.3. Example — Ratio Method

The following is an example of calculating the absorption factor using the ratio of two spectra. The results of the spectrum analysis without an absorber is shown in Fig. 250. The ^{154}Eu peaks are used because they are distributed over the range of interest.

The results with an absorber are shown in Fig. 251. The intensity (activity) columns from both figures have been transferred to Table 10, which also shows the ratio of the two sets of intensities and the logarithm of the ratio.

The logarithm values and the energies were entered into the absorption table. The absorption file records were saved in the “absorber-in” spectrum.

The spectrum was energy and efficiency calibrated using the point source (SRM 4275). The results of the analysis of the three conditions (no absorber, uncorrected absorber, and corrected absorber) are shown in Table 11.

NUCLIDE	PEAK CENTROID CHANNEL	ENERGY	BACKGROUND COUNTS	NET AREA COUNTS	INTENSITY CTS/SEC	UNCERT 1 SIGMA %	FWHM keV
EU-154	205.56	42.83	21567.	81517.	81.52	.56	1.386s
EU-154	600.95	123.08	3702.	63228.	63.23	.46	1.096
EU-154	1216.09	247.92	2387.	7803.	7.80	1.93	1.172
EU-154	1240.28	252.83	842.	66.	.07	77.62	.431s
EU-154	2909.92	591.69	1386.	3309.	3.31	3.67	1.490
EU-154	3516.06	714.71	1248.	258.	.26	47.25	1.071s
EU-154	3558.06	723.24	1344.	11503.	11.50	1.45	1.577
EU-154	4296.98	873.20	920.	5748.	5.75	2.21	1.631
EU-154	4902.96	996.19	869.	4710.	4.71	2.33	1.685
EU-154	4944.77	1004.67	987.	7712.	7.71	1.81	1.841
EU-154	6273.55	1274.35	77.	10292.	10.29	1.02	2.028
EU-154	7860.55	1596.44	4.	296.	.30	6.21	1.297s

s Peak fails shape tests.
D Peak area deconvoluted.

Figure 250. No Absorber Analysis.

NUCLIDE	PEAK CENTROID CHANNEL	ENERGY	BACKGROUND COUNTS	NET AREA COUNTS	INTENSITY CTS/SEC	UNCERT 1 SIGMA %	FWHM keV
EU-154	205.11	42.74	13258.	27358.	27.36	1.12	1.407s
EU-154	600.85	123.06	4562.	40707.	40.71	.68	1.090
EU-154	1215.85	247.88	2402.	5359.	5.36	2.56	1.230
EU-154	1244.33	253.66	1757.	208.	.21	43.82	.317s
EU-154	2910.12	591.73	1334.	2679.	2.68	4.42	1.569
EU-154	3517.08	714.92	1205.	278.	.28	38.89	.354s
EU-154	3558.02	723.23	1185.	8792.	8.79	1.47	1.628
EU-154	4296.72	873.15	602.	4686.	4.69	2.01	1.697
EU-154	4903.03	996.20	718.	3682.	3.68	2.62	1.690
EU-154	4944.84	1004.69	799.	6249.	6.25	2.00	1.824
EU-154	6273.41	1274.33	85.	8654.	8.65	1.13	2.100
EU-154	7860.54	1596.44	0.	256.	.26	6.25	1.780s

s Peak fails shape tests.
D Peak area deconvoluted.

Figure 251. Absorber-In Analysis.

All three isotopes in the sample are affected by the correction (see columns 3 and 4). The ^{154}Eu and ^{125}Sb are corrected to the no-absorber value. The ^{155}Eu activity is not corrected enough because all the lines used in the analysis of ^{155}Eu are below the lowest energy in the absorption table and the program uses a linear interpolation between the table values and linear extrapolation outside the table values. This underestimates the correction below the lowest energy because the attenuation is logarithmic in form.

Table 10. Absorption.

Energy	Without	With	Ratio	Log(ratio)
123.14	63.23	40.71	1.553	0.440
248.04	7.80	5.36	1.455	0.375
591.74	3.31	2.68	1.235	0.211
723.3	11.50	8.79	1.308	0.269
873.20	5.75	4.69	1.226	0.204
1004.76	7.71	6.25	1.234	0.210
1274.45	10.29	8.65	1.190	0.174

Table 11. Results — Measured Correction.

Nuclide	No Absorber	Uncorrected Absorber	Corrected Absorber
^{154}Eu	12750 Bq	10900 Bq	12750 Bq
^{155}Eu	8020	4813	7621
^{125}Sb	2900	2190	2890

6.10.6.4. Example — Table Values

The same spectrum example can be used to show the calculated coefficients. Using the mass attenuation coefficients table[33] for silicon and oxygen, the linear attenuation coefficients can be calculated for the sand absorber. Any other materials in the sand are ignored in this case, but might not be in the general case. Table 12 shows the mass attenuation coefficients for oxygen, silicon and sand (SiO_2).

The sand value can be calculated using the mass ratios. In this case it is also given in the handbook tables. The density of the sand was measured to be 1.67 g/cm^3. The fifth column in the table is the coefficient in column 4 multiplied by the density. These numbers are entered into the SOR table. This is the linear attenuation factor in 1/cm.

In the analysis, the absorption factor is entered as 1.6, because this is the thickness of the sand in cm. The result of the analysis using this table is shown in Table 13. Note that the calculated

[33]"Radiological Health Handbook," January 1970, U.S. Dept. of Health, Education and Welfare.

correction is more accurate below 100 keV than the measured correction so ^{155}Eu is more accurately corrected. Figure 252 shows the two correction files. The vertical scales have been adjusted to account for the difference in the input factor of 1.6.

Table 12. Calculated Coefficients.

	mu/rho			mu
Energy	**Oxygen**	**Silicon**	**Sand**	**Sand**
30	.372	1.41	.859	1.43
40	.257	.696	.463	.773
50	.213	.437	.318	.531
60	.191	.322	.252	.421
80	.168	.224	.194	.324
100	.156	.184	.169	.282
150	.136	.145	.140	.234
200	.124	.128	.126	.210
300	.107	.108	.108	.180
400	.0957	.0962	.0959	.160
500	.0873	.0875	.0874	.146
600	.0808	.0808	.0808	.135
800	.0708	.0707	.0707	.118
1000	.0637	.0635	.0636	.106
1500	.0518	.0518	.0518	.0865
2000	.0446	.0448	.0447	.0746

Table 13. Results — Calculated Correction.

Nuclide	No absorber	Uncorrected absorber	Corrected absorber
^{154}Eu	12750 Bq	10900 Bq	12450 Bq
^{155}Eu	8020	4813	7965
^{125}Sb	2900	2190	2776

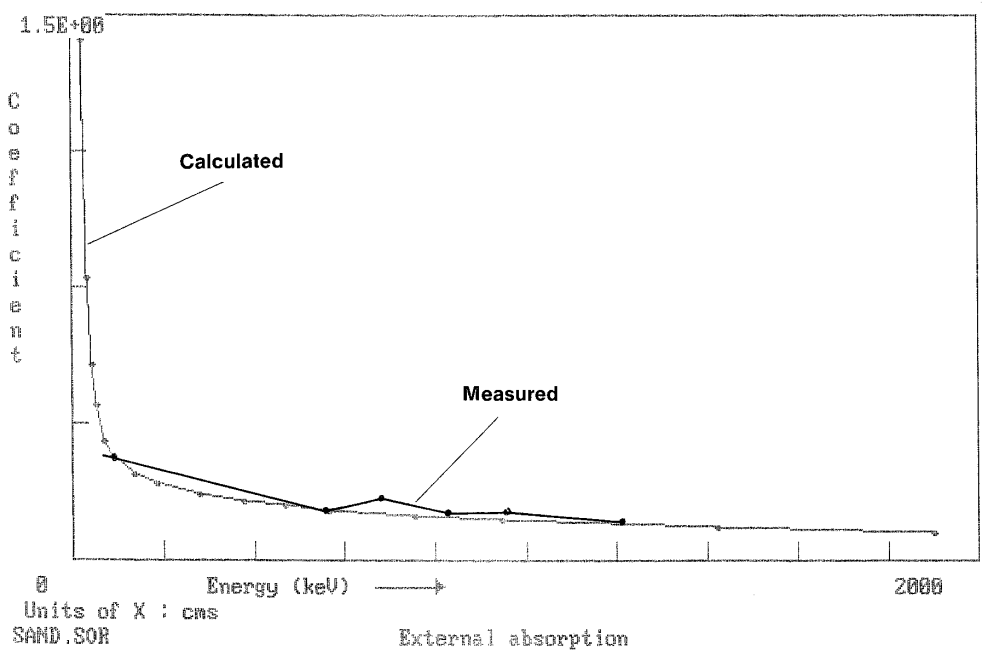


Figure 252. Comparison of Measured and Calculated Absorption Factors.

6.11. Random Summing

If more than one gamma-ray photon signal is absorbed by the detector during a pulse sampling cycle, the sum of the energies of the two (or more) is recorded in the spectrum. Since the two gamma rays are not related in any way, this is random coincidence. Random coincidence sum peaks can be formed at double the energy of the primary peaks (Fig. 253). Any full-energy photon that is summed with another pulse is not recorded in the single photon peak and represents a loss of counts or efficiency. This loss is count-rate dependent.

The random summing correction factor is:

$$RSF = \frac{1}{1 - \frac{\Sigma\, Ct}{F * LT_l}} \qquad \textbf{(91)}$$

where:

RSF = the random summing factor (multiplier)
Ct = the contents of all channels
F = the user-entered slope of the correction curve
LT_l = the live time

This value is set to 1.0 if it is calculated at less than or equal to zero.

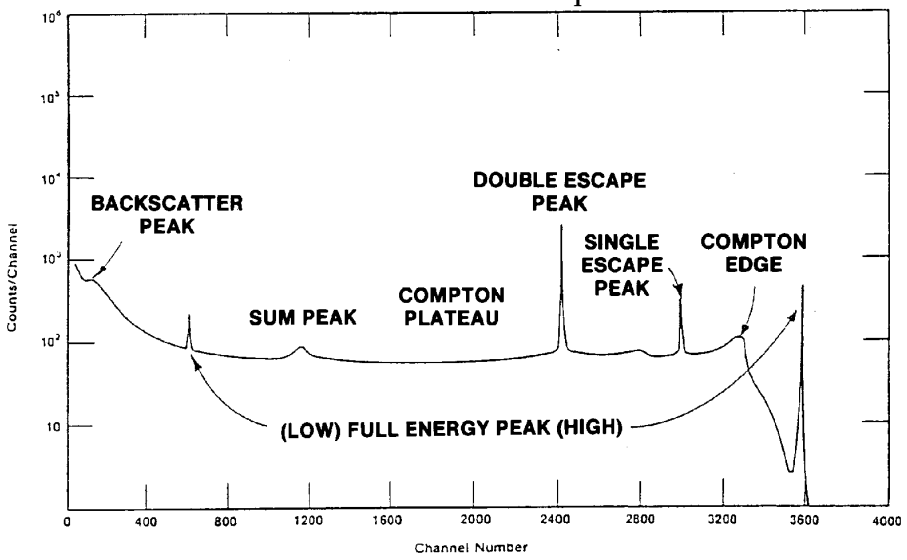


Figure 253. Random Summing. The Sum Peak Is the Sum of Two Coincident Low Full-Energy Peaks.

6.11.1. Random Summing Correction

The uncorrected peak area is multiplied by *RSF* to obtain the corrected peak area. This is done before the peak area is converted to activity.

The slope of the correction curve is dependent on the detector and the source/detector geometry. It is experimentally determined by the following simple procedure. The procedure requires two radioactive sources: one of low activity and high energy, and one of high activity and a lower energy. The energy of the high-activity source must be chosen so that it will not interfere with the high-energy peak, i.e., it should be less than half the energy. Two such sources are ^{88}Y and ^{137}Cs.

Position the high-energy source in front of the detector so that the count rate is low and collect a spectrum with a small counting statistical error (e.g., 100000 counts in the peak area). Measure the net peak area of the high energy gamma ray and the total counts in the spectrum (see Section 5.4.3, **Calculate/Peak Info...**). Now position the low-energy source in front of the detector to increase the count rate and collect a second spectrum for the same live time as the first spectrum. Again measure the net peak area and total counts in the spectrum. More spectra can be collected by moving the low-energy source closer to the detector to increase the count rate.

For example, six spectra were collected and the results are shown in Table 14.

Table 14. Random Summing Data.

Count Rate	Peak Area	Ratio
200	100000	1.00
2000	98850	0.98
4000	97200	0.97
6200	95900	0.95
8000	94800	0.94
9500	93700	0.937

Using the lowest and highest count rate values, the slope is calculated as:

$$SLOPE = \frac{200 - 9500}{1.0 - 0.937} = -147619 \quad \textbf{(92)}$$

The negative of this slope is the factor you enter as the **Random Summing** factor on the Sample tab under **Analyze/Settings/Sample Type...**.

6.12. Reported Uncertainty

The uncertainty printed on the report can be either counting or total uncertainty. They can be printed at 1, 2, or 3 sigma. The counting uncertainty is the uncertainty of the peak area due to statistical uncertainty, and was discussed earlier. For a peak net area, the counting uncertainty can be expressed in percent of the peak area. This same percent is used to express the percent counting uncertainty in the activity values.

6.12.1. Total Uncertainty Estimate

The total uncertainty estimate (1 sigma) is determined by summing in quadrature the individual uncertainties from the various analysis components.

$$\sigma_t = \sqrt{\sigma_{count}^2 + \sigma_{nor}^2 + \sigma_{rsum}^2 + \sigma_{abs}^2 + \sigma_{nuc}^2 + \sigma_{eff}^2 + \sigma_{geo}^2 + \frac{\sigma_{sys}^2}{3} + \sigma_{adl}^2 + \sigma_s^2} \quad \textbf{(93)}$$

where:

σ_{count} = counting uncertainty estimate (Section 6.3.4). If PBC is enabled, this term includes the PBC uncertainty calculated per Section 6.12.12.
σ_{nor} = additional normally distributed uncertainty estimate (Section 6.12.3)
σ_{rsum} = random summing uncertainty estimate (Section 6.12.4)
σ_{abs} = absorption uncertainty estimate (Section 6.12.5)
σ_{nuc} = nuclide uncertainty estimate (Section 6.12.6)
σ_{eff} = efficiency uncertainty estimate (Section 6.12.7)
σ_{geo} = geometry uncertainty estimate (Section 6.12.8)
σ_{sys} = systematic (uniformly distributed) uncertainty estimate (Section 6.12.9)
σ_{adl} = additional user-defined uncertainty factor (Section 6.12.10)
σ_{s} = sample size uncertainty (Section 6.12.11)

All components of uncertainty estimates except σ_{uni} are computed at the 1-sigma level. The uncertainty estimate for a uniformly distributed error is used at the full range. If a correction factor is not used, the uncertainty estimate is zero for that component.

6.12.2. Counting Uncertainty Estimate

This is discussed in Section 6.3.4.

6.12.3. Additional Normally Distributed Uncertainty Estimate

$Input_{nor}$ is obtained based on the **Random** setting in the **Additional Error** section of the Analysis tab of the Sample Types Settings dialog. This is saved in the .SDF file.

$$\sigma_{nor}^{2} = \left(\frac{Input_{nor}}{100} \right)^{2} \quad \textbf{(94)}$$

where:

σ^{2}_{nor} = variance of additional normally distributed uncertainty (% 1 sigma)
$Input_{nor}$ = user input for normally distributed uncertainty (% 1 sigma)

6.12.4. Random Summing Uncertainty Estimate

$$\sigma_{rsum}^{2} = \frac{|CF_{rs} - 1|}{100} \quad \textbf{(95)}$$

where:

σ^2_{rsum} = variance of random summing error estimate
CF_{rs} = random summing correction factor

6.12.5. Absorption Uncertainty Estimate

$$\sigma_{abs}^{2} = \frac{|CF_{ab} - 1|}{100} \quad \textbf{(96)}$$

where:

σ^2_{abs} = variance of attenuation error estimate
CF_{ab} = absorption correction factor

6.12.6. Nuclide Uncertainty Estimate

$$\sigma_{nuc}^{2} = \left(\frac{Input_{nuc}}{200} \right)^{2} \quad \textbf{(97)}$$

where:

σ^2_{nuc} = variance of nuclide error estimate
$Input_{nuc}$ = user uncertainty input for nuclide (% 2 sigma). This is the uncertainty in the yield (branching ratio) for the first gamma ray in the library for each nuclide.

6.12.7. Efficiency Uncertainty Estimate

The efficiency uncertainty is computed differently depending on the type of fit used for the efficiency calculation. The components used for efficiency include the errors due to uncertainty of the calibration source, uncertainty of the calibration fit, and the counting uncertainty of the calibration.

The total efficiency uncertainty, σ_{eff}, is calculated as:

$$\sigma_{eff}^2 = \sigma_c^2 + \sigma_p^2 \quad (98)$$

where σ_c is the calibration fit uncertainty and σ_p is the calibration counting uncertainty, both discussed in the sections below.

6.12.7.1. Calibration Counting Uncertainty

When an efficiency calibration is performed, the counting uncertainty is calculated and stored in the calibration record. In general, there is an above-the-knee counting uncertainty and a below-the-knee counting uncertainty, both calculated and saved to the calibration data record.

For polynomial and TCC-polynomial type calibrations, the counting uncertainty above the knee is calculated as the averaged counting uncertainty of all calibration peaks involved, regardless of the knee energy, as shown below:

$$\sigma_{ca} = \frac{1}{N}\sum_{i=1}^{N}\sigma_{ci} \quad (99)$$

where σ_{ci} is the counting uncertainty of the i-th calibration peak, and N is the total number of calibration peaks used. The counting uncertainty below the knee is always set to zero for these two calibration types:

$$\sigma_{cb} \equiv 0 \quad (100$$

For all other calibration types, the above-the-knee counting uncertainty is calculated as the averaged counting uncertainty of all the calibration peaks with energy greater than or equal to the knee energy, as shown below:

$$\sigma_{ca} = \frac{1}{N1}\sum_{i=1}^{N1}\sigma_{ci}, \qquad with\ E_i \geq E_{knee} \quad (101)$$

where $N1$ isthe number of calibration peaks whose energies are greater than or equal to the knee energy.

The below-the-knee counting uncertainty is calculated as the averaged counting uncertainty of all the calibration peaks with energy less than the knee energy:

$$\sigma_{cb} = \frac{1}{N2}\sum_{j=1}^{N2}\sigma_{ci}, \qquad with\ E_j < E_{knee} \tag{102}$$

where *N2* is the number of calibration peaks with energies less than the knee energy. If *N2* is zero, the counting uncertainty is zero.

For polynomial and TCC-polynomial type calibrations, the calibration counting uncertainty σ_p is always equal to the counting uncertainty above the knee:

$$\sigma_p = \sigma_{ca} \tag{103}$$

For all other calibration types, σ_p is calculated as:

$$\begin{aligned} \sigma_p &= \sigma_{cb}, \quad E > E_{knee} \\ \sigma_p &= \sigma_{ca}, \quad E \le E_{knee} \end{aligned} \tag{104}$$

NOTE For calibrations performed before GammaVision 7, the above-and below-the-knee counting uncertainties are both zero. To take into account the counting uncertainty discussed here, update the efficiency calibration with GammaVision 7 so the new uncertainties will be calculated and stored in the calibration file. Then, when a spectrum is analyzed, the final reported activity uncertainty will take into account the added uncertainty in calibration.

6.12.7.2. TCC-Polynomial

The calibration variance is the averaged variance of all the calibration points in the certificate file:

$$\sigma_c = \sqrt{\frac{\sum_{i=1}^{N}\sigma_i^{\,2}}{N}} \tag{105}$$

where:

σ_C = the calibration uncertainty
σ_i = the uncertainty of the i^{th} calibration point from the certificate
N = the total number of calibration points

6.12.7.3. Interpolative

For this calculation, the calibration points are sorted in ascending order by energy. If energy E is less than the first (lowest-energy) calibration point, E_i and E_{i+1} are the two lowest-energy calibra

tion points. If energy E is greater than the last (highest-energy) calibration point, E_i and E_{i+1} are the two highest-energy calibration points. For all other cases, $E_i < E < E_{i+1}$:

$$\sigma_c = \frac{\sigma_i(E_{i+1} - E) + \sigma_{i+1}(E - E_i)}{(E_{i+1} - E_i)} \quad \textbf{(106)}$$

where:

σ_i = the uncertainty (*not* the fractional uncertainty) associated with energy E_i from the certificate.

This calculation is also used when energy E is less than the first calibration point, the efficiency fit is polynomial, and the detector is N-type.

6.12.7.4. Linear, Quadratic or Polynomial

In general, the efficiency curve (or efficiency fit) can be expressed as:

$$\ln \varepsilon = \sum a_k x^n, \quad k = 1, \ldots, m \quad \textbf{(107)}$$

where:

ε = the efficiency at energy E

a_k = the k^{th} fitting parameter

The parameters x, n, and m depend on the type of efficiency curves:

- For linear/quadratic fits:

$$\begin{aligned} x &= \ln E \\ n &= k - 1 \\ m &= 2 \text{ (}\textit{linear}\text{) } \textit{or } 3 \text{ (}\textit{quadratic}\text{)} \end{aligned} \quad \textbf{(108)}$$

- For polynomial fits:

$$\begin{aligned} x &= E \\ n &= 2 - k \\ m &= 6 \end{aligned} \quad \textbf{(109)}$$

If the energy x is lower than the lowest two calibration points, the analysis engine performs an interpolated fit instead of a polynomial fit. The summation in Eq. 107 is the sum over all the fitting parameters, $k = 1, ..., m$, not the sum over all the calibration points.

Now let us define a parameter y as $y = ln\ \varepsilon$. This yields:

$$y = \sum a_k x^n, \quad k = 1, ..., m \tag{110}$$

The fitted efficiency at any point x_i (as defined in Eqs. 108 and 109 above) is:

$$y_i(x_i) = \sum a_k x_i^n, \quad k = 1, ..., m \tag{111}$$

Matrix Solution

Equation 111 above is Eq. 7.12 in Bevington,[34] except that the function $f_k(x_i)$ has been replaced by x_i^n, a particular type of polynomial:

$$f_k(x_i) = x_i^n \tag{112}$$

where x_i and n are defined in Eqs. 108 and 109.

From Eq. 7.14 in Bevington, the â matrix is calculated using Eq. 112 above:

$$\beta_k = \sum (1/\sigma_i^2)\ y_i\ x_i^n, \quad i = 1, ..., N \tag{113}$$

where σ_i and N are defined in Eq. 105, y_i is defined in Eq. 111, and x_i is defined in Eqs. 108 and 109.

From Eq. 7.15 in Bevington, the α matrix is calculated by:

$$\alpha_{nk} = \sum (1/\sigma_i^2)\ x_i^{(n_1+k_1)}, \quad i = 1, ..., N \tag{114}$$

where for a linear/quadratic fit:

$n_1 = n - 1$

$k_1 = k - 1$

[34]Bevington, Philip R. and D. K. Robinson. *Data Reduction and Error Analysis for the Physical Sciences*, 2nd ed., McGraw-Hill, 1992.

and for a polynomial fit:

$n_1 = 2 - n$

$k_1 = 2 - k$

The σ_i factor is the fractional uncertainty at the i^{th} calibration point (as defined for Eq. 105). σ_i is not the absolute uncertainty because the actual curve being fitted is not the efficiencies themselves but the natural log of the curve.

Matrix Inversion

From Eq. 7.20 in Bevington, the n^{th} fitting parameter in our Eq. 110 or Eq. 107 can be calculated as:

$$a_n = \sum \beta_k \delta_{kn}, \quad k = 1, \ldots, m \tag{115}$$

where ä is the *inverse matrix* of á:

$$\delta = \alpha^{-1} \tag{116}$$

The ä matrix is called the *error matrix* because its diagonal elements are the variances of the fitting parameters, and the off-diagonal elements are the covariances of the fitting parameters (see Eq. 7.25 in Bevington):

$$\sigma^2_{a_i a_j} = \delta_{ij}, \qquad i, j = 1, \ldots, m \tag{117}$$

If $i = j$, $\sigma^2_{a_i a_j}$ is the variance for the fitting parameter a_i. If $i \neq j$, $\sigma^2_{a_i a_j}$ is the covariance between the fitting parameter a_i and a_j.

Uncertainty of the Fit

From Eq. 3.13 in Bevington, the polynomial fit uncertainty is given by:

$$\sigma_y^2 = \sum \sum \delta_{ij} (\partial y / \partial a_i)(\partial y / \partial a_j) \qquad i, j = 1, \ldots, m \tag{118}$$

where y is the polynomial given in Eq. 110 and a_i is the i^{th} fitting parameter. The error matrix δ_{ij} has been used instead of $\sigma^2_{a_i a_j}$ for clarity. Equation 118 does not use the factor 2 before the covariance terms, as is done in Bevington Eq. 3.13. This is due to the double-summation notation used in Eq. 118 and because the error matrix is symmetric ($\delta_{12} = \delta_{21}$, ...). The diagonal elements are not double-counted in the above equation. (In Bevington Eq. 3.13, $\sigma^2_{a_i a_j}$ is denoted as $\sigma^2_{a_i}$.)

From Eq. 110, since $\partial y/\partial a_i = x^{i_1}$, we have:

$$\sigma_y^2 = \sum\sum \delta_{ij}\, x^{(i_1+j_1)} \qquad i, j = 1, \ldots, m \tag{119}$$

where for a linear/quadratic fit:

$i_1 = i - 1$
$j_1 = j - 1$

and for a polynomial fit:

$i_1 = 2 - i$
$j_1 = 2 - j$

Finally, the calibration uncertainty is:

$$\sigma_c = \varepsilon\, \sigma_y \tag{120}$$

where ε is the fitted efficiency at energy E (from Eq. 107), and σ_y is calculated from Eq. 119. If σ_c is zero, then the "sigma above" (σ_a) or "sigma below" (σ_b) value described in the following paragraphs is used.

If the fit type is neither polynomial nor TCC-polynomial, the calibration uncertainty is calculated as:

$$\sigma_c = \sigma_a \qquad for\ E > E_{knee} \tag{121}$$

$$\sigma_c = \sigma_b \qquad for\ E \le E_{knee} \tag{122}$$

where σ_a and σ_b are defined as follows.

If the energy $E > E_{knee}$,

$$\sigma_a^2 = \frac{\sum [(\varepsilon_i - f_i)/f_i]^2 - \left(\sum |(\varepsilon_i - f_i)|/f_i \sum |(\varepsilon_i - f_i)|/f_i\right)/N_a}{N_a - 1} \quad \textbf{(123)}$$

If $E \le E_{knee}$,

$$\sigma_b^2 = \frac{\sum [(\varepsilon_i - f_i)/f_i]^2 - \left(\sum |(\varepsilon_i - f_i)|/f_i \sum |(\varepsilon_i - f_i)|/f_i\right)/N_b}{N_b - 1} \quad \textbf{(124)}$$

where:

ε_i = the measured efficiency at energy E_i
f_i = the calculated efficiency at E_i from Eq. 107
E_{knee} = the efficiency knee energy

N_a is the number of efficiency points above the knee energy and N_b is the number of efficiency points below the knee energy. Both N_a and N_b must be greater than 1. If σ_a or σ_b is zero, the default uncertainty of 1.5% is used.

If the fit type is polynomial but not TCC-polynomial, the calibration uncertainty is calculated as:

$$\sigma_c = \sigma_a \quad \textbf{(125)}$$

For polynomial fits, E_{knee} is always ignored.

Sometimes, the efficiency pairs might be missing from the calibration file but the fit parameters and fit type are stored in the file. In these cases, the σ_a or σ_b value is used.

6.12.8. Geometry Uncertainty Estimate

This value, σ_{geo}^2,.is based on the geometry uncertainty estimate entered on the geometry correction sidebar (Fig. 153):

$$\sigma_{geo}^2 = \left(\frac{Input_{geo}}{100}\right)^2 \quad \textbf{(126)}$$

If the uncertainty is 0 or no value is entered, or if using a .GEO file from an earlier version of GammaVision, a fixed value of 1.5% is used.

6.12.9. Uniformly Distributed Uncertainty Estimate

$Input_{sys}$ is obtained based on the **Systematic** setting in the **Additional Error** section of the Analysis tab of the Sample Types Settings dialog. This is saved in the .SDF file.

$$\sigma_{sys}^{2} = \left(\frac{Input_{sys}}{100} \right)^{2} \quad \textbf{(127)}$$

where:

σ^2_{sys} = uncertainty estimate for a uniformly distributed uncertainty estimate
$Input_{sys}$ = user input for full range (%)

6.12.10. Additional User-Defined Uncertainty Factors

On the Uncertainties tab (Fig. 144) you can optionally define up to nine uncertainty values σ_{usr1} through σ_{usr9}, which are added quadratically to the total relative uncertainty, σ_t, as the additional user-defined uncertainty factor σ_{adl} as follows:

$$\sigma_{adl}^{2} = \sigma_{usr1}^{2} + \sigma_{usr2}^{2} + \sigma_{usr3}^{2} + \sigma_{usr4}^{2} + \sigma_{usr5}^{2} + \sigma_{usr6}^{2} + \sigma_{usr7}^{2} + \sigma_{usr8}^{2} + \sigma_{usr9}^{2} \quad \textbf{(128)}$$

Both the field description and its corresponding non-zero value must be defined for an uncertainty entry or it is not used. These values are stored in the .SDF file as well as .SPC spectrum files, and are reported individually in the Analysis Parameters table.

6.12.11. Sample Size Uncertainty

The value σ_s^2 is based on the sample size uncertainty entered on the System tab.

$$\sigma_s^2 = \left(\frac{Input_s}{100} \right)^2 \quad \textbf{(129)}$$

If using an .SDF file from an earlier version of GammaVision, a fixed value of 1.5% is used.

6.12.12. Peaked Background Correction and Uncertainty Calculations

6.12.12.1. Single PBC Subtraction

If the PBC net count rate at energy E is R_p (in cps), the live time is LT (in seconds), and the fractional uncertainty of the net PBC peak count rate is σ_p, then the corresponding PBC counts N_p and the associated absolute uncertainty σ_{absp} in counts can be calculated from the following:

$$N_p = LT * R_p \quad \textbf{(130)}$$

$$\sigma_{absp} = N_p * \sigma_p \quad \textbf{(131)}$$

If N_0 is the peak area in counts before PBC, σ_0 is the corresponding fractional uncertainty, and σ_{abs0} is the corresponding absolute uncertainty for the net peak area before PBC (see Eq. 48, page 251), the absolute peak area uncertainty before PBC is:

$$\sigma_{abs0} = N_0 * \sigma_0 \quad \textbf{(132)}$$

The PBC corrected peak area N (in counts) is calculated as:

$$N = N_0 - N_p \quad \textbf{(133)}$$

If, after PBC, the net peak area is <0, it is set to 0 unless **Directed Fit** is enabled (because negative peak area is not physical). After PBC, the subtracted PBC area is added to the peak background. If B_0 is the peak background before PBC, the peak background after PBC is:

$$B = B_0 + N_p \quad \textbf{(134)}$$

After PBC, the variance of the peak net area counts has contributions from the PBC subtraction as well as from the change in the peak background discussed above. The variance from the PBC subtraction is simply σ_{absp}^2.

The variance due to the change in the peak background is taken to be the increase in the peak background, N_p. Therefore, after PBC, the total absolute uncertainty (in counts) for the net peak area is calculated as:

$$\sigma_{absN} = \sqrt{\sigma_0^2 + \sigma_{absp}^2 + N_p} \quad \textbf{(135)}$$

Note that for PBC, only the absolute uncertainties (not relative) are added in quadrature. After the PBC correction, the relative uncertainty in percent is calculated as:

$$\sigma_N = \sigma_{absN} / Abs(N), \qquad if\ N<>0 \quad \textbf{(136)}$$

If the PBC corrected area is exactly zero, the relative uncertainty is set at 1000% (or 10.0), the default value used in all cases where the activity is zero.

Note that when PBC is enabled, the counting uncertainty for a peak always has PBC contributions. That is, the counting uncertainty calculated before PBC (σ_0 in Eq. 132) is not saved in the .UFO file. The same holds for the peak area; it is always the PBC corrected value, and the net peak area before PBC is not saved in the .UFO file.

6.12.12.2. Multiple PBC Subtraction

If there are multiple PBC peaks under a peak, that peak is subject to multiple PBC subtractions. The sum of the PBC net areas is simply the sum of individual PBC areas (for comparison, see Eq. 130 for single PBC subtraction):

$$N_p = \sum_{i=1}^{m} \left(LT * R_{p-i} \right) \quad \textbf{(137)}$$

where LT is the live time, R_{p_i} is the PBC count rate for the i-th PBC, and m is the total number of PBC peaks.

The total PBC uncertainty is calculated from the following (compare to Eq. 131):

$$\sigma_{absp}^{\ 2} = \sum_{i=1}^{m} \sigma_{absp-i}^{\ 2} \quad \textbf{(138)}$$

where ó$_{absp_i}$ is the absolute uncertainty of each PBC peak in counts. After calculating N_p and σ_{absp} for the combined PBC subtraction with multiple PBC the rest of the calculations can be applied the same way as for a single PBC (that is, all equations in this section except Eqs. 130 and 131 can be applied the same way for both single and multiple PBC subtractions).

6.13. EBAR — Average Energy

The average energy calculation (EBAR) represents the sum of the average beta-gamma emission energy per disintegration for the identified radionuclides in the sample. The nuclides must be in the analysis library and the EBAR table (i.e., the .EBR file). The weighting factors of the activity of each isotope are usually defined by the plant chemistry procedures or can be calculated based on data found in radioactive-decay tabulations such as DOE/TIC-11026[35] or ORNL/NUREG/TM-102.[36]

The EBAR formula is:

$$EBAR = \frac{\sum_{i=1}^{n} E_i A_i}{\sum_{i=1}^{n} A_i} \quad \textbf{(139)}$$

where:

$EBAR$ = the sum of the average beta and gamma energies in keV/disintegration
E_i = $e^{\beta}{}_i + e^{\gamma}{}_i$, the average energy/disintegration for an individual nuclide
A_i = the activity for nuclide i
n = the number of nuclides

The average energy for a given nuclide is the sum of the product of the energy of the gamma ray and the abundance of that ray, plus the product of the energies of the electrons (1/3 the maximum for beta decay), plus the abundance of that ray.

[35]DOE/TIC-11026, United States Department of Energy, Office of Scientific and Technical Information, Oak Ridge, Tennessee.

[36]Technical Manual TM-102, Nuclear Regulatory Commission Guide, Oak Ridge National Laboratory, Oak Ridge, Tennessee.

As an example, consider the decay scheme for ^{133}Xe–^{133}Cs in Fig. 254.

The maximum beta energy is given as 346 keV, which gives 267 keV and 45 keV for the energies of the transitions to the 160 keV and 382 keV states in ^{133}Cs. In addition to beta-decay electrons, the internal conversion electrons must also be included. The K-conversion electron has an energy of 45 keV and an abundance of 54%; the L electron has an energy of 75 keV and an abundance of 7%.

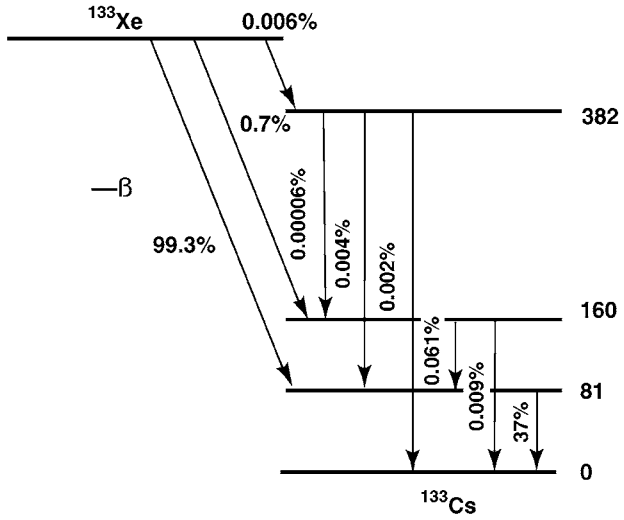


Figure 254. Decay Scheme.

Thus, for the betas, the energy is:

	$346 \times 0.993 \times 1/3$	=	114.5	
+	$267 \times 0.007 \times 1/3$	=	1.9	0.6
+	$45 \times 6.0 \times 10^{-5} \times 1/3$	=	0	
+	45×0.534	=	24.1	
+	45×0.09	=	6.8	
			146.0	

For the gamma rays, each gamma energy is multiplied by its abundance. In addition, the x-ray fluorescence from the internal conversion must also be included. For the two electrons (K and L), the x-ray energies are 36 keV and 6 keV, respectively. The same abundances as above are used.

The gammas yield the following:

	81×0.37	=	30.0
+	$79 \times 6\times10^{-4}$	=	0
+	$100 \times 9\times10^{-5}$	=	0
+	$220 \times 6\times10^{-7}$	=	0
+	$302 \times 4\times10^{-5}$	=	0
+	$382 \times 2\times10^{-5}$	=	0
+	36×0.534	=	19.2
+	6×0.09	=	0.5
			49.7 keV/disintegration

Adding the values for the electron energy and gamma energy gives the total average energy of 195.7 keV/disintegration for ^{133}Xe.

In the calculation of the average energy value for a nuclide, care must be taken to ensure that all radiations are counted.

NOTE Be sure the isotope identifiers (e.g., “Xe-133") in the average energy table match the identifiers in the analysis library, otherwise, GammaVision will be unable to calculate this value correctly.

6.14. IEQ — Iodine Equivalence

The iodine equivalence (Dose Equivalent Iodine-131) calculation is used to calculate that concentration of ^{131}I which alone would produce the same thyroid dose as the quantity and isotopic mixture of ^{131}I, ^{132}I, ^{133}I, ^{134}I, and ^{135}I actually present. The thyroid dose conversion factors are given in Table III of TID-14844[37] or Table E-7 of NRC NUREG 1.109 Rev. 1.[38] Table 15 shows the IEQ values from TID-14844.

Table 15. IEQ Table.

Nuclide	^{131}I Equiv
^{131}I	1.00000
^{132}I	3.610000E−02
^{133}I	0.270300
^{134}I	1.690000E−02
^{135}I	8.380000E−02

The IEQ value is the sum of the products of the isotopic abundance and the corresponding factor for all the isotopes in both the analysis library and the table.

[37]TID-14844, United States Department of Energy, Office of Scientific and Technical Information, Oak Ridge, Tennessee.

[38]Guide Number 1.109 Rev. 1, United States Nuclear Regulatory Commission, Washington, DC. October 1977.

The value is:

$$I = \sum_{i=1}^{l} A_i F_i \quad \textbf{(140)}$$

where:

A_i = the activity for the i^{th} isotope
F_i = the i^{th} factor
l = all the isotopes

The units of IEQ are the units specified in the report. If decay correction is specified, both the decay-corrected equivalent activity and the time-of-count equivalent activity are reported. Isotopes that are not found (those whose MDAs are reported) are not included in the reported value. If the decay correction is more than 12 half-lives, the decay-corrected value is not included in the reported value.

NOTE Be sure the isotope identifiers (e.g., “I-133") in the average energy table match the identifiers in the analysis library, otherwise, GammaVision will be unable to calculate this value correctly.

6.15. DAC or MPC

The DAC or MPC calculation is a measure of the fraction of the allowed activity or concentration in the current sample. The allowed activity or concentration values are stored in a table (see Section 5.5.1.8). A value of 1 (or 100%) means the sample had 100% of the allowed value.

NOTE Be sure the isotope identifiers (e.g., “Xe-133") in the table match the identifiers in the analysis library, otherwise, GammaVision will be unable to calculate this value correctly.

For cases where nuclides are identified in the analysis but not explicitly included in the DAC table, you can optionally add a nuclide named “Default” with an associated DAC value to the DAC table for use in the calculation. If no “Default” entry is included, then nuclides with activity reported that do not match a nuclide name in the DAC table will not affect the DAC calculation.

The value is defined as:

$$DAC = \frac{A_i * 100}{D_i} \quad \textbf{(141)}$$

where:

A_i = the activity of isotope *i*
D_i = the allowed value for isotope *i*
DAC = the fractional allowed value in percent

The value is not calculated for MDA values.

6.16. True Coincidence Correction

In the case where a nuclide emits multiple cascade gamma rays when it decays, these multiple gamma rays can be detected individually or together as one gamma ray. An example decay is ^{60}Co, as shown in Fig. 255. The two gamma rays (1173.2 and 1332.5 keV) are emitted in cascade or one after another. The lifetime of the intermediate state is very short so that it appears that the two gamma rays are emitted in coincidence (i.e., at the same time). Since the two gamma rays can interact in the detector in a time short compared to the response time of the detector and the resolving time of the electronics, the two gamma rays are recorded as a single gamma ray.

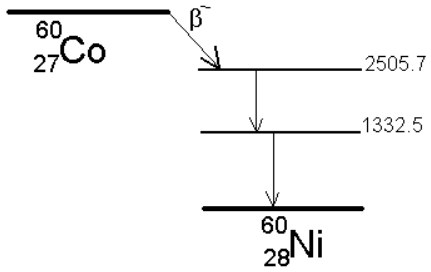


Figure 255. ^{60}Co Decay to ^{60}Ni.

When the two gamma rays are detected as one, it effects the spectrum in two ways. One way is the creation of a "sum" peak that is the sum of the amplitudes of the two individual full-energy peaks. The second way is to remove counts from the full-energy peak. The first creates extra peaks in the spectrum. The second reduces the peak area of these gamma rays and thus the reported activity of the nuclide.

The reduction of the peak area due to summing is more important than the creation of the "sum peak." The sum peak requires the addition of two full-energy pulses to get the summed energy. The reduction of the peak area only requires that there be a full-energy interaction at the same time as another interaction from the other members of the cascade. Recall that most of the interactions in the detector do not produce full-energy peaks, but produce partial-energy interactions (the Compton background). A summing with any of the partial-energy signals will result in the full-energy pulse being removed from the full-energy peak. Further details can be found in many

references.[39,40,41]

The *true coincidence correction* (TCC) is the correction necessary to account for all of the pulses removed from the full-energy peak. This correction is a simple divisor of the net peak area, that is the net peak area is increased by the correction factor. The correction factor is detector and sample geometry dependent. The correction factor depends on the full-energy efficiency, that is the ability of the detector to detect the total energy of the gamma ray, and the total efficiency, that is the ability of the detector to detect any part of the gamma ray energy. The full-peak efficiency is determined in the efficiency calibration (**Calibrate/Efficiency**) and the total efficiency is determined in the TCC part of **Calibrate/Calibration Wizard...**.

6.17. ISO NORM Implementation in GammaVision

This section details the implementation of the ISO-11929:2010 standard referred to as ISO NORM in GammaVision.

6.17.1. The ISO NORM Model in GammaVision

The ISO NORM model is described mathematically as:

$$y = (x_1 - x_2 x_3 - x_4) * \xi \quad \textbf{(142)}$$

where:

y = peak activity (A)
x_1 = gross counts (G)
x_2 = background counts (B)
x_3 = shielding factor (egual to 1 in GammaVision)
x_4 = additional background correction term (zero in GammaVision)
ξ = conversion factor from net counts to activity as described in Equation 60.

This formula simplifies to A=N * ξ which is described in Equation 59.

6.17.2. Peak Calculation Details

[39] Glenn F. Knoll, *Radiation Detection and Measurement*, 3rd edition, p. 323, Wiley and Sons, 2000.

[40] Gilmore, G., and J.D. Hemingway, *Practical Gamma-Ray Spectrometry*, p. 156, Wiley and Sons, 1995.

[41] "Calibration and use of Germanium Spectrometers for the measurement of gamma-ray emission rates of radionuclides," ANSI N42.14-1991.

6.17.2.1. Critical Level or Decision Threshold

Critical peak area N_{CL} is calculated as follows when Net Counts is presumed to be zero:

$$N_{CL} = \left(k_{1-\alpha}\right)\sqrt{B + \sigma_B^{\,2}} \quad \textbf{(143)}$$

where:

$k_{1-\alpha}$ is the quantile of the normal distribution for the probability α

If the uncertainty of the background is taken as the square root of the peak background, and if $k_{1-\alpha}$ is 1.645, then the ISO NORM Critical Level calculation is similar to the Critical Level MDA Method (Section 6.9.2.2):

$$N_{CL} = 2.33\sqrt{B} \quad \textbf{(144)}$$

6.17.2.2. Peak MDA or Peak Detection Limit

ISO NORM MDA is calculated as follows:

$$MDA = \frac{\xi * (b + \sqrt{v})}{2 * c} \quad \textbf{(145)}$$

where:

$$b = 2 * N_{CL} + k_{1-\beta}^2 \quad \textbf{(146)}$$

Uncertainties in the MDA Equation

$$v = b * b - 4 * \left(1 - k_{1-\beta}^2 * \left(\sigma_\xi\right)^2\right) * \left(1 - \frac{k_{1-\beta}^2}{k_{1-\alpha}^2}\right) * N_{CL}^2 \quad \textbf{(148)}$$

$$c = 1 - k_{1-\beta}^2 * \left(\sigma_\xi\right)^2 \quad \textbf{(147)}$$

The uncertainty of the conversion factor takes into account all of the total uncertainty parameters

without the counting uncertainty term:

$$\sigma_\xi = \sqrt{\sigma_A^2 - \sigma_{count}^2} \quad \textbf{(149)}$$

where:

σ_A = Peak Activity total uncertainty (Section 6.12).
σ_{count} = Peak Counting uncertainty (Section 6.3.4)

Special Cases

Under special conditions when both error probabilities are the same:

$$k_{1-\alpha} = k_{1-\beta} = k \quad \textbf{(150)}$$

So, the MDA is:

$$MDA = \left(\frac{k^2 + 2k\sqrt{B + \sigma_B^2}}{c} \right) * \xi \quad \textbf{(151)}$$

If we further assume the error probability is at 5% and the variance of the background is background B itself:

$$\sigma_B^2 = B, \qquad k = 1.645 \quad \textbf{(152)}$$

then the MDA is as follows (similar to MDA Method 12 which is derived from Currie):

$$MDA = \left(\frac{2.71 + 4.66 * \sqrt{B}}{c} \right) * \xi \quad \textbf{(153)}$$

MDA to Critical Level Ratio

When the critical level, in counts, is much greater than $k_{1-\alpha}^{2}$, the MDA can be calculated from the following equation:

$$N_{MDA}/N_{CL} = f\left(1+\sqrt{1-\frac{1}{f}\left(1-\frac{1}{\left(k_{1-\alpha}\sigma_{\xi}\right)^{2}}\left(1-\frac{1}{f}\right)\right)}\right) \quad \textbf{(154)}$$

where f is defined as:

$$f = \frac{1}{1-k_{1-\beta}^{2}*\left(\sigma_{\xi}\right)^{2}} \quad \textbf{(155)}$$

If we define the above MDA ratio as R:

$$R \equiv N_{MDA}/N_{CL} \quad \textbf{(156)}$$

and define X and A as:

$$X = 1/f, \qquad A = \frac{1}{k_{1-\beta}^{2}*\left(\sigma_{\xi}\right)^{2}} \quad \textbf{(157)}$$

then the MDA ratio R becomes:

$$R \approx f*\left(1+\sqrt{1-X*\left(1-A*\left(1-X\right)\right)}\right) \quad \textbf{(158)}$$

For a given R and A, the corresponding f can be obtained as follows:

$$f = (R^{2}+A)/(2R+A-1) \quad \textbf{(159)}$$

If the beta risk error and the alpha risk error are the same ($k_{1-\alpha} = k_{1-\beta} = k$), then no matter the value of k and the uncertainty, R is twice the value of factor f:

$$R \approx 2 * f \quad \textbf{(160)}$$

Maximum MDA Ratio

If the uncertainties are extremely small so that A is very large, then the MDA correction factor f should be close to 1.0 and the MDA ratio R approaches a value of 2.0. Note that this is true even though the beta and alpha errors are not the same. Therefore, the minimum MDA ratio should be set to 2.0 as well. Under typical conditions, the following are true:

$$\begin{aligned} A &>> 1 \\ f &\approx 1 \\ R &\approx 2 \end{aligned} \quad \textbf{(161)}$$

However, when the uncertainty is increased, A becomes smaller and f becomes larger such that the ratio can approach infinity if the denominator for f is zero ($A \approx 1$). When the uncertainty is further increased, both f (or R) and the MDA become negative.

The MDA is prevented from going negative or to infinity by reducing the beta risk error so there is an upper limit for the ratio R:

$$R \leq R_{Max} \quad \textbf{(162)}$$

The steps for limiting the ratio are:

1) Calculate the MDA ratio using the original alpha and beta risk error.

2) If the calculated R is greater than R_{Max}, force the ratio R to the value of R_{Max} to calculate an MDA correction factor f_{max} as shown below:

$$f_{max} = (R_{Max}^2 + A) / (2R_{Max} + A - 1) \quad \textbf{(163)}$$

3) To reduce the MDA correction to the value f_{max}, the beta risk error must be increased to decrease the $k_{1-\beta}$ value. The new beta risk error can be calculated from:

$$(k_{1-\beta})_{max} = \frac{1}{\sigma_\xi} * \sqrt{(1 - 1/f_{max})} \quad \textbf{(164)}$$

If the upper limit of R is set to 3, the corresponding maximum MDA correction factor is about 1.5. In GammaVision, R_{Max} can be any value from 2 to 1000 for the “Maximum ISO NORM

MDA Ratio factor" in the b30winds.ini (n30winds.ini for NAI32) file. Any value outside this range will result in using the default value of 3.

Maximum MDA Report

If R_{Max} is 3.0, the uncertainty to reach the maximum correction is about 35.1% with all parameters at default values. When the actual uncertainty is larger than this a new $k_{1-\beta}$ is calculated so the MDA ratio R remains at R_{Max}. If the uncertainty is extremely large, the asymptotic value of $k_{1-\beta}$ is zero and the corresponding value for the beta risk factor is 50%.

When the maximum MDA ratio has been reached, an "I" flag is reported next to the isotope name as shown here:

```
AM-241 I     5.7471E+03   6.7293E-01%   6.0850E+01%   1.000E+4
             5.7471E+03   5.6712E+03    5.8230E+03    5.791E+01   6.729E-01%
```

At the end of the ISO NORM table, the flags are defined as:

```
I - ISO NORM MDA ratio at maximum for one or more peaks
```

Note that the "I" flag supercedes other nuclide flags (A, B, C, F, and H). If there is more than one peak defined in the library for an isotope, it is possible that the ISO NORM MDA for one peak is limited even though the MDA is not capped for other peaks of the same isotope. But the isotope would still have the "I" flag assigned. However, if the nuclide is not present and the MDA is reported as the activity, the less-than flag may supercede all other flags, including the "I" flag, since that flag is of higher importance to the users. At default values, the uncertainty corresponding to the maximum MDA ratio is about 35%. The best estimated uncertainty can be used as an indication of whether the maximum MDA ratio has reached.

6.17.2.3. The Best Estimated Activity

The best estimated activity is calculated as:

$$A_h = \xi * N_s * \left(Q + \frac{\left[e^{\left(-\frac{Q^2}{2} \right)} \right]}{\omega} * \sqrt{2\pi} \right) \quad \textbf{(165)}$$

where:

$$Q = \frac{N}{N_s} \quad \textbf{(166)}$$

$$N_s = \frac{\sigma_A}{\xi} \quad \textit{when Reporting Total Uncertainty}$$

$$N_s = \sigma_N \quad \textit{when Reporting Counting Uncertainty}$$

and the parameter ω is defined as follows (see Eq. 31 or F.18 in ISO NORM):

$$\omega = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{Q} e^{(-v^2/2)}\, dv \quad \textbf{(167)}$$

The integration is from $-\infty$ to Q. In Eq. 165, the second term comes from the biased estimator used in ISO NORM.

The uncertainty of the best estimated net peak area counts, based on Eq. 34 in ISO NORM, is:

$$\sigma_{N_h} = \sqrt{N_s{}^2 - (N_h - N)\ N_h} \quad \textbf{(168)}$$

where all quantities have been defined before. From Eq. 165, because the best estimated peak area N_h is always greater than the net peak area N, the uncertainty of the best estimated peak area is always less than the uncertainty of the net peak area. If this value is zero, it is set to the best estimated net peak area.

If the isotope activity is zero or negative, and if the best estimated activity is more than three times the uncertainty of the best estimated activity, the best estimated activity and the associated

uncertainty are set to zero.

6.17.2.4. The Lower and Upper Limits of the Activity

From ISO NORM Eq. 29, the lower limit of the peak area is:

$$N_{<} = N - k_p N_s, \qquad p = \omega - \omega\,\gamma/2 \tag{169}$$

All the quantities have been defined earlier except $^{(\tilde{a})}$, which is related to the confidence interval and $1-^{(\gamma)}$ is the probability that the measured value is within the confidence limits calculated (the typical value of $^{(\tilde{a})}$ is 0.05 for 95% confidence).

According to ISO NORM Eq. 30 or F.17, the upper limit of the peak area is:

$$N_{>} = N + k_q N_s, \qquad q = 1 - \omega\,\gamma/2 \tag{170}$$

If the uncertainty is small compared to the net peak area (i.e., when Q is large), then ω is very close to 1. Under those conditions, N is in the middle of the confidence limits. When Q is small, k_p is less than k_q, so N is closer to the lower limit than the upper limit. If the peak area uncertainty is zero (typically this happens when the net peak area is zero), the lower and upper confidence limits are set to zero. Conversion from peak area limits to the corresponding activity limits is per Equation 59.

6.17.3. Nuclide Calculation Details

The nuclide activity and its associated uncertainty are the branching-ratio weighted average of all the "qualifying" peaks of the nuclide (i.e., those that meet the criteria in Section 6.7.1 for inclusion in the average activity calculation). For all ISO NORM quantities (CL, MDA, etc.), if those qualifying peaks are found, then the ISO NORM results are also weighted using the branching ratios. Otherwise, ISO NORM quantities are calculated from the "MDA" line, which is typically the line used by GammaVision to calculate the MDA in regular analysis reports.

6.17.3.1. Nuclide Activity

The final activity of the nuclide is the average of the peak activity of the qualifying peaks as described in Section 6.7.1.

6.17.3.2. Nuclide Activity Counting Uncertainty

Nuclide Counting Uncertainty is calculated as described in Section 6.7.2.

6.17.3.3. Nuclide Best Estimated Activity

The nuclide best estimated activity is given by:

$$A_{Ah} = \frac{\sum_{i}^{m} A_{hi}\, Br_i}{\sum_{i}^{m} Br_i} \qquad \textbf{(171)}$$

where A_{hi} is the best estimated activity for the i^{th} qualifying peak calculated from Eq. 165. If no appropriate peaks are found, the MDA peak is used.

6.17.3.4. Nuclide Best Estimated Activity Uncertainty

The 1-sigma uncertainty of the best estimated nuclide activity is given by:

$$\sigma_{Ah} = \frac{\sum_{i}^{m} \sigma_{Ahi}\, Br_i}{\sum_{i}^{m} Br_i} \qquad \textbf{(172)}$$

where σ_{Ahi} is the uncertainty of the best estimated activity for the i^{th} qualifying peak. If 2 sigma or 3 sigma is selected on the Report tab, this value will be multipled respectively by 2 or 3.

6.17.3.5. Nuclide Critical Level

The nuclide critical level is given by:

$$A_{ACL} = \frac{\sum_{i}^{m} A_{CLi}\, Br_i}{\sum_{i}^{m} Br_i} \qquad \textbf{(173)}$$

where A_{CLi} is the critical level of the i^{th} peak.

6.17.3.6. Nuclide MDA

The nuclide MDA is given by:

$$A_{MDA} = \frac{\sum_{i}^{m} A_{MDAi}\, Br_i}{\sum_{i}^{m} Br_i} \quad \textbf{(174)}$$

where A_{MDAi} is the MDA for the i^{th} qualifying peak.

6.17.3.7. Nuclide Lower and Upper Activity Limits

The lower activity limit is given by:

$$A_{A<} = \frac{\sum_{i}^{m} A_{<i}\, Br_i}{\sum_{i}^{m} Br_i} \quad \textbf{(175)}$$

and the upper activity limit is given by:

$$A_{A>} = \frac{\sum_{i}^{m} A_{>i}\, Br_i}{\sum_{i}^{m} Br_i} \quad \textbf{(176)}$$

where $A_{<i}$ and $A_{>i}$ are the lower and upper activity limit of the i^{th} qualifying peak.

6.17.3.8. Total Reported Activity

Total reported activity represents the summed activity calculated for all nuclides found in the sample. It is calculated as follows and printed in the analysis report immediately after the Summary of Nuclides table, or the Summary of Nuclides (ISO NORM) table if the **ISO NORM report** checkbox is marked on the Report tab.

$$A_{tot} = \sum_{n=1}^{Nuclides} A_{An} \quad \textbf{(177)}$$

where A_{An} is the calculated nuclide activity for the n-th nuclide.

Note that if an MDA is reported for A_{An} for a particular nuclide, that nuclide's contribution is not included in A_{tot}. In addition, any nuclide with the "Activity Not In Total" flag set is always excluded. Also note that this total activity is typically different from the total activity calculated for the standard GammaVision report. This is because the MDA values (which in turn might be used as the nuclide activity values) are calculated differently in ISO NORM due to the differences in background variance calculations.

6.17.4. GammaVision / ISO NORM Unique Calculations

6.17.4.1. Negative Peak Area and Confidence Interval

The ISO NORM standard does not make clear how negative peak areas should be handled. However, it can be shown that for the confidence interval, the peak area can be negative.

Lower Confidence Limit

The lower confidence limit can be rewritten as:

$$N_{<} = (Q - k_p)\,\sigma_N, \qquad p = \omega - \omega\,\gamma/2 \tag{178}$$

From Eq. 167 it is clear that Q is just k_ω. Because the probability p is always less than ω, to get a smaller probability, k_p (the horizontal axis in Gaussian function) must be less than k_ω.

$$k_p < k_\omega, \quad or \quad k_p < Q \tag{179}$$

Therefore, it can be concluded that no matter the value of Q (positive or negative), the following is always true:

$$N_{>} \geq 0 \tag{180}$$

Upper Confidence Limit

The upper confidence limit, k_q, is defined in Eq. 170 (ISO NORM Eq. 30 or F.17). The probability q is always greater than p because:

$$q - p \equiv 1 - \omega\gamma/2 - (\omega - \omega\gamma/2) = 1 - \omega \geq 0 \quad (\omega \leq 1) \tag{181}$$

Calculating the difference of the two limits:

$$N_> - N_< = (k_q + k_p)\,\sigma_N \tag{182}$$

From the Gaussian distribution, if the probability *1 - q* is less than the probability *p*, then $k_q + k_p$ should be greater than zero.

$$p - (1 - q) \equiv \omega - \omega\gamma/2 - (1 - (1 - \omega\gamma/2)) = \omega(1 - \gamma) \geq 0 \tag{183}$$

Thus, it can be concluded that :

$$k_q + k_p \geq 0 \tag{184}$$

Finally, it can be concluded that even in case of negative peak area, the following is always true:

$$0 < N_< < N_> \tag{185}$$

The Best Estimated Activity

The best estimated activity is calculated from Eq. 165. Because $Q = N / \sigma_N$, Eq. 165 can be rewritten as:

$$N_h = \sigma_N \left(Q + e^{(-Q^2/2)} / \omega / \sqrt{2\pi} \right) \tag{186}$$

The best estimated activity is always positive and the following is true:

$$0 < N_< < N_h < N_> \tag{187}$$

Uncertainty of the Best Estimated Activity

If for any reason the uncertainty cannot be calculated (due to negative operand in Eq. 28), σ_{Nh} will be set to the maximum best estimated activity uncertainty of 100%.

6.17.4.2. Peak Area Uncertainty

If the relative peak area uncertainty has been calculated, then the peak area uncertainty is simply:

$$\sigma_N = Abs(N) * Pkunct \quad \textbf{(188)}$$

where *Pkunct* is the relative peak area uncertainty reported in the GammaVision analysis report. If *Pkunct* is zero and if the activity uncertainty of the isotope is not zero, then σ_N is calculated by converting the activity uncertainty in Bq back to uncertainty in counts:

$$\sigma_N = \sigma_A / \xi \quad \textbf{(189)}$$

where σ_A is the nuclide activity. If σ_A is still zero, then the gross counts under the peak is calculated and the area uncertainty determined as:

$$\sigma_N = \sqrt{G + \sigma_B^2} \quad \textbf{(190)}$$

where G is the gross counts under the peak, and σ_B^2 is the peak background uncertainty.

6.18. EDF Gamma Total Analysis

6.18.1. Geometry (K-Factor) Calculation

1) Measure the background between 100 keV and 2 MeV.

2) Calculate the *K* coefficient, based on the measurement of a ^{137}Cs source, as follows:

$$K = 100 \times 0.852 \times \frac{T_R \times A_s}{\left(A_g - A_{bkg}\right) \times 100} \quad \textbf{(191)}$$

where

K = *K* coefficient

T_R = Real time, in seconds
A_s = Source activity at the time of measurement, in Bq
A_g = Gross area between the chosen range of the source spectrum (100 keV–2 MeV), in counts
A_{bkg} = Gross area between the chosen range of the background spectrum (100 keV–2 MeV), in counts. Choose the background spectrum on the Gamma Total setup dialog (Section 5.5.1.9).

6.18.2. Gamma Total (Cesium Equivalence) Activity

$$A_{Cs} = \frac{\left(A_g - A_{bkg}\right) \times K}{T_R} \quad \textbf{(192)}$$

where
K = K coefficient
T_R = Real time, in seconds
A_g = Gross area between the chosen range of the source spectrum (100 keV–2 MeV), in counts
A_{bkg} = Gross area between the chosen range of the background spectrum (100 keV–2 MeV), in counts. Choose the background spectrum on the Gamma Total setup dialog (Section 5.5.1.9).

[Intentionally blank]

7. ANALYSIS REPORT(V)

This chapter covers the contents of the GammaVision analysis report, which is based on the entries in the Sample Type Settings dialog under **Analyze/Settings/Sample Type...** (Section 5.5.1.1). The report details depend on the analysis engine and setting, spectrum, calibration, and library content, as described below.

7.1. Report Header

The two-line report header (Fig. 256) is repeated on every page.

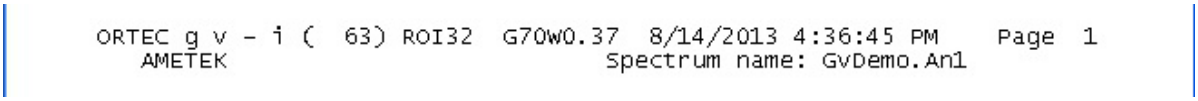


Figure 256. Two-line Report Header.

The first line contains the program name, analysis code in parenthesis (63 in this example), analysis Engine name and version code (ROI32 G70W0.37 in this example), analysis date/time, and page number. The second line contains the Laboratory Name and Spectrum filename.

The analysis code is an integer that defines various conditions applied or encountered during the analysis. The number is decoded into binary with the following bit usage:

Bit 1	True if the spectrum is energy calibrated
Bit 2	True if the spectrum is efficiency calibrated
Bit 3	True if the library is a valid gamma-ray library
Bit 4	True if the isotopic abundance will be reported
Bit 5	True if the isotopic matrix will be reported
Bit 6	True if the Unidentified Peak Summary, Identified Peak Summary, or Summary of Library Usage table is reported
Bit 7	True if DAC/MPC is enabled
Bit 8	True if the PBC has been used
Bit 9	True if absorption correction is enabled
Bit 10	True if geometry correction is enabled
Bit 11	True is peak stripping (library or manual based) is enabled
Bit 12	True if the directed fit has been enabled

For example, an analysis code of 63 (which is binary 0000 0011 1111, digit numbers read from right to left) means that the spectrum is (1) energy calibrated, (2) efficiency calibrated, (3) valid library found, (4) isotopic abundance is reported, (5) isotope matrix is reported, (6) peak/energy matrix is reported, (8) PBC not used, and (12) Directed Fit not used.

Normally, this code just confirms that the proper analysis was performed, but it can be useful when troubleshooting a particular analysis when the reported results are not as expected.

7.2. Sample, Detector, and Acquisition Parameters

The first four sections of the report (Fig. 257) contain the sample description; the full path to the spectrum; acquisition information including the start date/time, live time, real time, and dead time.

The Sample Description may include two lines of text as entered in the Sample Description field before analyzing the spectrum. The Detector Description is displayed under the Detector System heading.

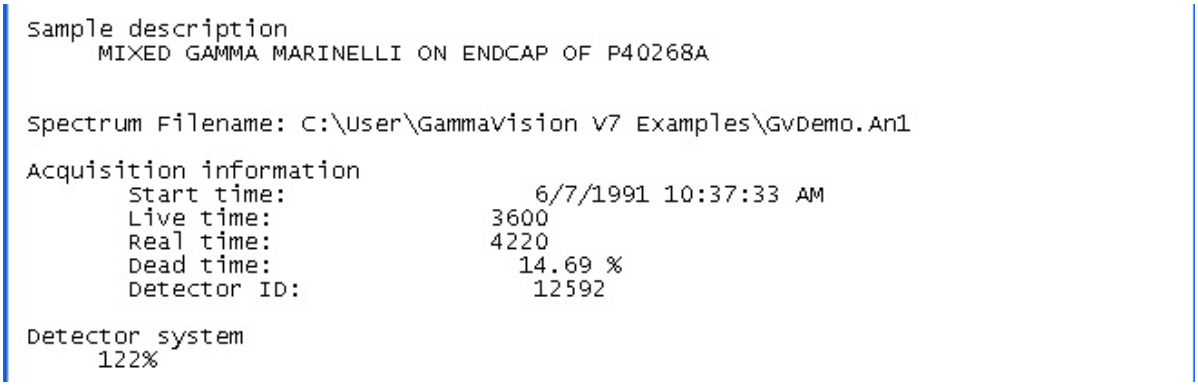


Figure 257. Sample Description, Filename, Acquisition, and Detector Report Sections.

7.3. Calibration Parameters

This section (Fig. 258) includes the calibration filename, internal description from the calibration file, efficiency calibration uncertainty, and the energy and efficiency calibration date/time and formula coefficients. The particular coefficients displayed for the efficiency calibration depend on the calibration type and knee settings (where applicable). Refer to Section 5.3 for details about efficiency calibration formulas and respective coefficients.

```
Calibration
        Filename:                    GvDemo.An1
     1L Marinelli on Detector 12592


        Energy Calibration
             Created:                4/5/1995 8:44:58 AM
             Zero offset:            3.771 keV
             Gain:                   0.162 keV/channel
             Quadratic:              2.447E-09 keV/channel^2

        Efficiency Calibration
             Created:                6/7/1991 10:37:33 AM
             Type:                   Polynomial
             Uncertainty:            2.112 %
             Coefficients:          -0.217759  -3.814522   0.571410
                                    -0.090628   0.005708  -0.000142
```

Figure 258. Calibration Report Section.

7.4. Library Parameters

This section (Fig. 259) displays the libraries used for analysis and the Library Match Width setting.

If **Manual Based Peak Stripping** is enabled on the Analysis tab, the **Second Library** specified on the Analysis tab is identified on the report as the “Stripping library,” and the **Third Library** specified on the Analysis tab is identified as the “Second analysis library.” The primary purpose of the stripping library is to define the interference while the second analysis library defines which nuclides are assigned the remaining peak area after peak stripping is applied. The stripping and second analysis libraries are omitted from the report if **Manual Based Peak Stripping** is not enabled. Refer to Section 6.5.5.2 for more information on peak stripping.

```
Library Files
        Main analysis library:      Lib01.Lib
        Library Match Width:        0.500
        Stripping library:          Lib02.Lib
        Second analysis library:    Lib03.Lib
```

Figure 259. Library Files Report Section.

7.5. Analysis Parameters

This section (Fig. 260) displays various analysis parameters used for the analysis, with the clarifications below.

```
Analysis parameters
       Analysis engine:            Wan32   G701W040
       Start channel:            200 (    36.07kev )
       Stop channel:           16000 (  2588.55kev )
       Peak rejection level:     50.000%
       Peak search sensitivity:   3
       Sample Size:               1.0000E+00
       Activity scaling factor:   1.0000E+00/(  1.0000E+00*  1.0000E+00) =
                                  1.0000E+00
       Detection limit method:    Traditional ORTEC method

       Random error:              1.0000000E+00
       Systematic error:          1.0000000E+00
       Uncertainty 1:             1.0000000E+00
       Uncertainty 2:             2.0000000E+00
       Uncertainty 3:             3.0000000E+00
       Uncertainty 4:             4.0000000E+00
       Uncertainty 5:             5.0000000E+00
       Uncertainty 6:             6.0000000E+00
       Uncertainty 7:             7.0000000E+00
       Uncertainty 8:             8.0000000E+00
       Uncertainty 9:             9.0000000E+00
       Fraction Limit:            0.000%
       Background width:          best method (based on spectrum).
       Half lives decay limit:   12.000
       Activity range factor:     2.000
       Min. step backg. energy    0.000
       Multiplet shift channel    2.000
       alpha, beta, gamma:        5.000E-02    5.000E-02    5.000E-02
       Max. ISO MDA ratio:        3.000E+00
```

Figure 260. Analysis Parameters Report Section.

- "Peak rejection level" is the same value as the **Peak Cutoff** on the Analysis tab. Peaks with 1-sigma counting uncertainty greater than this value are not used in the analysis except in the special case when **Directed Fit** is enabled, which will generate an activity result for every nuclide in the library even if no peaks for that nuclide pass the **Peak Cutoff** criteria.

- The "Activity scaling factor" is the multiplier applied to the total sample activity to calculate the specific activity. This parameter includes the **Multiplier**, **Divisor**, and sample **Size** from the System tab.

- The additional uncertainty parameters, "Uncertainty 1" through "Uncertainty 9" in Fig. 260, reflect the respective entries on the Uncertainties tab. These fields are reported only if a non-zero uncertainty is entered. If no label or non-zero uncertainty value is specified, the respective field is omitted from the report.

- The "Background width" is a description of the **Background Type** specified on the Sample tab. (In this example, "best method [based on spectrum]" refers to the **Auto** background type.)

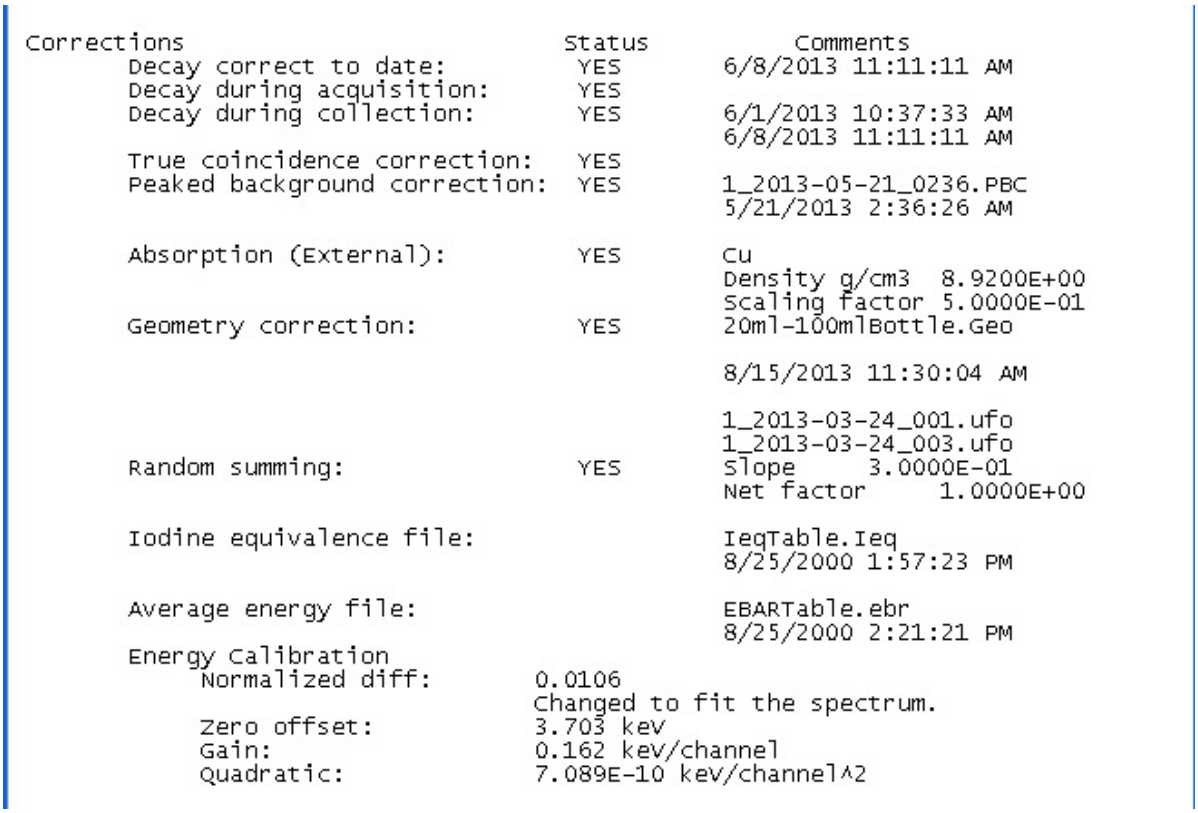
- All parameters from "Half lives decay limit" to the end of the list are specified in the b30winds.ini (n30winds.ini for NAI32) file (Section A.2.2).

- The "alpha, beta, gamma" and "Max ISO MDA ratio" fields are only displayed if the **ISO**

NORM section of the report is enabled on the Report tab.

7.6. Correction Parameters

This section (Fig. 261) displays the corrections applied during the analysis for decay, coincidence and random summing, geometry and attenuation/absorption, peak background, and automatic energy recalibration (if enabled). The Status column displays a “YES” when a correction is enabled, followed by additional information related to the correction in the “Comments” column. The Status is listed as “NO” for disabled corrections.



Corrections	Status	Comments
Decay correct to date:	YES	6/8/2013 11:11:11 AM
Decay during acquisition:	YES	
Decay during collection:	YES	6/1/2013 10:37:33 AM
		6/8/2013 11:11:11 AM
True coincidence correction:	YES	
Peaked background correction:	YES	1_2013-05-21_0236.PBC
		5/21/2013 2:36:26 AM
Absorption (External):	YES	Cu
		Density g/cm3 8.9200E+00
		Scaling factor 5.0000E-01
Geometry correction:	YES	20ml-100mlBottle.Geo
		8/15/2013 11:30:04 AM
		1_2013-03-24_001.ufo
		1_2013-03-24_003.ufo
Random summing:	YES	Slope 3.0000E-01
		Net factor 1.0000E+00
Iodine equivalence file:		IeqTable.Ieq
		8/25/2000 1:57:23 PM
Average energy file:		EBARTable.ebr
		8/25/2000 2:21:21 PM
Energy Calibration		
Normalized diff:	0.0106	
	Changed to fit the spectrum.	
Zero offset:	3.703 keV	
Gain:	0.162 keV/channel	
Quadratic:	7.089E-10 keV/channel^2	

Figure 261. Corrections Report Section.

- “Decay correct to date” should normally be set to the “Decay during collection” end time if both are enabled on the Decay tab.

- “Decay during collection” displays the collection start and stop date/time.

- “Peaked background correction” displays the PBC file name entered on the Corrections tab and the date/time the file was created, PBC By Energy or Nuclide, and the PBC Match Width.

- Absorption displays either database information as shown in Fig. 261 (material, density or mass, internal or external, and scaling factor [the latter is the **Length** value entered on

the Corrections tab]) or the file information (file name, date/time created, .UFO file name used to generate the attenuation table, and the scaling factor [again, the **Length** value entered on the Corrections tab]).

- "Random summing" displays the slope value entered in the **Random Summing** field on the Sample tab; and the Net factor, which is the Random Summing Factor calculated per Section 6.11.

- The "Iodine equivalence" and "Average energy" fields are only displayed if these options are enabled on the Isotopes tab.

- The "Energy Calibration" section displays the "Normalized difference," a measure of how well the spectrum peak energies match those in the library (see Section 6.3.6). This can range from 0.0 to 1.0, with 0.0 being the best and 1.0 the worst. High values may be due to a poor calibration or to analyzing very small peaks that do not have statistically good shape. If the automatic energy recalibration is enabled and the criteria specified in Section 6.3.6 are satisfied, a message indicates that the energy calibration was changed to fit the spectrum, and the new energy calibration coefficients used for the analysis are displayed.

7.7. Peak and Nuclide Tables

This section covers the various peak and nuclide tables GammaVision can report, based on the analysis engine used; see the following table. The content of a particular table may vary depending on the settings in the Sample Type Settings dialog or (.SDF) file, and in the b30winds.ini (n30winds.ini for NAI32) analysis parameters file, which is discussed in detail in Section A.2.2.

Section / Peak or Nuclide Table		Analysis Engine			
		ENV32, NPP32, NAI32	WAN32	ROI32	GAM32
7.7.1	ROI Peak Summary			✓	
7.7.2	Summary of ROI Peak Usage			✓	
7.7.3	Summary of ROI Nuclides			✓	
7.7.4	Background Correction	✓	✓	✓	✓
7.7.5	Summary of Peaks in Range	✓			
7.7.6	Unidentified Peak Summary	✓	✓	✓	✓
7.7.7	Identified Peak Summary	✓	✓	✓	✓
7.7.8	Summary of Library Peak Usage	✓	✓	✓	✓
7.7.9	Discarded Isotope Peaks	✓	✓	✓	
7.7.10	Summary of Discarded Peaks	✓	✓	✓	✓
7.7.11	Summary of Nuclides in Sample	✓	✓	✓	✓
7.7.12	Summary of Nuclides (ISO-NORM)	✓	✓	✓	✓
7.7.13	Iodine Equivalence and Average Energy	✓	✓	✓	✓
7.7.14	DAC Table	✓	✓	✓	✓

7.7.1. ROI Peak Summary (ROI32 Engine Only)

This table (Fig. 262) displays information for ROIs marked in the spectrum, with the clarifications below.

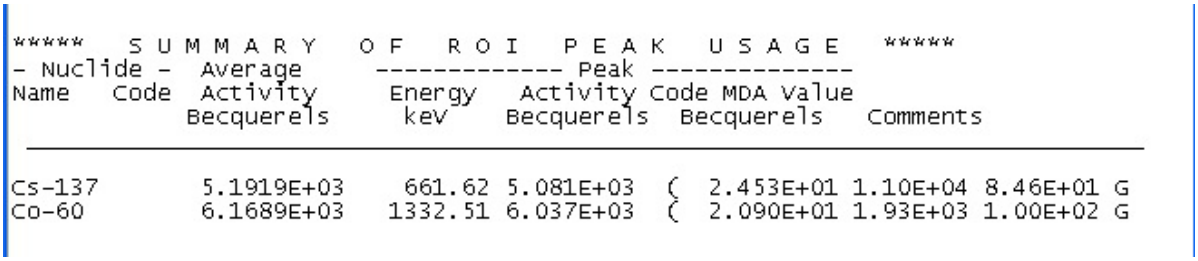
********** R O I P E A K S U M M A R Y **********

Nuclide	Peak Channel	Centroid Energy	Background Counts	Net Area Counts	Intensity Cts/Sec	Uncert 1 Sigma %	FWHM keV	
Cs-137	4073.06	661.64	41890.	609977.	169.438	0.17	1.407	s
Co-60	8225.61	1332.46	11935.	460983.	128.051	0.17	1.846	

s - Peak fails shape tests.
D - Peak area deconvoluted.

Figure 262. ROI Peak Summary Report Section.

- ROI parameters are calculated per Section 6.2.1.5.
- Peaks in this table are arranged in ascending energy order based on ROIs marked in the spectrum when the analysis is run.
- Only ROIs with calculated uncertainty lower than the peak cutoff are included in the table.
- If the peak centroid cannot be calculated, then the peak channel is set to 0 (zero).
- The peak centroid energy is listed in units of keV.
- Peak flags are displayed to the right of the FWHM column. The designators for Deconvolution, Shape, and Multiplets (as applicable) can be modified in the b30winds.ini (n30winds.ini for NAI32) file.



```
******   S U M M A R Y   O F   R O I   P E A K   U S A G E   ******
- Nuclide -  Average      ------------ Peak --------------
Name   Code  Activity      Energy   Activity Code MDA Value
            Becquerels      keV    Becquerels  Becquerels   Comments
 ------------------------------------------------------------------------

Cs-137       5.1919E+03    661.62 5.081E+03  (  2.453E+01 1.10E+04 8.46E+01 G
Co-60        6.1689E+03   1332.51 6.037E+03  (  2.090E+01 1.93E+03 1.00E+02 G
```

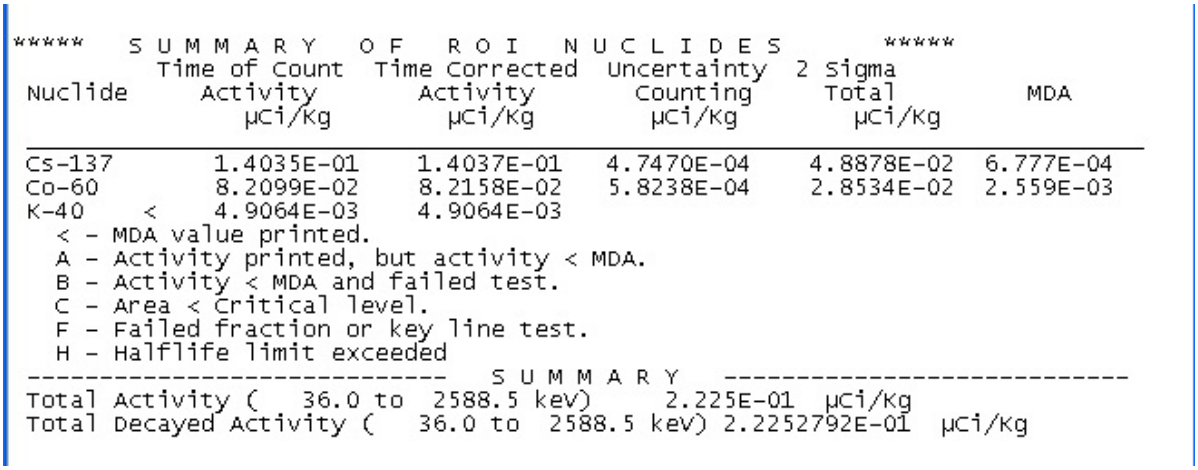
Figure 263. Summary of ROI Peak Usage Report Section.

7.7.2. Summary of ROI Peak Usage (ROI32 Engine Only)

The content of this table (Fig. 263) is similar to the Summary of Library Peak Usage table described in Section 7.7.8, except that the analysis data are related only to peaks identified by ROIs marked in the spectrum. See Section 7.7.8 for a complete explanation of this table content.

7.7.3. Summary of ROI Nuclides (ROI32 Engine Only)

The content of this table is similar to the Summary of Nuclides in Sample table described in Section 7.7.11, except that the analysis data are related only to nuclides with peaks identified by ROIs marked in the spectrum. See Section 7.7.11 for a complete explanation of this table content.



```
******   S U M M A R Y   O F   R O I   N U C L I D E S      ******
         Time of Count  Time Corrected  Uncertainty  2 Sigma
Nuclide     Activity       Activity       Counting     Total          MDA
               µCi/Kg         µCi/Kg         µCi/Kg       µCi/Kg
 ------------------------------------------------------------------------
Cs-137       1.4035E-01    1.4037E-01   4.7470E-04    4.8878E-02  6.777E-04
Co-60        8.2099E-02    8.2158E-02   5.8238E-04    2.8534E-02  2.559E-03
K-40    <    4.9064E-03    4.9064E-03
  < - MDA value printed.
  A - Activity printed, but activity < MDA.
  B - Activity < MDA and failed test.
  C - Area < Critical level.
  F - Failed fraction or key line test.
  H - Halflife limit exceeded
----------------------------   S U M M A R Y   ----------------------------
Total Activity (   36.0 to  2588.5 keV)     2.225E-01  µCi/Kg
Total Decayed Activity (   36.0 to  2588.5 keV) 2.2252792E-01  µCi/Kg
```

Figure 264. Summary of ROI Nuclides Report Section.

7.7.4. Background Correction

This table displays all peaks that were affected by peak background correction. The content of this table will vary depending on the type of background correction and library content as described below.

********** B A C K G R O U N D C O R R E C T I O N **********

Peak Energy	PBC Energy	Area Counts	Uncert (%)	PBC Area	Corr Area	Corr CR Cts/Sec	Corr Unc (%)	Nuc
186.15	186.10	207003.0	0.39	75746.0	131257.0	1.646E+00	0.66	

Figure 265. - PBC By Energy with Null Library

********** B A C K G R O U N D C O R R E C T I O N **********

Peak Energy	PBC Energy	Area Counts	Uncert (%)	PBC Area	Corr Area	Corr CR Cts/Sec	Corr Unc (%)	Nuc
185.72	185.72	92535.0	0.88	75746.0	92535.0	1.161E+00	0.88A	U235
186.21	185.72	114468.0	0.70	75746.0	38722.0	4.856E-01	2.18	RA226

Figure 266. - PBC By Energy with U-235 185.72 peak area derived

********** B A C K G R O U N D C O R R E C T I O N **********

Peak Energy	PBC Energy	Area Counts	Uncert (%)	PBC Area	Corr Area	Corr CR Cts/Sec	Corr Unc (%)	Nuc
185.72	185.72	130408.0	0.71	37873.0	92535.0	1.161E+00	0.88	U235
186.21	186.10	76595.0	1.07	37873.0	38722.0	4.856E-01	2.18	RA226

Figure 267. - PBC By Nuclide Peak with U-235 185.72 peak area derived

- "Peak Energy" is the actual peak centroid for both unidentified and library peak.
- "PBC Energy" is the PBC file energy when one PBC energy is applied to one spectrum peak as shown in Figure 267. When using the "By Energy" option multiple PBC peaks may be combined if they are within the peak energy acceptance range as shown in Fig. 265 and 266.
- "Area Counts" is normally the full peak area before background correction (i.e. Corrected Area plus PBC Area). When using the "By Energy" PBC option derived peaks (i.e., those derived by Peak Stripping as described in Section 6.5.5) the derived area and uncertainty is used for both the full and corrected values. These peaks will also display the "A" (Derived Area) flag similar to the Identified Peak Summary after the Corrected Uncertainty value. See Fig. 266.

- "Uncert (%)" is the uncertainty of the full peak area and will usually be somewhat lower than the background corrected peak area. See exception noted previously for Derived Peaks when PBC "By Energy" is enabled.

- "PBC Area" is the calculated area based on peak count rate in the PBC file and count time for the sample. When using the "By Nuclide Peak Energy" PBC option the area is determined by the corresponding nuclide peak energy from the PBC table. When using the "By Energy" PBC option the area is the sum of all PBC peaks associated with the spectrum peak as described in Section 6.10.4.

- "Corr Area" is the peak area after background correction, or the derived peak area if Peak Stripping was implemented as described in Section 6.5.5.

- "Corr CR cts/sec" is the "Corr Area" divided by Live Time.

- "Corr Unc (%)" is the uncertainty of the background corrected peak area. When using the "By Energy" background correction option, peaks with corrected uncertainty greater than the Peak Cutoff do not pass the peak acceptance test and would not be used in the remainder of the analysis process.

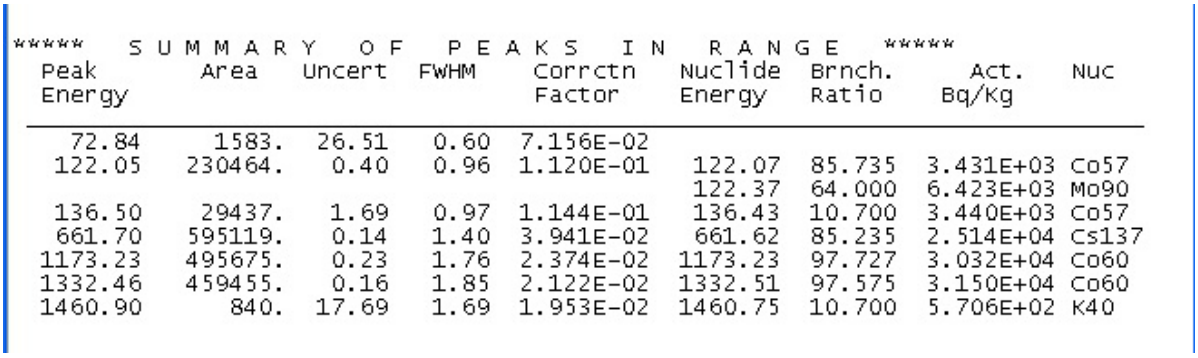
- "Nuc" is the nuclide name for Identified Peaks. Unidentified Peaks that have background correction applied will be displayed as shown in Figure 265 when using the "By Energy" background correction option.

- Figures 265 and 266 are examples of PBC "By Energy" as compared to Figure 267 which uses the PBC "By Nuclide Peak". Both of the PBC peaks shown in Figure 267 are combined as one background correction in Figures 265 and 266 because the energies fall within the "By Energy" acceptance range for this analysis.

- Figures 266 and 267 represent the same analysis with PBC "By Energy" and "By Nuclide Peak" respectively. The corrected peak areas and uncertainties are the same in both cases, but the uncorrected peak area and uncertainty, and PBC area are different because of how the background correction is applied with each method.

7.7.5. Summary of Peaks in Range (ENV32 and NPP32 Only)

This table (Fig. 268) displays all of the peaks that were found during the analysis process with the clarifications below.



***** SUMMARY OF PEAKS IN RANGE *****

Peak Energy	Area	Uncert	FWHM	Corrctn Factor	Nuclide Energy	Brnch. Ratio	Act. Bq/Kg	Nuc
72.84	1583.	26.51	0.60	7.156E-02				
122.05	230464.	0.40	0.96	1.120E-01	122.07	85.735	3.431E+03	Co57
					122.37	64.000	6.423E+03	Mo90
136.50	29437.	1.69	0.97	1.144E-01	136.43	10.700	3.440E+03	Co57
661.70	595119.	0.14	1.40	3.941E-02	661.62	85.235	2.514E+04	Cs137
1173.23	495675.	0.23	1.76	2.374E-02	1173.23	97.727	3.032E+04	Co60
1332.46	459455.	0.16	1.85	2.122E-02	1332.51	97.575	3.150E+04	Co60
1460.90	840.	17.69	1.69	1.953E-02	1460.75	10.700	5.706E+02	K40

Figure 268. Summary of Peaks In Range Report Section.

- The **Library peak list** option must be enabled on the Report tab for this table to be displayed.

- The peak data and nuclide activity are based a peak search run with no library peaks (i.e., a Mariscotti peak search) and no peak stripping (interference correction) applied. Any peaks identified using the Library Directed Peak Search that do not overlap those found using the Mariscotti search are also included in this table.

- The “Uncert” (uncertainty) value is 1-sigma counting uncertainty, which is directly comparable to the **Peak Cutoff** acceptance criterion. Only peaks with1-sigma counting uncertainty below the **Peak Cutoff** value are reported.

- The “Corrctn Factor” (correction factor) is the effective efficiency at the specified energy and takes into account any geometry or attenuation corrections enabled.

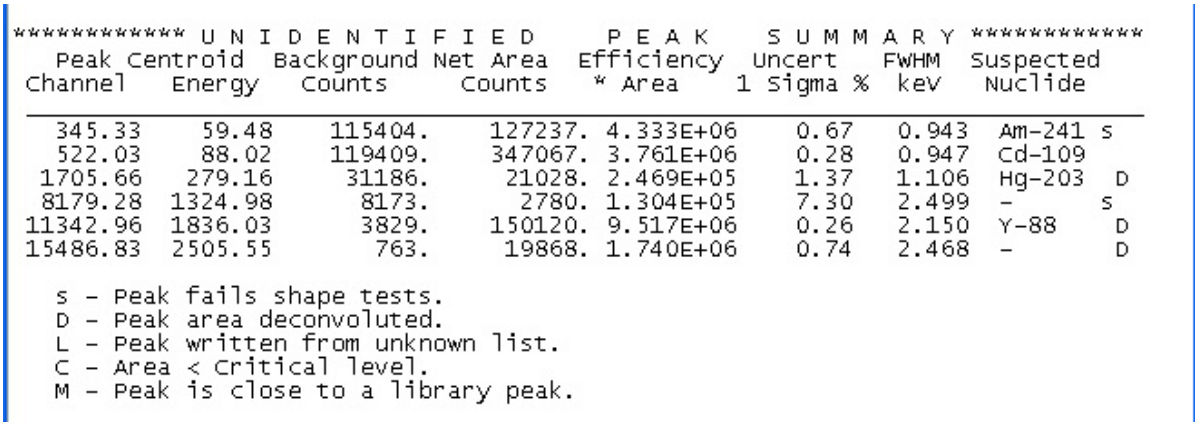
- The nuclide names (“Nuc”) have all non-alphanumeric characters removed for table formatting.

- All nuclides that have a photon energy within the Match Width × Calibration FWHM of a listed peak are listed as a possible source candidate along with the peak energy, branching ratio, calculated activity, and nuclide name. The specific activity for each potential nuclide candidate is calculated under the assumption that the full peak area was generated entirely by that nuclide such that all applicable correction factors (decay, efficiency, branching ratio, sample size, etc.) are applied except for any potential peak interferences. The nuclide activity values from this table may be substituted for nuclide activity reported in the Summary of Nuclides in Sample if it is determined that the peak was mis-

identified or misinterpreted due to peak interferences. This type of correction may be desired in some cases for manual interference calculations, reporting of conservative activity results, or to correct for inaccurate nuclide identification. The data from this table can also be used to compare the results of the Mariscotti vs Library Directed Peak Search and fitting to help identify where library or analysis option changes may be needed. Note that background correction is only applied to peaks in this table when **PBC By Energy** is enabled. When using **PBC By Nuclide** energy the peaks in the Summary of Peaks in Range do not have background correction applied because the associated correction could be different for each nuclide.

7.7.6. Unidentified Peak Summary

This table (Fig. 269) displays peaks found in the spectrum that were not associated with a library nuclide, with the clarifications below.



********** U N I D E N T I F I E D P E A K S U M M A R Y **********

Peak Channel	Centroid Energy	Background Counts	Net Area Counts	Efficiency * Area	Uncert 1 Sigma %	FWHM keV	Suspected Nuclide	
345.33	59.48	115404.	127237.	4.333E+06	0.67	0.943	Am-241	s
522.03	88.02	119409.	347067.	3.761E+06	0.28	0.947	Cd-109	
1705.66	279.16	31186.	21028.	2.469E+05	1.37	1.106	Hg-203	D
8179.28	1324.98	8173.	2780.	1.304E+05	7.30	2.499	-	s
11342.96	1836.03	3829.	150120.	9.517E+06	0.26	2.150	Y-88	D
15486.83	2505.55	763.	19868.	1.740E+06	0.74	2.468	-	D

s - Peak fails shape tests.
D - Peak area deconvoluted.
L - Peak written from unknown list.
C - Area < Critical level.
M - Peak is close to a library peak.

Figure 269. Unidentified Peak Summary Report Section.

- The **Unknown peaks** option must be enabled on the Report tab for this table to be displayed.
- Only peaks with1-sigma counting uncertainty below the Peak Cutoff value are reported.
- The uncertainty displayed is based on the **Confidence level** selected on the Report tab.
- The “Suspected Nuclide” is determined by selecting the nuclide from the suspect library that has the closest peak energy to the unidentified peak energy and is within the b30winds.ini (n30winds.ini for NAI32) file “Range Multiplier” parameter multiplied by the peak FWHM. The Range Multiplier is normally set to 2.0 but you can modify this. If there are no nuclides with peak energies in the specified range, the “Unknown Suspect” text from the b30winds.ini (n30winds.ini for NAI32) file is displayed in this column.

- If the b30winds.ini (n30winds.ini for NAI32) parameter “Unidentified Peak Summary and Library Peak Usage Format flag” is set to “T” (true), then the fifth column is labeled “Efficiency * Area” and displays the Net Area divided by the effective efficiency (which includes any Geometry or Attenuation corrections). If this parameter is set to “F”, then the fifth column is labeled “Intensity Cts/Sec” and displays the net count rate as shown in Fig. 270.

********** U N I D E N T I F I E D P E A K S U M M A R Y **********

Peak Channel	Centroid Energy	Background Counts	Net Area Counts	Intensity Cts/Sec	Uncert 3 Sigma %	FWHM keV	Suspected Nuclide	
8179.28	1324.98	8173.	2780.	0.772	21.90	2.499	-	sM
15486.83	2505.55	763.	19868.	5.519	2.21	2.468	-	D

Figure 270. Unidentified Peak Summary with Intensity Report Section.

- The designators for peaks flags (Deconvolution, Shape, and Multiplets as applicable) can be modified in the b30winds.ini (n30winds.ini for NAI32) file.

- The L, C, and M flags are applicable only to the NPP32 and ENV32 analysis engines.

7.7.7. Identified Peak Summary

This table (Fig. 271) displays peaks that were found in the spectrum and associated with a library nuclide, with the clarifications below.

********** I D E N T I F I E D P E A K S U M M A R Y **********

Nuclide	Peak Channel	Centroid Energy	Background Counts	Net Area Counts	Intensity Cts/Sec	Uncert 2 Sigma %	FWHM keV	
Co-57	732.81	122.07	52140.	213398.	59.277	0.58	0.977D	
Mo-90	734.66	122.37	237520.	39718.	11.033	3.62	0.977D	
Co-57	822.16	136.50	37910.	28373.	7.881	2.82	0.971	
Cs-137	4072.92	661.62	38686.	577307.	160.363	0.30	1.402D	
Co-60	7239.96	1173.23	25353.	475933.	132.204	0.33	1.757	
Co-60	8225.91	1332.51	11804.	453528.	125.980	0.34	1.859D	

s - Peak fails shape tests.
D - Peak area deconvoluted.
A Derived peak area.

Figure 271. Identified Peak Summary Report Section.

- The **Library peak list** option must be enabled on the Report tab for this table to be displayed.

- If the library is not found or the spectrum is not calibrated, this table is suppressed.

- If **Manual Library Based Peak Stripping** is enabled on the Analysis tab (WAN32 only), a separate table for peak data associated with each library is reported with the library name displayed at the beginning of the table.

- The designators for Deconvolution, Shape, and Derived Area (as applicable) can be modified in the b30winds.ini (n30winds.ini for NAI32) file.

- If the b30winds.ini (n30winds.ini for NAI32) parameter "Zero Area Identified Peak flag" is set to "F" (false), then only peaks with 1-sigma counting uncertainty below the **Peak Cutoff** and those resulting from **Directed Fit** (when enabled on the Analysis tab) are included in this table. If this parameter is set to "T" (true), additional peaks that did not pass the **Peak Cutoff** may be included in the list based on the analysis engine as follows:

  — **WAN32 and ROI32**: Peak data are displayed for all peaks in the library.

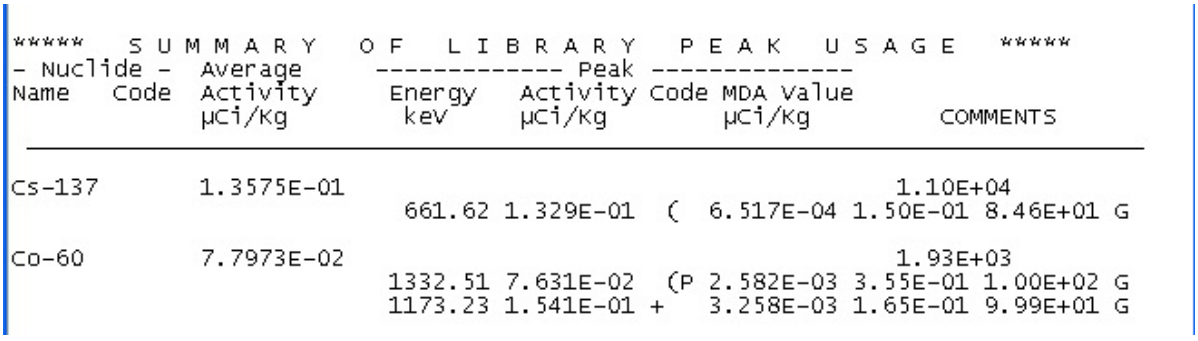
  — **GAM32**: Peak data are displayed for all peaks reported, but all library peaks may not be reported depending on peak quality, library content, and analysis settings.

  — **NPP32**: Deconvoluted peaks that are rejected may not be included in the peak list. Only the peak background and FWHM are displayed for peaks that do not meet the peak cutoff criteria.

  — **ENV32 and NAI32**: Some rejected peaks may be included in the list, but peak data are not available.

7.7.8. Summary of Library Peak Usage

This table (Fig. 272) displays peaks that were found in the spectrum and associated with a library nuclide with the clarifications below.



```
******   S U M M A R Y   O F   L I B R A R Y   P E A K   U S A G E   ******
- Nuclide -  Average      ------------- Peak --------------
Name   Code  Activity      Energy    Activity Code MDA Value
             µCi/Kg         kev      µCi/Kg         µCi/Kg          COMMENTS
 ------------------------------------------------------------------------------

Cs-137       1.3575E-01                                        1.10E+04
                          661.62 1.329E-01  (  6.517E-04 1.50E-01 8.46E+01 G

Co-60        7.7973E-02                                        1.93E+03
                         1332.51 7.631E-02  (P 2.582E-03 3.55E-01 1.00E+02 G
                         1173.23 1.541E-01  +   3.258E-03 1.65E-01 9.99E+01 G
```

Figure 272. Summary of Library Peak Usage Report Section.

- The **Library peak matrix** option must be enabled on the Report tab for this table to be

displayed.

- If the library is not found or the spectrum is not calibrated, this table is suppressed.

- If **Manual Library Based Peak Stripping** is enabled on the Analysis tab, a separate table for data associated with each library is reported with the library name displayed at the beginning of the table.

- The table format and content are based on the analysis engine as follows:

  — **NPP32, ENV32, and NAI32**:

  - Average Nuclide Activity and Peak Activity values have corrections applied including the activity scaling factor (based on the **Multiplier**, **Divisor**, and sample **Size** entered on the System tab) and decay.

  - The column to the right of the Peak MDA is the peak 1-sigma counting uncertainty in percent.

  - The first nuclide peak is one line below the applicable nuclide data.

  - If the b30winds.ini (n30winds.ini for NAI32) “Zero Activity Isotope flag” flag is set to “T” (true), rejected nuclides and associated peaks are included in the table. The activity values are set to zero, but peak flags, MDA, and counting uncertainty are displayed (as well as branching ratio and half-life if applicable based on the “Unidentified Peak Summary and Library Peak Usage Format flag” flag setting). Uncertainty values may be set to a default value of zero (NPP32) or 1E+03 (ENV32) for peaks that are rejected. This may be due to the nuclide being rejected prior to the Library Directed Fit process, the inability to physically fit a peak in the spectrum, or other peak rejection criteria. If this parameter is set to “F” (false), rejected nuclides are not displayed in this table.

  - If **Directed Fit** is enabled on the Analysis tab, peak fit data associated with Directed Fit are displayed in this table. When using ENV32, all nuclides should be reported with an activity value. When using NPP32, nuclides that fail the Key Line or Fraction Limit tests, or have interferences at key peaks, can still be reported with zero activity.

  - Peak energies are listed in the library order regardless of the b30winds.ini (n30winds.ini for NAI32) parameter “Sort Nuclide Peaks by Energy flag” setting.

  - If the b30winds.ini (n30winds.ini for NAI32) parameter “Zero Area Library Peak

flag" is set to "T" (true), display all nuclide library peaks even if they did not pass the analysis settings criteria. If this flag is set to "F" (false), only the peaks that passed the analysis settings criteria will be displayed, and a message summarizing how many of the library peaks were found will be displayed below the nuclide peak list (i.e., X of Y peaks found).

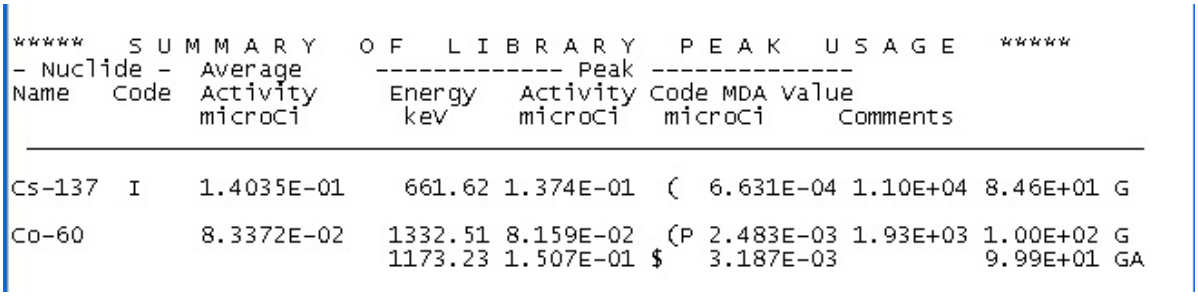
— **WAN32, GAM32, and ROI32**:

- Average Nuclide Activity is reported as Time of Count Total Activity in either ì Ci or Bq as selected on the System tab. This value has all corrections applied except for activity scaling factor (based on the **Multiplier**, **Divisor**, and sample **Size** entered on the System tab) and decay.

- Peak Activity is reported as Time of Count Total Activity in either ì Ci or Bq as selected on the System tab. This value has all corrections applied except for activity scaling factor (**Multiplier**, **Divisor**, and sample **Size**), decay, and Random Summing.

- Peak uncertainty is not reported.

- The first nuclide peak is on the same line as the nuclide data as shown in Fig. 273.



```
******   S U M M A R Y   O F   L I B R A R Y   P E A K   U S A G E   ******
- Nuclide -  Average     ------------- Peak --------------
Name   Code  Activity      Energy    Activity Code MDA Value
             microCi        kev      microCi   microCi     Comments
 ------------------------------------------------------------------------

Cs-137  I    1.4035E-01     661.62 1.374E-01  (  6.631E-04 1.10E+04 8.46E+01 G

Co-60        8.3372E-02    1332.51 8.159E-02  (P 2.483E-03 1.93E+03 1.00E+02 G
                           1173.23 1.507E-01 $   3.187E-03           9.99E+01 GA
```

Figure 273. Summary of Library Peak Usage Report Section showing first nuclide peak.

- All nuclides are reported even when they are not identified (i.e., zero activity) regardless of the b30winds.ini (n30winds.ini for NAI32) "Zero Activity Isotope flag" parameter setting.

- If **Directed Fit** is enabled on the Analysis tab, peak fit data associated with Directed Fit are displayed in this table. When using WAN32, nuclides that fail the Key Line or Fraction Limit tests, or have interferences at key peaks, can still be reported with zero activity.

- If the b30winds.ini (n30winds.ini for NAI32) "Sort Nuclide Peaks by Energy flag"

flag is set to “T” (true), then nuclide peaks are listed in order of energy. If this parameter is set to “F” (false), then nuclide peaks are listed in the library order.

- All nuclide library peaks are displayed regardless of the b30winds.ini (n30winds.ini for NAI32) “Zero Area Library Peak flag” setting.

— All analysis engines:

- If the b30winds.ini (n30winds.ini for NAI32) “Unidentified Peak Summary and Library Peak Usage Format flag” parameter is set to “T” (true), the nuclide half-life (in days) is displayed under the COMMENTS header on the same line as the nuclide data, and the peak branching ratios are displayed in the right-most column before the peak flags. If this parameter is set to “F”, the nuclide half-life and branching ratios are omitted.

- If the b30winds.ini (n30winds.ini for NAI32) “Use Internal TCC Library Peaks” parameter is set to “T” (true), the nuclide peaks in this table (and throughout the analysis process) will be based on the internal TCC library including the peak list and peak order which may (and likely will) differ from the original analysis library. Additionally, any peak flags set in the library are discarded. This configuration may not generate optimal results for some applications. If this parameter is set to “F”, the peak list, peak order, and peak flags from the original library are used for analysis. Only the Branching Ratio is adjusted for the coincidence summing correction. This configuration allows for improved optimization of the analysis results.

- The legend of Nuclide Codes shown after the nuclide name, Peak Codes shown at the far right, and Peak Flags shown after the Peak Activity are reported after this table. These are explained in the following section.

7.7.8.1. Summary of Library Peak Usage Flags

This table (Fig. 274) is displayed after the Summary of ROI Peak Usage and Summary of Library Peak Usage sections of the report. The Nuclide and Peak Codes listed at the bottom of the table are based on flags set in the analysis library. The Peak Flags are defined as follows:

(This peak was used in the average nuclide activity calculation (even if any other symbols are displayed). For more information on the Weighted Average Nuclide Activity, see Section 6.7.1.

* The peak FW10M and FW25M were wider than the calibrated shape by more than 20% which would indicate that this might be a multiplet. However, deconvolution was not

possible because only one peak was in the library.

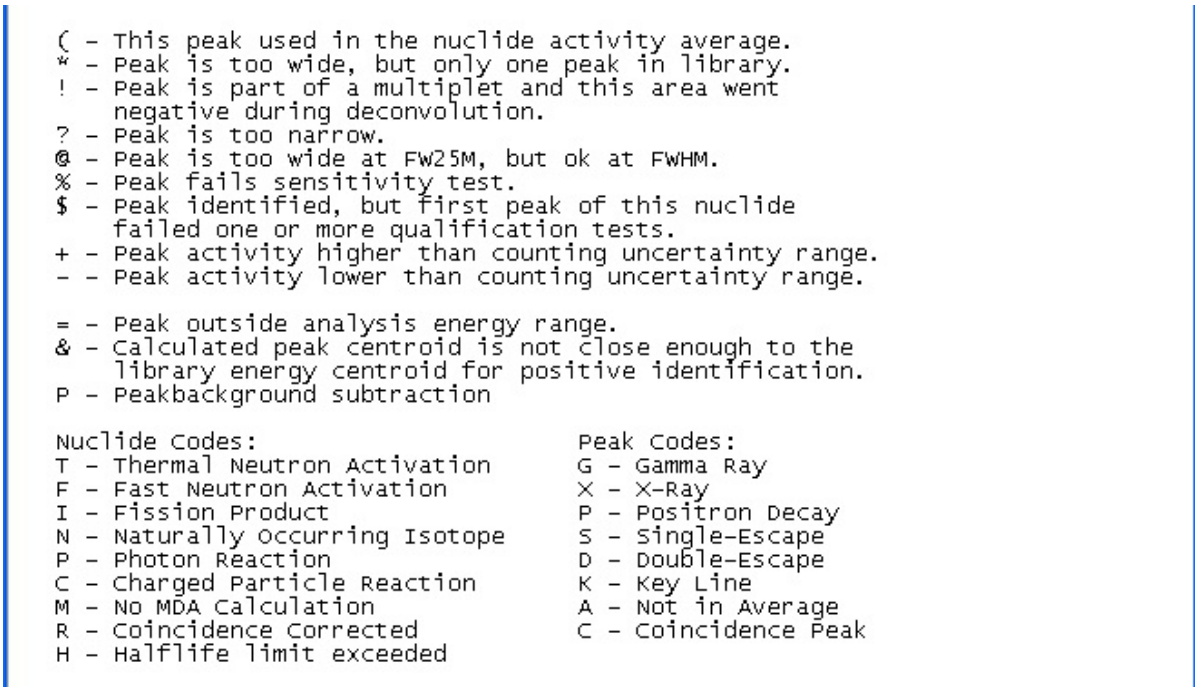


Figure 274. Summary of Library Peak Usage Flags.

! This peak was in an area that was deconvoluted and the area of this component was zero or negative. The peak was then removed as a component and the deconvolution redone. This usually indicates the peak was not present or the energy calibration needs adjustment.

? The peak FW25M is less than 80% of the calibration FW25M. This usually indicates that the peak has poor shape.

@ The peak FW25M was wider than the calibrated shape by more than 20%, but the FWHM was within 20% of the calibrated FWHM. This indicates there might be a small peak near the main peak that may need to be included in the library.

% The 1-sigma counting error was greater than the **Peak Cutoff** value set on the Analysis tab.

$ This peak was identified as belonging to this nuclide, but the first non-interfered peak for this nuclide was not identified or was disqualified. This may indicate that this peak was not generated by the respective nuclide.

+ The abundance for this peak was higher than the running average of those included at this point. For more information on the Weighted Average Nuclide Activity, see Section 6.7.1.

- The abundance for this peak was lower than the running average of those included at this point. For more information on the Weighted Average Nuclide Activity, see Section 6.7.1.

= This peak was outside the user-specified limits for the analysis.

& When the library-directed centroid was recalculated after background subtraction, the centroid value was outside the energy limits such that the peak could not be attributed to this nuclide. This may occur with very small peaks where the peak shape is not well defined, when the energy calibration needs adjustment, or if the library peak energies need to be corrected.

} The peak area for this peak was derived using other peaks for this nuclide. This is enabled by the library-based peak stripping option.

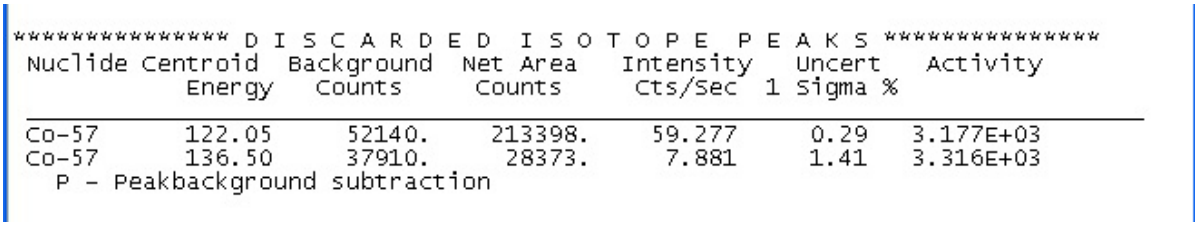
P Peak Background Subtraction was applied to this peak. (See Section 6.10.4 for details on peak background subtraction.)

7.7.9. Discarded Isotope Peaks

This table (Fig. 275) displays peaks associated with a nuclide that was rejected during the analysis due to a failed Key Line or Fraction limit test, with the clarifications below.

- Isotopes may be discarded when using WAN32, ROI32, and NPP32 analysis engines because the rejection criteria are evaluated after the Library Directed Peak Search has associated peaks with a nuclide. For GAM32 and ENV32 analysis engines, this table should be empty because the Key Line and Fraction Limit tests are implemented during the Library Reduction step at the beginning of the analysis process before the Library Directed Peak search, which assigns nuclide peaks.

- If the b30winds.ini (n30winds.ini for NAI32) parameter “Print Discarded Peak Table flag” is set to “T” (true), this table is displayed for all analysis engines except for GAM32. If this parameter is set to “F” (false), this table is suppressed.



********** D I S C A R D E D I S O T O P E P E A K S **********

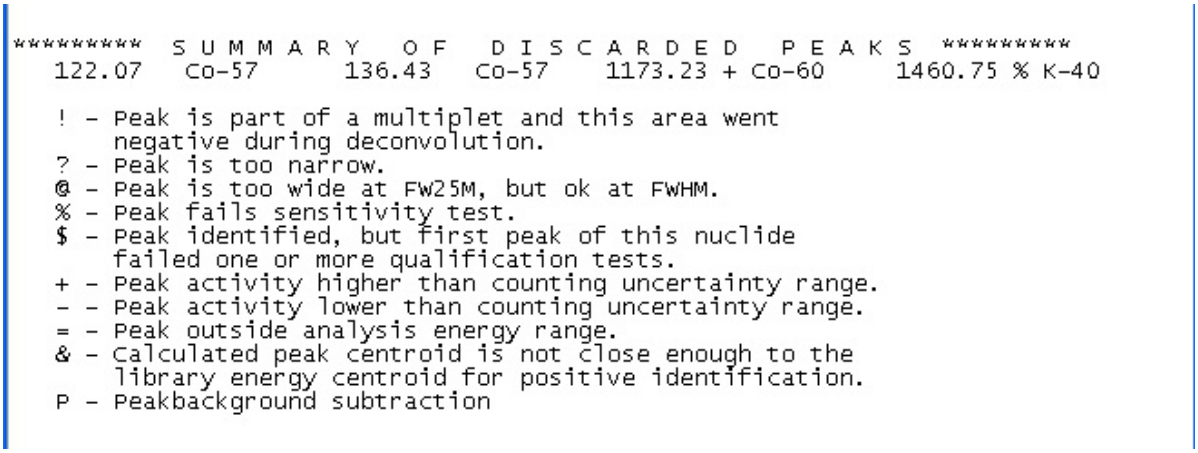
Nuclide	Centroid Energy	Background Counts	Net Area Counts	Intensity Cts/Sec	Uncert 1 Sigma %	Activity
Co-57	122.05	52140.	213398.	59.277	0.29	3.177E+03
Co-57	136.50	37910.	28373.	7.881	1.41	3.316E+03

P - Peakbackground subtraction

Figure 275. Discarded Isotope Peaks Report Section.

7.7.10. Summary of Discarded Peaks

This table (Fig. 276) displays peaks that were evaluated during the Library Directed Peak Search and rejected from use in calculating Nuclide Activity, with the following notes:



```
**********  S U M M A R Y   O F   D I S C A R D E D   P E A K S  **********
   122.07   Co-57      136.43   Co-57    1173.23 + Co-60     1460.75 % K-40

   ! - Peak is part of a multiplet and this area went
       negative during deconvolution.
   ? - Peak is too narrow.
   @ - Peak is too wide at FW25M, but ok at FWHM.
   % - Peak fails sensitivity test.
   $ - Peak identified, but first peak of this nuclide
       failed one or more qualification tests.
   + - Peak activity higher than counting uncertainty range.
   - - Peak activity lower than counting uncertainty range.
   = - Peak outside analysis energy range.
   & - Calculated peak centroid is not close enough to the
       library energy centroid for positive identification.
   P - Peakbackground subtraction
```

Figure 276. Summary of Discarded Peaks Report Section.

- A peak may be rejected due to failing a peak test, rejection of the nuclide due to key line or fraction limit tests, peak activity outside the uncertainty range for the nuclide average activity, as well as other factors.

- This table is displayed only when the **Library peak matrix** option is *disabled* on the Report tab.

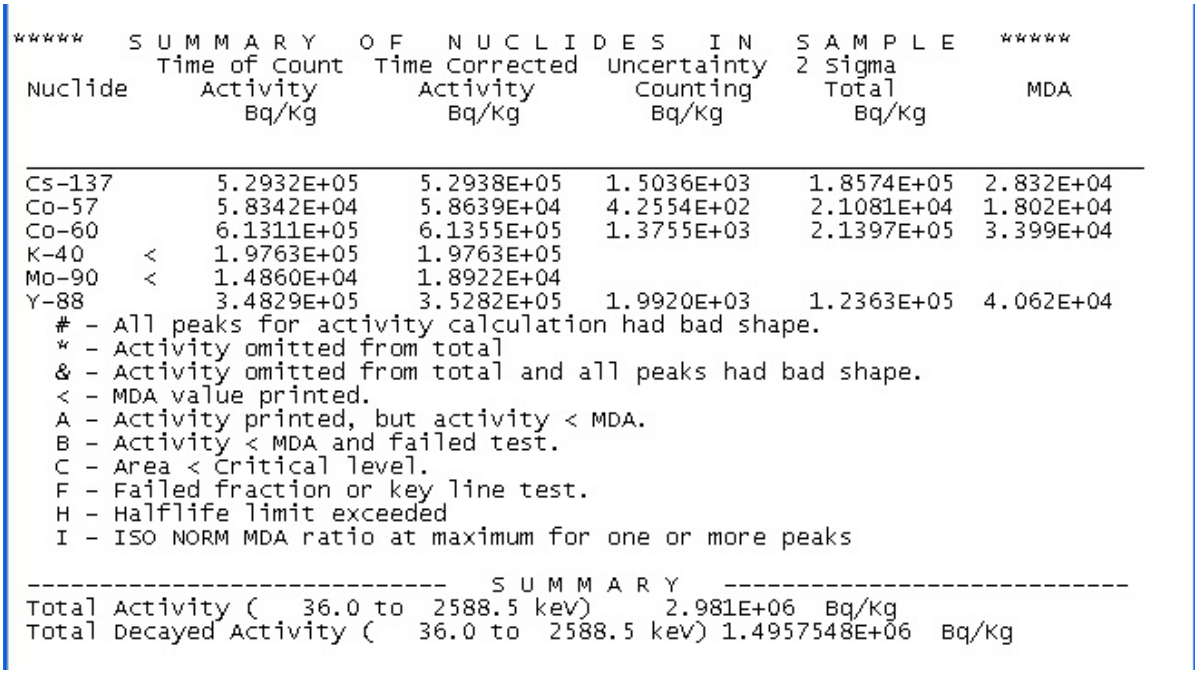
- See Section 7.7.8.1 for peak flag descriptions.

7.7.11. Summary of Nuclides in Sample

This table (Fig. 277) displays the final nuclide activity results with the clarifications below.

- The **Nuclide abundance** option must be enabled on the Report tab for this table to be displayed.

- If the library is not found or the spectrum is not calibrated, this table is suppressed.



****** S U M M A R Y O F N U C L I D E S I N S A M P L E ******

Nuclide		Time of Count Activity Bq/Kg	Time Corrected Activity Bq/Kg	Uncertainty Counting Bq/Kg	2 Sigma Total Bq/Kg	MDA
Cs-137		5.2932E+05	5.2938E+05	1.5036E+03	1.8574E+05	2.832E+04
Co-57		5.8342E+04	5.8639E+04	4.2554E+02	2.1081E+04	1.802E+04
Co-60		6.1311E+05	6.1355E+05	1.3755E+03	2.1397E+05	3.399E+04
K-40	<	1.9763E+05	1.9763E+05			
Mo-90	<	1.4860E+04	1.8922E+04			
Y-88		3.4829E+05	3.5282E+05	1.9920E+03	1.2363E+05	4.062E+04

- All peaks for activity calculation had bad shape.
* - Activity omitted from total
& - Activity omitted from total and all peaks had bad shape.
< - MDA value printed.
A - Activity printed, but activity < MDA.
B - Activity < MDA and failed test.
C - Area < Critical level.
F - Failed fraction or key line test.
H - Halflife limit exceeded
I - ISO NORM MDA ratio at maximum for one or more peaks

S U M M A R Y

Total Activity (36.0 to 2588.5 keV) 2.981E+06 Bq/Kg
Total Decayed Activity (36.0 to 2588.5 keV) 1.4957548E+06 Bq/Kg

Figure 277. Summary of Nuclides in Sample Report Section.

- Nuclide Activity Notes:

  — The “Time of Count” Activity column is weighted by the peak branching ratios as described in Section 6.10.2, and includes all corrections except for decay during collection and decay to collection time. Note that this includes **Decay During Acquisition**, which is set on the Decay tab.

  — The “Time Corrected Activity” column is weighted by the peak branching ratios as described in Section 6.10.3, and has all corrections applied including decay. It is only displayed in this table when **Decay During Collection** or **Decay to Collection Time** is enabled on the Decay tab.

- Uncertainty Notes:

  — Uncertainty Counting and Total Uncertainty data are reported in either percent or activity units as specified on the Report tab.

  — The Total Uncertainty column is only displayed if the Total Uncertainty option is specified on the Report tab.

  — If activity is set to zero, which may occur when using **Directed Fit**, the default percent uncertainty is 1000%.

  — Uncertainty is omitted, or set to zero for some analysis engines, if the nuclide activity

is reported with the "<" flag (i.e., less than the calculated MDA value.)

- MDA Notes:

  — Nuclides that have the "No MDA Calculation" flag set in the library will not calculate an MDA value. If an activity value is not calculated, these nuclides will be omitted from this table.

  — When a nuclide is reported with the "<" flag, the MDA values are displayed in the Time of Count and Time Corrected Activity columns as applicable.

  — For all analysis engines except for GAM32, if the b30winds.ini (n30winds.ini for NAI32) parameter "Print MDA flag" is set to "T" (true), the MDA value is reported in the far right column for nuclides that have an activity value calculated. If this parameter is set to "F" (false), nuclide MDA is not reported for nuclides that have an activity value calculated. The GAM32 analysis engine does not report MDA values when nuclide activity is calculated regardless of this flag setting.

  — The MDA Column header is determined by the b30winds.ini (n30winds.ini for NAI32) parameter "Nuclide Summary MDA Header," which is set to "MDA" by default.

- Total Activity and Total Decayed Activity at the bottom of the table are the sum of the respective nuclide activity columns except that nuclides marked with the following flags are not included in the totals: *, &, <, B, F, (H for Decay Activity only).

- Some nuclide flags may not be reported if no nuclides in the list meet the specified criteria. Nuclide flags are defined as follows:

  # - All peaks for the activity calculation had bad shape. This does not invalidate the nuclide activity, but may indicate that the peaks may have interference, few counts (as may also be accompanied with high uncertainty), tails due to detector performance, or other anomalies that may warrant investigation.

  * - This nuclide activity was omitted from the total activity because the "Activity Not in Total" flag was set for this nuclide in the library.

  & - This nuclide activity was omitted from the total activity because the "Activity Not in Total" flag was set for this nuclide in the library, and all of the peaks had bad shape. This flag is a combination of the # and * flag conditions.

< - The nuclide MDA is reported in the Time of Count and Decay Corrected activity columns as applicable.

A - The nuclide activity is lower than the calculated MDA value. This condition does not necessarily mean that the nuclide activity is invalid or that the true activity must be below the detection limit. This condition may be due to a liberal peak acceptance criterion (i.e., **Peak Cutoff**), using **Directed Fit** in the analysis options for nuclides with no substantial peaks, or when nuclide activity is near the detection level depending on the MDA method specified on the System tab. Further investigation may be warranted for this condition.

B - This flag is a combination of the "A" and "F" flags. Activity is less than the calculated MDA, and the Key Line or Fraction limit test failed.

C - The nuclide activity is lower than the Critical Level MDA method, which is based on the MDA Method 2 described in Section 6.9.2.2. This condition may be due to a liberal peak acceptance criteria (i.e., **Peak Cutoff**), or when using **Directed Fit** in the analysis options for nuclides with no substantial peaks. Further investigation may be warranted for this condition.

F - The Fraction Limit or Key Line test failed for this nuclide. Normally, nuclides that fail one of these tests would be reported as <MDA, but some conditions (i.e., **Directed Fit** or when using the WAN32 analysis engine) may result in nuclide activity being reported.

H - The number of half-lives specified in the b30winds.ini (n30winds.ini for NAI32) file for the "Half lives decay cutoff" parameter has been exceeded for this nuclide. If this occurs, the Time of Count Activity is reported as ">X Halflives" and the Time of Count Activity is reported based on the analysis engine as follows:

- **WAN32, ROI32, ENV32, and NAI32**: Time of Count activity is reported.
- **GAM32**: The "<" flag and MDA value are reported.
- **NPP32**: Time of Count activity is omitted.

I - This flag is only applicable when the ISO NORM table is enabled on the Report tab. It is displayed if the b30winds.ini (n30winds.ini for NAI32) parameter "Maximum ISO NORM MDA ratio factor" is exceeded. When this factor is exceeded, the ISO NORM Detection Limit (MDA) is also limited to a maximum value, as described in Section 6.17.2.1.

7.7.12. Summary of Nuclides (ISO-NORM)

This table (Fig. 278) displays the final ISO NORM compliant nuclide activity results, with the clarifications below.

****** S U M M A R Y O F N U C L I D E S (ISO - NORM) ******

All activity units are in Bq/Kg
Uncertainty in activity units at 2 sigma.

Nuclide		Activity Act_Best	Corrected_Act Act_Low	Counting_Unc Act_High	Total_Unc Det_Thres.	Det_Limit Unc_Best
Cs-137		5.2932E+05 5.2938E+05	5.2938E+05 5.2791E+05	1.5036E+03 5.1952E+05	1.857E+05 4.787E+02	1.047E+03 1.504E+03
Co-57	F	5.8342E+04 5.8639E+04	5.8639E+04 5.8221E+04	4.2554E+02 5.7498E+04	2.108E+04 3.955E+02	8.679E+02 4.255E+02
Co-60		6.1311E+05 6.1355E+05	6.1355E+05 6.1164E+05	1.3755E+03 6.0231E+05	2.140E+05 5.939E+02	1.299E+03 1.946E+03
Y-88		3.4829E+05 3.5282E+05	3.5282E+05 3.5087E+05	1.9920E+03 3.4268E+05	1.236E+05 6.273E+02	1.376E+03 1.992E+03

Figure 278. ISO-NORM Report Section.

- If the library is not found or the spectrum is not calibrated, this table is suppressed.
- If all peaks for a nuclide are outside of the analysis range, only the nuclide name and flags (if any) are reported.
- Each nuclide has two rows of data with the respective headers shown at the top of the table.
- **Activity** is the same as the “Time of Count Activity” reported in the Summary of Nuclides in Sample section.
- **Corrected_Act** is the same as the “Time Corrected Activity” reported in the Summary of Nuclides in Sample Section. This field is omitted and the remaining columns shifted to the left if **Decay During Collection** and **Decay to Collection** are not enabled on the Decay tab. If either of these decay options are enabled, and the b30winds.ini (n30winds.ini for NAI32) parameter “Half lives decay cutoff” is exceeded, the message “>X Halflives” is displayed and none of the other nuclide data is included in this table.
- **Counting_Unc** is the same as the “Counting Uncertainty” reported in the Summary of Nuclides in Sample section.

- **Total_Unc** is the same as the "Total Uncertainty" reported in the Summary of Nuclides in Sample section. This field is omitted and the remaining columns shifted to the left if **Total Uncertainty** is not enabled on the Report tab.

- **Det_Limit** is calculated per Section 6.17.2.2 for MDA Method 19, "ISO 11929 Detection Limit (MDA)," even if a different MDA method is specified on the System tab for reporting in all other sections of the report.

- **Act_Best** (Activity based on best estimate of peak area [A_h]) is calculated per Section 6.17.3.3.

- **Act_Low** (Lower Limit of peak area [$A_<$]) is calculated per Section 6.17.3.7.

- **Act_High** (Upper Limit of peak area [$A_>$]) is calculated per Section 6.17.3.7.

- **Det_Thres.** (Critical Level or Decision Threshold [A_{CL}]) is calculated per MDA Method 18, "ISO Decision Threshold (CL)"; see Section 6.17.2.1.

- **Unc_Best.** (Uncertainty of the best estimate activity [σA_h]) is calculated per MDA Method 19, "ISO Detection Limit (MDA)"; see Section 6.17.2.2.

7.7.13. Iodine Equivalence and Average Energy Calculations

These parameters (Fig. 279) are displayed after the nuclide summary tables when the applicable calculation is enabled on the Isotopes tab and the nuclide summary section of the report is enabled on the Report tab. Refer to Section 6.14 for details on Iodine Equivalence and Section 6.13 for details on Average Energy.

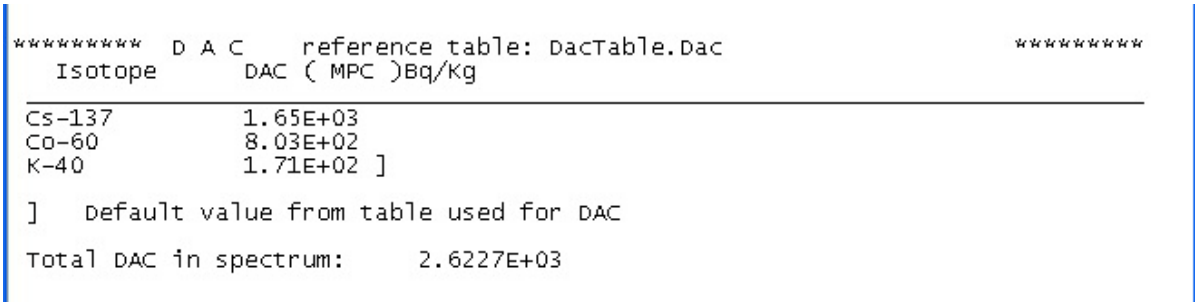
```
Iodine equivalence
       Time of count:    8.37582E+04
     Decay-corrected:    8.38035E+04

 Average energy
       Time of count:    1.45112E+00
     Decay-corrected:    1.45098E+00
```

Figure 279. Iodine Equivalence and Average Energy Report Sections.

7.7.14. DAC Calculations

This section (Fig. 280) is displayed after the nuclide summary tables when the calculation is enabled on the Isotopes tab. Refer to Section 6.15 for details on the DAC calculation.



```
**********  D A C    reference table: DacTable.Dac                    **********
   Isotope      DAC ( MPC )Bq/Kg
 ------------------------------------------------------------------------------
 Cs-137         1.65E+03
 Co-60          8.03E+02
 K-40           1.71E+02 ]

 ]   Default value from table used for DAC

 Total DAC in spectrum:     2.6227E+03
```

Figure 280. DAQ Calculations Report Section.

7.8. The EDF Special Application Report

The EDF Special Application Report (see Section 5.5.1.9) is appended to the end of the standard GammaVision report. This table lists the Gamma Total settings used in the analysis, and the quantitative results.

Figures 281 and 282 shows representative Gamma Total background and Gamma Total Reporting analyses.

```
********** EDF Special Application Report **********

Report path: C:\User\GammaTotal\
```

Gamma total reporting:	NO
Germanium reporting:	NO
Gamma total calculation:	NO
EDF table only:	NO
Count background	YES
Count Cs-137	NO
Write background report	NO
Write maintenance report	NO
Background spectrum:	Null.Spc
Cs137 spectrum:	Null.Spc
Geometry file name:	Null.Txt
Integration range (keV):	1.00E+02, 2.00E+03
Total and germanium sequence:	1, 0
Sample gross counts:	156103
Background CPS:	4.336E+001
Sample Background counts:	156103
Cs-137 gross counts:	0
Cs-137 background counts:	0
Cs-137 activity (Bq):	0.000E+000
K coefficient:	0.000E+000
Gamma total (Bq):	0.000E+000

Figure 281. Gamma Total Background Report.

```
********** EDF Special Application Report **********

Report path: C:\User\GammaTotal\
```

Gamma total reporting:	YES
Germanium reporting:	NO
Gamma total calculation:	YES
EDF table only:	YES
Count background	NO
Count Cs-137	NO
Write background report	NO
Write maintenance report	NO
Background spectrum:	An12717bk.Spc
Cs137 spectrum:	An1271ECs.Spc
Geometry file name:	Geo01.txt
Integration range (keV):	1.00E+02, 2.00E+03
Total and germanium sequence:	1, 0
Sample gross counts:	38367
Background CPS:	8.190E+001
Sample Background counts:	4077
Cs-137 gross counts:	197000
Cs-137 background counts:	4067
Cs-137 activity (Bq):	3.380E+004
K coefficient:	8.956E+000
Gamma total (Bq):	5.118E+003

Figure 282. Gamma Total Report.

[Intentionally blank]

8. QUALITY ASSURANCE(V)

CAUTION Running the MCB Configuration program can affect the continuity of your QA measurements in GammaVision. *Be sure to read Section 2.4!*

8.1. Introduction

The accuracy and reproducibility of results of a data acquisition system should be verified on a periodic basis. Quality Assurance (QA) in GammaVision supplies a means for doing this in accordance with ANSI N13.30 and N42.14. The detector-shield background, detector efficiency, peak shape, and peak drift can be tracked with warning and acceptance limits. The latter use a check source. These results are stored in a database and can be displayed and charted. The database can be accessed with commercially available database products, including Microsoft Access. The information stored in the database for each detector includes:

- **Total Background** — The count rate (counts/sec), over the entire spectrum, of the environmental background (that is, with no source present).

$$Total\ Background = Total\ Counts / Live\ Time$$

- **Total Activity** — The sum of the decay-corrected activities of the nuclides measured in the source, as defined in the analysis library.

$$Total\ Activity = \sum_{x=1}^{N} (DC_x \times A_x)$$

where:

N = the number of nuclides in the analysis library
DC = the decay correction factor for nuclide x in the analysis library
A = the calculated activity, in becquerels, for nuclide x in the analysis library

- **Average FWHM Ratio** — The sum of the ratio of each peak's measured FWHM vs. its calibrated FWHM, divided by the total number of peaks, for all peaks defined in the analysis library.

$$Average\ FWHM\ Ratio = \frac{\sum_{x=1}^{P} (FWHM_{Meas_x} / FWHM_{Cal_x})}{P}$$

where:

P = the number of identified peaks in the spectrum
$FWHM_{Meas}$ = the measured FWHM of analysis library peak x, in keV
$FWHM_{Cal}$ = the calibrated FWHM of analysis library peak x, in keV

- **Average FWTM ratio** — The sum of the ratio of each peak's measured FWTM vs. its effective calibrated FWTM, divided by the total number of peaks, for all peaks defined in the analysis library.

$$Average\ FWTM\ Ratio = \frac{\sum_{x=1}^{P} (FWTM_{Meas_x} / FWTM_{EffCal_x})}{P}$$

where:

P = the number of identified peaks in the spectrum
$FWHM_{Meas}$ = the measured FWTM of analysis library peak x, in keV
$FWHM_{EffCal}$ = the effective calibrated FWTM of analysis library peak x, in keV

- **Average Library Peak Energy Shift** — The average of the deviation of the measured peak enegy from the expected peak energy, for all energies defined in the analysis library.

$$Average\ Peak\ Energy\ Shift = \sum_{x=1}^{E} \frac{|E_{Meas_x} - E_{Lib_x}|}{E}$$

where:

E = the number of identified peak energies in the spectrum
E_{Meas} = the measured peak energy corresponding to analysis library energy x, in keV
E_{Lib} = the expected peak energy x from the analysis library, in keV

The background should be monitored to verify that the detector and shield have not been contaminated by radioactive materials. The value stored is the total count rate which is independent of the count time and any specific isotopic contamination. A background analysis report can be printed after the analysis completes.

The total activity of a calibration or check source will check the efficiency calibration currently in use and the general operating parameters of the system, including source positioning, contamination, library values, and energy calibration. This activity calculation uses the general analysis program to ensure that the total system is checked.

NOTE Use nuclides with long half-lives for your QA measurements. Short-lived nuclides will develop poor peak shapes as they decay.

ORTEC Application Note 55 contains more information and help on starting and running QA for gamma spectroscopy.

The FWHM and FWTM values will check the electronic noise and pole-zero adjustment of the amplifier. The peak shift checks to verify that the system gain and zero offset have not changed.

8.1.1. Using QA Results to Diagnose System Problems

A gradual deterioration of the $FWHM_{Meas}/FWHM_{Cal}$ ratio usually means the detector leakage current has increased.

A sudden deterioration of the $FWHM_{Meas}/FWHM_{Cal}$ ratio suggest that additional noise has been introduced into the system. Commonly, this can arise from:

- A noisy motor introduced into the ac line
- RF interference
- Electronic failure of a component in the detector, preamplifier, or MCB

Generally, these problems will also cause the FW.1M ratio check to fail.

If the FW.1M ratios fail but the FWHM ratios are acceptable, this could indicate:

- Incorrect pole zero
- Neutron or other radiation damage to the detector

8.2. QA Submenu(v)

Figure 283 shows the **QA** submenu under the **Acquire** menu. These commands allow you to accomplish the three major QA functions in GammaVision:

Figure 283. QA Submenu.

The three parts of QA in GammaVision are:

1) Establishing and entering the settings, or “ground rules,” for QA.

2) Measuring background and sample. You perform this periodically, and it is automatically logged into a database by the program.

3) Analyzing the QA database and generating reports. This includes GammaVision's **Status** and **Control Chart** features, which allow you to view the current status of measurements for the Detector and/or view and print the data stored in the database as a control-chart display.

8.2.1. Settings...

The QA settings include the upper and lower radionuclide activity limits which, when exceeded, indicate that the system is not operating correctly. There are two levels of limits. The ***warning*** limits are determined by the settings in the **Low** and **High** fields in the Quality Assurance Settings dialog in Fig. 284. The ***alarm*** limits those outside of the **Minimum** and **Maximum** fields. If the result of a QA measurement is outside the warning limits, a warning dialog is displayed. If the QA result is outside the alarm limits, a violation dialog is displayed. Moreover, if the **Lock Acquire on Violation(s)** box is marked, the violation must be corrected and the QA measurement repeated before the out-of-limits Detector can be used to collect more data.

Generally, after setup, these levels should not be changed without careful consideration.

NOTE If the "Unable to Access QA Database" message is displayed when you issue the **Settings...** command, the QA database file GvQa32.Mdb is not currently located in the folder in which it was originally created (i.e., it has been moved, renamed, or deleted). See Section 8.4.

8.2.1.1. Establishing QA Settings

Click **Settings...** to open the **Quality Assurance Settings** dialog shown in Fig. 284. This dialog contains three main data-entry areas:

- **BACKGROUND Acquisition** time and **Count Rate Limits**
- **SAMPLE Type Analysis Settings File**
- **SAMPLE Analysis Parameter Limits**

Several preliminary steps must be taken to determine the QA settings:

1) Backgrounds must be counted to determine reasonable levels.

2) Samples must be counted for total activity to obtain expected values, since total activity is detector and QA source dependent.

3) A QA library containing only the nuclides in the QA source must be created using the nuclide library editor (see Section 5.6).

4) A sample type settings file (.SDF) must be created which contains the defaults for the QA acquisition and analysis (see Section 5.5.1.1).

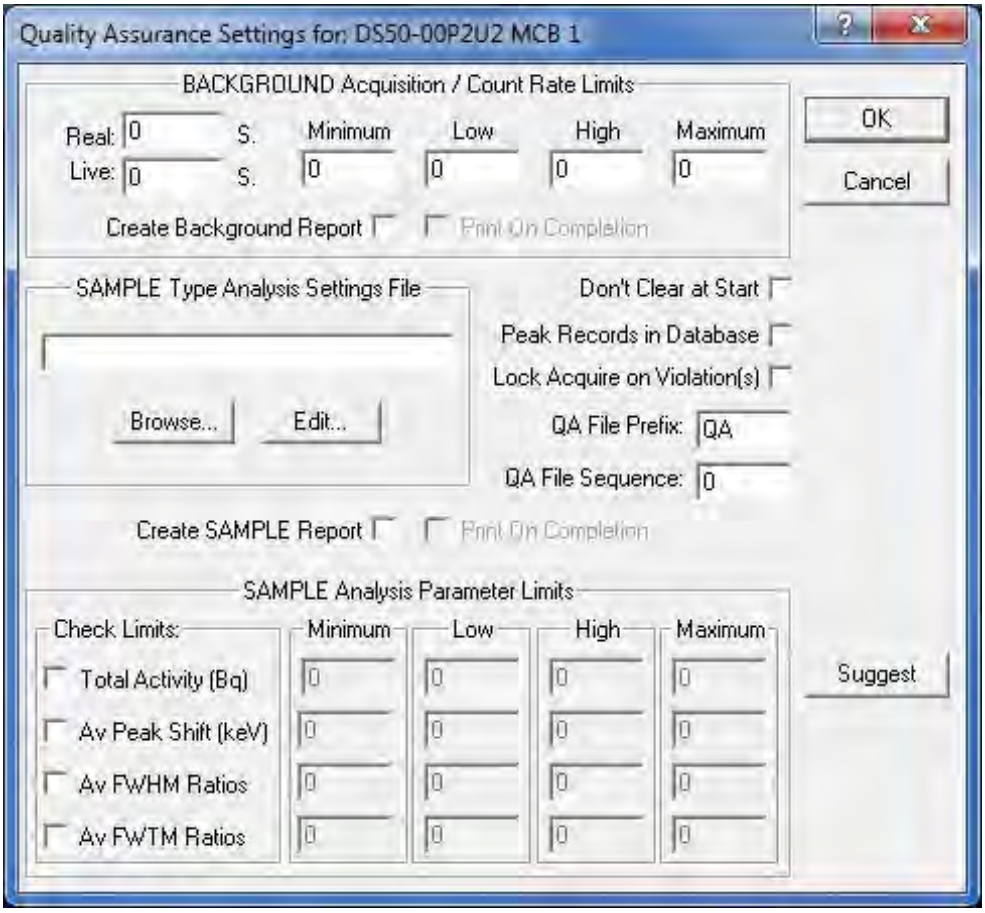


Figure 284. QA Settings Dialog.

5) A QA database file must exist. The GammaVision QA database, GvQa32.Mdb, is installed as part of the standard GammaVision installation, and should be located in the \User directory on the drive where GammaVision was installed. However, if you select the **Settings...** command and GammaVision cannot find GvQa32.Mdb (or if the database file cannot be used for some reason), a warning message will ask if you wish to create a QA database. Click **OK** to start the QA database setup wizard and go to Section 8.4 for instructions. When the database has been successfully created, you will be automatically returned to the Quality Assurance Settings dialog.

All the information gathered in preliminary Steps 1–4 can be entered in the Quality Assurance Settings dialog.

The **BACKGROUND Acquisition** time and **Count Rate Limits** are entered using the information gathered in Step 1 above. Enter the **Real** time or **Live** time in seconds; for background spectra, the dead time is near zero, so these are usually equal.

The **Minimum** and **Maximum** count-rate limits are the ***acceptance thresholds*** for the alarm limit. Acceptance thresholds are used to indicate that the system is operating far from the expected conditions, and can be used to prevent data acquisition from being performed at all until the condition is corrected. If the **Lock Acquire on Violation(s)** box is marked and an acceptance threshold is exceeded, the Detector is automatically locked out from use until the problem is corrected and QA is rerun. The **Low** and **High** count-rate limits are the warning limits, and exceeding them will cause warning messages to be displayed.

The Background Report is printed after the analysis if you mark the **Create Background Report** checkbox. The report can either be saved to disk or printed.

The **SAMPLE Type Analysis Settings File** is the .SDF file created for QA in Step 4 using **Analyze/Settings/Sample Type...**. Click **Browse...** to select the .SDF file. To edit the .SDF file, click **Edit...**. This will open the Analysis Options dialog (see Section 5.5.1.1). Especially relevant sample type settings include:

- Sample type **description**
- Acquisition **presets**
- **QA nuclide library** file (the one created in Step 3)

If you wish to save or print a SAMPLE Report after the analysis, mark the **Create SAMPLE Report** box.

On the left of the **SAMPLE Analysis Parameter Limits** section are checkboxes for marking the limits to be tracked. **Total Activity (Bq)**, **Av**erage **Peak Shift (keV)**, **Av**erage **FWHM Ratios**, and **Av**erage **FWTM Ratios** are the choices. Mark the limits to be tracked. The first time GammaVision QA is set up, click the **Suggest** button (on the right) to enter factory-set limits. After this, use the **Suggest** button with caution, because clicking on it again will reset all the limits to the previously defined settings. The actual limits can be determined from the samples counted in Step 2 above.

Click **OK**. GammaVision will check the measurement limits to determine if they are set consistently. If they are, the dialog will close; if not, a message will be displayed on the Marker Information Line and the dialog will remain open so the limits can be changed. QA data can now be collected using **Acquire/QA/Measure Background** and **Acquire/QA/Measure Sample**.

8.2.2. Measure Background

This command opens the dialog in Fig. 285, to verify that all sources have been removed from the Detector before proceeding. Confirm that all sources have been removed for a background measurement, click **OK–Start**. The remaining functions are performed automatically.

Figure 285. Begin Background QA Count.

Mark the **Overwrite (repeat) previous background measurement** checkbox (by clicking on it) if the previous measurement was in error. If a sample QA has been run since the background QA, the previous background run cannot be overwritten. For example, if a problem was detected, fixed, and this run is to verify the repairs, check the box so the “bad” value is not kept in the database. Click **OK**.

If the background is outside the set limits, a warning similar to Fig. 286 is displayed.

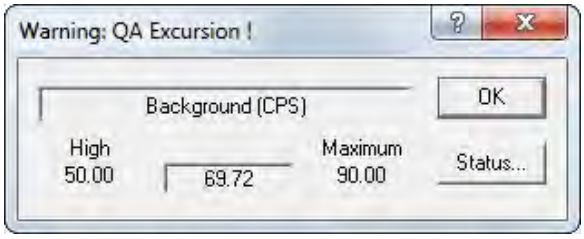


Figure 286. Background Warning Message.

8.2.3. Measure Sample

This command opens the Sample QA Measurement dialog (Fig. 287). It is a reminder to place the QA source on the Detector. Click **Overwrite** to replace the last measurement. Click **OK–Start** to begin the count.

The QA source spectra are collected for the preset time and analyzed automatically. The analysis results are compared with the limits. If the result is outside the limits, a warning is displayed. The results are also stored in the QA database.

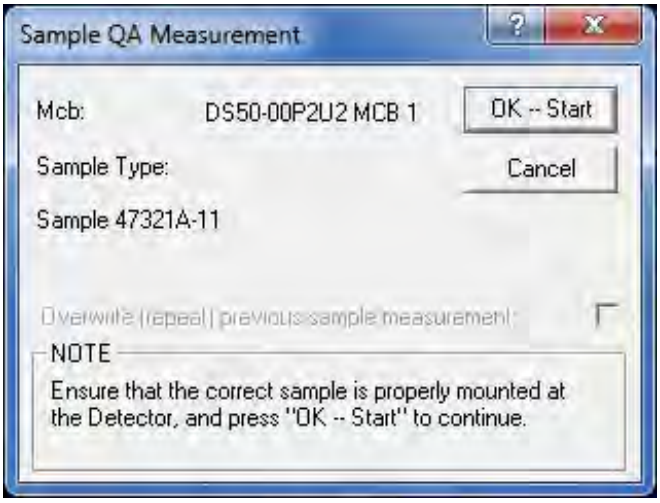


Figure 287. Starting Sample Type QA Measurement.

8.2.4. Status...

The QA status for the currently selected Detector is displayed as shown in Fig. 288. Click **OK** to close the dialog.

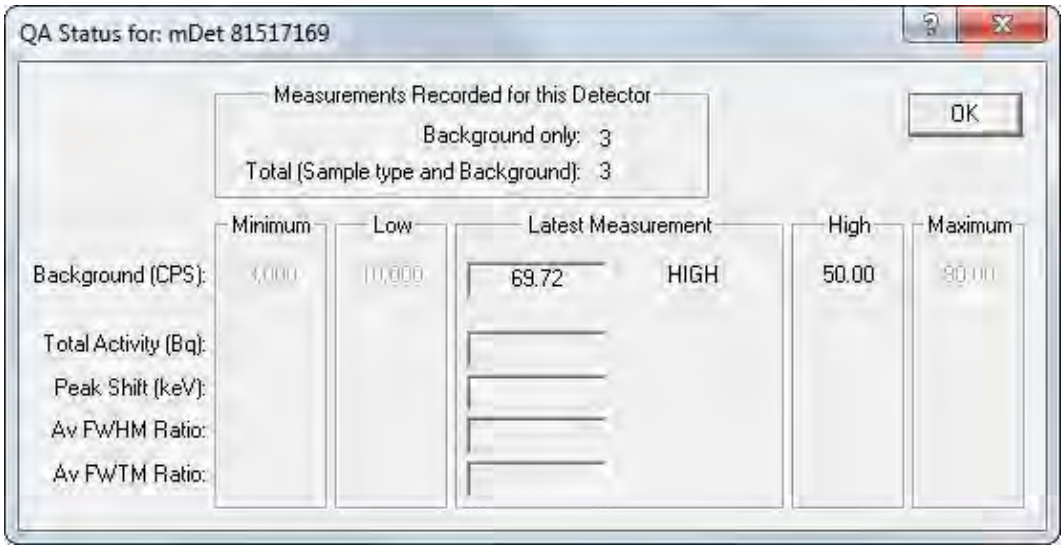


Figure 288. Showing Status of QA Measurements for a Detector.

8.2.5. Control Charts...

The **Control Chart...** functions display the data stored in the QA database as a control chart. The displayed data can be scrolled backward or forward across the screen so that all collected data can be viewed. A typical chart is shown in Fig. 289. The short dashed lines represent the warning limits and the long dashed lines represent the acceptance threshold limits. Note that if you call this command before any QA settings are established in the GammaVision QA database, you will receive an error message. Acknowledge the message and set up your detectors in the QA database.

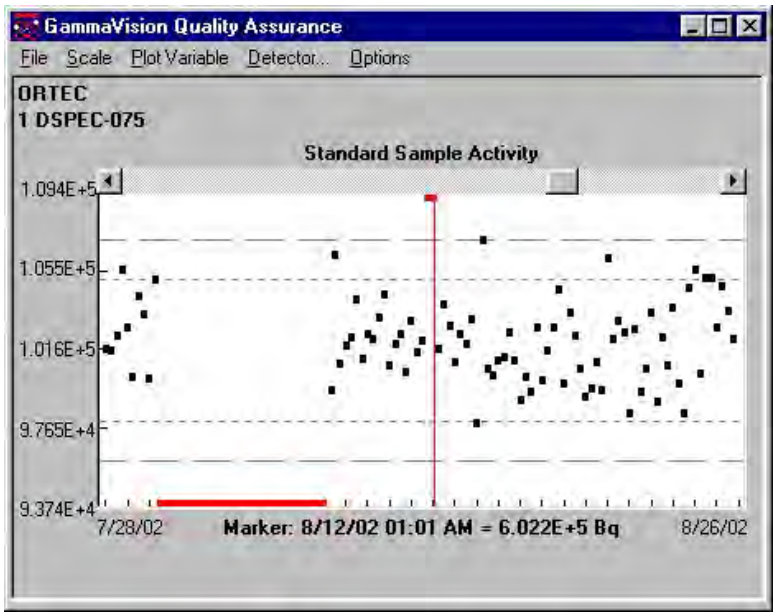


Figure 289. Control Chart Example.

Figure 290 shows the control chart **File** menu, which contains the **Print Graph** command for printing the current graph on the current

printer; a standard Windows **Print Setup...** command for selecting the printer and its setup features, such as landscape vs. portrait layout, paper size, number of copies, and device control options; the **Exit** command for closing the QA Chart Program (this duplicates the dialog's upper-right Close box); and an **About** box providing version information about the chart program.

Choose the chart time period (**Week**, **Month**, or **Quarter**) from the **Scale** menu (Fig. 291).

The **Plot Variable** menu (Fig. 292) contains functions for selecting **Activity**, **Peak Energy**, **Peak Width @ Half Max**, **Peak Width @ Tenth Max**, or **Background**.

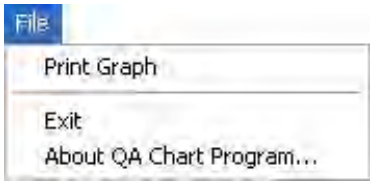


Figure 290. QA Chart File Menu.

Figure 291. Scale Menu.

Figure 292. Plot Variable Menu.

The **Detector** menu item opens the list of Detectors for which background and sample measurements have been made (Fig. 293). Select a Detector for this control chart and click **OK**.

Offline processing of the QA data-base (including detailed trend analyses) can be done outside of GammaVision. The database format used is well-documented and compatible with a number of popular software products including Microsoft Access.

NOTE ***We strongly recommend that you back up any GammaVision database files before performing manipulations on them outside of GammaVision.***

Figure 293. Detector Pick List.

The **Options** menu (Fig. 294) includes an **Always On Top** command, which keeps the QA window on top of all other windows, no matter which window (in GammaVision or any other program) might be active.

Figure 294. QA Chart File Menu.

The **Fixed Vertical Scale** command adds flexibility in displaying control charts both onscreen and on printouts, for comparison with other charts.

- **Fixed Vertical Scale Off** (no check mark) — In this mode, the vertical scale of the graph is adjusted so that all points are shown to scale. All points are black. If one or more data points are substantially out of range, the graph may be quite compressed vertically.

- **Fixed Vertical Scale On** (check mark) — In this mode, the vertical scale of the graph is set to show the upper and lower alarm limits as full scale. The data points within the alarm limits are colored black. Out-of-range points are displayed in red at the lower or upper limits of the graph, at the proper horizontal coordinate. The out-of-range points are printed as a question mark (**?**).

To switch between the two display modes, click the menu item to mark it with a checkmark or unmark it.

Figures 295 through 298 show the screen and printout for a QA data set with **Fixed Vertical Scale** on, then off. Compare the location of the points that exceed alarm limits in Figs. 295 and 296 to the location of the question marks in Figs. 297 and 298.

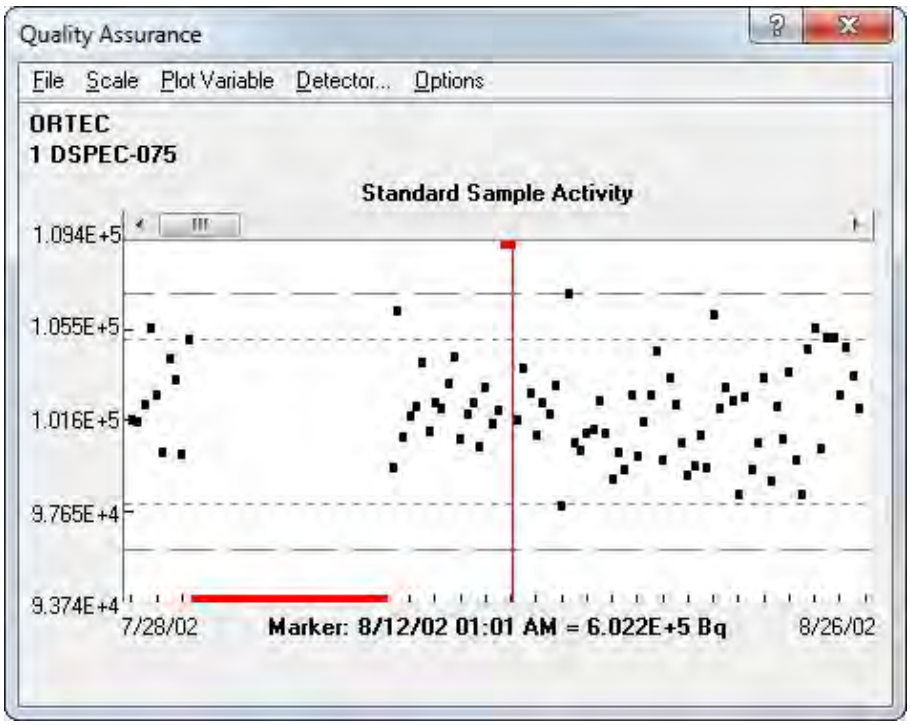


Figure 295. Control Chart On Screen with Fixed Vertical Scale On.

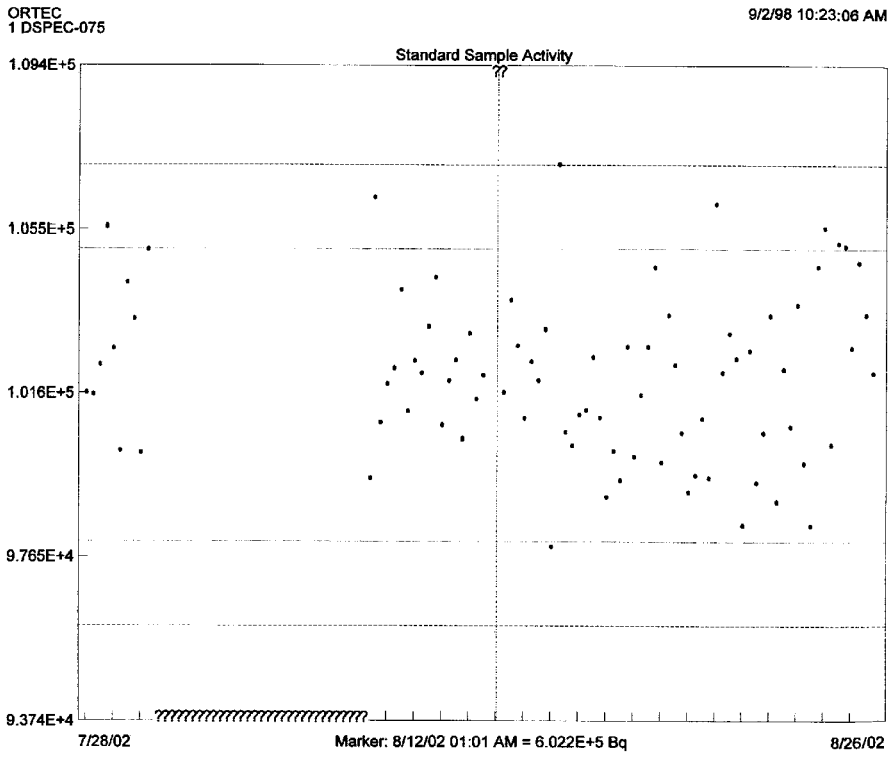


Figure 296. Printout of Control Chart with Fixed Vertical Scale On.

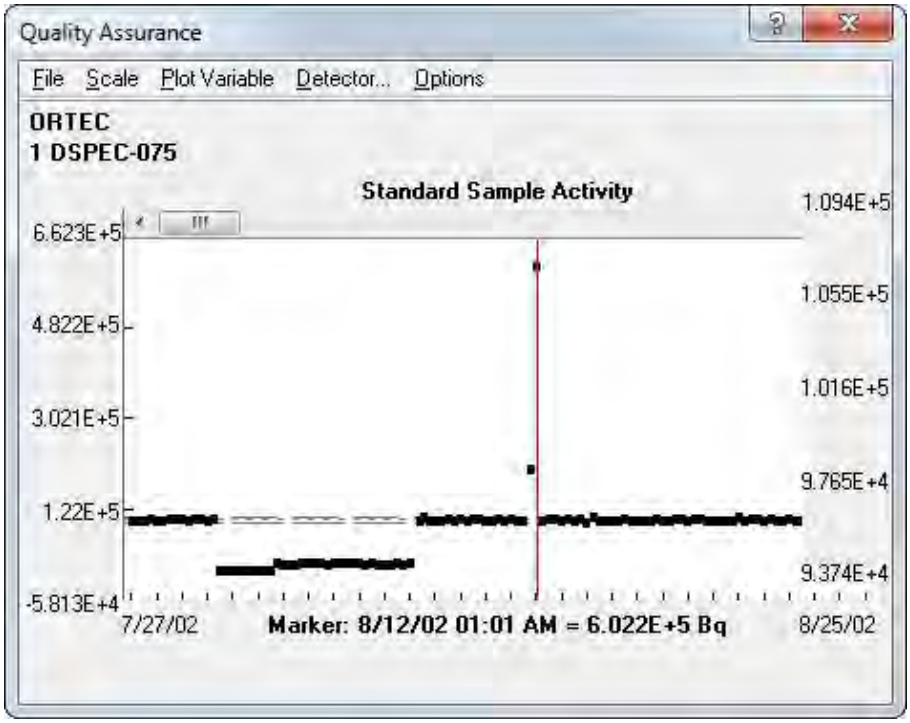


Figure 297. Control Chart On Screen with Fixed Vertical Scale Off.

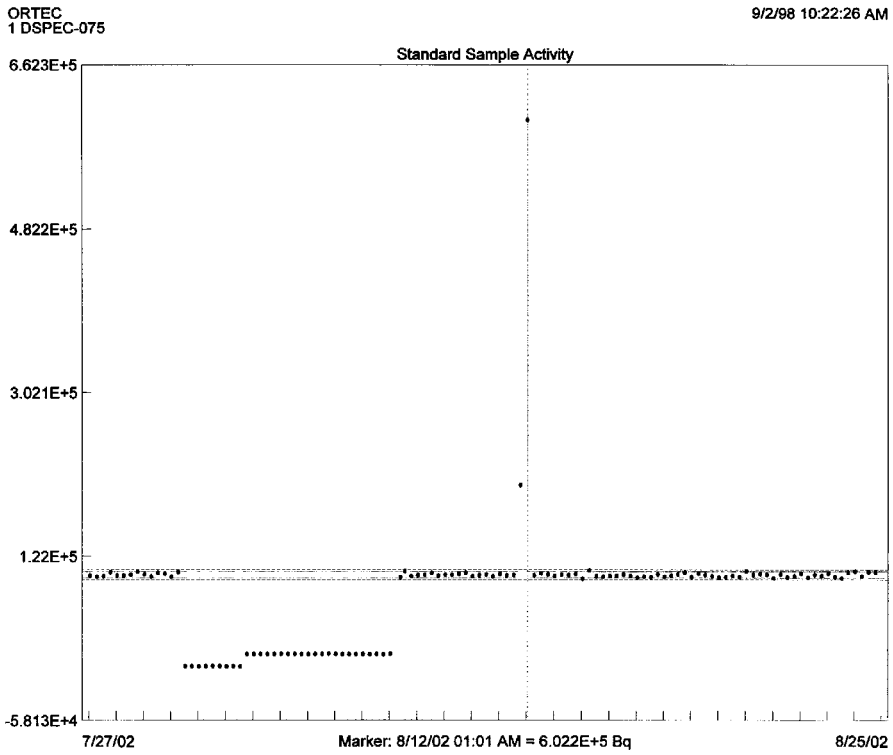


Figure 298. Printout of Control Chart with Fixed Vertical Scale Off.

8.3. Quality Assurance Example

This section discusses how to set up QA for a new detector in GammaVision, then perform background and check-source measurements for the detector.

1) From the detector droplist on the toolbar, select the MCB that has the new detector. This MCB will now be displayed in the active spectrum window.

2) We will assume our check source was calibrated at 1.0 ì Ci of ^{60}Co activity and 2.0 ì Ci of ^{137}Cs activity on June 27, 2000. The total expected activity measured today and decay-corrected back to the calibration date is 3.0 ì Ci. We will count the source in the same position for 10 minutes each day to verify the detector efficiency and calibration have not changed. It is unlikely the actual detector efficiency has changed, but the calibration file might have changed or electronic noise might be interfering with the spectrum collection. We will count background for 120 seconds to verify the detector is not contaminated (if the detector were contaminated with the same isotopes as in the QA source, the QA activity would be incorrect) .

3) Use the GammaVision Library Editor on the **Library** menu to prepare a QA library containing only ^{60}Co and ^{137}Cs, and save it the library as QA.lib.

4) Select **Acquire/QA/Settings...** to display the Quality Assurance Settings dialog for this detector (Fig. 299), then go to the **SAMPLE Type Analysis Settings File** section and click the **Edit** button. This will open the Analysis Options dialog (Fig. 300), which will allow us to create a sample defaults (.SDF) file for analyzing the QA acquisitions for this detector.

5) We will now enter the following analysis options for this .SDF file:

   - On the Sample tab, click the **Presets** button to open the Presets dialog for this MCB type, then enter a **Live Time** preset of 600 seconds.

   - In the **Nuclide Library** section, unmark the **Internal** box, then browse to retrieve the newly created QA.lib file.

   - Click the Decay tab. Mark the **Collection** checkbox and enter 06/27/2000 as the **Date** and 12:00:00 as the **Time**. The format for the date and time will be determined by the Windows settings for the host computer.

   - Return to the Sample tab, click **Save As...**, and save this file as QA.SDF.

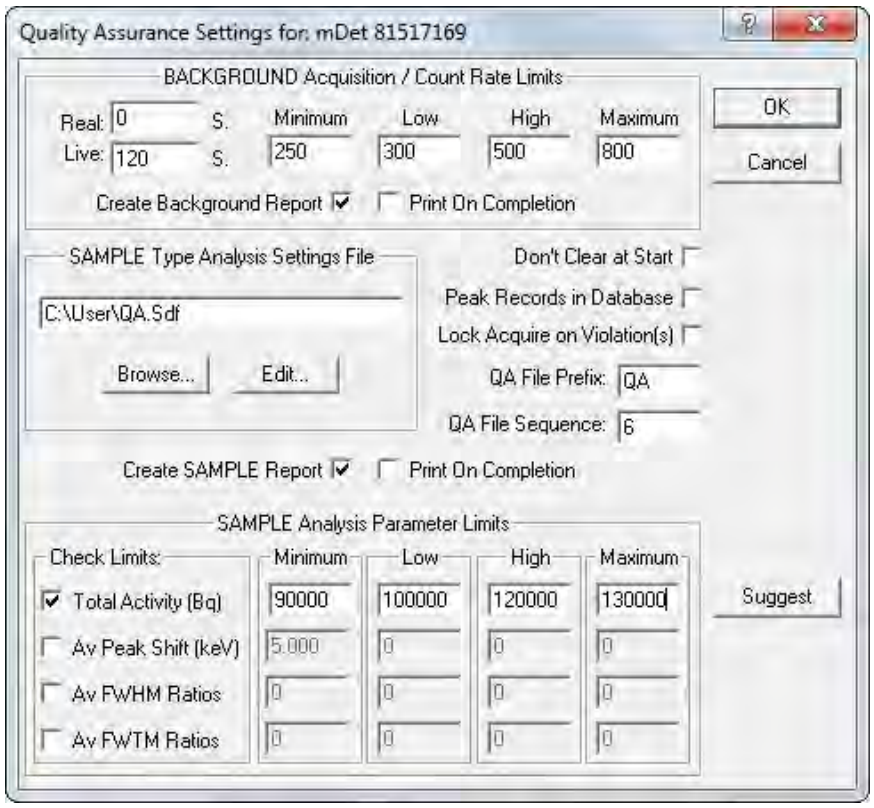


Figure 299. Example of Quality Assurance Settings.

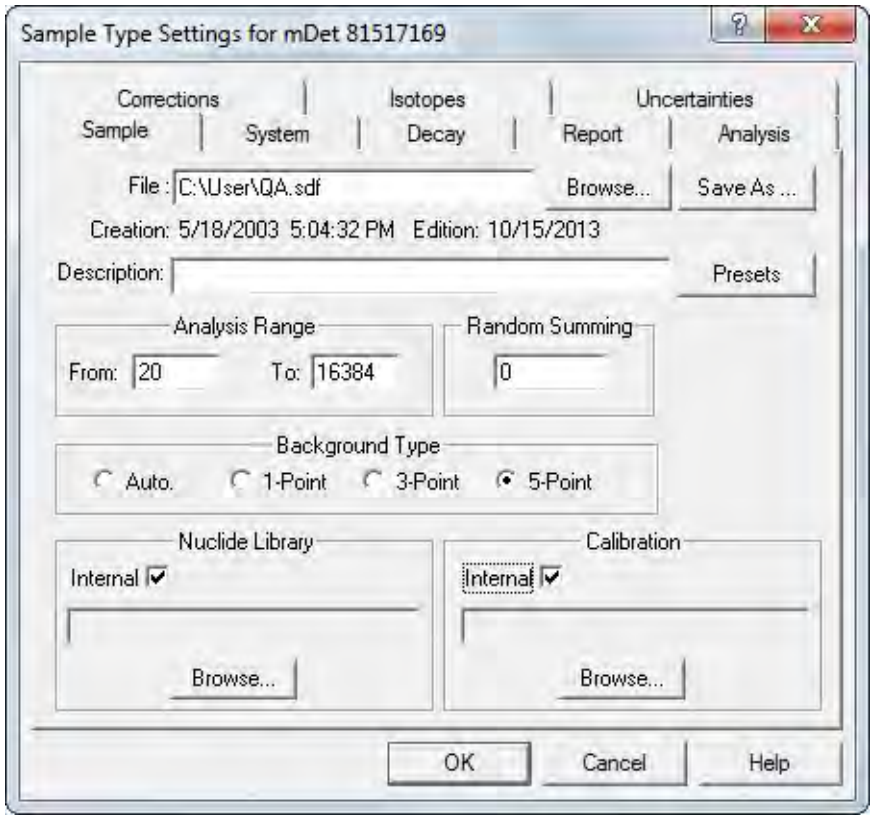


Figure 300. Typical Settings for Quality Assurance Analysis.

- Click **OK** to close the Analysis Options dialog. This will return you to the Quality Assurance Settings dialog.

6) In the **BACKGROUND Acquisition** section, enter a **Live Time** preset of 120 seconds. Enter arbitrary count-rate values for the **Low** and **High** background settings until you know what the realistic numbers should be. Do not use zero for the **Low** limit; if you do, you will not receive a warning if the detector is not counting (for instance, if it is disconnected). Remember that these values are count rates, so are independent of the counting time.

7) Select the QA.SDF file in the **SAMPLE Type Analysis Settings File** section.

8) The expected value of the activity of the sample is 1.1E+5 Bq (3.0 ì Ci). Scale this up and down by 10% for **Low**/**High** and 20% for **Minimum**/**Maximum** into activity fields. These values are shown in the **SAMPLE Analysis Parameter Limits** section in Fig. 299.

You are now ready to collect data for the QA background followed by the QA check source measurements.

9) Select **Acquire/QA/Measure Background...** to start the background process. You will be prompted to remove all the sources from the detector and click **OK-Start**. The background spectrum will be collected and summed, and stored in the QA database, GvQa32.Mdb. If any limits were exceeded, a warning message will be displayed.

10) Select **Acquire/QA/Measure Sample...** to start the sample process. You will be prompted to place the QA source in the proper place on the detector and click **OK-Start**. The sample spectrum will be collected and analyzed, and the results stored in the QA database. If any limits were exceeded, a warning message will be displayed.

11) Note the **Lock Acquire on Violation** checkbox in the QA settings dialog. If this box is marked and a limit is exceeded, GammaVision will display a QA warning each time you try to use the detector until the QA problem is corrected.

12) The background and sample spectra will automatically be stored according to the **QA File Prefix** and **QA File Sequence** number entered in Fig. 299.

You have now completed a QA setup and system verification, and have stored the results in the QA database.

8.4. Creating a QA Database

If you select the **Settings...** command on the **QA** sub-menu and the "Unable to Access QA Database" message is displayed (Fig. 301), GammaVision cannot find the QA database file GvQa32.Mdb in the folder in which it was originally created (i.e., it has been moved, renamed, or deleted). By default, GammaVision creates the QA database file in C:\User.

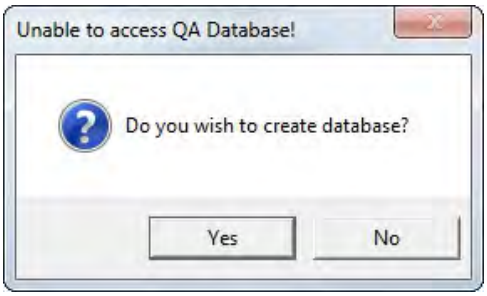


Figure 301. Cannot Find QA Database; Do You Wish to Create a New One?

If you have moved the QA database file to another folder, you can either (1) reestablish connection with it and its contents, or (2) create a new, empty QA database. *If you choose to create a new QA database, we recommend that you modify the name of the old database file to prevent data loss due to overwriting.*

To create a new, empty copy of GvQa32.Mdb, answer **Yes**. This will open the Select Database File dialog (Fig. 302). Click **OK** to accept the default filename and location; or select a new location and/or filename, then click **OK**. A blank Settings dialog will open, as described in Section 8.2.1, so you can establish new settings for the currently selected detector.

To reconnect to your existing QA database file, answer **Yes** to open the Select Database File dialog, and click **Browse**. This will open a standard Windows file-open dialog. Locate the desired QA database file, click **Save**, and confirm that you wish to overwrite the file. *Note that this does not overwrite (delete) the contents of your database file.* The Settings dialog will open, as described in Section 8.2.1, and will display the settings for the currently selected detector.

Figure 302. Accept Default Settings or Choose Location and Name of New QA Database File.

9. KEYBOARD FUNCTIONS

This chapter describes the GammaVision accelerator keys. The keys described in this section are grouped primarily according to location on the keyboard and secondarily by related function.

9.1. Introduction

Table 16 provides a quick reference to all of the GammaVision keyboard and keypad functions. These accelerators are also illustrated in Fig. 303, and discussed in more detail in the remainder of the chapter.

The accelerators are available only in the GammaVision window. The title bar must be high-lighted with the active title bar color (as set up in Windows Control Panel). In addition, the active cursor — or input *focus* — must be in one of the spectrum windows. Similar to other Windows applications, the focus can be switched between GammaVision and other applications by clicking on the Windows Taskbar, pressing **<Alt + Tab>**, or, if the inactive window is visible, pointing with the mouse at some spot in the inactive window and clicking.

The multi-key functions, such as **<Alt + 1>** or **<Shift + →>**, are executed by holding down the first key (e.g., **<Alt>**, **<Shift>**, or **<Ctrl>**) while pressing the key that follows the "+" sign in the brackets, then releasing both keys simultaneously. Functions that use the keypad keys begin with the word **Keypad**, e.g., **Keypad<5>**.

As usual for any Windows application, the menus are accessed by clicking on them with the mouse, or by using the **Alt** key plus the key that matches the underlined letter in the menu item name. For example, the multi-key combination to activate the **File** menu is **<Alt + F>**.

Note that the GammaVision accelerator keys do not interfere with Windows menu operations or task switching. For example, when a menu is active (i.e., pulled down), the <←>/<→> and <↑>/<↓> keys revert to their normal Windows functions of moving across the menu bar and scrolling up/down within a menu, respectively. As soon as the menu is closed, they behave as GammaVision accelerators again.

9.2. Marker and Display Function Keys

9.2.1. Next Channel <→>/<←>

When not in rubber-rectangle mode, the right and left arrow keys move the marker by one displayed pixel in the corresponding direction. This might represent a jump of more than one spectral data memory channel, especially if the horizontal scale in channels is larger than the width in pixels of the window (see the discussion in Section 4.2).

Table 16. Quick Reference to GammaVision Keyboard Commands.

Key	Function
<↓> or <F5>	Change vertical scale so spectrum peaks appear smaller (vertical zoom out).
<↑> or <F6>	Change vertical scale so spectrum peaks appear larger (vertical zoom in).
<→>	Move marker to higher channel.
<←>	Move marker to lower channel.
<–> or <F7>	Narrow the horizontal scale.
<+> or <F8>	Widen the horizontal scale.
<Ctrl + →>	Jump to next higher peak.
<Ctrl + ←>	Jump to next lower peak.
<Shift + →>	Jump to next higher ROI. In rubber rectangle mode, shift rectangle right (to higher energy/channel) one pixel.
<Shift + ←>	Jump to next lower ROI. In rubber rectangle mode, shift rectangle left (to lower energy/channel) one pixel.
<Shift + ↑>	Shift the Compare spectrum up. In rubber rectangle mode, shift rectangle up (away from baseline) one pixel.
<Shift + ↓>	Shift the Compare spectrum down. In rubber rectangle mode, shift rectangle down (toward baseline) one pixel.
<Alt + →>	Advance to next library entry.
<Alt + ←>	Move back to previous library entry.
<PageUp>	Jump to higher channel number in 1/16th-screen-width increments.
<PageDown>	Jump to lower channel number in 1/16th-screen-width increments.
<Home>	Jump to first channel of the full spectrum.
<End>	Jump to last channel of the full spectrum.
<Ctrl + Fi>	Select Detector i (i = 1 to 12, in pick list order).
<F2>	Switch ROI bit control from OFF to SET to CLEAR.
<F3>	In MCBs with ZDT Mode, switch between the two spectra stored in ZDT mode.
<Shift + F3>	In Compare mode when comparing ZDT spectra, hold the initial spectrum in its current ZDT view (ERR or ZDT) and toggle the Compare spectrum between its ZDT views.
<F4> or <Alt + 6>	Switch between displaying selected Detector and buffer.
<F5> or <↓>	Change vertical scale so spectrum peaks appear smaller (vertical zoom out).
<F6> or <↑>	Change vertical scale so spectrum peaks appear larger (vertical zoom in).
<F7> or <–>	Change the horizontal scale so peaks appear narrower (horizontal zoom out)
<F8> or <+>	Change the horizontal scale so peaks appear wider (horizontal zoom in)
<Alt + F7>	Reset both horizontal and vertical scaling to view complete spectrum.
Keypad<–>	Zoom out.
Keypad<+>	Zoom in.
Keypad<5>	Center expanded display on cursor.
Keypad</>	Switch between logarithmic and linear vertical scaling.
Keypad<*>	Switch to auto vertical scale.
Insert<Ins>	Mark the peak region around the cursor as an ROI.
Delete<Del>	Clear the ROI.
<Alt + 1>	Start acquisition in selected Detector.
<Alt + 2>	Stop acquisition in selected Detector.
<Alt + 3>	Clear data in selected Detector.
<Alt + 5>	Copy data in the selected Detector to the buffer.
<Alt + 6> or <F4>	Switch between displaying selected Detector and buffer.
<Alt + –>	Decrease amplifier fine gain by smallest increment (where supported).
<Shift + Alt + –>	Decrease amplifier fine gain by several increments.
<Alt + +>	Increase amplifier fine gain by smallest increment.
<Shift + Alt + +>	Increase amplifier fine gain by several increments.
<PrintScreen>	Capture screen to Windows Clipboard.

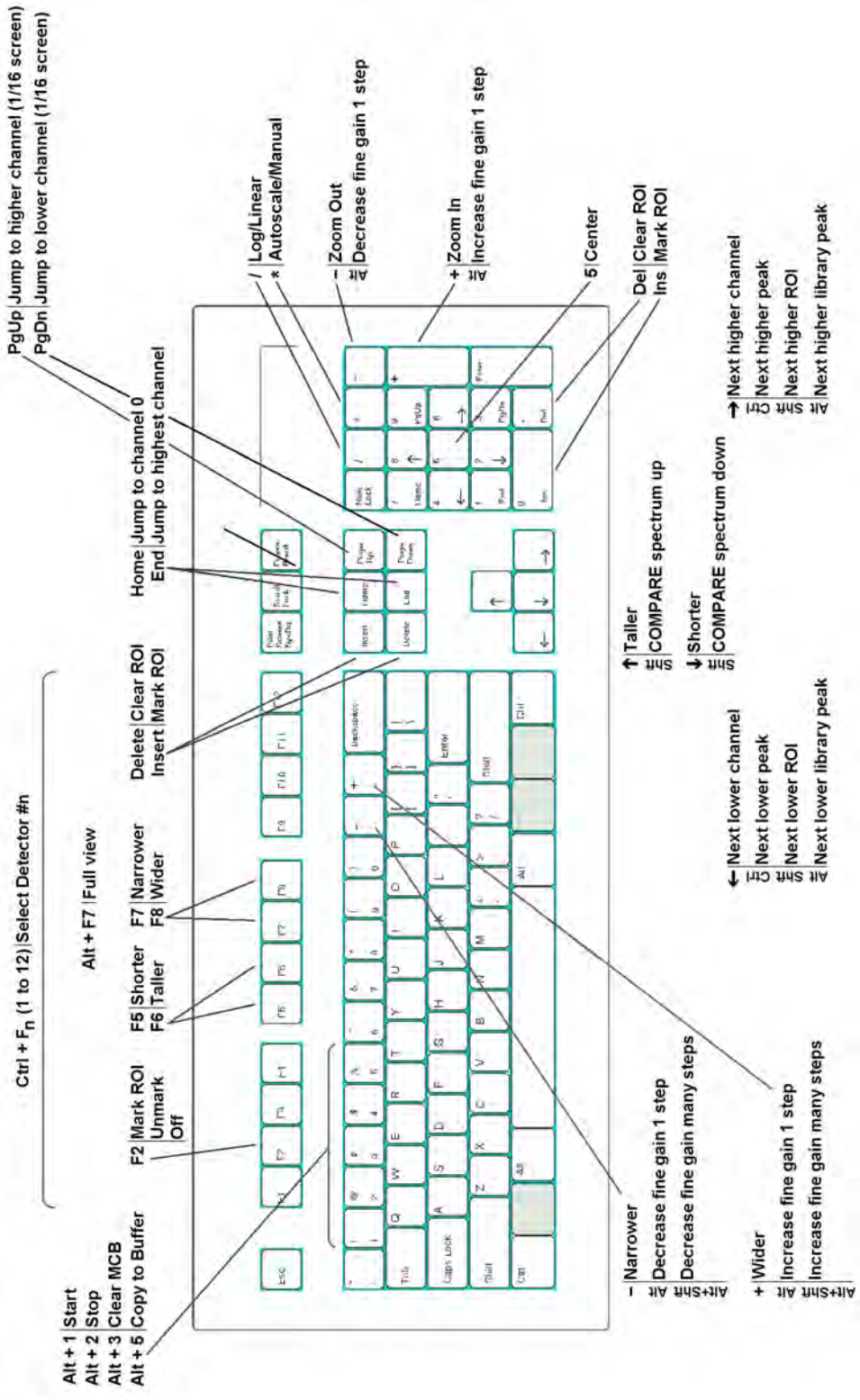


Figure 303. GammaVision Keyboard and Keypad Accelerators.

If the horizontal scale is expanded, when the marker reaches the edge of the spectrum window, the next key press past the edge shifts the window to the next block of channels in that direction such that the marker is now in the center of the display.

When the ROI mode is set to **Mark**, the <→>/<←> keys cause the channels to be marked as the marker moves. Similarly, they clear the ROI bits while the ROI mode is **UnMark**. (See Section 5.8.)

9.2.2. Next/Previous ROI <Shift + →>/<Shift + ←>

The **<Shift + →>** or **<Shift + ←>** move the marker to the beginning of the next higher channel ROI, or the end of the preceding ROI, respectively, of the displayed spectrum. These functions are duplicated by the **ROI** indexing buttons on the Status Sidebar.

9.2.3. Next/Previous Peak <Ctrl + →>/<Ctrl + ←>

The **<Ctrl+ →>** and **<Ctrl+ ←>** keys perform a peak search on the spectrum in the higher or lower channel direction, respectively, and move the marker to the first peak found. If no peak is found, the program displays the "**Can't find any more peaks!**" message and the marker does not move. If the spectrum is energy-calibrated and the library loaded, the system displays the best match from the library within two FWHMs of the peak centroid. If there is no match within this range, the "**No Close Library Match**" message is displayed. These functions are duplicated by the **Peak** indexing buttons on the Status Sidebar.

9.2.4. Next/Previous Library Entry <Alt + →>/<Alt + ←>

These keys move forward or backward through the nuclide library to the next closest library entry. Each button press advances to the next library entry and moves the marker to the corresponding energy. Also, instead of indexing from a previously identified peak, the marker can be positioned anywhere in the spectrum and these keys used to locate the entries closest in energy to that point. If a warning beep sounds, it means that all library entries have been exhausted in that direction, or that the spectrum is not properly calibrated for reaching the energy with the marker. In any case, if an appropriate peak is available at the location of the marker, data on the peak activity are displayed on the Marker Information Line. These functions are duplicated by the **Library** indexing buttons on the Status Sidebar.

9.2.5. First/Last Channel <Home>/<End>

These keys move the marker to the first or last channel of the spectrum.

9.2.6. Jump (Sixteenth Screen Width) <PageDown>/<PageUp>

<PageDown> and **<PageUp>** jump the marker position to the left (to lower channel numbers) or right (to higher channel numbers), respectively, 1/16 of the window width, regardless of the horizontal scale. The status of the ROI bit is not altered when the marker is moved with these keys, that is, the **Mark/UnMark/Off** state is ignored. The marker channel contents and Marker Information Line are continuously updated as the marker jumps, so when the jump is complete, the marker information is up-to-date for the current channel.

9.2.7. Insert ROI <Insert> or Keypad<Ins>

These keys mark an ROI in the spectrum, at the marker position, in one of two ways:

1) If the spectrum is calibrated, the region is centered on the marker with a width of three times the calibrated FWHM. There does not need to be a peak at the marker position.

2) If the spectrum is not calibrated, the region is centered on the peak, if any, located within two channels of the marker and is as wide as the peak. If the peak search fails, or if the peak is not well-formed, no ROI is marked. There is no limit on the size of a peak or ROI; therefore, in some uncalibrated spectra, large ROIs could be marked.

These accelerators duplicate the function of the **Mark ROI** toolbar button and the **ROI/Mark Peak** menu selection (see Section 5.8).

NOTE **<Insert>** and **Keypad<Ins>** work conveniently in combination with **<Ctrl +** ←**>** and **<Ctrl +** →**>** to rapidly set peak ROIs.

9.2.8. Clear ROI <Delete> or Keypad<Del>

<Delete> and **Keypad<Del>** clear the ROI bits of all ROI channels contiguous to the channel containing the marker. These accelerators duplicate the function of the **Clear ROI** button on the toolbar and the **ROI/Clear** menu selection (see Section 5.8).

9.2.9. Taller/Shorter <↑>/<↓>

The <↑> and <↓> keys decrease or increase the vertical full scale of the displayed spectrum so the peaks appear taller or shorter, respectively. The minimum is 32 counts-full-scale; the maximum is 1024 million counts. Each successive key press doubles or halves the full scale until the maximum or minimum is reached. Whenever the maximum full-scale value is reached, the next <↑> key press switches to logarithmic scale. If the display is already in logarithmic scale, the display switches to linear scale. In either case, the vertical full-scale value is always shown on the toolbar.

Note that if the number of counts exceeds the full-scale value, the data points will be displayed at the full-scale value.

These keys duplicate the function of the **<F6>/<F5>** keys.

9.2.10. Move Rubber Rectangle One Pixel <Shift + ↑, ↓, →, ←>

In rubber-rectangle mode (see Section 4.4.3), the **<Shift + Arrow>** keys move the rubber rectangle one channel or one pixel at a time.

9.2.11. Compare Vertical Separation <Shift + ↑>/<Shift + ↓>

In Compare mode, the **<Shift** + ↑> or **<Shift** + ↓> keys decrease or increase the vertical separation between the two spectra. Each successive key press will increase or decrease the separation by moving the spectrum read from disk. The spectrum from disk can be moved below the first spectrum if it has fewer counts.

9.2.12. Zoom In/Zoom Out Keypad<+>/<->

Keypad<+> increases the scale of both axes in the Expanded Spectrum View so the peaks appear larger, while **Keypad<->** does the opposite, making the peaks look smaller. The scale value for both axes is always shown on the toolbar.

These functions are duplicated by the **Zoom In**/**Zoom Out** buttons on the toolbar and **Zoom In** and **Zoom Out** under the **Display** menu. See Section 4.2 for a more detailed discussion.

9.2.13. Fine Gain <Alt + +>/<Alt + ->

These accelerators step the internal amplifier up or down by one increment of fine gain on the selected Detector, if it has a software-controlled amplifier. The new fine gain setting is shown on the Supplemental Information Line at the bottom of the screen. If the gain stabilizer is active, the display of the histogram data might not change.

The fine gain can also be set with **Acquire/MCB Properties...** (Section 5.2.11), **<Shift + Alt + +>/<Shift + Alt + ->** on the keyboard, and **Keypad<Alt** + +>/**<Alt** + **->**.

9.2.14. Fine Gain (Large Move) <Shift + Alt + +>/<Shift + Alt + ->

<Shift+Alt+ +> and **<Shift+Alt+ ->** step the internal amplifier of the selected Detector (if it has a software-controlled amplifier) up or down by a large increment of fine gain. If the gain stabilizer is active, the display of the histogram data might not change.

The fine gain can also be set using **Acquire/MCB Properties...** (Section 5.2.11), **<Alt+ +>/ <Alt+ ->** on the keyboard, and **Keypad<Alt + +>/ <Alt + ->**.

9.2.15. Screen Capture <PrintScreen>

The **<PrintScreen>** key captures the entire monitor display to the Windows Clipboard, where it is available for use in other applications such as word processors and Windows Paint. Some older keyboards require **<Alt + PrintScreen>** or **<Shift + PrintScreen>**.

A typical usage would be to set up the display as desired for the snapshot (you might wish to use **Display**/**Preferences**/**Spectrum Colors...** to select black or white for all areas rather than colors, since they produce clearer printouts), then press **<PrintScreen>**. Start the desired graphics or word processing application. Copy the image from the Clipboard with **<Ctrl + V>** or **Edit**/**Paste** (refer to the documentation for the graphics or word processing program). See the FullShot manual for other screen-capture and screen-printing methods.

9.3. Keyboard Number Combinations

NOTE Only the key*board* numbers will function in the following combinations. The key*pad* number keys will *not* perform these functions.

9.3.1. Start <Alt + 1>

<Alt + 1> starts the acquisition in the selected Detector. Any presets desired must be entered before starting acquisition. This accelerator duplicates the **Start** toolbar button, the **Start** command on the right-mouse-button menu, and **Acquire**/**Start**, discussed in Section 5.2.2.

9.3.2. Stop <Alt + 2>

<Alt + 2> stops acquisition in the selected Detector. This duplicates the **Stop** toolbar button, the **Stop** command on the right-mouse-button menu, and **Acquire**/**Stop**, discussed in Section 5.2.4.

9.3.3. Clear <Alt + 3>

<Alt + 3> clears the displayed Detector's histogram data and its descriptors (e.g., real time, live time). This accelerator duplicates the **Clear Spectrum** toolbar button, the **Clear** command on the right-mouse-button menu, and **Acquire**/**Clear**, discussed in Section 5.2.5.

9.3.4. Copy to Buffer <Alt + 5>

<Alt + 5> copies the histogram data from the selected Detector to the buffer, along with its descriptors (e.g., live time, real time), and displays the spectrum in a new window. This

duplicates the **Copy to Buffer** command on the right-mouse-button menu and **Acquire**/**Copy to Buffer** (Section 5.2.6).

9.3.5. Detector/Buffer <Alt + 6>

<Alt + 6> switches the display between the histogram of the spectrum in the selected Detector and the spectrum in the buffer. The buffer will have the memory size of the spectrum that was last transferred from Detector or disk file.

The Detector list on the right side of the toolbar indicates whether the buffer or a particular Detector is currently displayed, and the Status Sidebar shows the presets for the displayed data.

This duplicates **<F4>** and **Display**/**Detector/Buffer**; see Section 4.6.2.

9.3.6. Narrower/Wider <+>/<->

The <+> key decreases the horizontal scale of the Expanded Spectrum View so the peaks appear wider, while the **<->** key increases the horizontal scale, making the peaks look narrower. The horizontal and vertical scale values are displayed on the toolbar. These functions are duplicated by **<F7>**/**<F8>**.

9.4. Function Keys

9.4.1. ROI <F2>

The **<F2>** key switches the ROI marker status among the **Mark**, **UnMark**, and **Off** conditions, so you can use the marker to set or clear the ROI bits for particular channels or groups of channels, or return the marker to normal usage. The current ROI marking status (**Marking**, **Unmarking**) is shown in at the extreme right of the menu bar (**Off** mode is shown as blank). ROI bits are changed by using the keyboard to move the marker to a channel, as follows:

- **Mark** The channel is marked (set) as an ROI with the marker.
- **UnMark** The channel is removed from the ROI (reset) with the marker.
- **Off** The ROI status is unchanged with the marker.

9.4.2. ZDT/Normal <F3>

For MCBs operating in ZDT mode, the **<F3>** key switches between the normal (LTC) or uncertainty (ERR) spectrum and the ZDT corrected spectrum. It duplicates the **Acquire/ZDT Display Select** command.

9.4.3. ZDT Compare <Shift+F3>

For ZDT-supporting instruments in Compare mode, this accelerator switches the compare spectrum between the ZDT spectrum and its accompanying LTC or ERR spectrum. Used in combination with **<F3>** or **Acquire/ZDT Display Select**, it allows you to display the normal-to-ZDT, uncertainty-to-ZDT, ZDT-to-normal, or ZDT-to-uncertainty comparisons.

9.4.4. Detector/Buffer <F4>

The **<F4>** key switches between the display of the data in the Detector and the data in the buffer. It duplicates the function of **<Alt + 6>** and **Display/Detector/Buffer**; see Section 9.3.5.

9.4.5. Taller/Shorter <F5>/<F6>

These keys decrease or increase the vertical full scale of the displayed spectrum so the peaks appear taller or shorter, respectively. They duplicate the function of the <↑> and <↓> keys. The vertical scale value is always shown on the toolbar.

9.4.6. Narrower/Wider <F7>/<F8>

These keys increase or decrease the horizontal scale of the data display so the peaks appear narrower or wider, respectively. They duplicate the function of **<->** and <+> keys. The horizontal scale value is always shown on the toolbar.

9.4.7. Full View <Alt + F7>

Full View adjusts the horizontal and vertical scaling to display the entire spectrum in the Expanded Spectrum View. This duplicates **Display/Full View**; see Section 5.9.10.

9.4.8. Select Detector <Ctrl + F1> through <Ctrl + F12>

These keys display the spectrum for the specified Detector **n** (where **n** = 1 to 12, corresponding to **<Ctrl+ Fn>**, in the order that the Detectors are defined in the Detector pick list; see Section 5.9.1). The selected Detector name (or the buffer) is shown on the toolbar.

These keys duplicate the function of the Detector pick list on the toolbar, and the **Detector...** dialog under the **Display** menu. However, you should be aware of which Detector numbers are available when using the function keys. An error message box will appear if the selected Detector is invalid. In systems with more than 12 Detectors, use **Display/Detector...** or the droplist on the toolbar.

9.5. Keypad Keys

9.5.1. Log/Linear Keypad</>

Keypad</> toggles the active spectrum window between logarithmic and linear vertical display. This is duplicated by the **Log** toolbar button. The vertical scale can be controlled with the **Zoom In**/**Zoom Out** toolbar buttons, **Keypad<+>/<->**, the <↑> and <↓> keys, and **<F7**/**F8>**.

9.5.2. Auto/Manual Keypad<*>

Keypad<*> switches the spectrum window between automatic and manual vertical full scale (see the discussion in Section 5.9.5). This is duplicated by the **Vertical Auto Scale** button on the toolbar.

9.5.3. Center Keypad<5>

Keypad<5> forces the marker to the center of the screen by shifting the spectrum without moving the marker from its current channel. This is duplicated by the **Center** button on the toolbar. For more information, see Section 5.9.9.

9.5.4. Zoom In/Zoom Out Keypad<+>/<->

Keypad<+> increases the scale of both axes in the Expanded Spectrum View so the peaks appear larger, while **Keypad<->** does the opposite, making the peaks look smaller. The scale value for both axes is always shown on the toolbar. These functions are duplicated by the **Zoom In**/**Zoom Out** toolbar buttons.

9.5.5. Fine Gain Keypad<Alt + +>/<Alt + ->

These accelerators step the internal amplifier up or down by one increment of fine gain on the selected Detector, if it has a software-controlled amplifier. The new fine gain setting is shown on the Supplemental Information Line at the bottom of the screen. If the gain stabilizer is active, the display of the histogram data might not change.

The fine gain can also be set with **Acquire**/**Adjust Controls...** (Section 5.2.11) and **Keypad<Shift + Alt + +>**/ **<Shift + Alt + ->**; and keyboard **<Alt + +>**/**<Alt + ->** and **<Shift + Alt + +>**/**<Shift + Alt + ->**.

10. JOB FILES

10.1. Introduction

The GammaVision .JOB file consists of one or more lines of ASCII text representing a series of commands that can automate most of the functions described earlier in this manual. The details of the commands and the required syntax are given in this chapter. A .JOB file can be created within GammaVision using the **Services/Job Control...** command or in Windows Notepad or any other ASCII editor. A .JOB file can be started from **Services/Job Control...**, or by including the name of the .JOB file (e.g., GVDEMO.JOB) on the command line when GammaVision is first started (see Section A.1).

.JOB files can be used for the following types of functions:

- Performing a repetitive task, such as running a sequence of experiments without user intervention.

- Defining initial conditions at startup (useful in preloading presets after a power loss for the 916/916A/917/918/918A each time GammaVision is run).

This version of GammaVision is compatible with.JOB files written for previous versions of GammaVision or MAESTRO. The text versions of these files will work on new Detectors as well as older models, with the exception of new or deleted commands.

10.1.1. JOB Command Functionality

10.1.1.1. Loops

GammaVision can run repetitive loops. Furthermore, the current loop count can be included as a variable in any string, including filenames, program parameters, and text. Data can thus be stored with unique filenames and labeled with unique descriptions.

In previous versions of GammaVision (and MAESTRO) JOB files, the macros $(Loop) and $(Loop1) were used to embed the Loop counter (zero- and one-based) into text strings. As of v7, GammaVision can add any offset to the loop counter with the $(LoopN) Macro.

For example, the following JOB commands:

```
LOOP 5
ASK_CONFIRM “The loop counters are: $(Loop), $(Loop10) and $(Loop25).”
END_LOOP
```

produce the following output:

```
The loop counters are: 0, 10 and 25.
The loop counters are: 1, 11 and 26.
The loop counters are: 2, 12 and 27.
The loop counters are: 3, 13 and 28.
The loop counters are: 4, 14 and 29.
```

Note that custom variable values cannot be embedded in custom variables. For example, the expression '$(Loop$(Variable))' is invalid.

10.1.1.2. Errors

If an error is encountered in running a .JOB file, the execution of the file stops and control returns to GammaVision. An error code appears in the **JOB Control...** dialog; these are described in Appendix C.

10.1.1.3. Ask on Start and Ask on Save

If the appropriate **Ask on Start** (see **Acquire/Acquisition Settings...**) or **Ask on Save** (see **File/Settings...**) fields are turned on, GammaVision will ask the corresponding questions when START or SAVE commands are executed in the .JOB file. This means that execution of the .JOB file stops until the entry is made.

The ASK commands will also stop the .JOB file and prompt you to enter the requested information. The .JOB file will continue when you click **OK** or press **<Enter>** on the dialog. The input is used or stored immediately, before the next JOB instruction, except for the ASK_SPECTRUM command.

NOTE If you choose **Cancel** when responding to an ask-on-start or ask-on-save prompt, the JOB will terminate at that point.

10.1.1.4. Password-Locked Detectors

When .JOB files are used with locked Detectors, the first time a destructive command is used on the locked Detector, you will be prompted for the password. Alternatively, you can use the ASK_PASSWORD command at the beginning of the JOB. From then on while the .JOB file executes, the password is retained and you will not receive a prompt. When the .JOB file quits, the password is forgotten.

10.1.1.5. .JOB Files and the Multiple-Detector Interface

GammaVision allows you to open eight Detector windows and eight buffer windows at one time. However, there is no limit on the number of Detectors that can be operated using .JOB files, and only one JOB at a time can run in a single instance of GammaVision. A Detector window opens

for each SET_DETECTOR command in the JOB, to a maximum of eight, and these windows function as follows:

- JOB streams use the SET_DETECTOR command to open Detector windows. If eight Detector windows are already open and SET_DETECTOR is issued to open a ninth window, the oldest displayed Detector window will be closed without prompting.

- The same buffer window is always selected by the commands in a JOB, therefore, a JOB does not open multiple buffer windows.

- When you start a JOB, a Detector window will open for each Detector called by the .JOB file. The JOB filename will be echoed on the main GammaVision title bar as well as on the title bars of all open spectrum windows.

Note that the JOB processor does not support the simultaneous, multiple-detector start, stop, start/save/report(ã), and clear functions that are available from the toolbar and menu commands.

10.1.2. JOB Command Structure

In the command descriptions in Section 10.4, a variable filename or text is enclosed in "**...**" and a variable number is enclosed in <**...**>; anything enclosed in square brackets [**...**] is optional.

10.2. .JOB File Variables

Variables have been added to the .JOB file features to allow more flexibility and control of the JOBS. These variables are defined by the program or by user entries. They can be used anywhere in the .JOB file.

For example:

```
$(FullPath)= D:\USER\SOIL\SAM001.SPC
```

then:

```
$(FullBase)  =     D:\USER\SOIL\SAM001
$(FileExt)   =     SPC
$(FileDir)   =     D:\USER\SOIL
$(ShortPath)       =  SAM001.SPC
$(ShortBase)       =  SAM001
```

The following variables are expanded in .JOB file strings:

$(FullPath)	Full pathname of the spectrum file
$(FullBase)	Full pathname of the spectrum without the "." and extension
$(FileExt)	File extension of the spectrum file without the "."
$(FileDir)	Directory of the spectrum file without the last backslash (\)
$(McaDir)	GammaVision directory without the last backslash
$(CurDir)	Starting (current) directory of GammaVision
$(Loop)	Current value of the loop counter (zero based)
$(Loop1)	Loop counter plus 1
$(Bel)	ASCII bell character
$(CR)	ASCII carriage return character
$(FF)	ASCII form feed character
$(LF)	ASCII line feed character
$(ESC)	ASCII escape character
$(AutoFile)	Create an automatic filename based on the **Start**/**Save**/**Report**(ã) settings
$(ShortPath)	Relative pathname of the spectrum file
$(ShortBase)	Relative pathname of the spectrum without the "." and extension
$(Password)	Value entered in ASK_PASSWORD command
$(Owner)	Value entered in ASK_PASSWORD command
$(Spectra)	Number of spectra in a multi-spectrum buffer. See "VIEW" Job command.

The filename variables are updated each time a READ operation is performed. The READ operations are:

ANALYZE "file"(ã)
ASK_CALIBRATION
ASK_LIBRARY
ASK_OPTIONS
ASK_PBC(ã)
ASK_SPECTRUM
CALIBRATE_EFFICIENCY
CALIBRATE_ENERGY
LOAD
RECALL
RECALL_CALIBRATION
RECALL_EFFICIENCY
RECALL_ENERGY
RECALL_OPTIONS
RECALL_ROI
STRIP

The filename is not updated for WRITE commands.

The following sample .JOB file will produce a set of files in which the last character of the filename is a digit that increments with each loop.

```
ASK_SPECTRUM
LOOP 5
SAVE "$(FULLBASE)$(LOOP1).$(FILEEXT)"
END_LOOP
```

10.3. JOB Programming Example

A common operation that is ideal for a .JOB file is the collection of many consecutive sample spectra without user intervention. An example of this is the collection of a series of spectra to show the radioactive decay in a particular sample.

This process can be described as follows:

1) Set the Detector parameters, such as live time.
2) Start the acquisition.
3) Wait for the acquisition to stop.
4) Integrate the nuclide peak.
5) Record the peak area.
6) Repeat this for the required number of samples.

By looking at the list of steps above and the explanations below, the necessary commands can be determined and written down.

The first step in the process is to initialize the Detector to the condition needed of 1000 seconds live time. These are:

```
SET_DETECTOR 1
SET_PRESET_CLEAR
SET_PRESET_LIVE 1000
CLEAR
```

Note that all the presets were cleared before setting the live-time preset. This is to ensure that no previous presets (left over from other users) will interfere with this analysis.

Now start the acquisition and wait for completion of the live time.

```
START
WAIT
```

During this time the display manipulation keys are active so that the spectrum can be studied while collection is taking place.

Now move the spectrum from the Detector to the buffer. Select the buffer for the computational step.

```
FILL_BUFFER
SET_DETECTOR 0
```

In this step, the nuclide peak of interest is being marked by reading in an .ROI file. This .ROI file has been previously defined by looking at the spectrum and marking the peak (or the region around the peak). This ROI data is saved on the disk under the name DECAYPK.ROI. This .JOB file will work on different peaks or nuclides just by changing the .ROI file.

```
RECALL_ROI “DECAYPK.ROI”
```

The peak areas of the marked peak or peaks is printed on the printer by this command.

```
REPORT “PRN”
```

This gives a list of the peak areas and count rates for the marked peak. If the library has a peak near this energy then the peak identity will also be printed.

The set of instructions, as written so far, will only collect and report once. There are two ways to make the process repeat itself for a series of samples. The first and hardest is to write one set of the above instructions for every sample in the series. A much more efficient way is to use the

LOOP command. To use this, put LOOP before CLEAR and END_LOOP after REPORT. The whole .JOB file now looks like this:

```
SET_DETECTOR 1
SET_PRESET_CLEAR
SET_PRESET_LIVE 1000
LOOP 10
CLEAR
START
WAIT
FILL_BUFFER
SET_DETECTOR 0
RECALL_ROI “DECAYPK.ROI”
REPORT “PRN”
SET_DETECTOR 1
END_LOOP
```

Note that an additional SET_DETECTOR 1 has been inserted after REPORT, *so the loop will operate on the desired Detector*.

Now select **Services/Job Control**. Click once on an existing .JOB filename then click the **Edit File** button. This will display the contents of that file in Windows Notepad. You can then *over-write* the existing instructions with the above set of commands. However, save the new instructions to a new file named SAMPDATA.JOB using the **File/Save As** function (do not use **Save** or the original file will be lost).

This new .JOB file can then be executed in GammaVision from the **Services** menu by selecting **Job Control...** to display the **Run JOB File** dialog. Select SAMPDATA.JOB from the list of files and click **Open**.

10.3.1. Improving the JOB

This .JOB file can be improved by adding a save step for each spectrum collected. This is done by inserting the SAVE command in the .JOB file. The spectrum sample description is also entered here. This sample description is saved with the spectrum and is printed by the REPORT command. Note that the loop counter (the ??? in the .JOB file text) is used in the SAVE and DESCRIBE_SAMPLE commands.

The new .JOB file is:

```
SET_DETECTOR 1
SET_PRESET_CLEAR
SET_PRESET_LIVE 1000
LOOP 10
CLEAR
START
WAIT
FILL_BUFFER
SET_DETECTOR 0
DESCRIBE_SAMPLE “This is sample ???.”
SAVE “DECAY???.CHN”
RECALL_ROI “DECAYPK.ROI”
REPORT “PRN”
SET_DETECTOR 1
END_LOOP
```

Spooling the report might take some time. To overlap the data collection with the analysis, the logic of the .JOB file needs to be modified to restart the acquisition after the data have been moved to the buffer. All of the analysis is performed on the buffer spectrum so the Detector spectrum can be erased and the next one started.

Insert CLEAR and START after FILL_BUFFER, as shown here:

```
SET_DETECTOR 1
SET_PRESET_CLEAR
SET_PRESET_LIVE 1000
CLEAR
START
LOOP 10
WAIT
FILL_BUFFER
CLEAR
START
SET_DETECTOR 0
DESCRIBE_SAMPLE “This is sample ???”
SAVE “DECAY???.CHN”
RECALL_ROI “DECAYPK.ROI”
REPORT “PRN”
SET_DETECTOR 1
END_LOOP
```

10.3.2. JOB Commands for List Mode

This section discusses the JOB commands for MCBs that support List Mode (which is discussed in Section 1.6). The SET_LIST and SET_PHA commands switch the selected Detector respectively between the PHA and List modes; the SAVE command supports the .LIS file type; and the SET_RANGE command retrieves a specified time slice of data from an existing .LIS file. Note that the SET_RANGE command has two syntaxes: A time slice can be recalled either by specifying an absolute date/time and the desired time-slice duration; or by specifying the starting real time and the desired time-slice duration. Note that while the **List Data Range** command on the **Calculate** menu (Section 5.4.2) can only retrieve time slices to a resolution of 1 second, the SET_RANGE command syntax supports fractional real time and duration.

The following example uses the commands discussed in the preceding sections plus the list-mode commands to switch “Detector 12" from the standard PHA mode to List Mode, collect data and save it in .LIS format as well as the three supported spectrum file formats, recall the .LIS file into a buffer, retrieve a time slice of data from the .LIS file using the two syntaxes of the SET_ RANGE command, save the time slices, and switch the Detector back to PHA mode.

```
REM First set change the Detector to List Mode and set the preset
REM
CLOSEMCBS
CLOSEBUFFERS
SET_DETECTOR 12
SET_LIST
SET_PRESET_CLEAR
SET_PRESET_REAL 60
```

```
REM
REM Next start a List Mode acquisition:
REM
CLEAR
START
WAIT
REM
REM Save the spectrum in the four supported file formats:
REM
SAVE “JobTest.Lis”
SAVE “JobTest.Chn”
SAVE “JobTest.Spc”
SAVE “JobTest.Spe”
REM
REM Close all windows and recall the list mode file just created:
REM
CLOSEMCBS
CLOSEBUFFERS
RECALL “JobTest.Lis”
REM
REM Recall a time slice of the data with the SET_RANGE command using the
REM absolute date/time and duration in whole seconds:
REM
SET_RANGE “6/29/2012", “14:05:00", 900
REM
REM Save the partial list mode file in the four supported file formats:
REM
SAVE “JobTest2.Lis”
SAVE “JobTest2.Chn”
SAVE “JobTest2.Spc”
SAVE “JobTest2.Spe”
SAVE
REM Close all buffer windows
REM
CLOSEBUFFERS
REM
REM Recall the original list mode file
REM
RECALL “JobTest.Lis”
REM
REM Recall a data time slice with SET_RANGE using a starting real time and duration:
REM
SET_RANGE “900", “900"
REM
SAVE “JobTest3.Lis”
SAVE “JobTest3.Chn”
SAVE “JobTest3.Spc”
SAVE “JobTest3.Spe”
REM
```

```
REM Set the MCB back to PHA mode:
REM
CLOSEBUFFERS
SET_DETECTOR 12
SET_PHA
```

10.4. JOB Command Catalog

ANALYZE ["spectrum filename"](ã)

This analyzes the spectrum in the same manner as the menu commands. With no argument, the spectrum in the display (either the MCB or the buffer) is analyzed according to the settings in the **Analyze/Settings/ Sample Type...** dialog. With a spectrum filename as argument, the spectrum on disk is analyzed according to the settings in the spectrum file. The filename can include any of the variables shown in Section 10.2.

To change the settings used in an analysis, load the spectrum into the buffer using the RECALL command, recall the new settings using the RECALL_SETTINGS command, then ANALYZE the spectrum in memory (no filename).

The .JOB file does not wait until the analysis is complete before proceeding to the next command, however the results will be automatically output according to the settings (printed, file or program) when the analysis is complete. To force the JOB to wait until the analysis is complete, put a WAIT "WAN32.EXE" command after the ANALYZE command.

The JOB command might exit after the ANALYZE command, but the QUIT command should not be used because the results will not be printed if GammaVision is not running.

ASK_CALIBRATION

This asks for the name of a file containing the calibration to be used as the internal calibration. After entering the filename, the file is read and the calibration is loaded.

ASK_COLLECTION

This asks for the date and time for the decay correction. It is the same as the date and time entry in the **Acquire/Acquisition Settings...** dialog. If any **Ask on Start** options are marked, the START command in the .JOB file will also open this dialog.

ASK_CONFIRM <"text">

This opens a dialog showing the text, and waits until you click **OK**.

ASK_DESCRIPTION

This asks for the sample description to be put in the spectrum file and on the report. It is the same as the sample description entry in the **Acquire/Acquisition Settings...** dialog and the sample description entry in the **File/Settings...** menu. If the **Ask on Start** option is marked, the START command in the .JOB file will also open this dialog. If the **Ask on Save** option is marked, the SAVE command in the .JOB file will also open this dialog.

ASK_GAMMATOTAL(γ)

This command opens the Gamma Total/EDF Report dialog as shown in Fig. 304 (see also Section 5.5.1.9).

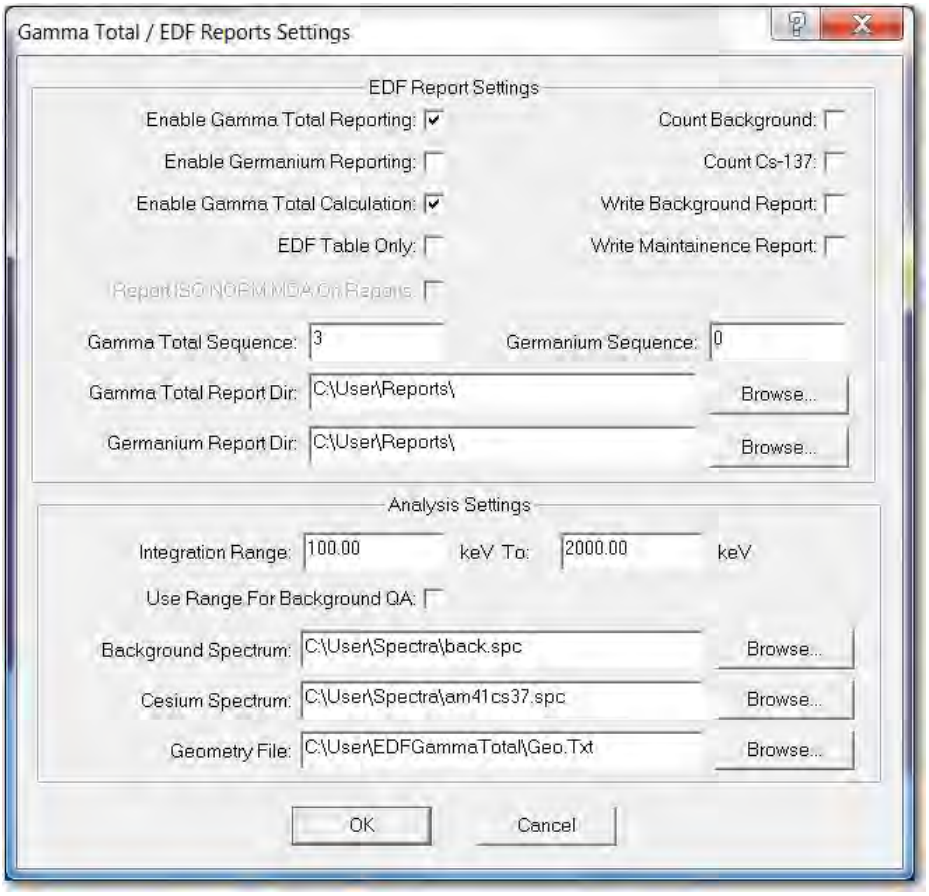


Figure 304. ASK_GAMMATOTAL Dialog.

NOTES

Individual parameters can be set in JOB files using the SET_SETTING or SET_OPTIONS commands. The following parameters are stored in the .SDF file and are loaded when an .SDF file is recalled:

GammaTotalReportingEnabled
GammaTotalGermaniumReportingEnabled
GammaTotalCalculationEnabled

GammaTotalEDFTableOnlyEnabled
GammaTotalReportIsoMdaOnReportsEnabled
GammaTotalCountBackgroundEnabled
GammaTotalCountCesiumEnabled
GammaTotalWriteBackgroundReportEnabled
GammaTotalWriteMaintenanceReportEnabled
GammaTotalAnalysisStartChannel
GammaTotalAnalysisEndChannel
GammaTotalUseRangeForBackgroundQAEnabled
GammaTotalBackgroundSpectrumPath
GammaTotalCesiumSpectrumPath
GammaTotalGeometryFilePath

ASK_LIBRARY

This asks for the name of the library to be used as the internal library. After entering the filename, the library file is loaded.

ASK_ONLYEFFICIENCY

Displays a dialog (Fig. 305) that asks for a calibration file. Once a file is selected, the command loads the Efficiency calibration but does not load the Energy or FWHM calibration. If you click **Cancel**, the JOB terminates with JOB Error 15 (Problem with Ask).

ASK_ONLYENERGY

Displays a dialog (Fig. 306) that asks for a calibration file. Once a file is selected, the command loads the energy calibration but does not load the FWHM calibration. If you click **Cancel**, the JOB terminates with JOB Error 15 (Problem with Ask).

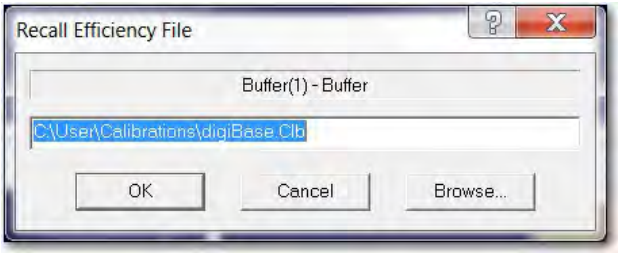


Figure 305. ASK_ONLYEFFICNCY Dialog.

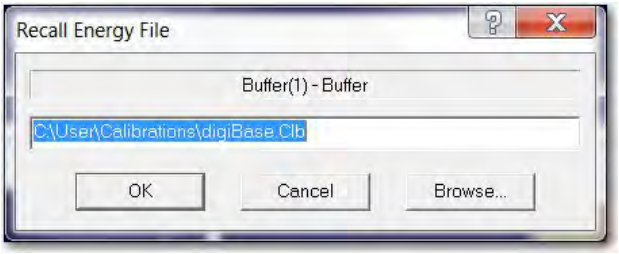


Figure 306. ASK_ONLYENERGY Dialog.

ASK_ONLYFWHM

Displays a dialog (Fig. 307) that asks for a calibration file. Once a file is selected, the command loads the FWHM calibration but does not load the Energy calibration. If you click **Cancel**, the JOB terminates with JOB Error 15 (Problem with Ask).

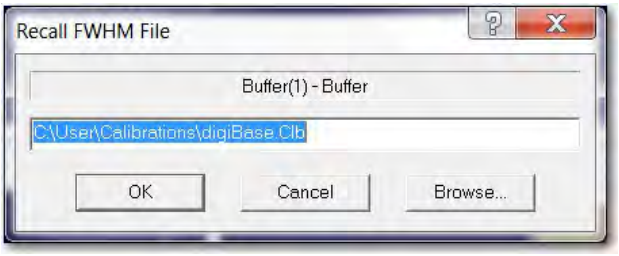


Figure 307. ASK_ONLYFWHM Dialog.

ASK_OPERATOR

Asks for the operator's name to be put in the spectrum file and on the report. It is also stored in the Registry.

ASK_OPTIONS

Asks for the .SDF (Sample Description File) filename of the analysis options. The .SDF file is created in the **Analyze/Settings/Sample Type...** dialog. It is the same as the sample type entry in the **Acquire/Acquisition Settings...** dialog. If **Ask on Start** is marked, the START command in the .JOB file will also open this dialog.

ASK_PASSWORD

Used to define the password to be used in the .JOB file. This command can be to lock an unlocked detector, unlock and use one that is locked, or lock one for the duration of the job and then unlock it. The actual lock/unlock is done with LOCK and UNLOCK, respectively.

This command is to set the internal password variable, $(Password), to the user input so the password will be available for use in the JOB. The $(Owner) variable is only used when locking detectors. Following is an example:

```
.
.
ASK_PASSWORD
LOCK "Password","Owner"
.
.
```

ASK_PBC[ã]

Asks for the name of the peak background correction to be used. After entering the filename, the Peak Background Correction file is loaded.

ASK_PRESET

Asks for the presets to be set in the Detector. It is the same as the preset entry in the **Acquire/ Acquisition Settings...** dialog. If **Ask on Start** is marked, the START command in the .JOB file will also open this dialog.

ASK_SPECTRUM

Asks for the spectrum filename to be used in the next and subsequent SAVE and RECALL commands. See SAVE command below. This is stored in the variables $(FullPath), $(FullBase), $(FileExt), and $(FileDir).

ASK_VARIABLE "VarName", "Label", "Format", "FileExtension"

This command displays a dialog box that asks for the JOB variable value. The arguments to this command are as follows:

VarName	The variable name can be up to 32 characters long. If the variable does not exist in the list of defined variables, a new one is created. This field is required.
Label	This optional field is used to provide a text prompt for data entry. If omitted, the label used is "Enter Value:"
Format	This optional field describes the variable type. Valid Format values are: "Integer", "Float", "String", "Date", and "Path". Based on this value, the value is checked for the specified type. If omitted, the Format used is "String".
FileExtension	This value describes the default file extension used for the "Path" format. A browse button is enabled so the user can select an existing file. If this field is omitted, the FileExtension used is "*." (i.e., all file types).

Figures 308 through 312 illustrate the ASK_VARIABLE dialogs for the different Format options. If you click **OK** to close the dialog without entering a value, an error message is displayed and you are prompted to select a value before closing the dialog. If you click **Cancel**, the JOB terminates with JOB Error 15 (Problem with Ask).

Figure 308. ASK_VARIABLE Integer Format.

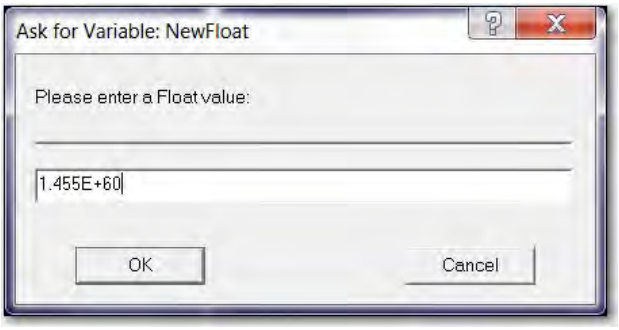


Figure 309. ASK_VARIABLE Float Format.

Figure 310. ASK_VARIABLE String Format.

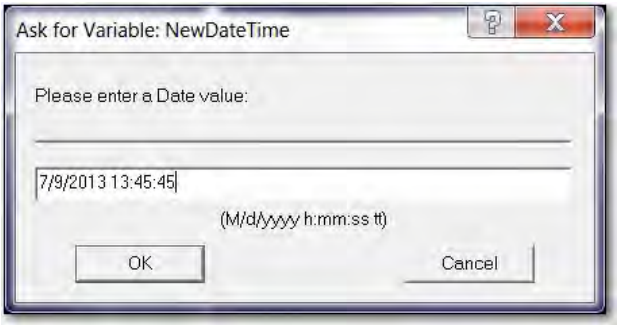


Figure 311. ASK_VARIABLE Date Format.

Figure 312. ASK_VARIABLE Path Format.

ASK_WEIGHT

ASK_WEIGHT prompts for the sample size or weight to be stored in the spectrum file and used in the analysis (the units are specified in the Sample Defaults File). In addition, it includes an optional 1-sigma sample size uncertainty (+/-) field, which accepts values from 0% to 1000%. This is the same as the sample size entry in the **Acquire/Acquisition Settings...** and **File/Settings...** dialogs. If **Ask on Start** is marked, the START command in the .JOB file will also open this dialog. If **Ask on Save** is marked, the SAVE command in the .JOB file will also open this dialog.

BEEP <freq>,<duration>

In PCs without a sound card, this produces an audible tone at a pitch of <freq> hertz lasting for <duration> milliseconds. Overridden (disabled) if computer has a sound card.

BEEP ID

A numerical ID is given based on a desired system event. For example, **BEEP** 7 will generate the "Exit Windows" sound, if one has been designated.

ID	Event
0	Beep Speaker
1	Default Beep
2	Start Windows
3	Asterisk
4	Exclamation
5	Critical Stop
6	Question
7	Exit Windows

BEEP "String"

String can be a .WAV file or any event defined in the Registry.

CALIBRATE_AUTO

This executes the automatic energy calibration on the active spectrum with the working library.

CALIBRATE_EFFICIENCY "file.eft"

Performs an efficiency calibration using the active spectrum and the data in file.eft. The filename can include any of the variables defined in Section 10.2.

CALIBRATE_ENERGY "file.ent"

Performs an energy calibration using the active spectrum and the data in file.ent. The filename can include any of the variables defined in Section 10.2. This performs the same function as the **Merge** button on the Energy Calibration Sidebar (see Section 5.3.2.4).

CALL "file.job"

Executes another .JOB file as a subroutine. The filename can include any of the variables defined in Section 10.2.

CHANGE_SAMPLE

This is used to control the CHANGE SAMPLE output and SAMPLE READY input BNC signals on the rear panel of most MCBs, and is intended to initiate a hardware handshake sequence for advancing a sample changer. The SET_OUTPUT_HIGH command is sent to the

currently selected Detector, then the sample-ready status is monitored (for at least 120 seconds) until the input is low, then finally the SET_OUTPUT_LOW command is sent and input is monitored until it returns to the high level again before proceeding.

Note that if the sample changer controls are not able to make the SAMPLE READY input go high very soon after the CHANGE SAMPLE signal is set (i.e., the normal state of the SAMPLE READY is low; it is expected to go high immediately after the CHANGE SAMPLE condition is set and remain high while the sample changer is moving, and returns to low when the sample changer is at its new position), then it might be necessary to use the SEND_MESSAGE command to send a SET_OUTPUT_HIGH command, then pause (with WAIT or some other time-consuming command), and then send the CHANGE_SAMPLE command. The following example demonstrates this:

```
SET_DETECTOR 1
LOOP 5
CLEAR
START
WAIT
FILL_BUFFER
SEND_MESSAGE “SET_OUTPUT_HIGH”
SET_DETECTOR 0
SAVE “MONTE???.CHN”
SET_DETECTOR 1
CHANGE_SAMPLE
END_LOOP
```

CLEAR

This clears (erases) the data, the real time and the live time for the selected Detector. The presets are not changed. This command has the same function as the CLEAR function under the ACQUIRE menu. The command would logically be preceded by the SET_DETECTOR commands as follows:

```
.
.
SET_DETECTOR 1
CLEAR
.
.
```

CLOSEBUFFERS

Closes all buffer windows.

CLOSEMCBS

Closes all Open Detector windows.

CLOSEWINDOW

Closes the active window if multiple windows are open. This command has no effect if there is only one open window.

CREATEPBC "file.ufo" , "file.pbc"(ã)

Generates a .PBC file when given a .UFO file as input. This is the same as the **Create PBC...** command under the **Analyze/Settings/Peak Background Correction** submenu.

DESCRIBE_SAMPLE "description"

Accepts a 63-character description of the sample being analyzed. This description is saved with the spectrum using the SAVE command function, and is included in the REPORT printout. Same function as the **Sample Description** function under the **Services** menu.

The loop count value can be included in any text by typing three question marks in the text where the loop count is to be inserted. The loop count replaces "???" with three characters wherever it appears.

END_LOOP — see **LOOP**

EXPORT "filename"

This executes the Export function with the filename specified. The remainder of the options are defined on the Export tab under **File/Settings...**. The filename can include any of the variables defined in Section 10.2.

FILL_BUFFER

This transfers the active Detector data to the buffer. This command has the same function as **Copy to Buffer** under **Acquire**.

IMPORT "filename"

This executes the Import function with the filename specified. The remainder of the options are defined on the Import tab under **File/Settings**. The filename can include any of the variables defined in Section 10.2.

LOAD_LIBRARY "filename.extension"

This loads the nuclide library specified, and duplicates the function of **Select File** under the **Library** menu. The filename can include any of the variables defined in Section 10.2.

LOAD_PBC "name.pbc"(ã)

This loads the Peak Background Correction specified, and duplicates the function of **Select PBC...** under **Analyze/Settings/Peak Background Correction**. The filename can include any of the variables defined in Section 10.2.

LOCK “Pwd” [,”Name”]

This locks the current Detector using “Pwd” as the password. If the optional “Name” parameter is missing, the Locked name defaults to “Job”.

This password is retained in the .JOB file and used with any .JOB commands so that the user does not need to re-enter the password.

LOOP <repetitions> **... END_LOOP**

This pair executes multiple times all the commands between LOOP and END_LOOP. The number of execution times is specified by <repetitions>. Each command must be given on a separate line. A value of 0 executes once. A LOOP with no END_LOOP statement executes once.

The loop count value can be included in any text by typing three question marks in the text where the loop count is to be inserted. The loop count replaces “???” with three characters using leading zeros if necessary.

The loop variables, $(Loop) and $(LOOP1), can be included in any text. The loop count will be inserted with leading zeros suppressed.

The following is an example:

```
SET_DETECTOR 1
SET_PRESET_LIVE 20
LOOP 3
SET_DETECTOR 1
CLEAR
START
WAIT
FILL_BUFFER
SET_DETECTOR 0
SAVE “TEST???.CHN”
END_LOOP
```

The above commands run three 20-second acquisitions and store the data on a disk in TEST001.CHN, TEST002.CHN, and TEST003.CHN.

If the SAVE command is replaced with SAVE “TEST$(Loop).CHN,” then the following files will be saved: TEST0.CHN, TEST1.CHN, and TEST2.CHN.

See also Section 10.1.1.1.

LOOP SPECTRA...END_LOOP

This executes the commands within the loop once for each spectrum stored in the Detector hardware. This command only works for hardware that supports Field Mode.

MARK_PEAKS

This command performs a Mariscotti-type peak search on the spectrum in the currently selected Detector or buffer window (see **Analyze/Peak Search**, Section 5.5.2, which performs the same function). The peak search sensitivity is chosen on the System tab under **Analyze/Settings/ Sample Type...** (page 152). Each peak found is marked with an ROI. If a calibration is loaded in the selected window, the width of the ROI is three times the calculated FWHM of the peak. If no calibration is loaded in the selected window, the width of the ROI equals the width of the peak as determined by the peak search function. Overlapping or close peaks might have contiguous ROIs. Existing ROIs are not cleared, therefore, you might wish to clear them before issuing this command.

The following is an example of the MARK_PEAKS command used with REPORT:

```
.
.
MARK_PEAKS
REPORT “TESTDAT.RPT”
.
.
```

The above procedure performs a peak-search, then writes to disk an **ROI Report** for the peaks found.

QABACKGROUND(γ)

This executes the background QA test without displaying prompts or violations.

QASAMPLE(ã)

This executes the sample QA test without displaying prompts or violations.

QUIT

This unconditionally terminates the GammaVision program and returns control to Windows.

RECALL “file.chn” or “file.spc”

This reads a disk filename to the buffer. The disk file must be in the format created by SAVE. Any DOS filename, including the drive and subdirectory, can be used. The resultant horizontal size of the buffer is the same as the file. If the spectrum file has calibration information, the calibration parameters in the spectrum file are used to set the calibration for the buffer.

This command has the same function as **Recall...** under the **File** menu.

The loop count value can be included in the above filename, as in any text, by typing three question marks in the text where the loop count is to be inserted. The loop count replaces "???" wherever they appear. The filename can include any of the variables defined in Section 10.2.

RECALL_CALIB "file "

This loads both the energy and efficiency calibration data from the specified file to the calibration data for the selected Detector. If the file is a pure calibration file (.CLB), then all the information, including any energy or efficiency tables, are replaced in the selected spectrum data memory. If the file is a spectrum data type file .CHN, only the calibration parameters from the calibration data stored with a spectrum are loaded.

The filename can include any of the variables defined in Section 10.2.

This command can be used in generating reports that include library nuclide identification. The following is an example:

```
.
.
RECALL_CALIB "CALIB001.clb"
MARK_PEAKS
REPORT "NEWDATA.RPT"
.
.
```

The report NEWDATA.RPT includes nuclide identification using the energy calibration contained in CALIB001.clb.

RECALL_EFFICIENCY "file "

This loads the efficiency calibration data from the specified file to the calibration data for the selected Detector. If the file is a pure calibration file (.CLB), then all the information, including any efficiency tables, are replaced in the selected spectrum data memory. The filename can include any of the variables defined in Section 10.2.

RECALL_ENERGY "file "

This loads the energy calibration data from the specified file to the calibration data for the selected Detector. If the file is a pure calibration file (.CLB), then all the information, including any energy tables, are replaced in the selected spectrum data memory. If the file is a spectrum data type file .CHN, only the calibration parameters from the calibration data stored with a spectrum are loaded. The filename can include any of the variables defined in Section 10.2.

RECALL_ONLYEFFICIENCY "File"

Recall efficiency calibration only, where "File" can be any GammaVision file that contains a valid efficiency calibration. This command is identical to the RECALL_ EFFICIENCY command and is provided for consistent naming.

RECALL_ONLYENERGY "File"

Recall energy calibration only, where "File" can be any GammaVision file that contains a valid energy calibration. This command does not recall the FWHM calibration from the file.

RECALL_ONLYFWHM "File"

Recall FWHM calibration only, where "File" can be any GammaVision file that contains a valid energy calibration. This command does not recall the energy calibration from the file.

RECALL_OPTIONS "file.sdf"

This loads the acquisition and analysis parameters into the working set for the selected Detector or buffer. This is the same as recalling a .SDF file in the **Analyze/Settings/Sample Type...** type menu. The filename can include any of the variables defined in Section 10.2.

RECALL_ROI "file.roi"

This marks the ROI channels in the selected data memory or Detector to conform to the table in the disk file, which can be an .ROI, .UFO, .SPC, or .LIB file. The data contents of the Detector or buffer are not altered by this operation. The previous ROIs are cleared. The filename can include any of the variables defined in Section 10.2.

This command has the same function as **Recall File**... under **ROI**.

This command can be used in generating reports that look for specific nuclides (library-directed as opposed to peak-search-directed). For example, a calibration spectrum is run containing ^{57}Co and ^{137}Cs, and ROIs marked on the 122 keV and 662 keV peaks.

The calibration is saved as spectrum file COBCS.CHN and as .ROI file COBCS.ROI. The command sequence is:

```
.
.
RECALL_CALIB "COBCS.CHN"
RECALL_ROI "COBCS.ROI"
REPORT "COBCS.RPT"
.
.
```

These commands report the values only for the 122 keV and 662 keV peaks. Compare with the example for MARK_PEAKS.

As usual, the loop count value can be included in any text by typing three question marks in the text where the loop count is to be inserted.

REM [Text]

This line is a comment (remark) and is ignored during command processing. The REM command allows entering descriptive comments into script files or disabling commands during testing of scripts.

REPORT "filename"

This command will produce a list of areas, activities, and peak shapes for all the ROIs marked in the spectrum. See **Analyze/ROI Report** (Section 5.5.3) for more information on the report format and contents. The ROI data will be presented in either columns or paragraphs, according to the format most recently selected in the ROI Report dialog (therefore, you can choose a format before executing the JOB file). If you do not specify a filename, the report will be sent to the default Windows printer for this computer. If you specify a filename, the report will be sent to an ASCII text file that can be used by other programs or printed later. The loop count value can be included in the filename by typing three question marks in the text where the loop count is to be inserted. The loop count replaces "???" in the filename. The filename can include any of the variables defined in Section 10.2.

RUN "program"

This executes an application named "program." This is typically an .EXE filename. Note that the program will not run to completion before returning to GammaVision, unless it is run at higher priority or the WAIT command is used. The filename can include any of the variables defined in Section 10.2. Any arguments to the program can be included in the quotation marks.

RUN_MINIMIZED "program"

Same as the RUN command above, except that the application is run initially as an icon (minimized), rather than as a normal window.

SAVE "[d:][\path\]file[.spc]" [,n]

This saves the active Detector or the selected data memory in a disk file. It has the same function as **Save As...** under the **File** menu. The file type is determined in the **File/Settings...** dialog. The disk filename (in quotation marks) can be any valid DOS filename; the drive [d:], path [\path\] and extension [.spc] are optional. If an extension is not supplied, the default extension is automatically determined by the file settings selection. Also, the current drive and directory are used by default when the optional path specification is not supplied. The loop count value can be included in the filename by typing three question marks in the text where the loop count is to be inserted. The loop count replaces "???" wherever it appears. The filename can include any of the variables defined in Section 10.2.

The optional argument n specifies the spectrum number to save for a .CHN or .SPE file. For the DSPEC Plus in ZDT mode zero, a value of zero will switch the display to the normal spectrum before the data is saved and a value of 1 will switch the spectrum to the ZDT spectrum before the save. For the DSPEC Plus in ZDT mode one, a value of 1 will switch the display to the ZDT spectrum before the data is saved and a value of zero will switch the spectrum to the Error spectrum before the save. This parameter is ignored if the DSPEC Plus is not in ZDT mode. This parameter is not used when saving data to an .SPC file since both spectra are automatically saved.

The **Ask on Save** questions as defined in **File/Settings...** will be asked each time a SAVE command is executed. This will stop execution of the .JOB file until the question is answered. Note that if you **Cancel** an ask-on-save prompt, the JOB will terminate. As with the **File/Save As** function, the real time, live time, start of acquisition, and, if available, calibration data, detector description, and sample description are stored with the spectrum.

If the **ASK_SPECTRUM** command has been executed in this .JOB file prior to this SAVE command, the filename is stored in $(FullPath).

SAVE_CALIBRATION "[d:][\path\]file[.clb]"

Saves the current working energy and efficiency calibrations to a .CLB file. It has the same function as **Save Calibration...** under the **Calibrate** menu. The contents of the spectrum are not altered by this operation. The disk filename (in quotation marks) can be any valid filename, with optional elements as described for the SAVE command, above. The default extension is .CLB. The loop count value can be included in the filename by typing three question marks in the text where the loop count is to be inserted. The loop count replaces "???" wherever it appears. The filename can include any of the variables defined in Section 10.2.

SAVE_ROI "[d:][\path\]file[.roi]"

Saves a table of channel numbers that have the ROI set for the active Detector or selected data memory in a disk file. It has the same function as **Save File...** under the **ROI** menu. The contents of the spectrum are not altered by this operation. The disk filename (in quotation marks) can be any valid filename, with optional elements as described for the SAVE command, above. The default extension is .ROI. The loop count value can be included in the filename by typing three question marks in the text where the loop count is to be inserted. The loop count replaces "???" wherever it appears. The filename can include any of the variables defined in Section 10.2.

SAVE_SPCIMAGE "ImageFile", "Type", "SettingsFile"

Saves the currently displayed histogram to the specified "ImageFile" in either .BMP or .JPG format. The optional argument "Type" may be either "Jpg" or "Bmp". If this argument is missing, the image format defaults to "Bmp" format. Additionally, a GVPlot settings file

(created in GVPlot with the **File/Save Settings As...** command) can also be passed in as an argument.

SEND_MESSAGE “command”

This is used to send MCB hardware commands to the active Detector. This can be used to perform any operations of the Detector that are desired. The text must be in the syntax expected by the Detector. If the response from the Detector does not end with a command-accepted message, then this command will exit with error.

Specific Detector commands and syntax are described in the technical manual associated with each specific Detector.

The following is an example of using this command to set the fine and coarse gain to a total value of 50 (the product of the fine [= 0.5] and coarse [= 100] gains):

```
.
.
SET_DETECTOR 1
STOP
CLEAR
SEND_MESSAGE “SET_GAIN_FINE 2048"
SEND_MESSAGE “SET_GAIN_COARSE 100"
.
.
```

SET_BUFFER

This selects the buffer. It is the same as SET_DETECTOR 0.

SET_DETECTOR <number>

This selects the active Detector or the buffer. The Detector number can be 1 to 999 according to the Detector configuration, or 0 for the buffer. Also, SET_DETECTOR without an argument is used to switch to the previously selected Detector. If a Detector is selected that does not exist, no change is made. The Detector number is the number shown on the toolbar and the Detector pick list.

The JOB processor expects one or more numerals as the argument to this command, entered with or without quotation marks (e.g., you can enter the numerals 1000 or the string “1000"). The JOB processor will also accept the loop counter as an argument to the function *as long as it is set in quotation marks*. For example, you could use “$(loop1)” to sequence through the detector list, provided the detector list is in numerical sequence.

This command (for values 1 to 12) has the same function as **<Ctrl+ F1>** through **<Ctrl+ F12>**. For value 0 or no argument at all, it duplicates the **Detector/Buffer** toggle under the **Display** menu, **<F4>**, and **<Alt+ 6>**.

See also the notes on SET_DETECTOR and the new GammaVision multi-detector interface in Section 10.1.1.4.

SET_LIST
Switches the currently selected Detector from PHA mode to LIST mode.

SET_NAME_STRIP “file.chn”
This can be used before STRIP to select a disk filename to be used subsequently by the STRIP command. (It is not necessary to use this command, because the filename can be supplied as part of the STRIP command itself; however, the command is included for backward compatibility.) No other action is taken by this command. The filename can include any of the variables defined in Section 10.2.

SET_OPTIONS “OptionsFile”, “SdfFile”
This command creates “SdfFile” based on the options specified in “OptionsFile”. The OptionsFile is a text file composed of single settings as defined in the SET_SETTINGS JOB command. An example file is shown in Fig. 313.

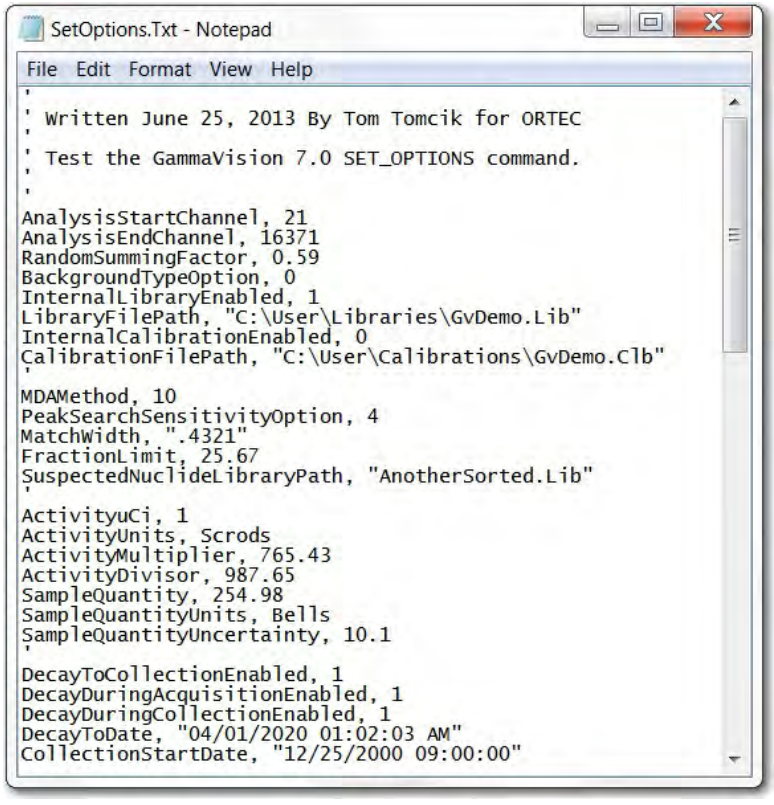


Figure 313. SET_OPTIONS Options file.

NOTES

- An invalid parameter name, data type, or file structure will generate an error and terminate the job.

- A single quote character at the start of a line indicates that the line is a comment, and the line is not parsed for Parameter/Data pairs.

- A blank line will terminate the parsing process, so the single quote character should be used if white space is desired to improve readability of the file content.

- The .SDF file does not store the following SET_SETTINGS parameters, so they cannot be included in the Options File.

Keyword	Storage Location
Operator	Stored in the Registry
Laboratory	Stored in the Registry
GammaTotalGammaTotalSequence	Stored in the Context File
GammaTotalGermaniumSequence	Stored in the Context File
GammaTotalReportDirectory	Stored in the Registry
GammaTotalGermaniumReportDirectory	Stored in the Registry

The following additional parameters can be used to set the Presets in the .SDF file, and they will be applied to the hardware when the .SDF file is loaded into GammaVision.

RealTimePreset	Float in seconds
LiveTimePreset	Float in seconds
ROIPeakPreset	Integer
ROIIntegralPreset	Integer
UncertaintyPresetPercent	Float in percent
UncertaintyPresetStartChannel	Integer
UncertaintyPresetWidth	Integer

Note that presets can also be modified when the Job is running by using the following GammaVision Job commands in lieu of saving presets to an .SDF file.

SET_PRESET_CLEAR
SET_PRESET_REAL
SET_PRESET_LIVE
SET_PRESET_COUNT
SET_PRESET_INTEGRAL
SET_PRESET_UNCERTAINTY

SET_PHA

Switches the currently selected Detector from LIST mode to PHA mode.

SET_PRESET_CLEAR

This clears the presets for the active Detector. The clearing should be done to ensure that unwanted presets are not used by the Detector when the Detector is started.

NOTE For the Models 916/17/18 Detectors, the new presets (including CLEAR) can be loaded at any time, but are not put into effect until the Detector goes from STOP to START. For most other MCBs, the presets can only be changed when the unit is not counting.

The Detector should be selected by the SET_DETECTOR commands before the SET_PRESET_CLEAR command is given, as in the following:

```
.
.
SET_DETECTOR 1
STOP
SET_PRESET_CLEAR
START
.
.
```

SET_PRESET_COUNT <counts>

This sets the ROI peak count preset for the active Detector. The preset is set to the entered value. With this preset condition, the Detector stops counting when any ROI channel's content reaches this value. If no ROIs are marked in the Detector, then that Detector never meets this condition. This command has the same function as the **ROI Peak Count** field on the Presets tab under **Acquire/MCB Properties...** (Section 5.2.11); refer to the discussion describing that dialog for additional information.

The JOB processor expects one or more numerals as the argument to this command, entered with or without quotation marks (e.g., you can enter the numerals 1000 or the string "1000"). The JOB processor will also accept the loop counter as an argument to the function *as long as it is set in quotation marks*. For example, you could use the loop counter to collect a series of spectra with increasing ROI peak counts by appending zeroes to the loop counter to obtain 1000 counts, then 2000, and so on.

SET_PRESET_INTEGRAL <counts>

This sets the ROI Integral Count preset value for the active Detector. The preset is set to the entered value. With this preset condition, the Detector stops counting when the sum of all counts in all channels marked with an ROI reaches this limit. If no ROIs are marked in the Detector, then that Detector never meets this condition. This command has the same function as the **ROI Integral** field on the Presets tab under **Acquire/MCB Properties...**

(Section 5.2.11); refer to the discussion describing that dialog for additional information.

The JOB processor expects one or more numerals as the argument to this command, entered with or without quotation marks (e.g., you can enter the numerals 1000 or the string “1000"). The JOB processor will also accept the loop counter as an argument to the function *as long as it is set in quotation marks*. For example, you could use the loop counter to collect a series of spectra with increasing ROI integral counts by appending zeroes to the loop counter to obtain 1000 counts, then 2000, and so on.

SET_PRESET_LIVE <seconds>

This sets the live-time preset for the active Detector. The preset is set to the entered value. With this condition, the Detector stops counting when the live time reaches this limit. The live time is the real time minus the dead time. This command has the same function as the **Live Time** field on the Presets tab under **Acquire/MCB Properties...** (Section 5.2.11); refer to the discussion describing that dialog for additional information.

The JOB processor expects one or more numerals as the argument to this command, entered with or without quotation marks (e.g., you can enter the numerals 1000 or the string “1000"). The JOB processor will also accept the loop counter as an argument to the function *as long as it is set in quotation marks*. For example, you could use the loop counter to collect a series of spectra with increasing live times by appending zeroes to the loop counter to obtain 1000 seconds, then 2000, and so on.

SET_PRESET_REAL <seconds>

This sets the real-time preset for the active Detector. The preset is set to the entered value. With this preset condition, the Detector stops counting when the real time reaches this limit. This command has the same function as the **Real Time** field on the Presets tab under **Acquire/MCB Properties...** (Section 5.2.11); refer to the discussion describing that dialog for additional information.

The JOB processor expects one or more numerals as the argument to this command, entered with or without quotation marks (e.g., you can enter the numerals 1000 or the string “1000"). The JOB processor will also accept the loop counter as an argument to the function *as long as it is set in quotation marks*. For example, you could use the loop counter to collect a series of spectra with increasing real times by appending zeroes to the loop counter to obtain 1000 seconds, then 2000, and so on.

SET_PRESET_UNCERTAINTY <limit>,<low chan>,<high chan>

This sets the statistical preset to the uncertainty based on the counts in the region between the low and high channels. Not supported by all MCBs. See Section 4.2.1.1 for details on the calculation. The low channel must be greater than 1 and the high channel must be greater than the low channel plus 7.

SET_RANGE "M/dd/yyyy", "hh:mm:ss", <t>
SET_RANGE "r", "t"
Displays a time slice of data from a .LIS file that has been recalled into a buffer.

SET_SETTING "Setting", "Value"
This command updates the analysis setting described by "Setting" to the value specified by "Value". Formatting for the Setting / Value combinations are shown below:

NOTE: A valid file path must be specified for the Correction options (i.e., PBC, Geometry, or Attenuation) prior to setting the "InternalEnabled" parameter to NO or the "Enabled" parameter to YES. If the file path is not valid then the associated correction will be automatically disabled.

Setting	Description
AnalysisStartChannel	Starting channel number
AnalysisEndChannel	Ending channel number
RandomSummingFactor	Floating point value allowed
BackgroundTypeOption	0 = Auto, 1 = 1Pt, 3 = 3Pt, 5 = 5pt, xP, x.xF x = # of points with the "P" suffix x.x = FWHM Factor with the "F" suffix
InternalLibraryEnabled	1 = Yes, Anything else = No
LibraryFilePath	Library pathname
InternalCalibrationEnabled	1 = Yes, Anything else = No
CalibrationFilePath	Calibration override pathname
Laboratory	Laboratory name
Operator	Operator name
MDAMethod	1 = Traditional ORTEC 2 = Critical Level ORTEC 3 = Suppress Output 4 = KTA Rule 5 = Japan 2-Sigma Limit 6 = Japan 3-Sigma Limit 7 = Currie Limit 8 = RISO MDA 9 = LLD ORTEC 10 = Peak Area 11 = Air Monitor – GIMRAD 12 = Reg. Guide 4.16 Method 13 = Counting Lab USA

	14 = DIN 25 482.5 Erkennungsgrenze 15 = DIN 25 482.5 Nachweisgrenze 16 = EDF – France 17 = Nureg 0472 18 = ISO Decision Threshold (CL) 19 = ISO Detection Limit (MDA)
PeakSearchSensitivityOption	1, 2, 3, 4, or 5
MatchWidth	Floating point (0.4 to 1.0)
FractionLimit	Floating point in percent
SuspectedNuclideLibraryPath	Full pathname to suspected nuclide library
ActivityuCi	1 = uCi, Anything else = Bq
ActivityUnits	Sample Activity Units descriptor
ActivityMultiplier	Sample amount multiplier
ActivityDivisor	Sample amount divisor
SampleQuantity	Sample amount
SampleQuantityUnits	Sample amount units
SampleQuantityUncertainty	Sample amount uncertainty in percent
DecayToCollectionEnabled	1 = Yes, Anything else = No
DecayDDuringAcquisitionEnabled	1 = Yes, Anything else = No
DecayDuringCollectionEnabled	1 = Yes, Anything else = No
DecayToDate	Date Time “YYYY-MM-DD HH:MM:SS”
CollectionStartDate	Date Time “YYYY-MM-DD HH:MM:SS”
CollectionEndDate	Date Time “YYYY-MM-DD HH:MM:SS”
ReportUnknownPeaksEnabled	1 = Yes, Anything else = No
ReportLibraryPeakListEnabled	1 = Yes, Anything else = No
ReportLibraryPeakMatrixEnabled	1 = Yes, Anything else = No
ReportNuclideAbundanceEnabled	1 = Yes, Anything else = No
ReportIsoNormEnabled	1 = Yes, Anything else = No
UncertaintyPercentOption	1 = Percent, Anything else = Activity
UncertaintyCountingOption	1 = Counting, Anything else = Total
UncertaintyConfidenceLevelOption	1 = 1-Sigma, 2 = 2-Sigma, 3 = 3-Sigma
DisplayAnalysisResultsEnabled	1 = Yes, Anything else = No

ReportOutputOption	1 = Printer, 2 = File, 3 = Program, 4 = Report Writer
ReportFilePath	File pathname
ReportProgramPath	Program pathname
ReportWriterTemplatePath	Template pathname
AnalysisEngine	'WAN32', 'GAM32', 'NPP32', 'ENV32', 'ROI32', 'NAI32', or user-defined name

NOTES

For GAM32 and ROI32, **Directed Fit**, **Library Based** peak stripping, and **Manual Based** peak stripping are disabled.

For NPP32, ENV32 and NAI32, **Library Based** peak stripping is enabled and **Manual Based** peak stripping is disabled.

AdditionalRandomError	Random error in percent
AdditionalSystemicError	Systemic error in percent
LibraryPeakStrippingEnabled	1 = Yes, Anything else = No
ManualPeakStrippingEnabled	1 = Yes, Anything else = No
SecondLibraryPath	Pathname to second library
ThirdLibraryPath	Pathname to third library
PeakCutoff	Peak cutoff in percent
TCCEnabled	1 = Yes, Anything else = No
DirectedFitEnabled	1 = Yes, Anything else = No
PBCEnabled	1 = Yes, Anything else = No
PBCInternalEnabled	1 = Yes, Anything else = No
PBCByEnergyEnabled	1 = Yes, Anything else = No
PBCFilePath	Full pathname to the PBC file
PBCMatchWidth	Positive floating point number
GEOEnabled	1 = Yes, Anything else = No
GEOInternalEnabled	1 = Yes, Anything else = No
GEOFilePath	Full pathname to the Geometry file
ATTEnabled	1 = Yes, Anything else = No
ATTInternalEnabled	1 = Yes, Anything else = No
ATTFromFilePath	Full pathname to ATT file
ATTFromDatabaseEnabled	1 = Yes, Anything else = No
ATTMaterial	Material name

NOTE: The ATTConfigurationOption must be set prior to setting the Material name.

ATTConfigurationOption	1 = Linear, Anything else = Mass
ATTLength	Length or Mass
ATTTypeOption	1 = Internal, Anything else = External
AvgEnergyEnabled	1 = Yes, Anything else = No
AvgEnergyInternalEnabled	1 = Yes, Anything else = No
AvgEnergyFilePath	Full pathname to the .EBR file
IEQEnabled	1 = Yes, Anything else = No
IEQInternalEnabled	1 = Yes, Anything else = No
IEQFilePath	Full pathname to the .IEQ file
DACEnabled	1 = Yes, Anything else = No
DACInternalEnabled	1 = Yes, Anything else = No
DACFilePath	Full pathname to the .DAC file
GammaTotalReportingEnabled	1 = Yes, Anything else = No
GammaTotalGermaniumReportingEnabled	1 = Yes, Anything else = No
GammaTotalCalculationEnabled	1 = Yes, Anything else = No
GammaTotalEDFTableOnlyEnabled	1 = Yes, Anything else = No
GammaTotalReportIsoMdaOnReportsEnabled	1 = Yes, Anything else = No
GammaTotalCountBackgroundEnabled	1 = Yes, Anything else = No
GammaTotalCountCesiumEnabled	1 = Yes, Anything else = No
GammaTotalWriteBackgroundReportEnabled	1 = Yes, Anything else = No
GammaTotalWriteMaintenanceReportEnabled	1 = Yes, Anything else = No
GammaTotalSequence	Integer number
GammaTotalGermaniumSequence	Integer number
GammaTotalReportDirectory	Directory path
GammaTotalGermaniumReportDirectory	Directory path
GammaTotalAnalysisStartChannel	Starting channel number
GammaTotalAnalysisEndChannel	Ending channel number
GammaTotalUseRangeForBackgroundQAEnabled	1 = Yes, Anything else = No
GammaTotalBackgroundSpectrumPath	Full pathname
GammaTotalCesiumSpectrumPath	Full pathname
GammaTotalGeometryFilePath	Full pathname
AdditionalUncertainty1Name	String description 37 chars max
AdditionalUncertainty2Name	String description 37 chars max
AdditionalUncertainty3Name	String description 37 chars max
AdditionalUncertainty4Name	String description 37 chars max
AdditionalUncertainty5Name	String description 37 chars max

AdditionalUncertainty6Name	String description 37 chars max
AdditionalUncertainty7Name	String description 37 chars max
AdditionalUncertainty8Name	String description 37 chars max
AdditionalUncertainty9Name	String description 37 chars max
AdditionalUncertainty1Value	Float between 0 and 1000%
AdditionalUncertainty2Value	Float between 0 and 1000%
AdditionalUncertainty3Value	Float between 0 and 1000%
AdditionalUncertainty4Value	Float between 0 and 1000%
AdditionalUncertainty5Value	Float between 0 and 1000%
AdditionalUncertainty6Value	Float between 0 and 1000%
AdditionalUncertainty7Value	Float between 0 and 1000%
AdditionalUncertainty8Value	Float between 0 and 1000%
AdditionalUncertainty9Value	Float between 0 and 1000%

SET_VARIABLE “VarName”, “VarValue”

This command sets the user defined JOB variable “VarName” to “VarValue”. Variable name are limited in length by 32 characters and variable values are limited to 256 characters. Up to 100 variables can be accessed in a JOB and variable 101 overwrites the first variable assigned.

To access any one of the user-defined variables, the macro expansion ‘$(VarName)’ can be used in any JOB command. For example, the following JOB commands load the sample type file stored in the variable ‘SDFPath’:

```
SET_VARIABLE “SDFPath, “C:\User\Sample Types\SetOptions.Sdf”
RECALL_OPTIONS $(SDFPath)
```

User-defined variables are shared across multiple jobs when they are nested using the CALL JOB command. The nested JOBs inherit all previously defined variables and their values at run time, and changes made to those variables or values added in nested JOBs are available when control returns to the calling JOB. The maximum limit of 100 user-defined variables is the total across all nested JOBs that are called from a main JOB.

SMOOTH

This command smooths the data in the active buffer window. Its function is the same as **Smooth** under the **Calculate** menu. A five-point, area-preserving, binomial smoothing algorithm is used. The original contents of the buffer are lost.

START

This initiates data collection in the selected Detector. This function is the same as **Start** under the **Acquire** menu.

The **Ask on Start** questions as defined in **Acquire/Acquisition Settings...** will be asked each time a START command is executed. This stops execution of the .JOB file until the question is answered. If you choose **Cancel** for an ask-on-start prompt, the JOB terminates.

START_OPTIMIZE

For MCBs that support this feature, this starts the optimize function for the Detector. See Section 4.2.3.5 for functional details.

START_PZ

This starts the PZ function for the detector. It is automatically included in the optimize function. This command is only available for MCBs with internal amplifiers.

STOP

This stops data collection in the active Detector. If the Detector has already been stopped, no operation occurs. This command has the same function as **Stop** under the **Acquire** menu.

STOP_PZ

This stops the PZ function for the detector. Note that the PZ function is not complete when this is used. The PZ function should be allowed to complete automatically. This command is only available for MCBs with internal amplifiers.

STRIP <factor>,[“file.chn”]

This strips the disk spectrum specified in the SET_NAME_STRIP command or in the command itself (either way is acceptable; the filename is optional in this command) from the spectrum in the buffer and stores the results in the buffer. The disk and selected data memory spectra must be the same size. The disk spectrum can be scaled up or down by <factor> (a constant) or, if <factor> is zero, by the ratio of the live times of the two spectra. The filename can include any of the variables defined in Section 10.2.

UNLOCK “Pwd”

This unlocks the current Detector using “Pwd” as the password.

VIEW “i”, [“Type”]

This moves the “i”th stored spectrum to position 0 (i.e., makes it active in the view). This command is only valid in MCBs with Field Mode or buffers containing N42 files that have multiple spectra. The optional “Type” argument specifies the spectrum type to view with valid options of “Any”, “Background”, “TimeSlice”, “LongCount”, “KnownSample”, or “BlankSample”. Any other Type options will generate an error.

The Job variable “$(Spectra)” is updated to reflect the number of spectra stored in a multiple spectrum file when the VIEW command is run. This variable can be used with the LOOP command to automatically process each spectrum as necessary. An example Job showing

how to extract all Background spectra to CHN files is shown below.

```
SET_BUFFER
RECALL “Detective-Pro.N42"
VIEW 1, “Background”
LOOP “$(Spectra)”
    RECALL “Detective-Pro.N42"
    VIEW “$(LOOP1)”, “Background”
    SAVE“Background$(LOOP1).chn”
END_LOOP
```

WAIT [<seconds>]

This suspends execution of the JOB to wait until either the active Detector stops counting (in the case where the <seconds> argument is not included), or for a fixed number of seconds.

WAIT “program”

This suspends execution of the JOB to wait until the named program stops execution. If the program does not stop, this JOB will not continue. It is good practice to put a WAIT 2 command between the RUN “program” and WAIT “program” commands to give Windows time to start the program before the status is checked. The “program” name must agree with the name used in Windows, and must include the .EXE extension.

WAIT_AUTO

For DSPEC only; this waits until the optimize function is complete.

WAIT_CHANGER

This waits until the sample ready signal on the rear panel is present. It is used in conjunction with the SEND_COMMAND function for more control over the sample changer than is provided by the CHANGE_SAMPLE command.

WAIT_PZ

This waits until the PZ function is complete.

WAIT_QA(ã)

This waits until QA is complete.

WAIT_SERIAL “Command”, timeout[,”Response”]

This is used to send and receive commands on the serial port of MCBs. It is designed to be used to control sample changers with RS-232 controls. “Command” are the characters sent to the changer to make it operate. Timeout is the maximum time to wait for a response before error. “Response” is the reply from the changer when it has finished the “Command.”

The first operation is to send "Command" out the serial port for the selected Detector. It then waits for a response or timeout according to these entries:

1. If a response string is provided, the length of the response string determines the exact number of characters to wait for.
2. If a response string is not provided, any character input will generate a success.
3. If a response string is provided, and the characters do not match, an Invalid Response message is generated and the JOB terminates.
4. If a timeout occurs, a Timeout Message is generated and the JOB terminates.

Example:

```
SET_DETECTOR 1
LOOP 3
    WAIT_SERIAL "$(Loop1)L$(CR)", 300, "$(BEL)"
    BEEP 5
END_LOOP
```

This code does the following:

1. Sends **1L**↩ and waits 5 minutes for an ASCII Bell Character. Beeps 5 after ASCII bell is received.
2. Sends **2L**↩ and waits 5 minutes for an ASCII Bell Character. Beeps 5 on success.
3. Sends **3L**↩ and waits 5 minutes for an ASCII Bell Character. Beeps 5 on success.

The ↩ is the $(CR) (carriage return) character.

ZOOM <i>

Changes the size of the GammaVision window. Selects one of icon, normal, or maximum according to the argument. The arguments are:

−1 = minimize (icon on Taskbar)
0 = normal (size determined by last use)
+1 = maximize (full screen)

ZOOM: <x,y,w,h>

Changes the position and size of the GammaVision window. The arguments are:

x = x position of upper-left corner of window (0 is left)
y = y position of upper-left corner of window (0 is top)
w = width of window in pixels, starting at x and going right
h = height in pixels, starting at y and going down

Since these arguments are in pixels, experimentation is the best way to determine the desired size.

[Intentionally blank]

11. UTILITIES

11.1. GVPlot

GVPlot replaces WinPlots as our program for printing any type of ORTEC spectrum file. In the interactive mode (it can also be run in command-line mode), a preview of the spectrum plot is displayed on the screen and updated as you adjust the display parameters. You can select the graph colors and symbols for the plot, the start and stop channels or energy range, the printer to be used, and logarithmic or linear vertical scaling. Optionally, you can save these display settings and recall them for later use. The sample, detector, and acquisition descriptions in the file can be printed or suppressed. In addition, you can save, recall, and display the spectrum file's corresponding analysis information; as well as ROIs stored in the spectrum file or in a separate .ROI file.

To start GVPlot, enter gv or gv[space]p in the "*search programs and files*" box then click the **Gv Plot** search result; or open the Windows Start menu and click **GammaVision** then **Gv Plot**. You can also run GVPlot in command line mode for use in .JOB files, or directly from other Windows programs (see Section 11.1.5). In this mode, you can either specify the settings or use the defaults.

The spectrum files are associated with GVPlot by the installation program, so double-clicking on a spectrum filename in Windows Explorer will start GVPlot and display that spectrum.

11.1.1. Screen Features

Figure 314 shows the major GVPlot screen features.

1) **Title bar**, shows the current spectrum filename. On the far right are the standard Windows Minimize, Maximize, and Close buttons.

2) **Menu Bar**, shows the available menu commands (which can be selected with either the mouse or keyboard); these functions are discussed in detail in the following sections.

3) **Toolbar**, beneath the menu bar, contains icons for recalling a spectrum, printing it, and adjusting the vertical and horizontal scale of the spectrum window. You can display or hide the toolbar from the **View** menu.

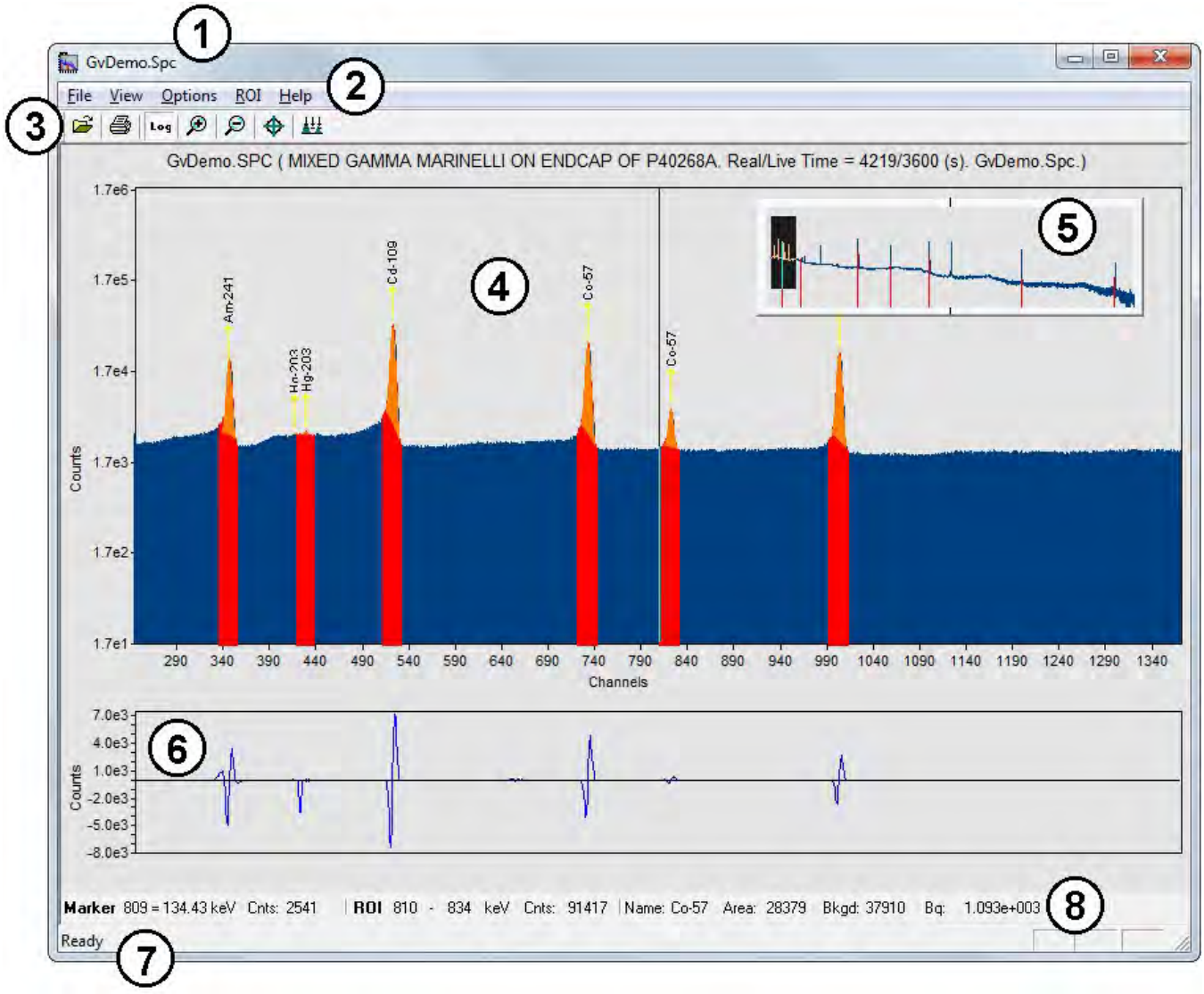


Figure 314. The Main GVPlot Display.

4) The **Expanded Spectrum Window** shows all or part of the full histogram; this allows you to zoom in on a particular part of the spectrum and see it in more detail. You can change the vertical and horizontal scaling, and perform a number of operations such as displaying peak information, marking and modifying ROIs, and displaying the residuals (see item 6 below). This window contains a vertical line called a *marker* that highlights a particular position in the spectrum. Information about that position is displayed on the Marker Information Line (see item 7 below). Right-clicking in this window opens a right-mouse-button menu, which is discussed in Section 11.1.4.

5) The **Full Spectrum Window** shows the full histogram from the file or the Detector memory. The vertical scale switches between logarithmic and linear in concert with the scaling in the expanded window. When you zoom in on part of the spectrum in the expanded window, the

Full Spectrum Window displays a rectangular area that reflects the portion of spectrum now visible in the Expanded Spectrum Window. To quickly move to different region in the spectrum, either click that region in the Full Spectrum Window or click and drag the rectangle to the new position, and the expanded display will update immediately at the new position. You can also zoom out by clicking and dragging a rubber rectangle over any portion of the Full Spectrum Window (the starting point for this operation must be outside of the current expanded-view indicator rectangle). The full-spectrum window can be moved and sized (see Section 4.4.4).

6) **Residuals**, which can be displayed in the lower section of the spectrum window, displays a comparison of the counts in each channel to the calculated counts for that channel as determined by the peak-fitting algorithm. This comparison can be displayed in counts (absolute residuals) or standard deviations (relative residuals). See the discussion on page 431.

7) **Status Bar**, below the Marker Information Line, displays program status information such as warning messages. You can display or hide the status bar from the **View** menu.

8) **Marker Information Line**, beneath the spectrum, shows the **Marker** channel, marker energy, and channel contents. The **ROI** section shows the boundaries of the ROI in energy (for calibrated spectra) or channels (for uncalibrated spectra), the number of counts in the ROI, and other information; see the discussion associated with Fig. 326 on page 433.

11.1.2. The Toolbar

The row of buttons below the menu bar provides convenient shortcuts to some of the most common GVPlot commands.

The **Recall** button retrieves an existing spectrum file. This is the equivalent of selecting **File/Recall Spectrum...** from the menu.

Print sends the current spectrum immediately to the default Windows printer without opening the standard Print dialog. If you wish to switch to another printer or adjust the default print properties, use the **File/Print...** command (Section 11.1.3.1).

Vertical Log/Lin Scale switches between logarithmic and linear scaling. When switching from logarithmic to linear, it uses the previous linear scale setting.

Zoom In decreases the horizontal full scale of the Expanded Spectrum Window so the peaks appear larger and broader. You can also access this command from the right-mouse-button menu (Section 11.1.4.2).

Zoom Out increases the horizontal full scale of the Expanded Spectrum Window so the peaks appear smaller and narrower. You can also access this command from the right-mouse-button menu (Section 11.1.4.3).

Center forces the marker to the center of the screen by shifting the spectrum without moving the marker from its current channel.

Baseline Zoom sets and keeps the baseline of the Expanded Spectrum Window at zero counts in **Linear** scale mode and 1.0E+0 counts in **Logarithmic** scale mode. When **Baseline Zoom** is off, the baseline can be offset to a higher value. This is useful to show small peaks on a high background.

11.1.3. Menu Commands

11.1.3.1. File

Figure 315 shows the **File** menu. Use these commands to select the spectrum, analysis, and ROIs to be displayed, recall or save GVPlot settings files, and print the spectrum.

Use the **Recall Spectrum...** command (Fig. 316) to open a spectrum file.

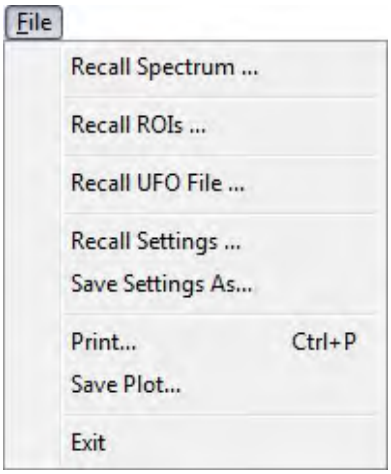


Figure 315. The File Menu.

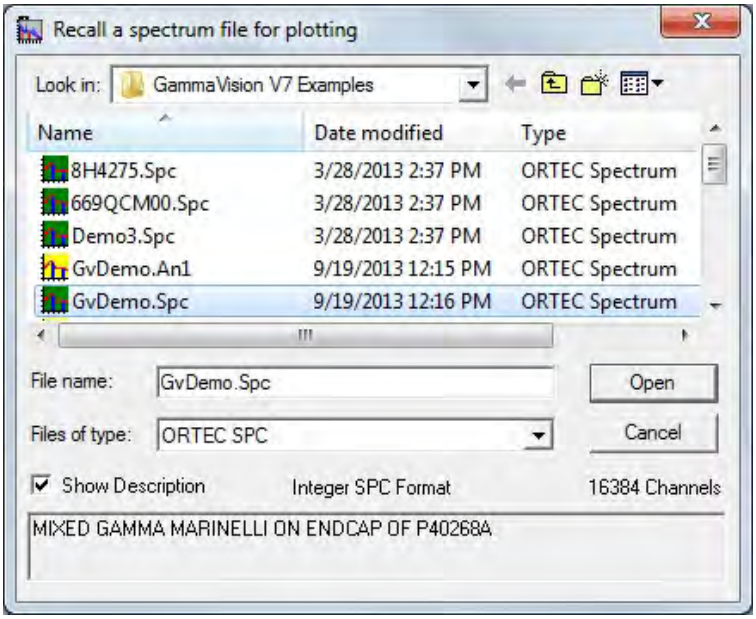


Figure 316. Open a Spectrum File.

When the **Show Description** checkbox at the bottom of the dialog is marked, you can click each spectrum filename and see its sample description, spectrum format, and number of channels as an aid in selecting the correct file.

The recalled spectrum will be displayed using the most recently selected graph color, symbol, and axis-scaling settings (which are set with the **Options/Graph...** command). These settings will also be used when you **Print** the spectrum or save it as a bitmap or jpeg image with **Save Plot...**

Once you have opened a spectrum file, **Recall ROIs** allows you to import the ROIs from an .ROI file. You can also open the corresponding analysis results (.UFO) file with **Recall UFO File**.

The graph colors, symbols, and axis parameters selected in **Options/Graph...** can be saved in an ASCII text file with the **Save Settings As...** command (which opens a standard Windows file-open dialog). The **Recall Settings** command allows you to recall a particular settings file so you can quickly and reproducibly adjust the appearance of the spectrum window. You can also call a settings file from the GVPlot command line to ensure the resulting plot(s) will be displayed according to your specifications.

The **Print...** dialog (Fig. 317) allows you to select a printer **Name** and specify the **Number of copies** to be printed (this number is reset to 1 after every print session). Click **Properties** to change print options such as paper size, orientation, and output resolution.

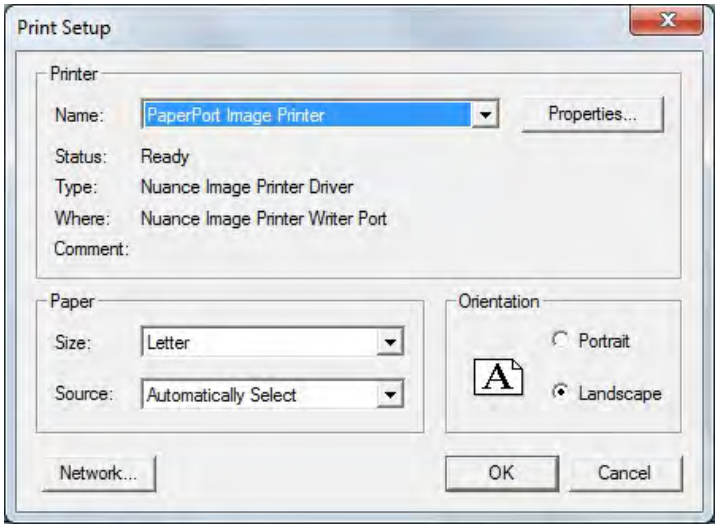


Figure 317. The Print Plot Dialog.

11.1.3.2. View

Figure 318 shows the **View** menu, which allows you to hide or display the **Toolbar** and **Status Bar**.

11.1.3.3. Options

The **Options** menu is shown below in **Figure 317**, **Figure 318**, **Figure 318**. These menu items govern the appearance of the spectrum window and printed output.

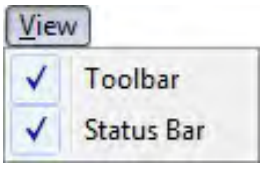


Figure 318.View Menu.

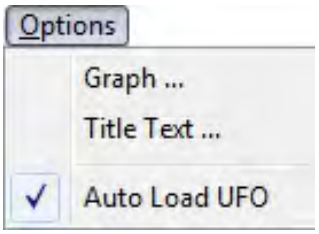


Figure 319. Options Menu.

Graph...

This command opens the dialog shown in Fig. 320, which lets you set the graph colors, symbol type, and axis scaling factors. These settings are stored when you exit GVPlot and reloaded the next time GVPlot is started. You can also save these settings in an ASCII text file using the **Save Settings As...** command, and retrieve them with **Recall Settings...**. **Graph...** is duplicated by the **Properties** item on the right-mouse-button menu.

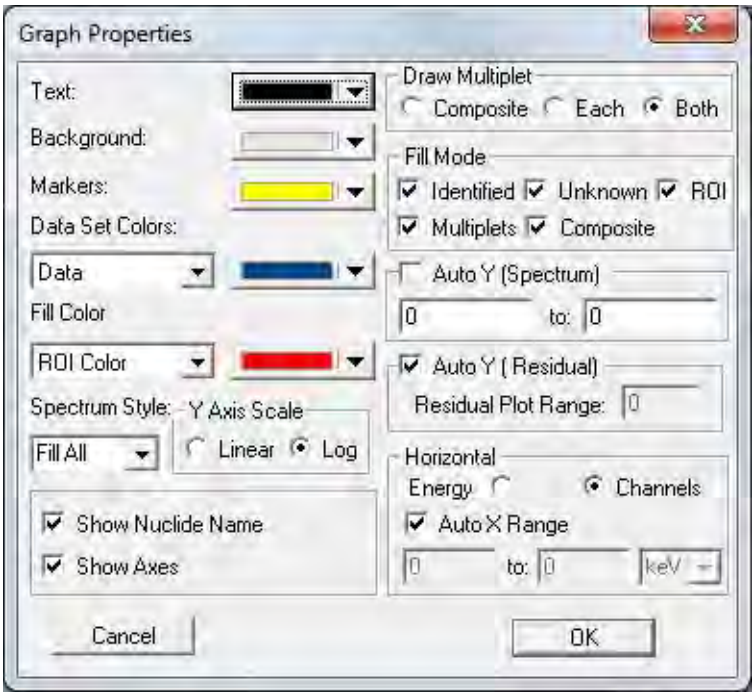


Figure 320. The Plot Options Dialog.

The droplists on the left side of the dialog control the screen and printout colors. As noted above, there are some differences between screen and printer fonts and colors. Also, if you do not have a color printer, the screen colors will be rendered in grayscale.

The **Text** color affects the color of the axes, axis labels, and spectrum title. **Background** controls the color of the spectrum background in both the full and expanded windows. **Markers** applies to the ROI bars.

Data Set Colors allows you to choose separate colors for spectrum **Data**, **Fit**ted peaks, and **Residual**s; select a data type from the left-hand droplist, then choose a color from the list on the right. Similarly, use **Fill Color** to control the colors of **ROI**s, **Nuclide Peak**s, **Unknown Peak**s, **Multiplet**s, and **Composite**s in both point and fill modes. **Spectrum Style** determines how the histogram data are represented (**Points**, **Line**, or **Fill All**).

The **Show Nuclide Name** checkbox allows you to hide or display the nuclide markers for an *analyzed* spectrum (an example of these markers is shown in Fig. 20, page 26). Turning the nuclide markers on or off slightly adjusts the graph's vertical scaling.

Clearing the **Show Axes** checkbox removes the axes so the portion of histogram shown in the Expanded Spectrum Window occupies the entire window without an inside border.

Set the **Y Axis Scale** of both the Full and Expanded Spectrum Windows to **Linear** or **Log**arithmic. You can also do this with the **Vertical Log/Lin Scale** button on the toolbar.

The **Draw Multiplet** radio buttons determine whether multiplets are drawn as a **Composite** curve, shown individually (**Each**), or displayed as individual peaks superimposed with the composite curve (**Both**). These modes are compared in Fig. 321. This display is most easily seen with all **Fill Mode**s turned off (checkboxes unmarked).

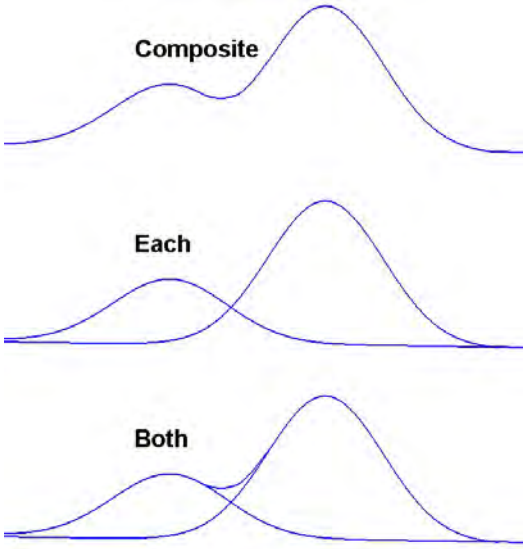


Figure 321. Draw Multiplet Modes.

The **Fill Mode** checkboxes allow you to determine which peak types, if any, will be displayed in fill mode rather than data-point mode.

Auto Y (Spectrum) allows you set up a fixed y-axis range for the Expanded Spectrum Window (**Auto Y** unmarked/off), or allow the program to autoscale the y-axis to accommodate the tallest peak currently displayed in the expanded view (**Auto Y** marked/on). The **Auto Y (Residual)** functions similarly for the residuals plot (which is displayed from the right-mouse-button menu, Section 11.1.4.1).

If the spectrum is calibrated, the **Horizontal** axis can be displayed in either **Energy** units or **Channel** numbers. If the spectrum is not calibrated, the horizontal axis is shown in channels and cannot be changed.

You can plot all or part of a spectrum by turning **Auto X Range** respectively on or off. Turning **Auto X Range** off activates the x-axis range fields that allow you to let the plot limits in either channels or keV (select units from the droplist). The plot limits are independent of the x-axis units of measure. This means that you can, if you wish, choose to display the x-axis in **Energy** units, then select the portion of the spectrum to be displayed as a range of channel numbers.

In order to easily compare spectra, the energy can be set to values below the first channel in the spectrum. In this case the data below channel 0 are plotted as 0.

NOTE Manually setting the range for one axis disables zooming for that axis only. If both axis ranges are manually fixed, all zooming is disabled.

Title Text

This dialog (Fig. 322) allows you to compose a title to be displayed at the top of the spectrum plot. In addition, you can choose whether or not to display the **Real and Live Time**, **Spectrum File Name**, and the sample or Detector description.

Auto Load UFO

When this feature is turned on (a checkmark is dis-played beside the command), recalling a spectrum file also recalls the corresponding .UFO file if it shares the same filename and drive/ folder location as the spectrum file. Note that if the analysis captured in the .UFO file covers only part of the spectrum, that portion of the spectrum, rather than the entire spectrum, will initially be displayed in the Expanded Spectrum View.

11.1.3.4. ROI

The **ROI** menu (Fig. 323) works in conjunction with the **Mark ROI** and **Clear Active ROI** commands on the right-mouse-button menu (Section 11.1.4).

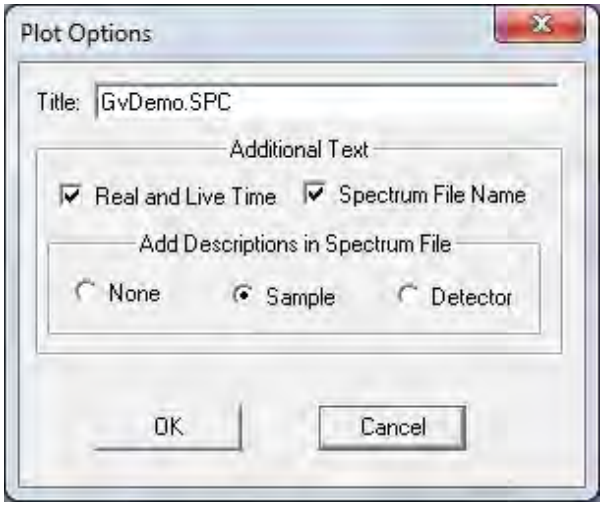


Figure 322. Compose the Plot Title.

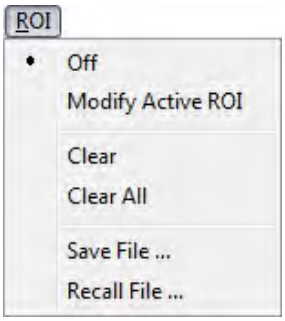


Figure 323. The ROI Menu.

Modify Active ROI/Off

This enables the **Modify Active ROI** mode, which lets you use the left/right arrow keys to add more channels to the currently active ROI (click inside the ROI to activate it). Pressing the left arrow shifts the low-energy boundary of the ROI to the left and pressing the right arrow shifts the high-energy side to the right; this shift might take a moment to occur. As you adjust the size of the ROI, the ROI boundary (and *ROI Bars*, if currently displayed; see Section 11.1.4.8) shifts and the Marker Information Line updates accordingly. When you select **Off**, the left/right arrow keys return to their original function of moving the marker through the spectrum. You can also adjust the size of the ROI by clicking and dragging the ROI bars.

Clear

This clears the ROI bits in all ROI channels that adjoin the channel containing the marker. This is duplicated by the **Clear Active ROI** command on the right-mouse-button menu.

Clear All

This resets all the ROI bits in the spectrum, removing all ROI markings from the spectrum.

Save File...

This command allows you to save to disk a table of the channel numbers, for the current spectrum, that have the ROI bit set. The contents of the spectrum are not changed. A standard Windows file-save dialog opens, allowing you to create a filename or overwrite an existing .ROI file.

Recall File...

Recall File... sets the ROIs in the spectrum according to the table in the disk file created by **ROI/ Save File...**. This command opens a standard file-open dialog, prompting you to select a filename. When you select a file, the ROIs in the currently displayed spectrum are set to conform to the table in the file. The previous ROIs are cleared. The spectrum data are not altered by this operation, only the ROI bits.

In .ROI files, the ROIs are saved by channel number. Therefore, if the spectrum peaks have shifted in position, the ROIs in the file will not correspond exactly to the spectrum data.

11.1.4. Right-Mouse-Button (Context) Menu Commands

Figure 324 shows the right-mouse-button menu that opens when you right-click in the Expanded Spectrum Window.

Figure 324. The Context Menu.

11.1.4.1. Show Residuals

Marking this menu item activates the **Plot Absolute Residuals** and **Plot Relative Residuals** modes. The Residuals section of the spectrum window (item 6 on page 425) displays a comparison of the counts in each channel (*Actual*) to the calculated counts for that channel as determined by the peak-fitting algorithm (*Fitted*). **Plot Absolute Residuals** displays the difference in each channel, in counts, between *Actual* and *Fitted* counts. **Plot Relative Residuals** displays the difference in each channel, in standard deviations (abbreviated **STD** on the screen), between *Actual* and *Fitted* counts divided by the square root of the *Actual* counts; that is, $(Actual - Fitted) / \sqrt{Actual}$.

The **Properties** command is equivalent to **Options/Graph...**; see Section 11.1.3.3.

11.1.4.2. Zoom In

Zoom In adjusts the horizontal and vertical scales in the Expanded Spectrum Window to view a smaller portion of the spectrum. This command is duplicated by the **Zoom In** button on the toolbar.

11.1.4.3. Zoom Out

Zoom Out adjusts the horizontal and vertical scales in the Expanded Spectrum Window to view a larger portion of the spectrum. This command is duplicated by the **Zoom Out** button on the toolbar.

11.1.4.4. Undo Zoom In

This will undo or reverse the last **Zoom In** operation done with the rubber rectangle. It restores the display to the horizontal and vertical expansion before the **Zoom In**. It is not the same as **Zoom Out**.

11.1.4.5. Full View

Full View adjusts the horizontal and vertical scaling to display the entire spectrum in the Expanded Spectrum View.

11.1.4.6. Mark ROI

This allows you to mark a peak as an ROI by clicking and dragging the rubber rectangle across a portion of the spectrum, then selecting **Mark ROI**. If **Show ROI Bars** is on (Section 11.1.4.8), the new ROI will be marked with the active ROI Bars until you either move to or create another ROI. Use the **Modify Active ROI** command on the **ROI** menu (Section 11.1.3.4) to widen the ROI boundaries, or click and drag the ROI bars to increase or decrease the number of channels in the ROI.

11.1.4.7. Clear Active ROI

This clears the ROI bits in all ROI channels that adjoin the channel containing the marker. This is the same as the **Clear** command on the **ROI** menu (Section 11.1.3.4).

11.1.4.8. Show ROI Bars

These are vertical markers that indicate the lower and upper boundaries of each ROI in the spectrum. The ROI bars for an inactive/unselected ROI have solid fill; when you click an ROI to activate it (only one is active at a time), the bars for the active ROI change to a diagonal fill (see Fig. 325). To display the ROI bars, right-click in the expanded window to open the right-mouse-button menu, then click **ROI Bars** to checkmark it. To hide the ROI bars, click the command again to clear the checkmark.

When you activate an ROI by clicking on it, the Marker Information Line (Fig. 326) displays the following information about the active ROI:

(a) The marker position, in channels and energy
(b) The counts in the marker channel
(c) The start and end points for the ROI, in channels for uncalibrated spectra and energy for calibrated spectra
(d) The total counts in the ROI
(e) The nuclide name, if identified
(f) The net peak area, in counts
(g) The peak background area, in counts
(h) The activity in the peak, in becquerels

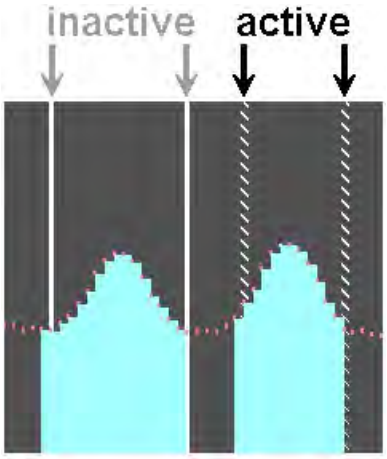


Figure 325. Inactive (solid) and Active (diagonal fill) ROI Bars.

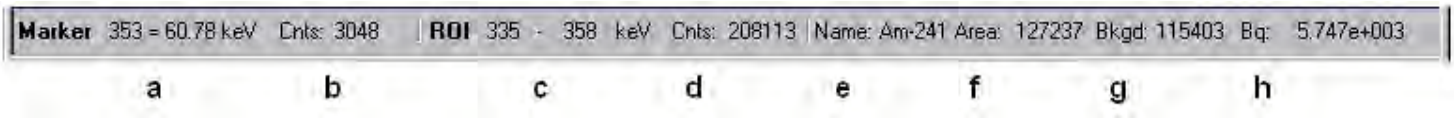


Figure 326. The GVPlot Marker Information Line.

You can shift the start or end channel of an ROI by moving the mouse over an ROI bar until the pointer changes to a double-arrow, then clicking and dragging the ROI bar to the desired location (allow a moment for the display to update). In addition, you can widen the ROI in the **Modify Active ROI** mode (Section 11.1.3.4).

Set the color of the ROI bars with the **Markers** droplist in the Graph Properties dialog (select **Properties** from the right-mouse-button menu or **Options/Graph...**).

11.1.4.9. Peak Info

This command opens a **Peak Info** box (Fig. 327) for the selected peak and leaves the box open until you click inside it. This command works for peaks loaded from a .UFO file and ROIs created within GVPlot or loaded from an .ROI file. The contents of the Peak Info box are described in Section 5.4.3. You can simultaneously display multiple Peak Info boxes as long as they do not overlap (opening a new Peak Info box closes any overlapping boxes). For very narrow peaks, you might find it useful to position the marker with the left/right arrow keys before calling the **Peak Info** command. When the marker is on a peak, the right side of the Marker Information Line will display a **Peak Area** readout.

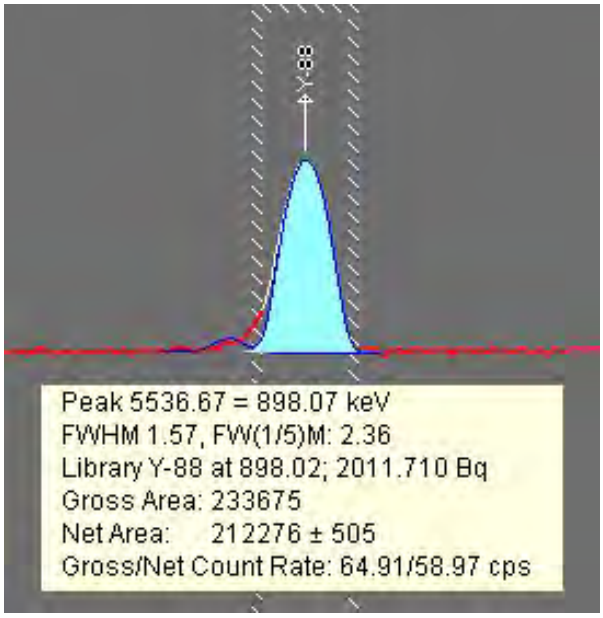


Figure 327. The Peak Info Window for an ROI.

11.1.4.10. Show Hover Window

When you select this command, a checkmark is displayed by this menu item to indicate that it is in hover-window mode. In this mode, the Peak Info window opens when the mouse pointer is paused over a peak for approximately 1 second, and closes when the pointer is moved away from the peak. To turn off hover mode, select **Show Hover Window** again to remove the checkmark.

11.1.4.11. Sum Spectrum

This sums the gross counts in the area selected with the rubber rectangle or, if you have not selected an area, the gross counts in the entire spectrum. The results are displayed on the status line, and indicate the span of channels summed.

11.1.4.12. Print Graph

This command prints performs a “quick print” of the contents of the Expanded Spectrum Window, using the currently selected printer and print settings (these will be either the default printer and print settings for this computer or the printer and settings used most recently during this GVPlot session). To change printers and/or print properties, use the **Print...** command on the **File** menu (page 427).

11.1.4.13. Properties

This opens the Graph Properties dialog, which is discussed in Section 11.1.3.3.

11.1.5. Command Line Interface

The GVPlot command line interface supports options available in the interactive mode as shown below:

```
GvPlot <spectrum> -U <ufofile> -R <roifile> -S <setfile> -P
```

where:

<spectrum>	Specifies the spectral data file (.SPC, .An1, or .CHN). The extension must be included.
-U <ufofile>	Specifies the .UFO file. The extension must be included.
-R <roifile>	Specifies the .ROI file. The extension must be included.
-S <setfile>	Specifies the settings file. The extension must be included.
-P	Print the plot to the PC's Windows default printer and exit automatically. Used mainly in .JOB files and **File/Export...**.

11.2. TRANSLT

The TRANSLT program (TRANSLT.EXE, located in your operating system's program files folder under \GammaVision) translates several different text files to and from .SPC or .CHN files. All operation is controlled from the command line. The command line is:

```
TRANSLT [-type] inname [[-type] outname] [-w] [-nc] [-col n] [-ni] [-nh] [-i]
```

where:

type	chn	The inname file is in CHN format.
	spc	The inname file is in SPC format.
	txt	The inname file is in ASCII text format.

The default is based on the filename extension and the i switch. Both chn and spc cannot be used together.

inname — The input spectrum file, no default; default extension is SPC. If the input file is a .TXT file, it must contain the live and real time in this format:

```
Real Time:  240.
Live Time:  120
```

Both values are in seconds.

The header information in the .TXT file will be converted and stored in the .SPC file if it is in the correct format. The correct format for the .TXT input file is the same as the .TXT format created as the output file.

type	chn	The outname file is in CHN format.
	spc	The outname file is in SPC format.
	txt	The outname file is in ASCII text format.

outname — The output spectrum file. The default is the inname with the extension changed. If the outname is not given, the spectrum file will not be overwritten by the default name. The length of the spectrum file converted from text will be the next higher power of two with the surplus channels set to 0.

w — Set the format output to 128 characters per line; default is 70 characters per line.

nc — Do not print channel as first number in line; default is to print the channel number. The channel number is followed by a colon (**:**) to separate it from the data.

col n — Number of data columns is n; default is 5. Error returned if line width will exceed available space.

ni — Do not write acquisition or analysis information in output file; default is to write this information.

nh — Do not write header information in output file; default is to write this information.

i — Import a text file and save as .SPC (or .CHN) file. If one filename is given, default is to convert that file to the other format, i.e., for AAA.SPC; the output will be AAA.TXT. If two filenames are given, the default is to convert the spectrum to text. The .TXT file will be overwritten even if the .SPC file is not located.

Example:

```
TRANSLT -SPC GOODSPEC -TXT TEXTSPEC -ni -nh -col 1
```

This will make a text file of one column with no header, no analysis information, and one channel per line.

APPENDIX A. STARTUP AND CONFIGURATION OPTIONS

To start GammaVision, enter gamm in the "*search programs and files*" box then click the **GammaVision** search result; or open the Windows Start menu and click **GammaVision**, and **GammaVision** (Fig. 328). You can also start GammaVision by entering run in the search box and choosing the **Run** search result; or (in XP) by selecting **Run...** from the Start menu. The Run option allows you to start up from the command line, with or without arguments, as described below.

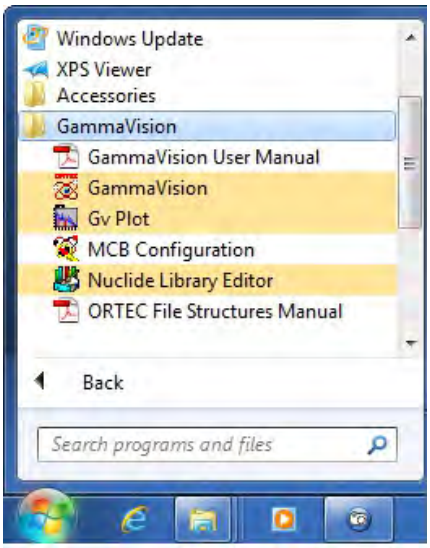


Figure 328. GammaVision Menu.

A.1. Command Line Options

GammaVision is run with the following command line properties:

GV32 [-d[n]] [-L file.lib] [-p listname] [-t] [-l] [-B] [-z] [file.job]

All of the arguments are optional; one or more can be omitted. Thus, at a minimum, GammaVision can be executed without any arguments at all, in which case certain defaults apply for the Detector list and nuclide library, as described below. Switches (e.g., -d, -z) can be uppercase or lowercase (e.g., -d or -D, -z or -Z).

[n] An optional parameter for the -d switch to enable debugging output mode at a specified level (values are 1 or 2; no argument is equivalent to 1). Default is no debugging. Debug mode is not recommended for general use.

file.lib An optional nuclide library (use with -L option) to be loaded at startup. The default is the library loaded when GammaVision exited.

-p listname Optionally uses listname as the Detector pick list name. The pick list name must be 5 characters or less. If a pick list is not specified, M32MCA.CFG — located in C:\ProgramData\ORTEC Shared\UMCBI — is used by default. The current pick list name is displayed above the Pick List column in the Detector List Editor dialog

(**Services/Edit Detector List...**). If the pick list name specified by `pick` does not exist then one is created. This new list will contain all available detectors included in the Master Detector List. If the pick list already exists, only the detectors defined in that list are displayed in the Detector droplist on the toolbar. Changes made to the pick list with the **Edit Detector List...** command are stored with the active pick list filename. Therefore, to create multiple pick lists, use the `-p` option with the pick list name and then edit the list to contain only the desired Detectors. The contents of the list can be overridden with the Edit Detector list function. The new list will be stored for use the next time this instance of GammaVision is run.

`-t` Forces GammaVision to be "Always on Top." The default is the normal Windows display.

`-1` Allows one and only one instance to run. This is the numeral one.

`-B` Start up with an open buffer window. This should be used if the computer is on a network and no MCBs are connected anywhere in the system.

`-z` The "zoom" switch with several variations:

`-z` or `-z:` With no arguments, causes the previously stored "ZOOM:" parameters (see page 421) to be used to position and size the GammaVision window.

`-z:x,y,w,h` Changes the position and size of the GammaVision window. The arguments (which are the same as for the ZOOM: profile variables, page 421) are:

`x` = x position of upper-left corner of window (0 is left)
`y` = y position of upper-left corner of window (0 is top)
`w` = width of window in pixels, starting at `x` and going right
`h` = height in pixels, starting at `y` and going down

`-z0` Forces position and size to be determined by Windows tiling algorithm.

`-z+1` Forces GammaVision to be maximized.

`-z-1` Forces GammaVision to be minimized (icon).

`file.job` An optional `.JOB` file to be executed at start-up.

Certain defaults apply if any one or more of these arguments is omitted. The initial Detector list is named M32MCA.CFG. The nuclide library is the last library used. And no JOB is automatically executed unless the file.job argument is included.

A.2. Analysis Setup(Y)

GammaVision includes two configuration files, b30winds.ini (n30winds.ini for NAI32) and b30win.txt, that allow advanced users to control several options in the analysis options and the report. If a configuration file is not found or cannot be read then GammaVision will use default settings. *These files should only be changed after careful consideration of the impact of the changes*.

A.2.1. WAN32, GAM32, NPP32, ENV32, ROI32, and NAI32

GammaVision's analysis engines are standalone programs which perform the complete spectrum analysis. The NAI32 analysis engine is used for low resolution (i.e., Sodium Iodide) spectrum analysis, and all of the others are used for high resolution (i.e., HPGe) spectrum analysis. These analysis engines are normally run within GammaVision, but they can also be run by other programs or by themselves using command line parameters as shown here for WAN32:

WAN32 file.SPC [DEBUG] [file.INI]

file.SPC — This is the spectrum filename and it must be the first argument. For a complete analysis it must contain all the analysis parameters and calibrations. The output files are the input file name with the extension of .UFO for the binary output and the extension of .RPT for the text output.

DEBUG — This optional parameter controls the output of debugging information in the analysis report file. GammaVision sets this parameter when GammaVision is run in debug mode. This produces considerable output and significantly slows the execution. It must be the second or third argument.

file.INI — This optional file overrides the default b30winds.INI or n30winds.INI settings.

A.2.2. B30winds.ini and N30winds.ini

The b30winds.ini file (Fig. 329) contains global analysis settings for all HPGe analysis engines. The NAI32 analysis engine has the same parameters in the n30winds.ini to allow for different settings associated with low resolution spectrum analysis.

If the specified file cannot be found in the same directory as the analysis engine then the \MESSAGE directory on the default drive is searched. If it is not found there or cannot be read, then the internal values are used.

NOTE These parameters are read sequentially from the file and none can be omitted even if they will not be used. Doing so would offset the parameters, and subsequent settings would be incorrectly interpreted.

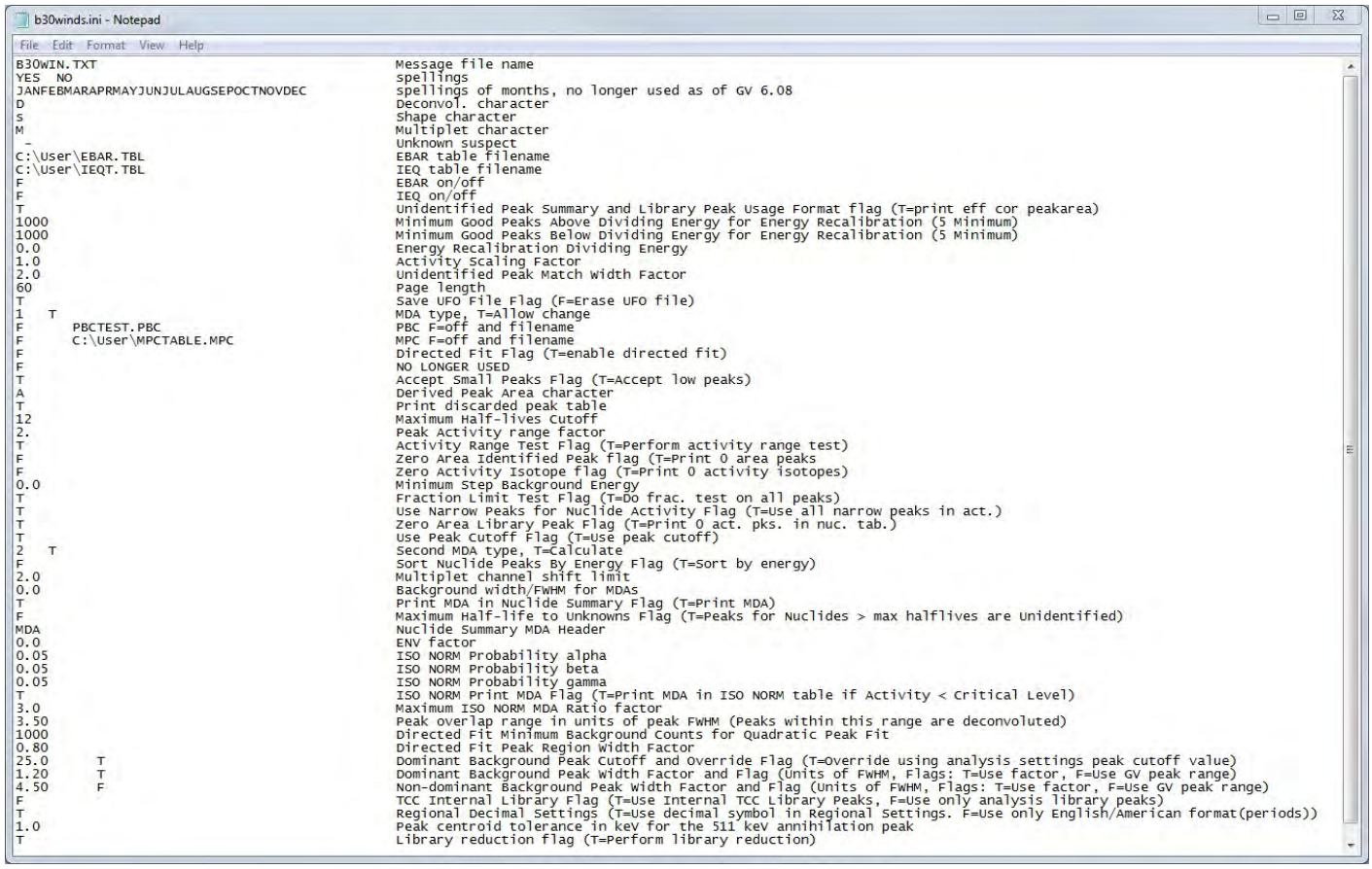


Figure 329. The b30winds.ini File in Notepad.

A.2.2.1. Contents

Except where indicated, all discussion of analysis settings refers to the current (working) settings on the **Analyze/Settings/Sample Type...** tabs or in the selected .SDF file.

Message file name

B30WIN.TXT — The name of the file that defines the standard analysis report format.

spellings

YES NO — Spelling of Yes and No displayed on analysis report under the Corrections Status column. Alternates to English can be substituted.

spellings of months

NO LONGER USED.

Deconvol. character

D — The character in the peak tables indicating that this peak is part of a deconvolution.

Shape character

s — Bad-peak-shape indicator in the peak tables.

Multiplet character

M — The peak table character indicating this peak is part of a multiplet.

Unknown suspect

– — The character in the unknown peak table indicating that this peak was not found in the Suspect Library.

EBAR table filename

C:\User\EBAR.TBL — Filename for the average energy table. The analysis setting overwrites this parameter in most cases. (Included for backward compatibility with older spectrum formats. This setting is used when analyzing .CHN spectra using the **Analyze/ Spectrum on Disk...**(γ) command or when the analysis is performed external to GammaVision.)

IEQ table filename

C:\User\IEQT.TBL — Filename for the iodine equivalence table. The analysis setting overwrites this parameter in most cases. (Included for backward compatibility with older spectrum formats. This setting is used when analyzing .CHN spectra using the **Analyze/ Spectrum on Disk...**(γ) command or when the analysis is performed external to GammaVision.)

EBAR on/off

F — Average Energy flag. The analysis setting overwrites this parameter in most cases. (Included for backward compatibility with older spectrum formats. This setting is used when analyzing .CHN spectra using the **Analyze/ Spectrum on Disk...**(γ) command or when the analysis is performed external to GammaVision.)

T = Perform average energy calculation.
F = Do not perform average energy calculation.

IEQ on/off

F — Iodine Equivalence flag. The analysis setting overwrites this parameter in most cases. (Included for backward compatibility with older spectrum formats. This setting is used when analyzing .CHN spectra using the **Analyze/ Spectrum on Disk...**(ã) command or when the analysis is performed external to GammaVision.)

T = Perform iodine equivalence calculation
F = Do not perform iodine equivalence calculation

Unidentified Peak Summary and Library Peak Usage Format flag

T

T = Print efficiency corrected peak area for unknown peaks instead of net peak count rate and include the nuclide half-life and peak branching ratios in the Library Peak Usage section.
F = Print net peak count rate for unknown peaks instead of efficiency corrected peak area and omit the nuclide half-life and peak branching ratios in the Library Peak Usage section.

Minimum Good Peaks Above Dividing Energy for Energy Recalibration (5 Minimum)

1000 — *This flag does not function in ROI32.* Number of good peaks above the energy calibration dividing point required for an automatic energy recalibration during analysis. The maximum value is 9999.

Minimum Good Peaks Below Dividing Energy for Energy Recalibration (5 Minimum)

1000 — *This flag does not function in ROI32.* Number of good peaks below the energy calibration dividing point required for an automatic energy recalibration during analysis. The maximum value is 9999.

Energy Recalibration Dividing Energy

0.0 — *This flag does not function in ROI32.* Energy calibration dividing point (energy). This value must include a decimal point.

Activity Scaling Factor

1.0 Scaling factor multiplied times nuclide activity in addition to the **Multiplier**, **Divisor**, and **Weight** values specified in the analysis settings. This value must include a decimal point.

Unidentified Peak Match Width Factor

2.0 Range multiplier for listing suspect nuclides in the unknown peak table. For peaks listed in the unknown peak table, the suspect nuclide in the unknown peak table is determined by choosing the closest energy match to the unknown peak that is within *Range Multiplier* * *FWHM* of each peak. This value must include a decimal point.

Page length

60 Page length (in lines) of analysis report.

Save UFO File flag

T If the .UFO file is deleted upon completion of the analysis, some features in GVPlot, the **Display Analysis Results...** command, and updating PBC files will not be not available because these functions rely on information stored in the .UFO file.

T = Do not delete .UFO file after analysis is complete.
F = Erase .UFO file after analysis is complete.

MDA Type, T = Allow change

1 T

T = Allow change and use the **MDA Type** specified in the analysis settings.
F = Do not allow change and always use the MDA number specified on this line, regardless of the analysis settings. The MDA number is based on the order in which MDA methods are listed on the System tab.

PBC F=off and filename

F PBCTEST.PBC

T = Use the PBC file specified here unless a different PBC file is given in the analysis settings. The file must include the full path and is limited to 32 characters total.
F = Do not use a PBC file unless one is specified in the analysis settings.

MPC F=off and filename

F C:\User\MPCTABLE.MPC

T = Use the specified MPC/DAC file unless a different MPC/DAC file is given in the analysis settings.
F = Do not use an MPC/DAC file unless one is specified in the analysis settings.

Directed Fit flag (T=enable directed fit)

F

T = Perform directed fit regardless of analysis setting.
F = Do not perform directed fit unless the option is turned on in the analysis settings.

F

NO LONGER USED

Accept Small Peaks flag

T

If the following three conditions are all true, then an MDA is reported for the peak. Otherwise, an activity calculation for the peak is attempted.

Condition 1 — The peak is too narrow (FWHM or FWTM too narrow)

Condition 2 — This condition is TRUE if the Narrow Peak for Activity Calculation flag is off.

Condition 3 — This condition is TRUE if any one of the following conditions is true:

a) If the area is less than 200 AND the Accept Small Peaks flag is off.
b) The peak area is greater than 300.
c) The background is more than twice the peak area.

Derived Peak Area character

A Character displayed in the unidentified and identified peak summaries.

Print Discarded Peak Table

T

T = Discarded Isotope Peaks table is displayed on the report for all analysis engines except GAM32. (See Section 7.7.9 for more detail related to the Discarded Isotope Peaks Table.)
F = Discarded Isotope Peaks table is suppressed.

Maximum Half-lives Cutoff

12 The Decay-Corrected Activity is flagged as exceeding the half-life cutoff instead of calculating a decay-corrected activity value. The same type of flag is displayed in the Summary of Peaks in Range section. The maximum value is 9999.

Peak Activity Range Factor

2.

This is the uncertainty multiplier used in determining the acceptable activity range per Section 6.7.1. This value must be followed by a decimal point.

Activity Range Test flag

T

T = Use the Activity Range Factor in the previous parameter to determine if a nuclide peak is used to calculate the weighted average nuclide activity.
F = Use all peaks that meet the uncertainty cutoff in determining the weighted average nuclide activity.

Zero Area Identified Peak flag

F

T = Show peaks that are not found in the spectrum (i.e., fail the Peak Cutoff test) in the Identified Peak Summary with the following qualifications for specific analysis engines:

- **WAN32 and ROI**32 — Peak data is displayed for all peaks in the library.
- **GAM32** — Peak data is displayed for all peaks reported, but all library peaks may not be reported depending on peak quality, library content, and analysis settings.
- **NPP32** — Deconvoluted peaks that are rejected may not be included in the peak list. Only the peak background and FWHM is displayed for peaks that do not meet the peak cutoff criteria.
- **ENV32 and NAI32** — Some rejected peaks may be included in the list, but no peak data are displayed.

F = Only show peaks in the Identified Peak Summary that meet the Uncertainty cutoff limit.

Zero Activity Isotope flag

F *This flag functions only for the NPP32, ENV32, and NAI32 analysis engines.* The GAM32, WAN32, and ROI32 analysis engines show all nuclides (even if zero activity) regardless of this flag setting.

T = Show nuclides with no activity reported in the Summary of Library Peak Usage table. This would include all nuclides in the library that were not found during analysis.

F = Only show nuclides in the Summary of Library Peak Usage table that were identified in the analysis. This includes nuclides that had zero activity because the associated peaks were found but moved to the Discarded Peaks Table.

Minimum Step Background Energy

0.0 Sets the lowest energy to use for a stepped background under a multiplet. Typically, this parameter is set greater than zero only when multiplet peaks are found on the rising edge of a peak or continuum that is not compatible with the stepped-background fitting methodology required for fitting small peaks on the high side of larger peaks. This value must include a decimal point.

Fraction Limit Test flag

T *This flag functions only in ENV32 and NAI32.*

T = All nuclide peaks are used for the fraction limit test.
F = Nuclide peaks flagged as “do not include in the average activity” in the library are not used for the fraction limit test.

Use Narrow Peaks for Nuclide Activity flag

T Operates in conjunction with the “Accept Small Peaks” flag (page 444).

Zero Area Library Peak flag

T *This flag applies only to the NPP32, ENV32, and NAI32 analysis engines.* The WAN32, GAM32, and ROI32 analysis engines always display all library peaks.

T = Show peaks with no area in the Summary of Library Peak Usage table. This would include all library peaks that did not pass the analysis settings criteria.
F = Only show peaks in the Summary of Library Peak Usage table that passed the analysis settings criteria, and summarize how many library peaks were found as compared to the number listed in the library for that nuclide (i.e., “X of Y peaks found”) under nuclide peak list.

Use Peak Cutoff flag

T

T = Use Peak Cutoff specified in the analysis settings file to limit peaks used in the analysis to only those that meet the Peak Uncertainty Cutoff limit.
F = Ignore the Peak Cutoff value in the analysis settings and use all peaks found regardless of uncertainty in the analysis.

Second MDA type, T=Calculate

2 T Second MDA Type (see MDA Type above). If set to T, the second MDA type is stored in the .UFO file but it is not printed on the analysis report.

Sort Nuclide Peaks By Energy flag

F *This flag applies only to the WAN32, GAM32, and ROI32 analysis engines.* The NPP32, ENV32, and NAI32 analysis engines always sort peak energy by the library order.

T = Sort peaks in the Summary of Library Peak Usage table by energy
F = Sort peaks in the Summary of Library Peak Usage table by library order.

Multiplet channel shift limit

2.0 The maximum number of channels that multiplet peaks can be shifted in the peak-fit optimization. This value must include a decimal point.

Background width/FWHM for MDAs

0.0 Use this value times the peak FWHM to determine the background area for calculating the MDA. If set to zero, the entire background area for the peak is used to calculate the MDA. (Use zero for old method.) This value must include a decimal point.

Print MDA in Nuclide Summary (T=Print MDA)

T *This parameter does not function in GAM32.* GAM32 does not report MDA for nuclides that have an activity value calculated.

T = Include the MDA in the Summary of Nuclides in Sample table when a nuclide activity value is calculated.
F = The nuclide MDA is not included in the Summary of Nuclides in Sample table when a nuclide activity is calculated.

Maximum Half-life to Unknowns flag

F

T = Treat peaks associated with nuclides exceeding the half-life limit as unknowns.
F = Treat peaks associated with nuclides that exceed the half-life limit as identified peaks rather than unknowns.

Nuclide Summary MDA Header

MDA — MDA column header in "Summary of Nuclides in Sample" section of report. This column header is displayed only if the nuclide MDA column is included in the Summary of Nuclides in Sample table (see the "Print MDA in Nuclide Summary" flag above).

ENV factor

0.0 — *This flag functions only in ENV32, GAM32, and NAI32.* Nuclide rejection factor. In the library reduction algorithm, it is used to remove nuclides from the analysis library. If set to a lower value, more nuclides will likely be removed/dropped from the library (see Section 6.2.3 for details on how this factor is used). This value must include a decimal point.

ISO NORM Probability alpha

0.05 — Probability variable á for the ISO NORM calculations. See also the "b30winds.ini" discussion on page 157. This value must include a decimal point.

ISO NORM Probability beta

0.05 — Probability variable â for the ISO NORM calculations. See also the "b30winds.ini" discussion on page 157. This value must include a decimal point.

ISO NORM Probability gamma

0.05 — Probability variable ä for the ISO NORM calculations. See also the "b30winds.ini" discussion on page 157. This value must include a decimal point.

ISO NORM Print MDA flag

T — T = Report the MDA if the critical level is greater than the activity.
F = Always report the activity and the associated uncertainty.

Maximum ISO NORM MDA Ratio factor

3.0 The maximum ratio of ISO NORM Detection Limit (MDA) to ISO NORM Decision Threshold (Critical Level). This ratio is used to calculate the “fmax” term, which limits the maximum ISO NORM Detection Limit (MDA); see page 318. This value must include a decimal point.

Peak overlap range in units of peak FWHM

3.5 Peaks within FWHM times the Peak Overlap Range Factor plus peak background points are deconvoluted. This value must include a decimal point. The minimum value is 1.0. Default for n30winds.ini is 2.0.

Directed Fit Minimum Background Counts for Quadratic Peak Fit

NO LONGER USED

Directed Fit Peak Region Width Factor

1.00 Range factor used in the Directed Fit peak width determination. See Section 6.3.2.2. This value must include a decimal point. The maximum value is 9999.

Dominant Background Peak Cutoff and Override flag

25.0 T If the peak uncertainty exceeds this value at 1 sigma, then background dominates with regard to the next two parameters below. The flag, True by default, specifies whether to override this value with the Peak Cutoff from the analysis options (i.e., same criterion as acceptable peak determination). To set a different criterion for Dominant Background, set the flag to False and specify the Dominant Background peak cutoff criterion. This value must include a decimal point.

Dominant Background Peak Width Factor and flag

1.20 T FWHM multiplier dictates the peak integration range (i.e., 1.2 * FWHM) when background is dominant. When the flag is set to True, the fixed width factor is used to determine peak background when the peak is not part of a multiplet. When the flag is set to False, the background is determined by the normal GammaVision peak integration calculation. The fixed width background is typically more representative when background is dominant. This value must include a decimal point.

Non-dominant Background Peak Width Factor and flag

4.5 F — FWHM multiplier dictates the peak integration range (i.e., 4.5 * FWHM) when background is not dominant. When the flag is set to True, the fixed width factor is used to determine peak background when the peak is not part of a multiplet. When the flag is set to False, the background is determined by the normal GammaVision peak integration calculation. The GammaVision peak integration is typically more representative when background is not dominant (i.e., when peaks meet the acceptance criteria). This value must include a decimal point.

TCC Internal Library Flag

F — T = Use Internal TCC Library Peaks
F = Use only peaks from the library in the analysis

Regional Decimal Settings

T — T = Use decimal symbol in Regional Settings.
F = Use period for the decimal symbol regardless of Regional Settings.

511 kev Peak Centroid Tolerance

1.0 — Peaks with a centroid in the range of 511 kev plus or minus this tolerance factor (in kev) use a FHWM wider than the calibration for the peak fit.

Library Nuclide Reduction Flag (GAM32, ENV32, and NAI32 Only)

T — T = Remove nuclides from the analysis that fail the key line or fraction limit test based on the initial Mariscotti Peak Search. The ENV Factor test is unaffected by this setting. (Default for b30winds.ini)
F = Library Nuclide Reduction by Key Line and Fraction Limit tests are disabled (Default for n30winds.ini)

Library Peak Reduction Flag (GAM32, ENV32, and NAI32 Only)

T — T = If the Library Nuclide Reduction Flag is set to True, then remove any peaks not found by the initial Mariscotti Peak Search from the analysis.
F = Library Peak Reduction is disabled (Default)

Library Peak Critical Level Test Flag (GAM32, ENV32, and NAI32 Only)

T — T = Secondary nuclide peaks that have a calculated area based on the nuclide average which is less than the calculated critical level at that energy will not be associated with the target nuclide. (Default for b30winds.ini)
F =Peaks will be associated with a nuclide even if the peak area is expected to be less than the critical level based on the average nuclide activity. (Default for n30winds.ini)

Non-Directed Fit Maximum Activity Range

100.0 This is the maximum activity range specified as a percentage of the first peak activity when Directed Fit is not enabled in the analysis settings. A value of zero disables the maximum range test. (See Section 6.7.1.)

Directed Fit Maximum Activity Range

0.0 This is the maximum activity range specified as a percentage of the first peak activity when Directed Fit is enabled in the analysis settings. A value of zero disables the maximum range test. (See Section 6.7.1.)

[Intentionally blank]

APPENDIX B. FILE FORMATS

This appendix describes the file structure for the GammaVision program files. See the *ORTEC Software File Structures Manual for DOS and Windows Systems* for complete descriptions of the formats for these files, including .SPC, .CHN, and .UFO files. The .LIS file format is instrument-specific; see the hardware manual for your MCB. The .SPE file format is based on the IAEA ASCII file format recommendation for gamma spectrometers; see the *File Structures Manual* for details.

B.1. GammaVision File Types

B.1.1. Detector Files

.CFG "ConFiGuration"; System Detector configuration information used by GV32.EXE; binary format.

.CXT "ConteXT"; For each Detector/Device a context file is automatically created to remember all extra information required for analyses and calibration; binary format.

.SDF "Sample type defaults"; Created by the **Analyze/Settings/Sample Type...** command; binary format.

B.1.2. Spectrum Files

.CHN "CHaNnels"; MAESTRO-style spectral data file; binary format.

.SPC "SPeCtrum"; spectrum with full analysis settings, calibration, descriptions, etc; "Inform" type binary format.

.AN1 Alternate name for spectrum files used for analysis, when the .SPC name is already in use; same format as .SPC.

B.1.3. Miscellaneous Files

.CLB "CaLibration"; full energy/efficiency calibration; "Inform" style binary format.

.LIB "LIBrary"; nuclide library; "Inform" style binary format.

.ROI "ROI"; channel pairs created by the **ROI/Save File...** function; binary format.

.UFO "UnFormatted Output"; analysis results; "Inform" style binary format.

.EFT "EFficiency Table"; used for efficiency **Calibrate/Recall Calibration...** function (and created with the **Save...** button on the Efficiency Calibration Sidebar); formatted ASCII text (also, lines that do not begin with numeric values are ignored).

.ENT "ENergy Table"; used for energy **Calibrate/Recall Calibration...** function (and created with the **Save...** button on the Energy Calibration Sidebar); formatted ASCII text (also, lines that do not begin with numeric values are ignored).

.RPT "RePorT"; output of analysis engine; ASCII text.

.TXT "TeXT"; general ASCII text files used by **File/Print...**.

.JOB ASCII text providing commands for **Services/JOB Control...** function.

.DAC "Derived Activity Calculation"; values for the DAC or MPC calculation.

.EBR Average energy tables for the EBAR calculation.

.ATT "ATTenuation" database files.

.GEO "GEOmetry correction"; used for geometry correction function.

.IEQ "Iodine EQuivalence"; table values for the IEQ calculation.

.PBC "Peak Background Correction"; table values for the PBC.

B.1.4. QA Database Files

.MDB Microsoft Access database file extension.

B.2. Database Tables for GammaVision QA

B.2.1. QA Detectors Detector Table

(Only one of these tables for entire database; one record for each detector being monitored for QA, with fields defined as follows.)

Field Name	SQL Data Type	Description
Detector	SQL_INTEGER	Detector ID number. (Primary Key)
DetName	SQL_CHAR (32)	Detector Pick List Name
DetDesc	SQL_CHAR (64)	Detector Description

Creation	SQL_TIMESTAMP	Date/Time this record created
NumMeas	SQL_INTEGER	Measurement counter (all types) for this detector
NumBack	SQL_INTEGER	Background type only Measurement counter for this detector
SamFile	SQL_CHAR (64)	Sample Type File Name
SamType	SQL_CHAR (64)	Sample Type Description
LibFile	SQL_CHAR (64)	Nuclide Library File Name
Setup	SQL_SMALLINT	Setup Flagword
Limits	SQL_SMALLINT	Limit Settings Flagword
MinBack	SQL_REAL	Min. Background CPS Acceptance Limit
LowBack	SQL_REAL	Low Background CPS Excursion Warning Level
BigBack	SQL_REAL	High Background CPS Excursion Warning Level
MaxBack	SQL_REAL	Max. Background CPS Acceptance Limit
MinActivity	SQL_REAL	Min. Total Activity Acceptance Limit
LowActivity	SQL_REAL	Low Total Activity Excursion Warning Level
BigActivity	SQL_REAL	High Total Activity Excursion Warning Level
MaxActivity	SQL_REAL	Max. Total Activity Acceptance Limit
MinShift	SQL_REAL	Min. Average Peak Shift Acceptance Limit
LowShift	SQL_REAL	Low Average Peak Shift Warning Level
BigShift	SQL_REAL	High Average Peak Shift Warning Level
MaxShift	SQL_REAL	Max. Average Peak Shift Acceptance Limit
MinFWHM	SQL_REAL	Min. Average FWHM Ratio Acceptance Limit
LowFWHM	SQL_REAL	Low Average FWHM Ratio Warning Level
BigFWHM	SQL_REAL	High Average FWHM Ratio Warning Level
MaxFWHM	SQL_REAL	Max. Average FWHM Ratio Acceptance Limit
MinFWTM	SQL_REAL	Min. Average FWTM Ratio Acceptance Limit
LowFWTM	SQL_REAL	Low Average FWTM Ratio Warning Level
BigFWTM	SQL_REAL	High Average FWTM Ratio Warning Level
MaxFWTM	SQL_REAL	Max. Average FWTM Ratio Acceptance Limit
Operator	SQL_CHAR(64)	User name last entered on the System tab under **Analyze/Settings/Sample Type...** at start of latest measurement

B.2.2. Application Information Table

(One of these tables for entire database; one record for GammaVision.)

Field Name	SQL Data Type	Description
ModelNumber	SQL_LONG	Product Model No.(i.e., 66)
SerialNumber	SQL_CHAR(32)	Product Serial No.
AppName	SQL_CHAR(16)	Application Name (i.e., "GammaVision")
AppVersion	SQL_CHAR(8)	Version/Revision (i.e., "2.22" or greater)
Laboratory	SQL_CHAR(64)	Laboratory name entered under GammaVision's system dialog

B.2.3. M...d Measurements Table(s)

(Where "...d" is the detector number in decimal from the Detectors table above. There is one of these tables for each detector, covering all measurements, whether background or standard sample type. The total number of records in this table is denoted by NumMeas in the Detectors table, which is also the measurement number of the last record in this table. The records are stored sequentially by measurement number.)

Field Name	SQL Data Type	Description
Measurement	SQL_INTEGER	Measurement Number (Primary key)
MeasTime	SQL_TIMESTAMP	Date/Time for this measurement
MeasType	SQL_SMALLINT	Activity analysis (1) or Background (0)
LiveTime	SQL_REAL	Acquisition Live Time in Seconds
CountRate	SQL_REAL	Background CPS (only for Background measurement)
Activity	SQL_REAL	Total Activity
PeakShift	SQL_REAL	Average Peak Shift
FWHMRatio	SQL_REAL	Average FWHM Ratio
FWTMRatio	SQL_REAL	Average FWTM Ratio

B.2.4. P...dmmmm Peaks Table(s)

(Where "...d" is the detector number in decimal, "mmmm" is the measurement number to 4 places. There is one of these tables for each measurement in the table above, but only if the output of actual centroid energies is enabled.)

Field Name	SQL Data Type	Description
PeakNumber	SQL_INTEGER	Peak No. counter (Primary key)
PeakFlags	SQL_INTEGER	Analysis Results Flags
Nuclide	SQL_CHAR(8)	Library Nuclide Name this peak belongs to
Energy	SQL_REAL	Library Energy
Centroid	SQL_REAL	Actual Centroid Energy
CalFWHM	SQL_REAL	Expected (Calibrated) FWHM at this energy
FWHM	SQL_REAL	Actual FWHM
FWTM	SQL_REAL	Actual FWTM
Area	SQL_REAL	Net counts in peak
Background	SQL_REAL	Background counts

[Intentionally blank]

APPENDIX C. ERROR MESSAGES

Errors are displayed in popup warning boxes, the lower-left corner of some MCB Properties dialogs, and the supplementary information line at the bottom of the window.

Acquisition Failure (JOB Error 11)
For some reason an acquisition function failed from a .JOB file.

Already started.
Detector already active when a Start Acquisition command was issued.

Altering Detector data.
Restoring data to a Detector would destroy the data already there.

Amplifier not pole-zeroed.
Warning from an MCB with automatic pole zero, indicating that the Detector should be pole-zeroed.

Analysis Completed for ...
WAN32.EXE has finished executing.

Analysis Error <n>
A call to DLAN1.DLL has been completed, but an error was encountered. The error code <n> has the following meaning:

Error #	Warning #	Reason
1	1	Read error in UFO peak record
1	2	Read error in UFO nuclide record
2	1	Write error in UFO peak record
2	2	Write error in UFO nuclide record
3	1	Invalid acquisition date and time
4	0	Illegal absorption correction
5	1	Read error in spectrum file

Analysis Failed!
WAN32.EXE has finished executing, but an error was encountered. Refer to the "WAN32 completion codes..." message.

Analysis Failed (Job Error 18)
The ANALYZE(ã) command failed (look for the WAN32 error code for specifics).

Analyzing (Please Wait) ...
Analysis via DLAN1.DLL is being executed.

Attempt to dynamically link to a task! (WinExec error 5)
Error encountered trying to spawn WAN32.EXE or some other application program.

Auto Calibration failed (Job Error 21)
An error occurred when the CALIBRATE_AUTO command was executed.

Auto PZ aborted.
The MCB Auto PZ function was aborted (by **<Esc>**).

Buffer and Detector not same size or segments.
Error when trying to restore data that does not match the Detector configuration.

Calibration per channel wrong.
Error when trying to calibrate spectrum, arising whenever the calibration slope would be 0, negative or greater than 100 units per channel.

Can't allocate memory for library.
Attempting to load a library for which there is not enough room in memory. Best dealt with by trying again or removing some other applications from memory.

Can't find any more peaks!
A peak could not be found in the direction indicated by the function button pressed.

Can't Find Any More ROIs.
Attempting to index to the next ROI in a direction for which no more ROIs can be located.

Can't read library file.
Attempting to open or read the library file resulting in some kind of file I/O error, usually because the file doesn't exist, but also possibly because the disk is defective.

Can't RESTORE to acquiring Detector.
Error preventing the Restore function from altering data in a Detector in which one or more segment(s) are actively acquiring data.

Can't Run Protected Mode Application in Real Mode!
(WinExec error 18)
Error encountered trying to spawn WAN32.EXE or some other application program.

Can’t Run Second Instance of this .EXE (multiple writeable data segments)! (WinExec error 16)

Error encountered trying to spawn WAN32.EXE or some other application program.

Can’t Run Second Instance of this .EXE (Non-shareable DLL in use)! (WinExec error 17)

Error encountered trying to spawn WAN32.EXE or some other application program.

Cannot get valid Spectral Data!

The File/Save function was not presented with valid spectral data; usually the result of problems obtaining data from a Detector.

Comm. Failure!

Detector communication failure, most likely resulting from a timeout (the Detector failed to respond within a reasonable period of time).

Configuration failed!

Attempted reconfiguration failed, most likely because of some conflict with Detectors physically installed.

Could not properly fit the peak.

Function requiring a fitted peak could not obtain an acceptable peak, probably because of too few counts, too narrow, or non-Gaussian peak shape, or bad statistics such as calculated sigma-squared less than zero.

Couldn’t get background subtracted ROI.

A function requiring a background subtracted ROI couldn’t obtain such, probably because there was no ROI at the point specified, or maybe because there weren’t statistically significant counts above background.

Default Printer Failed! Undefined at Control Panel?

The REPORT or PRINT function was aborted because the default system printer has not been properly set up. Go to the Printers function in Windows Control Panel, install the appropriate printer, and select it as outlined in the Microsoft Windows documentation.

Detector #.. ; ..... ; Error ... (Macro) ... (Micro)

An unresolved error originating in the Detector. The offending Detector command is shown, together with the macro and micro error codes. If the error persists, the error codes should be recorded and the factory should be contacted. These error codes are explained in the hardware manual for the Detector.

Detector busy or Segment not responding.

This indicates the Detector was unable to respond within a certain time limit, due to other activities, such as multiple instances of GammaVision accessing the Detector at the same time, or otherwise heavy use of the Detector interface.

Detector does not support Field Mode (Job Error 19)

An attempt was made to execute the LOOP_SPECTRA or VIEW command on a Detector that does not support Field Mode.

Detector Error!

The selected Detector could not be STARTed or STOPped due to some unresolved error condition.

Detector Not Located.

A Detector could not be located at the configured address.

Do you want to save buffer?

A function that would destroy the buffer (such as COPY or EXIT) queries the user unless the buffer has not been modified since last being saved.

Do you want to save Library?

The nuclide library has been modified by the library editor, but the user has not yet saved the changes.

DOS 4.0 Application! (WinExec error 13)

Error encountered trying to spawn WAN32.EXE or some other application program.

Error opening file.

If trying to write a file, this would indicate a disk controller problem such as a full disk. If trying to read a file, this would indicate that the filename specified could not be found.

Error reading file -- STRIP aborted.

Could not read the file requested for stripping.

Error reading file.

File read error is usually a result of damaged media.

Error writing file.

File write error is usually a result of damaged media or full disk.

.EXE for earlier version of Windows! (WinExec error 15)

Error encountered trying to spawn WAN32.EXE or some other application program.

Failure obtaining ROI (or Peak).

A function that requires a defined ROI (or Peak, in the case of the Calibrate function) when the marker is not placed in a channel with an ROI bit set (and if a Peak is not very close by).

Failure of Detector function (JOB Error 12)

This error arises from a JOB that encounters an error when trying to access a Detector.

File already exists!

If the file output function requested would write a file with the same name as another file that already exists, the user is prompted for confirmation of the operation by this warning. See also “OK To Overwrite Existing File?”

File is wrong size Can’t STRIP.

The STRIP function requires a compatible file for stripping from the spectrum in memory; i.e., must contain the same number of channels.

File Not Found! (WinExec error 2)

Error encountered trying to spawn WAN32.EXE or some other application program.

Fine gain is at limit of ...

This message appears in the Information Line when an attempt is made to change the MCB gain setting with the keyboard function, but while the MCB cannot be decreased or increased any further.

FWHM Fit Error Exceeds 25%.

The peaks entered in an energy calibration produced a FWHM fit with an error on at least one peak greater than 25%.

Hardware failure!

This message appears as the result of a Detector execution error with micro code 137, indicating a hardware failure.

High voltage not enabled.

START was attempted on a 92X while the high voltage was not enabled.

Illegal Entry!

Certain values are not permitted in manual dialog entries or tables.

Illegal Detector.

The Detector number for the requested function was not identifiable as part of the active configuration.

Incorrect Windows Version! (WinExec error 10)

Error encountered trying to spawn WAN32.EXE or some other application program.

Insufficient memory.

System memory has been exhausted. Usually, this error arises when the buffer cannot be created due to insufficient available memory in the system. Sometimes this error can be eliminated by attempting the buffer operation again, but this is not recommended due to the marginal state of the system, which might result in other errors.

Invalid Argument (Job Error 17)

The ROI limits in SET_PRESET_UNCERTAINTY command were invalid. The VIEW command specified a spectrum that was not stored in the Detector. The ZOOM command did not specify valid integers.

Invalid Command or Missing Argument. (JOB Error 4)

A syntax error in a JOB, meaning that a command could not be interpreted; usually the result of misspelling.

Invalid Device or Segment!

This message arises as a result of a Detector execution error with micro code 134, indicating that an invalid device or Segment was selected.

Invalid .EXE file! (WinExec error 11)

Error encountered trying to spawn WAN32.EXE or some other application program.

Invalid File Format!

A function to recall a file could not obtain data in the proper format.

Invalid library format!

An attempt was made to load a nuclide library from a file that was not in the proper format.

Invalid LOOP count. (JOB Error 7)

The LOOP statement could not be executed properly in a JOB.

Invalid Start Date/Time -- Battery Backup Lost??

A 919 or 92X Detector contained an unrecognizable start date. This is usually an indication that the backup power was lost.

Invalid Start Record.

No valid Start Record file could be found to provide the start date/time for an installed 917 or 918 Detector.

JOB Aborted or Premature EOF (JOB Error 1)

A JOB was aborted by the user, or an End-of-File was encountered while trying to obtain a command from the executing .JOB file.

JOB Error.

A generic error message indicating that an error was encountered while executing a .JOB file. Usually some explanatory phrase is given.

Library requires separate data segments for each task!
(WinExec error 6)

Error encountered trying to spawn WAN32.EXE or some other application program.

Library too large to load.

Library files larger than 65,000 bytes are not admissible as internally resident libraries. (However, any size library can be used for Master Library.)

Multiple-device Detector added.

While performing the CONFIGURATION dialog function ADD, a 919 device type was specified, and there is room to add up to four Detectors for each 919 device added; the ADD function is automatically repeated for each possible Detector number.

Must have a value greater than zero!

Certain analysis or library table entries require values greater than 0.0.

Must have valid calibration!

Certain analysis functions cannot be performed if the calibration is invalid.

Must select 92X type Detector!

This error results from an attempt to perform a function available for only 92X-type Detectors.

Need an ROI at the desired peak location.

The Stabilizer function requires a valid ROI at the desired peak.

No Buffer to RESTORE from!

The RESTORE function requires a valid spectrum in buffer.

No close library match.

The REPORT function could not obtain a library entry close enough to the located peak.

No File Name.

A file function was requested without specifying the filename adequately.

No more library peak energies!

A peak search was attempted in a direction where no more can be found.

No more multiplets!

The multiplet finding sidebar function in Analysis Results display mode cannot find any more multiplets in the direction indicated.

No more peaks for this nuclide!

The “peaks within nuclide” sidebar function in Analysis Results mode cannot find any more peaks within the selected nuclide.

No more unknown peaks!

The unknown peak finding sidebar function in Analysis Results display mode cannot find any more unknown peaks in the direction indicated.

No peaks found!

The peak search function could not find any valid peaks in the spectrum.

No ROI found to report!

The REPORT function could not find any ROIs in range.

No ROI There To Clear.

The **Clear ROI** function (the **<Del>** or **<Delete>** key) requires at least one channel at the marker with the ROI bit set.

No segment selected.

The Detector function could not be performed because no Segment was selected.

Not Allowed During Acquisition!

An execution error (micro 135) arising from the Detector, indicating that the Detector command is not allowed while acquisition is in progress.

Not Allowed During Current Mode!

An execution error arising from the Detector (micro 136), indicating that the Detector command attempted is not allowed in the current mode of operation.

Not enough data points for fit.

Efficiency calibration fit for specified type requires a minimum number of table entries for that type; e.g., for a polynomial fit, six or more points are required.

Not enough memory STRIP aborted.

The STRIP function temporarily allocates enough memory to read the file, but the allocation failed in this case, probably due to insufficient available memory in the system. The STRIP function is discontinued.

Not enough memory for COMPARE.

The COMPARE mode could not be executed due to insufficient memory for the second spectrum.

NOTE: Settings for SEGMENT <n>

GammaVision is informing the user in the case of multi-segment Detector that he is performing settings (e.g., through an ASK function) on a specific segment only.

OK to add another device?

When a 919 device is being added in the CONFIGURATION dialog, the user is prompted for confirmation before automatically proceeding with the addition of up to four Detector numbers.

OK to attempt another instance?

Attempt to start an analysis (via WAN32.EXE) while a previous analysis has not yet finished, or had been aborted abnormally. GammaVision is asking the user to allow it to continue with this operation in case it is not properly sensing the state of the previous analysis. If the user permits this to continue (by answering Yes), but if the previous instance was actually still running, then another "WinExec()..." error will occur.

OK to destroy contents of Detector?

The RESTORE function prompts the user for confirmation before writing the contents of the buffer into the Detector.

OK to overwrite '...' ?

A file output function discovered that the specified filename already exists, and will only overwrite the file after the user confirms his intentions. See also "File already exists!"

OK to save changes?

The user is being prompted to allow the system to save a modified file such as a library file, table file, or sample-type defaults file.

OK to use it anyway?

A new configuration was applied but failed due to some conflict with the Detectors physically present; it is possible to use the configuration anyway by answering Yes to this query.

OS/2 Application! (WinExec error 12)

Error encountered trying to spawn WAN32.EXE or some other application program.

Out of Memory! (WinExec error 0)

Error encountered trying to spawn WAN32.EXE or some other application program.

Path Not Found! (WinExec error 3)

Error encountered trying to spawn WAN32.EXE or some other application program.

Peak rejected for asymmetry.

Peak statistics could not be obtained for the function due the calculated non-Gaussian asymmetry of the obtained peak.

Preset already reached.

Acquisition START was attempted on a Detector or Segment that had already satisfied the preset condition(s) in some way.

Presets can’t be changed during acquisition.

Changes in the preset condition(s) are not allowed while the Detector is actively acquiring.

Presets not programmed to Detector correctly!

Usually a failure of the selected Detector to accept the commands from GammaVision to program presets. Often the result of improper configuration or faulty interface.

Previous analysis did not run to completion!

Attempt to start an analysis (via WAN32.EXE) while a previous analysis has not yet finished, or had been aborted abnormally. See “OK to attempt another instance?”

Problem with Buffer. (JOB Error 2)

A JOB error resulting from some problem with the buffer, usually indicating insufficient memory to create or enlarge the buffer as needed.

Problem with Calculation. (JOB Error 13)
A JOB error resulting from a problem with a calculation.

Problem with RECALL. (JOB Error 10)
The RECALL statement could not be executed in a JOB.

Problem with REPORT. (JOB Error 14)
The REPORT function could not be exercised in a JOB.

Problem with SAVE. (JOB Error 9)
The SAVE function could not be executed in a JOB.

QA failed (Job Error 22)
An error occurred when the QASAMPLE(ã) or QABACKGROUND(ã) command was executed.

Sample Changer Hardware Failure. (JOB Error 16)
The Sample Changer hardware handshake failed in some way; usually the result of too much time before SAMPLE READY is obtained.

Start/Save/Report sequence aborted!
Start/Save/Report(ã) sequence aborted (usually by manual intervention, but also resulting from certain errors.)

Start/Save/Report waiting for completion of previous analysis...
A status message indicating that the **Start/Save/Report**(ã) sequence has been suspended while waiting for completion of an ongoing analysis.

Table is Full!
A limit of 96 entries is allowed in the calibration table.

There are no stored spectra to view (Job Error 20)
An attempt was made to execute the LOOP_SPECTRA or VIEW command on a Detector that does not have any stored spectra.

The Serial I/O Command timed out (Job Error 24)
The WAIT_SERIAL command timed out before receiving a response from the selected Detector.

The Serial I/O Response did not match (Job Error 25)
The WAIT_SERIAL command did not time out, however, the actual and expected responses did not match.

The WAIT program was not started by GammaVision (Job Error 23)

All programs "WAITed for" have to be started by GammaVision.

Token Error.

A token error in a JOB, meaning that some argument to the command was invalid or out of context.

Unable to CALL -- Invalid file name. (JOB Error 8)

A JOB error resulting from a problem with the CALL function (usually because the file does not exist).

Unable to COMPARE files of different sizes.

The COMPARE function requires compatible files.

Unable to cut peak or peak not selected!

The library editor **Cut** function or Analysis Results **Delete** library peak function is complaining that it cannot cut or delete a peak from the library for some reason, usually because a peak is not selected.

Unable to open file -- STRIP aborted.

The STRIP function is aborted if the file cannot be read.

Unable to open file for COMPARE.

The COMPARE function is aborted if the second spectrum cannot be read.

Unable to Read Specified File. (JOB Error 3)

A file input/output error encountered while executing a JOB.

Unable to RUN non-executable program. (JOB Error 6)

The specified program could not be RUN from a JOB.

Unable to strip Detector memory.

The stripping function must be performed in the buffer.

Unknown .EXE type! (WinExec error 14)

Error encountered trying to spawn WAN32.EXE or some other application program.

Unknown (misspelled) Command. (JOB Error 5)

A command in a .JOB file could not be executed because it could not be interpreted as a valid command (usually a result of misspelling).

WAIT program was not started by GammaVision (JOB Error 23)

All programs "WAITed for" have to be started by GammaVision. In 32-bit Windows, the 32-bit programs are completely independent.

WAN32 completion codes: i=<i> errnum=<e> warnum=<w>

The following numbers are returned by the analysis routines and displayed on the information line.

Error #	Warning #	Reason
1	?	Invalid spectrum filename
1	1	Read error in UFO peak record
1	2	Read error in UFO nuclide record
1	3	Read error in spectrum non-data record
1	4	Read error in UFO file
1	200	Attempt to read start channel after stop channel
1	201	Read error on disk for .CHN files
1	202	Read error on disk for .SPC files
1	203	Attempt to read invalid spectrum file type
2	0	Illegal filename
2	1	Write error in UFO peak record
2	2	Write error in UFO nuclide record
2	3	Write error in other UFO records
2	4	Invalid record for UFO file
2	7	Write error on report file
2	8	Invalid record request for table file
3	0	Invalid acquisition date and time
4	0	Illegal absorption correction
4	3	Spectrum not found
5	0	Read error in spectrum file
5	3	Spectrum wrong file type
6	1	Library not sorted
6	2	Read error on library
6	3	Invalid record request for library
6	4	Library not found
10	Error #	System error (e.g., math overflow)

Warning 128.
Warning 64.
Warning 8.

All three of the above messages are the result of Detector Start or Stop warnings and are hardware dependent.

Warning: Buffer was modified.

When the program is being closed, this message will appear if the buffer spectrum had been modified but not yet saved to disk. Thus the user is prompted for confirmation of possibly saving the buffer before proceeding to terminate the application.

Warning: File Changes.

The table editor sensed that modifications were made, but the user had not saved the file. See “OK to save changes?”

Warning: Library was modified.

The library was edited or modified for analysis but not yet written to a file. See “OK to save changes?”

Warning: Sample Type Defaults changed

Sample type defaults have been modified but not yet written to selected file. See “OK to save changes?”

WinExec() Error <n>!

Error encountered trying to spawn WAN32.EXE or some other application program; refer to Windows SDK documentation for meaning of code <n>.

[Intentionally blank]