

# QuantaSmart™

for the Tri-Carb® Liquid Scintillation Analyzer

(Models 4810TR, 4910TR, 5110TR, and Quantulus™ GCT  
6220)

## Reference Manual



**PerkinElmer®**

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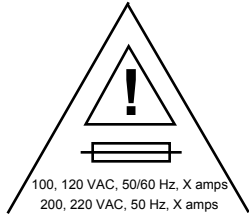
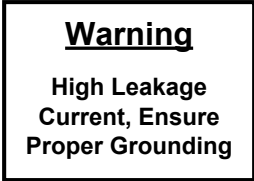




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## Explanation of Symbols

## Signification des symboles

## Erklärung der Symbole

Symbol	Symbol	Symboles	Beschreibung
	Alternating current	Courant alternatif	Wechselstrom
	Protective Earth Ground	Mise à la terre	Schutz - Erdung
	On (Supply)	Marche (alimentation)	Ein
	Off (Supply)	Arrêt (alimentation)	Aus
	Caution - Risk of Electrical Shock	Attention: Risque de choc électrique	Vorsicht - Gefährliche Spannung
	Caution (refer to accompanying documents)	Attention: Voir les documents ci-joints	Vorsicht - Siehe Begleitinformation
	Serial Out	Sortie série	Serieller Ausgang
	Printer	Imprimante	Drucker
	Monitor	Moniteur	Bildschirm

Symbol	Symbol	Symboles	Beschreibung
	Fuse Label / Current Warning	Étiquette d'avertissement relatif au type et au courant du fusible	Sicherung/ Stromstärke
	Warning High Leakage Current, Ensure Proper Grounding	Avertissement: Courant de fuite élevé, Mettre correctement à la terre	Warnung: Hoher Leckstrom- Ordnungsgemäße Erdung sicherstellen
	Warning Laser Product Avoid Direct Exposure to Beam	Avertissement: Appareil à laser exposition au faisceau dangereuse	Warnung: Laserstrahlung, nicht in den lichtstrahl blicken, unsicht bare laserstrahlung.
	Pinch Hazard	Pincement Hasard	Vorsicht- Verletzungsgefahr!
	Hot Surface	Surface Chaude	Heiße Oberfläche
	Waste Electrical & Electronic Equipment	Dispositions Relatives à La Composition Des Équipements Électriques et Électroniques	Überschüssige elektrische und elektronische Ausrüstung

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## Regulatory Compliance

This equipment must be used only by authorized personnel, in a controlled laboratory environment.

Refer all detailed questions to the PerkinElmer, Inc., Operation and Reference manuals.

This equipment must only be used with IEC listed accessories (computer, printer, monitor, etc.).

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## RFI Compliance

This equipment has been tested and found to comply with the limits of IEC 61326-1: Edition 2.0 2012.

Any changes or modifications not expressly approved by PerkinElmer, Inc., could adversely affect compliance.

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Use only shielded interface cables with this equipment.

If the instrument is received in a damaged condition, request an immediate inspection by the carrier and local technical service representative. PerkinElmer, Inc., is not responsible for damage occurring during transit. However, PerkinElmer, Inc., will assist in ensuring a satisfactory settlement from the carrier.

Upon receipt of all damage/inspection reports, PerkinElmer, Inc., will arrange for either instrument repair or replacement.

For proper ventilation of this equipment, a distance of 15cm must be maintained from this unit to any other surface.



*Warning: If the equipment is used in a manner not specified herein, the protection provided by the equipment may be impaired.*

---

Ce matériel doit être utilisé seul par Personnel autorisé, a commandé dans un l'environnement du Laboratoire.

Reportez à toutes questions détaillées au PerkinElmer, Inc., et manuels de la Référence.

Reportez à tout service, a formé à un PerkinElmer, Inc., le personnel du service seul.

Ce matériel, faut seul est utilisé avec IEC a Inscrit des Accessoires. (Ordinateur, Imprimeur, Moniteur, [etc]).

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## RFI Acquiescement

Ce matériel a été testé et a trouvé conformer à avec les limites de IEC 61326-1: Edition 2.0 2012.

Tous changements ou modifications pas expressément approuvé Instrumente par PerkinElmer, Inc., pouvait, [incorrigeable] effectue l'acquiescement.

Utilisez seul a protégé des câbles de l'interface avec ce matériel.

Si l'instrument est reçu dans une condition endommagée, demande une inspection immédiate par le porteur et représentant du service local technique. PerkinElmer, Inc., n'est pas responsable pour dégât produit pendant passage. De quelque manière que, PerkinElmer, Inc., aidera dans assurer un règlement satisfaisant du porteur.

Rapporte sur reçu de toute inspection du dégât, PerkinElmer, Inc., arrangera la réparation de l'instrument a l'un ou l'autre ou remise en place.

Pour ventilation adéquate de ce matériel, une distance de 15cm doit être maintenue, de cette unité à toute autre surface.



*Avertissement: Si cet appareil est utilisé d'une façon non spécifiée dans le présent document, la protection qu'il procure pourrait s'en trouver altérée.*

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Bitte nur gleichwertige Ersatzsicherungen des angegebenen Typs verwenden.

Das Gerät erst nach der Einarbeitung durch einen von PerkinElmer, Inc., geschulten Vertreter benutzen.

Reparatur- und Servicearbeiten sind nur von durch PerkinElmer, Inc., geschulten Personen durchzuführen.

An das Gerät darf nur IEC-registriertes Zubehör angeschlossen werden (Computer, Drucker, Monitor usw).

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## **Funktstörung**

Das Gerät wurde getestet und entspricht den Vorschriften von IEC 61326-1: Edition 2.0 2012.

Durch Änderungen oder Umbauten, die nicht ausdrücklich von PerkinElmer, Inc., genehmigt wurden, wird die Zulassung u.U. hinfällig.

Mit diesem Gerät nur isolierte Schnittstellenkabel verwenden.

Weist das Gerät bei der Entgegennahme Schäden auf, verlangen Sie bitte eine sofortige Inspektion durch den Spediteur und den zuständigen Kundendienstvertreter. PerkinElmer, Inc., ist für Transportschäden nicht haftbar,

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setzt sich jedoch gern dafür ein, mit dem Spediteur eine befriedigende Lösung auszuarbeiten.

Nach Eingang aller Schadens- und Inspektionsberichte veranlaßt PerkinElmer, Inc., entweder die Reparatur oder den Umtausch des Geräts.

Für ordnungsgemäße Ventillation darf dieses Gerät nicht näher als 15cm von einer Wand entfernt aufgestellt werden.



*Warnung: Wird das Gerät auf eine Weise benutzt, die hierin nicht angegeben wird, kann der vom Gerät gebotene Schutz beeinträchtigt werden.*

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## Safety Compliance

This equipment has been tested and found to comply with the IEC 61010-1-Edition 3.0 2010. Any changes or modifications not expressly approved by PerkinElmer, Inc., could adversely affect compliance.

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## conformité de sécurité

Cet équipement a été testé et déclaré conforme à la norme CEI 61010-1, troisième édition (2010) norme de sécurité.

Les changements ou modifications non expressément approuvés par PerkinElmer, Inc., pourraient nuire à la conformité.

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## Sicherheitsrichtlinien

Dieses Gerät wurde getestet und mit dem IEC 61010-1, dritte Ausgabe (2010) Sicherheitsstandard entsprechen.

Alle Änderungen oder Modifikationen, die nicht ausdrücklich von PerkinElmer, Inc. genehmigt wurde, könnte sich negativ auf die Compliance.



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# Chapter 1

## About the Tri-Carb

The Tri-Carb<sup>®</sup> liquid scintillation counter relies on interactions between radioactive decay energy and a scintillator, a component of the “scintillation cocktail.” The scintillator converts ionizing radiation from the radionuclide into photons of light (scintillation). The intensity of light produced during scintillation is proportional to the initial energy of the beta particle.

By placing a vial containing a radionuclide and scintillation cocktail into a dark detection enclosure (the instrument’s detector), the scintillation counter can measure photon intensity. A Photomultiplier Tube (PMT) amplifies the light emitted from sample vials and the amplified signal is converted to pulses of electrical energy registered as counts. The counts accumulated during this process are sorted into separate channels, with the amplitude of the signal determining the energy channel (keV) into which the counts are sorted, and used to generate a sample spectrum. Using this spectrum, the system can perform various count correction calculations and determine Counts Per Minute (CPM) for each sample.

To calculate Disintegrations Per Minute (DPM), the instrument determines a counting efficiency of each sample, and using a quench curve, compares the quench index for samples to that for quench standards. This determines sample counting efficiency, and calculates DPM for unknown samples.

Figure 1-1 and Figure 1-2 provide an overview of this process:

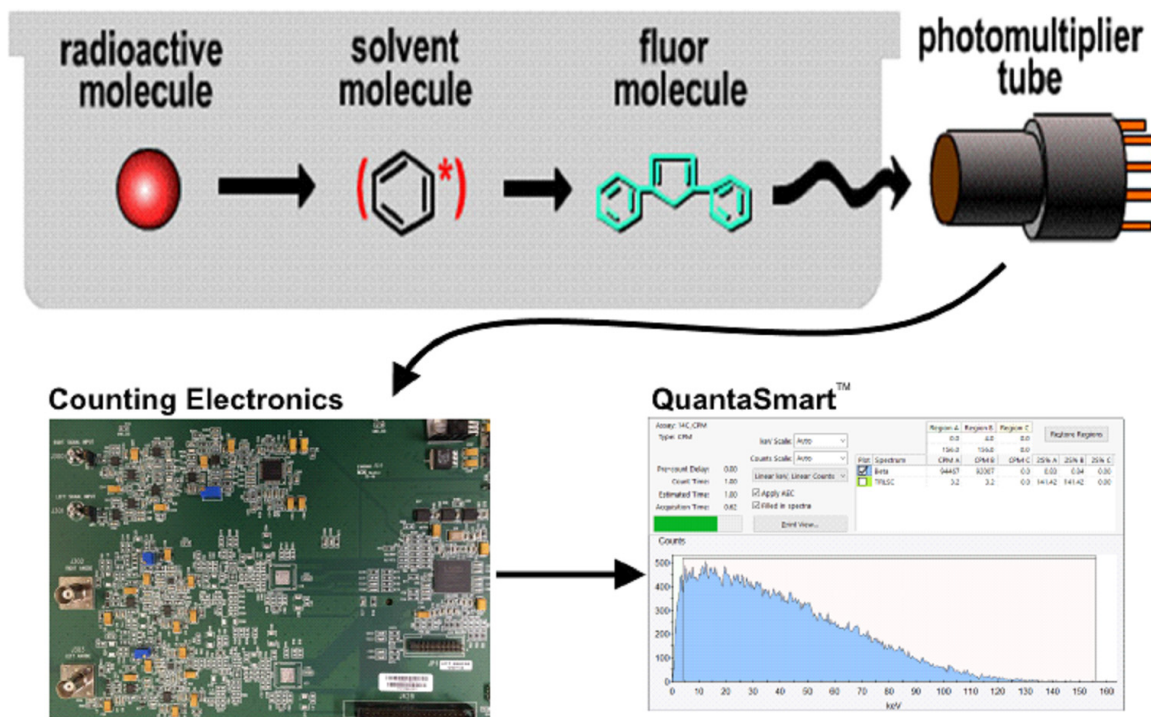


Figure 1-1. Overview of the Scintillation Counting Process (1 of 2).

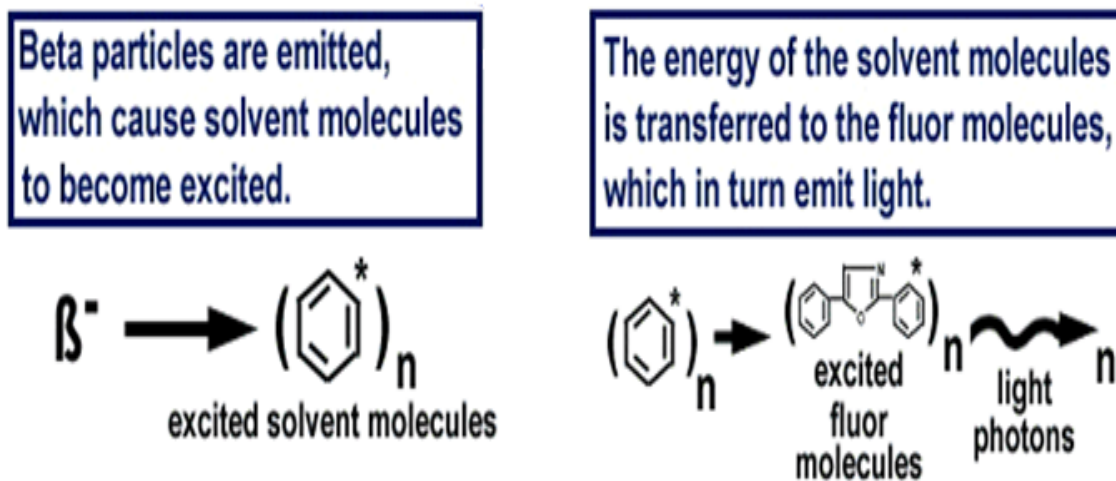


Figure 1-2 Overview of the Scintillation Counting Process (2 of 2).

The remainder of this chapter discusses the following topics about the Tri-Carb system:

- Instrument Specifications (page 3)
- Recommended Safety Procedures (page 10)
- Customer Service (page 11)
- Moving the Tri-Carb Instrument (page 11)
- Decontamination (page 12)
- Preventative Maintenance (page 12)
- Overview of System Hardware (page 12)

## Instrument Specifications

All Tri-Carb instrument specifications are developed using sources whose activity is referenced to NIST source activity, and PerkinElmer reference methods. Depending on the instrument placement in your laboratory, some specifications may differ from those in this chapter.

The specifications for your Tri-Carb system are defined in the following sections.

These specifications include the following:

- Physical Dimensions (page 4)
- Electrical Requirements (page 4)
- Environmental Requirements (page 4)
- Energy Range (page 5)
- Efficiency (page 5)
- Chi-Square (page 5)
- Detectors (page 6)
- Sample Changer (page 6)
- External Standard (page 6)
- Sample Cassettes (page 6)
- Protocol Flags (page 7)
- Bar Code Reader (page 8)
- Shielding (page 8)
- Sample Vials (page 9)

## Physical Dimensions

<b>Height:</b>	19 inches (48 cm)
<b>Width:</b>	40.6 inches (103 cm)
<b>Depth:</b>	32.36 inches (82 cm)
<b>Weight:</b>	470 pounds (214 kg) without refrigeration unit 515 pounds (234 kg) with refrigeration unit

## Electrical Requirements

### Instrument:

	60 Hz	50 Hz
<b>Voltage (VAC):</b>	100, 120	200, 240
<b>Amperage (Amps):</b>	1.0	0.5
Installation Category II, Pollution Degree 2		
<b>Fuse (Amps):</b>	4.0 (type S) (5 X 20 mm)	2.5 (type T) (5 X 20 mm)
<b>Wattage (Watts):</b>	125	125

### Refrigeration Unit (Optional):

	60 Hz	50 Hz
<b>Voltage (VAC):</b>	117	240
<b>Amperage (Amps):</b>	2.5	1.5
<b>Fuse (Amps):</b>	Circuit Breaker	Circuit Breaker
<b>Wattage (Watts):</b>	500	500

## Environmental Requirements

<b>Operating Ambient Temperature:</b>	15°C to 35°C (59°F to 95°F)
<b>Operating Relative Humidity:</b>	30% to 85% (Non-condensing; system for indoor use only)
<b>Altitude:</b>	Up to 2000 meters (6561 feet)

## Energy Range

This table represents the preset regions for the following nuclides:

Preset Regions (keV)	
<b>Tritium</b>	0–18.6
<b>Carbon-14</b>	0–156
<b>Phosphorus-32</b>	5–1700
<b>Iodine-125</b>	0–70

You can define preset regions for any nuclide in the Sample Nuclides Library. Refer to Sample Nuclides Library (page 152) for more information.

## Efficiency

For Tritium ( $^3\text{H}$ ) in the range 0–18.6 keV, the minimum acceptable efficiency is 63% (58% for Model GCT 6220). For Carbon-14 ( $^{14}\text{C}$ ) in the range 0–156 keV, the minimum acceptable efficiency is 95% (94% for Model GCT 6220). These values were generated by PerkinElmer. Exact values obtained at other instrument locations may vary. Counting Efficiency is a parameter measured as part of Instrument Performance Assessment (IPA).

Counting efficiencies, backgrounds and Figure of Merit are determined in IPA using optimized window settings of 1–18.6 keV for Tritium and 4–156 keV for  $^{14}\text{C}$ . These windows will yield slightly lower counting efficiencies. To determine a full range counting efficiencies, CPM assays with counting regions of 0–18.6 keV for Tritium and 0–156 keV for  $^{14}\text{C}$  must be utilized.



*Note: This feature may be optional. Contact your PerkinElmer representative for details.*

## Chi-Square

Chi-Square acceptable range: 7.63 to 36.19, performed as 20, 0.5 minute repeat counts, and tested at the 99% confidence limits. Chi-Square is a parameter measured as part of IPA.



*Note: This feature may be optional. Contact your PerkinElmer representative for details.*

## Detectors

Two diametrically opposed high performance Photomultiplier Tubes (PMTs) are coupled to a light-tight, reflective optical chamber. These detectors are located below the sample changer at the rear of the instrument.

## Sample Changer

The sample changer automatically moves samples into position, and load them into the detector for counting. After the count is completed, the sample is automatically unloaded, and the next sample is loaded.

The sample changer typically moves cassettes in a forward (counterclockwise) direction using a pair of synchronously driven transport belts. If necessary, these belts can run in the reverse (clockwise) direction, such as during recovery from a power failure.

The instrument can hold up to (depending on the configuration):

- 408 large vials
- 720 small vials
- 720 4 mL vials

The Varisette™ option allows users to count large vial and small vial samples in dedicated cassettes. This feature may be optional; Contact your PerkinElmer representative for details.

## External Standard

$^{133}\text{Ba}$ , nominal less than  $20\mu\text{Ci}$  (for all Tri-Carb models except Quantulus GCT).

$^{133}\text{Ba}$ , nominal less than  $1\mu\text{Ci}$  (for Tri-Carb Quantulus GCT models).

## Sample Cassettes

Cassettes are plastic racks that hold sample vials, and allow them to be moved on the sample changer deck. Samples are placed into cassettes that accommodate standard or small vials without adapters (4 mL vials require cassettes with adapters). A standard vial cassette can accommodate up to 12, 15–20 mL vials, and the mini-vial cassettes up to 18, 6–7 mL mini-vials. A protocol flag attached to the cassette identifies protocol and assay conditions defined for use with samples. Individual cassettes are identified by unique numbers (cassette IDs) located at the end of each cassette. The protocol flag and cassette ID are automatically read by the instrument to provide Positive Sample Identification (PID) when using Worklists.



Figure 1-3. Sample Cassette with Vials

## Protocol Flags

Protocol flags are numbered, plastic devices that contain an encoded, reflective metal that the instrument uses to identify appropriate assay counting parameters for a sample set. The counting parameters that the instrument uses correspond to the parameters defined during the assay definition process (predefined by PerkinElmer for the Direct DPM assay). These assay parameters become a functional part of a protocol once an assay is associated to a protocol number.

Prior to counting samples, attach the correct protocol flag (e.g. the protocol flag number associated to the assay) to the first cassette to be counted. Verify the cycle flag is in the reset position (Figure 1-3). When a protocol number is recognized, a cycle flag at left indicates the assay is being counted for the first time. If multiple cycles are defined for an assay, the cycle counting starts over. The system will push the cycle flag to the right after the cassette is counted. Subsequent protocol counting is considered to be the following cycles of the same samples. Reset the cycle flag each time new samples are placed in the cassette(s).

## Bar Code Reader

The 2D Bar Code Reader is an optional feature providing automated sample tracking for the Tri-Carb system. To use the reader, a 2D bar code is placed on a sample's vial cap, and the label read before the sample is loaded. Refer to the following sections for more information about the Bar Code Reader option:

- *Configure Barcode Reader* on page 83
- *Barcode Settings* on page 150
- *Sample Name* on page 145 (part of the **Worklist** tab description)
- *2D Bar Code Reader Option* on page 221



*Note: Linear 1D bar codes are also supported, provided they can fit onto the top of a vial cap. Use the bar code reader's software to configure the reader to accommodate linear 1D bar codes (see the software's help for instructions). Disable all other bar codes not used for maximum speed and efficiency.*

## Shielding

The detector assembly is surrounded by two inches (minimum) of lead.



## Sample Vials

Vials and caps must conform to the following sizes. Caps must not exceed the diameter of the vials.

<b>Large Vials</b>	<b>Minimum</b>	<b>Maximum</b>
Vial Height:	58.4 mm	63.0 mm
Vial Diameter:	26.0 mm	28.1 mm
Cap Diameter:	22.0 mm	≤ vial diameter
<b>Small Vials</b>	<b>Minimum</b>	<b>Maximum</b>
Vial Height:	53.0 mm	58.0 mm
Vial Diameter:	14.5 mm	17.8 mm
Cap Diameter:	13.0 mm	≤ vial diameter
<b>4 mL Vials</b>	<b>Minimum</b>	<b>Maximum</b>
Vial Height:	53.0 mm	58.0 mm
Vial Diameter:	12.7 mm	14.5 mm
Cap Diameter:	12.0 mm	≤ vial diameter

## Recommended Safety Procedures

To ensure personal safety and to maximize the life of the Tri-Carb instrument, do the following:

1. The AC power cord used to connect the Tri-Carb instrument to the AC mains must be rated for the appropriate input voltage (see page 4 for voltage information). Also use a grounded outlet. The system provides automatic recovery after a power failure.  
  
Once the power cord is properly connected, the instrument can be turned on and off using the power switch on the right side of the instrument (Figure 1-6, page 15). The power switch also powers the internal computer.
2. Power to the temperature control unit should not be supplied through a power strip. Connect the temperature control unit's power cord only to a grounded wall outlet with the appropriate voltage (see page 4 for more information).
3. For proper ventilation, a distance of 15 cm (5.9 in) must be maintained from this unit to any other surface.
4. If the equipment is used in a manner not specified by the manufacturer, the protection provided by the equipment may be impaired.
5. Do not attempt to make internal adjustments or replacements in the Tri-Carb instrument. Servicing should only be performed by trained PerkinElmer service personnel.
6. Verify that all connections to the Tri-Carb instrument are secure. See page 15 for more information.
7. Do not operate the Tri-Carb instrument or its components in water or any other liquid or fluid.
8. Do not allow flammable materials to contact the Tri-Carb instrument.
9. Keep the Tri-Carb instrument away from sources of radiation (e.g. X-ray equipment, radiation storage vaults, etc.).
10. Do not allow direct sunlight or unshielded fluorescent light to enter the sample changer. Direct sunlight affects optical sensors within the sample changer, and can cause erratic operation. Direct sunlight can also induce fluorescence within your samples, causing erratic results.
11. The Tri-Carb calibration sources contain  $^{14}\text{C}$  and/or Tritium standards, and the Tri-Carb instrument also contains a Barium-133 source for use as an external standard. If it is necessary to dispose of these items, do so according to Good Laboratory Practices (GLP).

If the Tri-Carb instrument appears damaged or unsafe, do not operate the instrument. The Tri-Carb may be unsafe if it exhibits any of the following conditions:

- Shows visible damage.
- Fails to perform the intended measurement.
- Has been subjected to prolonged use or storage in unfavorable conditions (refer to *Environmental Requirements* on page 4 for proper operating conditions).
- Has been subjected to severe transport stresses.

If the Tri-Carb appears damaged or in need of repair, contact your PerkinElmer service technician.

## Customer Service

### Company Name and Address:

PerkinElmer  
710 Bridgeport Ave.  
Shelton, CT 06484 USA  
Telephone: (800) 762-4000  
Internet: [www.perkinelmer.com](http://www.perkinelmer.com)

Supplies, accessories, and replacement parts can be ordered directly from PerkinElmer. To place an order, request a free catalog, or to review current information on part numbers, product brochures, spare parts, and application notes, refer to the PerkinElmer website ([www.perkinelmer.com](http://www.perkinelmer.com)).

## Moving the Tri-Carb Instrument

If necessary to move the Tri-Carb instrument a short distance, do the following:

- Remove power to the Tri-Carb instrument.
- Disconnect any cables in the way when moving the instrument (see page 15 for the location of Tri-Carb connectors - left and right).
- Use a cart to transport the Tri-Carb instrument.
- Use at least two people to lift the instrument onto the cart.
- Use caution when transporting the Tri-Carb instrument on the cart.
- When finished moving the instrument, position the Tri-Carb for proper ventilation (ensure a distance of at least 15 cm (5.9 in) between the Tri-Carb and other surfaces).

## Decontamination

Decontamination is a necessary precaution when shipping a potentially contaminated system (or parts from that potentially contaminated system) to another site.

- For decontamination instructions, visit:  
<http://www.perkinelmer.com/deconprocedure>
- To obtain a copy of the decontamination certificate, visit  
<http://www.perkinelmer.com/deconcertificate>

If you have any questions about the decontamination process or certificate, contact your PerkinElmer service representative.

## Preventative Maintenance

With the exception of inspection and cleaning, there are no preventative maintenance procedures that users should perform. For more information, refer to page 223 of Chapter 8.

## Overview of System Hardware

The following sections contain information about the Tri-Carb instrument's hardware:

- System Computer
- Front of Tri-Carb (page 13)
- Back of Tri-Carb (page 14)
- Right Side of the Tri-Carb (page 15)

## System Computer

The instrument is controlled by an internal Windows-based computer. USB ports are located on the left side of the instrument. All RS-232 communication uses a USB to a RS-232 converter. The instrument can be attached to a network using the Ethernet port connection on the left side. Only IEC 60950 approved devices (monitors, printers, etc.) can be connected to the Tri-Carb instrument. The devices sold with a Tri-Carb instrument are IEC 60950 approved.

## Front of Tri-Carb

Figure 1-4 shows the front of the Tri-Carb Liquid Scintillation Analyzer.



**Figure 1-4. Front of Tri-Carb.**



*Note: The left side of the instrument has four USB ports, plus a network and DVI video connection.*

*In the front center of the Tri-Carb is a status light which indicates the current state of the instrument:*

- *White – Idle, instrument is not in use*
- *Green – Running, instrument is measuring or moving samples*
- *Red – Error, instrument needs attention*

## Back of Tri-Carb

Figure 1-5 shows the back of the Tri-Carb system—both with and without the refrigeration unit (*Contact your PerkinElmer representative for details.*).

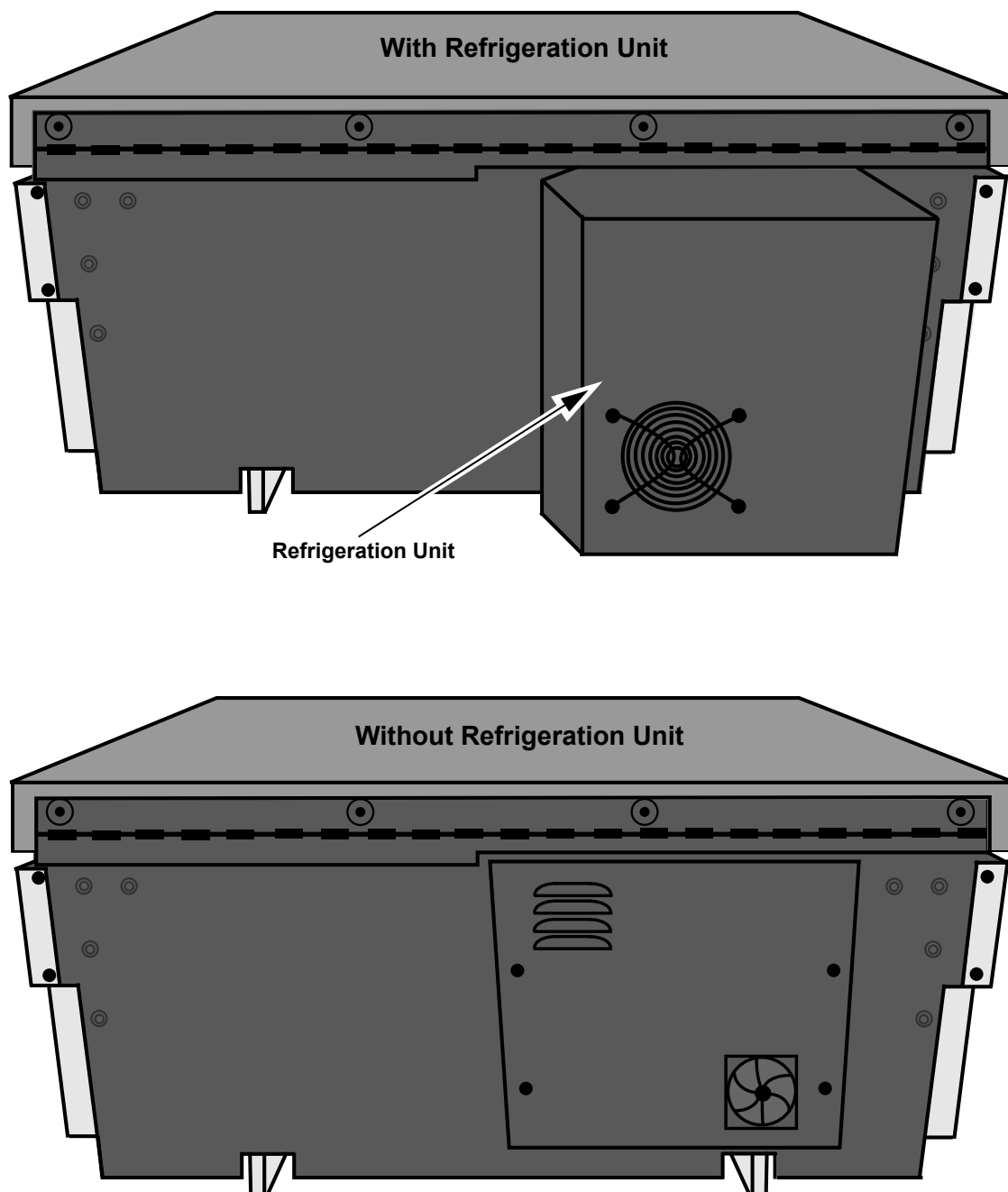
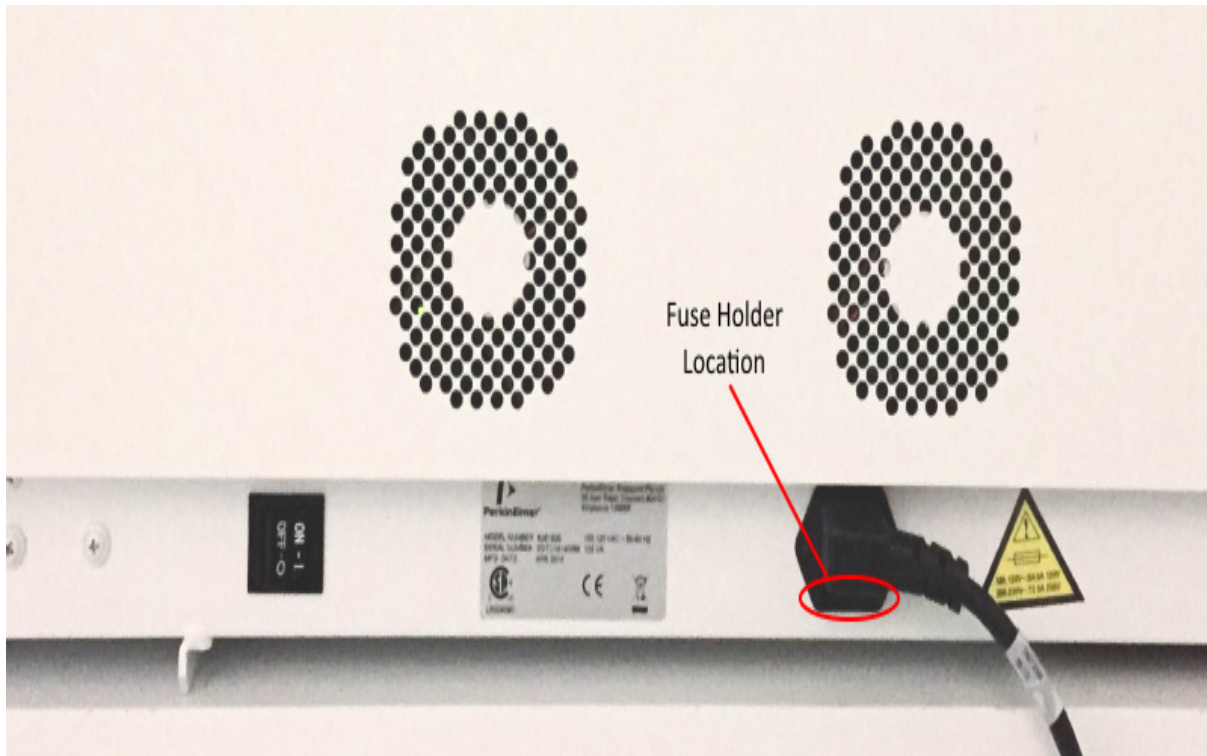



Figure 1-5. Back of Tri-Carb.

## Right Side of the Tri-Carb

Figure 1-6 shows the location (on the right-hand side of the Tri-Carb) of the power switch, power connector, and fuse holder.



**Figure 1-6. Right Side View of Tri-Carb.**

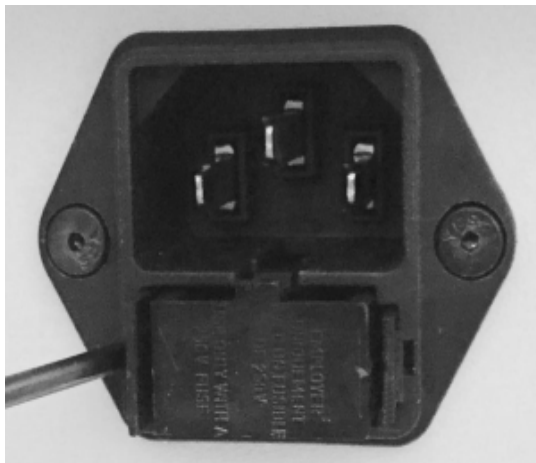
 *Note:* Leave room on the right-hand side of the Tri-Carb to easily access the power switch.

### Replacing a Fuse

The fuse holder is located on the right side of the Tri-Carb instrument (Figure 1-6). To replace a fuse, do the following:

1. Power the Tri-Carb instrument off, and disconnect the power cord from the Tri-Carb power connector.

2. Insert a small screwdriver (or similar tool) between the power connector and fuse holder (Figure 1-7). Then, carefully pull the fuse holder out of the instrument.



**Figure 1-7. Removing the Fuse Holder.**

3. Remove and replace the fuse (or both fuses) in the fuse holder. Always replace a fuse with a new one of the same type (see *Electrical Requirements* on page 4 for the fuse type).
4. Insert the fuse holder back into the Tri-Carb instrument.



## Chapter 2

### How To...


This chapter presents an overview of common tasks performed with QuantaSmart™ software.

The following tasks are discussed:

- How to Get Started (page 18)
- How to Perform Self-Normalization and Calibration (SNC) (page 19)
- How to Create an Assay (page 22)
- How to Create a Password To Protect Assays (page 25)
- How to Associate an Assay to a Protocol (page 27)
- How to Count Samples (page 30)
- How to Disassociate an Assay from a Protocol (page 31)
- How to Edit an Assay (page 32)
- How to Print an Assay (page 33)
- How to Manually Print a Report (page 33)
- How to Link a Quench Set to a Sample Nuclide (page 34)
- How to Set Up a Quench Standards Assay (page 36)
- How to use Alpha/Beta Detection Mode (page 37)
- How to Use the Replay Feature (page 50)
- How to Calculate Radioactive Decay (page 52)

## How to Get Started

When ready to begin a counting procedure, do the following tasks:

1. Normalize and calibrate the instrument. See *Normalization, Calibration, and IPA* on page 177.
  - 1.0.1 Select an assay type: Alpha/Beta, Alpha/Beta Standards, CPM Assay, DPM Single, DPM Dual, DPM Triple, FS DPM, Direct DPM, Quench Standards, or Single Photon Counting. See *Assays* on page 97.
  - 1.0.2 For any DPM assay (except Direct DPM), create quench data. See page 99 for information on performing a DPM assay.
  - 1.0.3 Define and save the new assay parameters. See *Defining an Assay* on page 115.
  - 1.0.4 Associate (link) the assay parameters to a protocol. See *How to Associate an Assay to a Protocol* on page 27.
  - 1.0.5 Attach the correct protocol flag to the first cassette to be counted, and load the cassette(s) with samples.
2. Click the green flag start button  at the top of the main window to begin counting.

## How to Perform Self-Normalization and Calibration (SNC)

1. Select **IPA | IPA Definition** from the menu bar.
  - 1.0.1 In the *IPA Definition* window (Figure 2-1), enter the date and activity of your standards (see page 179).

The screenshot shows the 'IPA Definition' dialog box with the following fields and options:

- IPA Parameters:**
  - 3H Standard DPM: 264300
  - 3H Reference Date: 22 April 2009
  - 14C Standard DPM: 132900
  - Background Count Time (min): 60.00
  - 3H FOM Threshold: 180
  - 14C FOM Threshold: 380
- Chi Square Tests:**
  - 3H
  - 14C
- RS-232:**
  - Transmit IPA Data
- IPA Data:**
  - Save copy of IPA data to a text file
  - File Name: C:\Packard\TriCarb\IpaData.txt
- Baselines:**
  - Number of Datapoints to Establish Baselines: 5
  - Mean and Limit columns for:
 

	Mean	Limit
3H Background:	In Progress	In Progress
3H Efficiency:	In Progress	In Progress
14C Background:	In Progress	In Progress
14C Efficiency:	In Progress	In Progress
  - Reset Baseline Values

Buttons at the bottom: Help, OK, Cancel.

**Figure 2-1. IPA Definition Window.**


- 1.0.2 Reset the SNC protocol flag to the reset position at far left when the plug is on the left end of the cassette (Figure 2-13, page 30).
- 1.0.3 Proceed to the following section (SNC Cassette Loading), and refer to the related procedures depending on instrument type (Quantulus GCT or Other Tri-Carb Models).

## SNC Cassette Loading



**CAUTION:** Do not use unpurged, Low Level standards to calibrate the instrument, even if using Low Level, High Sensitivity, or Super Low Level count mode.

### Quantulus GCT Instruments

1. Load the cassette with a purged, unquenched  $^{14}\text{C}$  standard.
  - 1.0.1 Load the cassette with an empty vial in the second vial position. This vial must be of the same type and material used to count low level samples.
  - 1.0.2 Load the cassette with a purged, unquenched Tritium standard (optional).
  - 1.0.3 Load the cassette with a purged background standard (optional).
  - 1.0.4 Load the instrument with cassettes.
2. Click the green flag start button  at the top of the main window to begin counting.

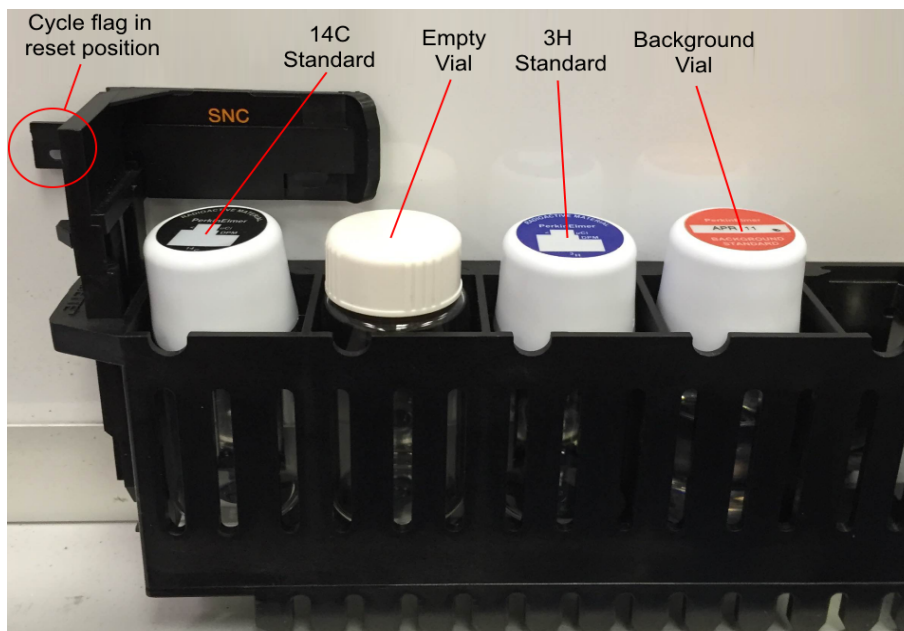

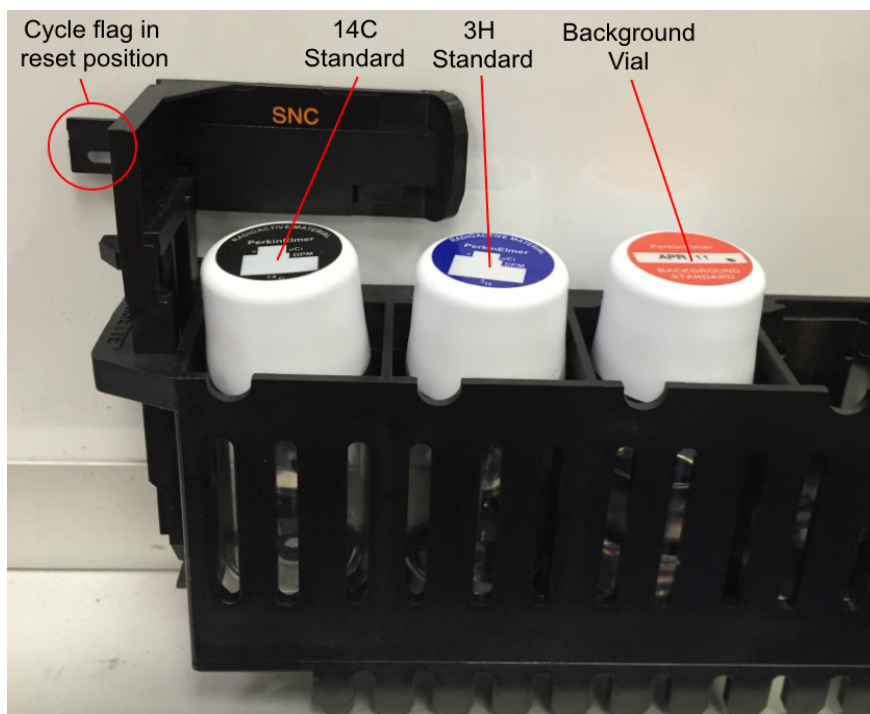


Figure 2-2 Quantulus GCT SNC Cassette Load (Sample).

### All Other Tri-Carb Models

1. Load the cassette with a purged, unquenched  $^{14}\text{C}$  standard.
  - 1.0.1 Load the cassette with a purged, unquenched Tritium standard (optional).
  - 1.0.2 Load the cassette with a purged background standard (optional).
  - 1.0.3 Load the instrument with cassettes.
2. Click the green flag start button  at the top of the main window to begin counting.



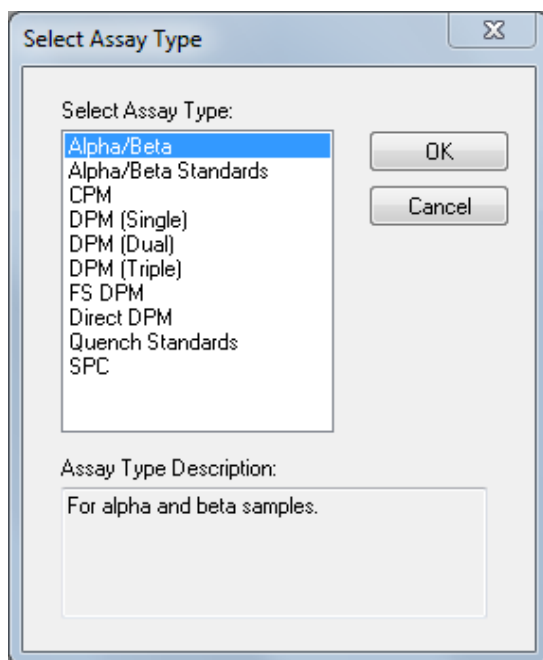
**Figure 2-3 General Tri-Carb SNC Cassette Load (Sample).**



*Note: For faster SNC processing, the background vial (or background and Tritium vials) may be left out of the cassette. The report at the end of the SNC will indicate if vials are not present.*

## How to Create an Assay

1. Select **File | New Assay** from the menu bar.
  - 1.0.1 In the *Select Assay Type* window (Figure 2-4), click on an assay type to select it, and then click **OK**. For more information on assay types, see page 97.



**Figure 2-4. Select Assay Type Window.**

- 1.0.2 When the *Assay Definition* window appears, define the individual assay parameters (as needed) on each of the window's seven tabs, then click **Save As** and save the assay using a descriptive name.
- 1.0.3 In the **Protocols** tree of the main window (Figure 2-5), right-click on the protocol flag number to associate with the assay. From the submenu displayed, select **Associate Assay**.



*Note:* Associate an assay with a flag by selecting (by clicking on) a flag, and then selecting **File | Associate Assay** from the menu bar.

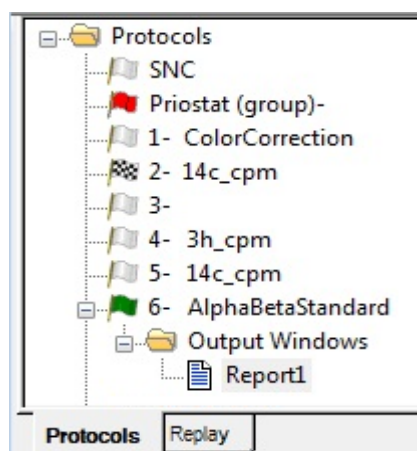


Figure 2-5. Protocols Tree.

- 1.0.4 When the *Associate Assay* window appears (Figure 2-6), select the assay to associate with the protocol flag number.
- 1.0.5 Click the **Open** button.

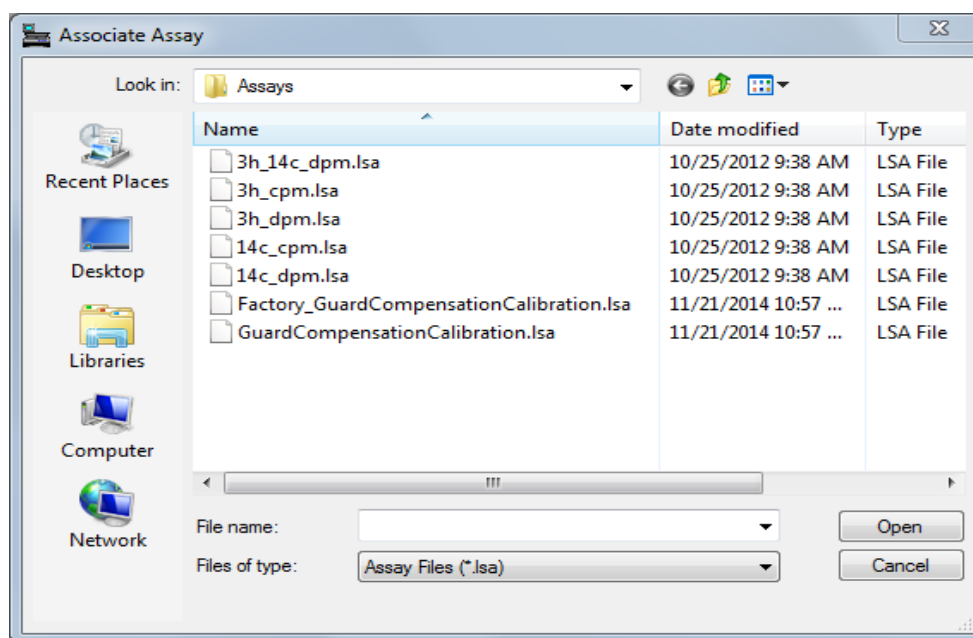
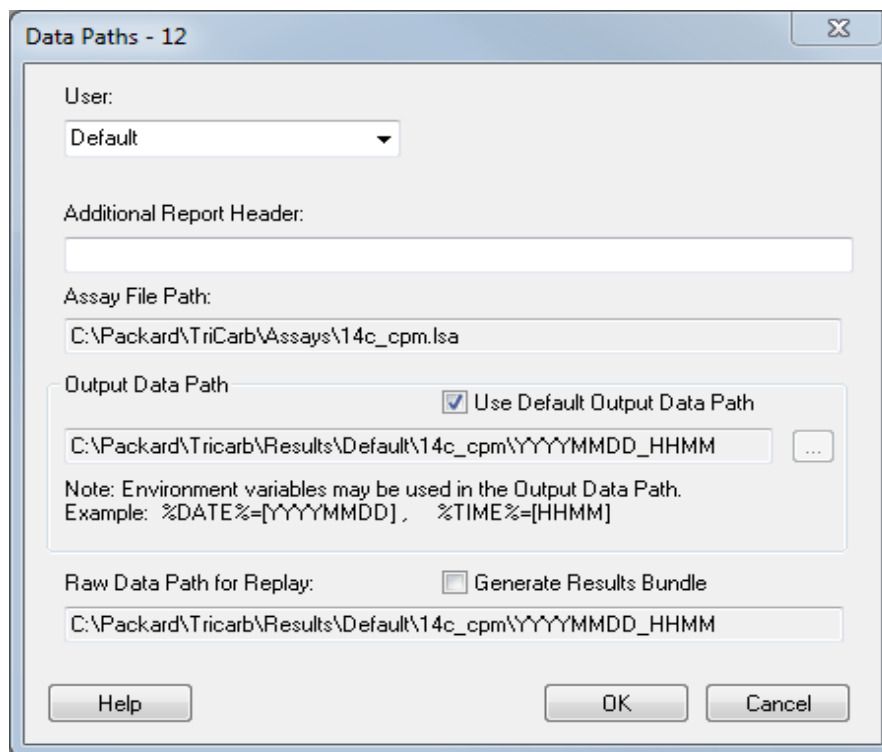


Figure 2-6. Associate Assay Window.


- 1.0.6 When the *Data Paths* window appears (Figure 2-7), do the following:
  - Select a **User** for the assay from the drop-down menu.
  - Type an **Additional Header**, if necessary.
  - Type an **Output Data Path**, to save data in a directory other than the

default.

In the example in Figure 2-7, the default path is  
C:\Packard\TriCarb\Results\Default\14c\_dpm



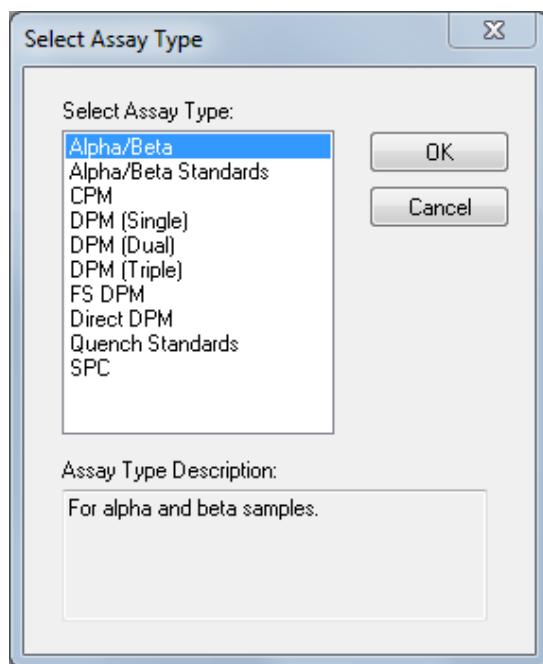
**Figure 2-7. Data Paths Window.**

- 1.0.7 Attach (to the cassette) the appropriate protocol flag in the reset position (Figure 2-13, page 30).
- 1.0.8 Load the cassette(s) with vial samples.
- 1.0.9 Load the instrument with cassettes.
2. Click the green flag start button  at the top of the main window to begin counting.



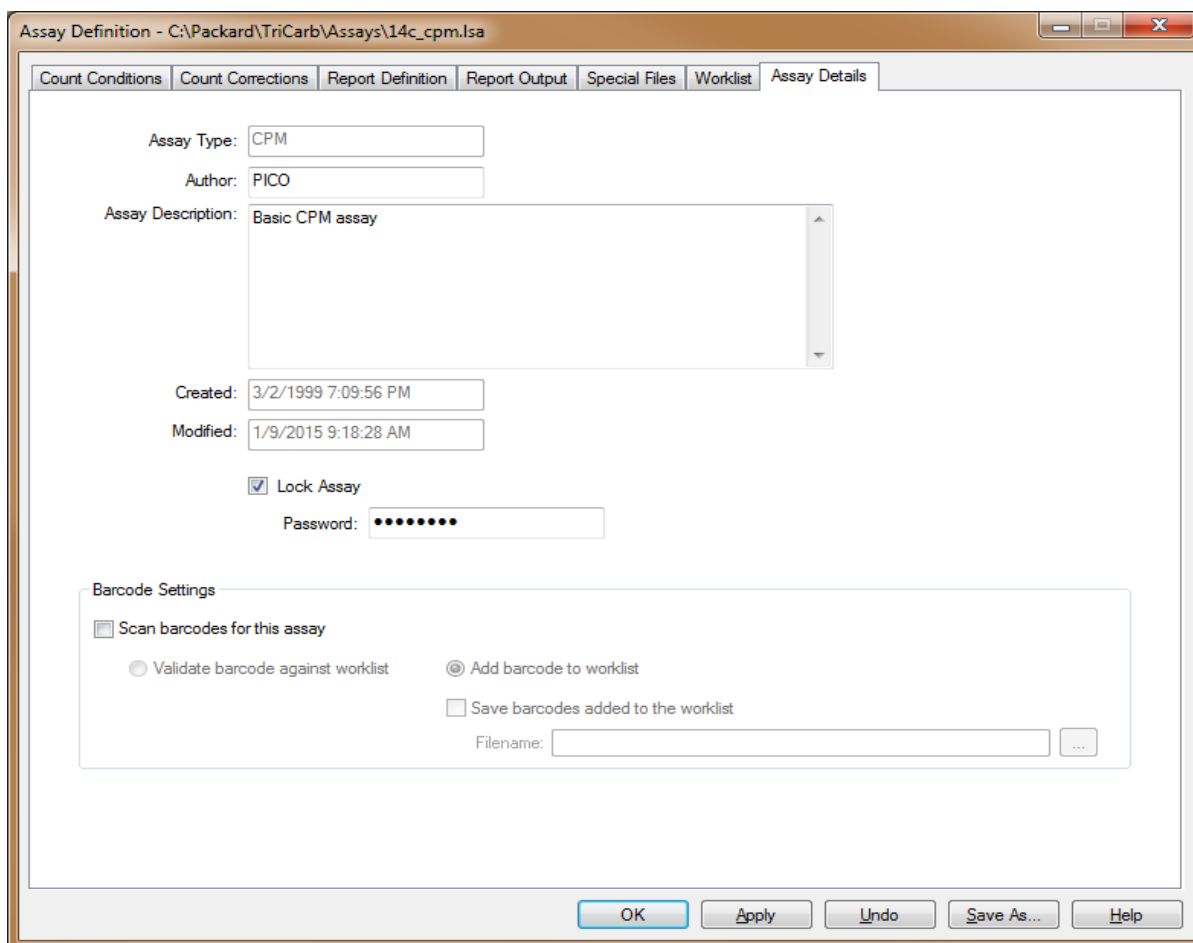
## How to Create a Password To Protect Assays

1. Select **File | New Assay** from the menu bar. The *Select Assay Type* window is displayed (Figure 2-8).
  - 1.0.1 From the assay list, click on the assay type to create, and then click **OK**.



**Figure 2-8. Select Assay Type Window.**

- 1.0.2 When the *Assay Definition* window appears (Figure 2-9), select the **Lock Assay** checkbox on the **Assay Details** tab. The **Password** field is now enabled.




**Figure 2-9. Assay Definition Window (Assay Details - Password).**

- 1.0.3 In the **Password** field, type a descriptive password.
- 1.0.4 In the seven tabs of the *Assay Definition* window, define the individual assay parameters (as needed). Refer to page 115 for more information.
- 1.0.5 When the assay definition process is completed, click the **Save As** button to save the assay. The password must be used to edit the assay after it is saved.

## How to Associate an Assay to a Protocol

1. In the **Protocols** tree of the main windowFigure 2-11, right-click on the protocol flag number to associate with an assay. From the menu displayed, select **Associate Assay**.

 *Note:* Associate an assay with a flag by selecting a flag, and then selecting **File | Associate Assay** from the menu bar.

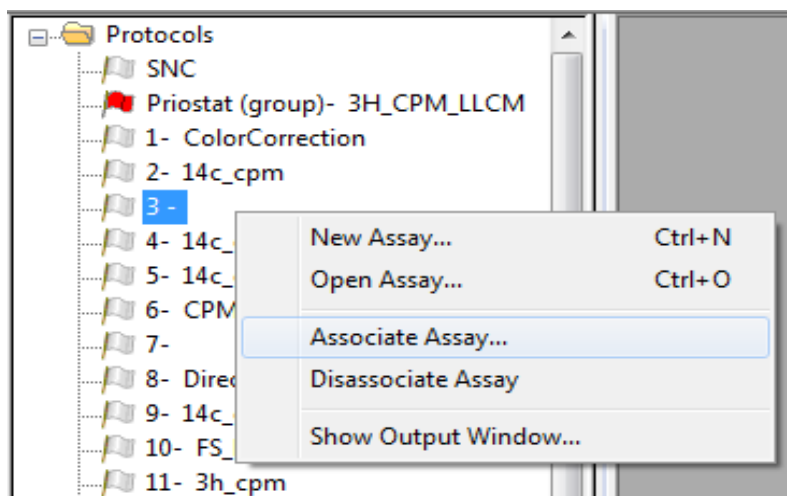


Figure 2-10 Associate Assay Option.

- 1.0.1 When the *Associate Assay* window opens, select the assay to associate with the protocol flag number, and then click the **Open** button.

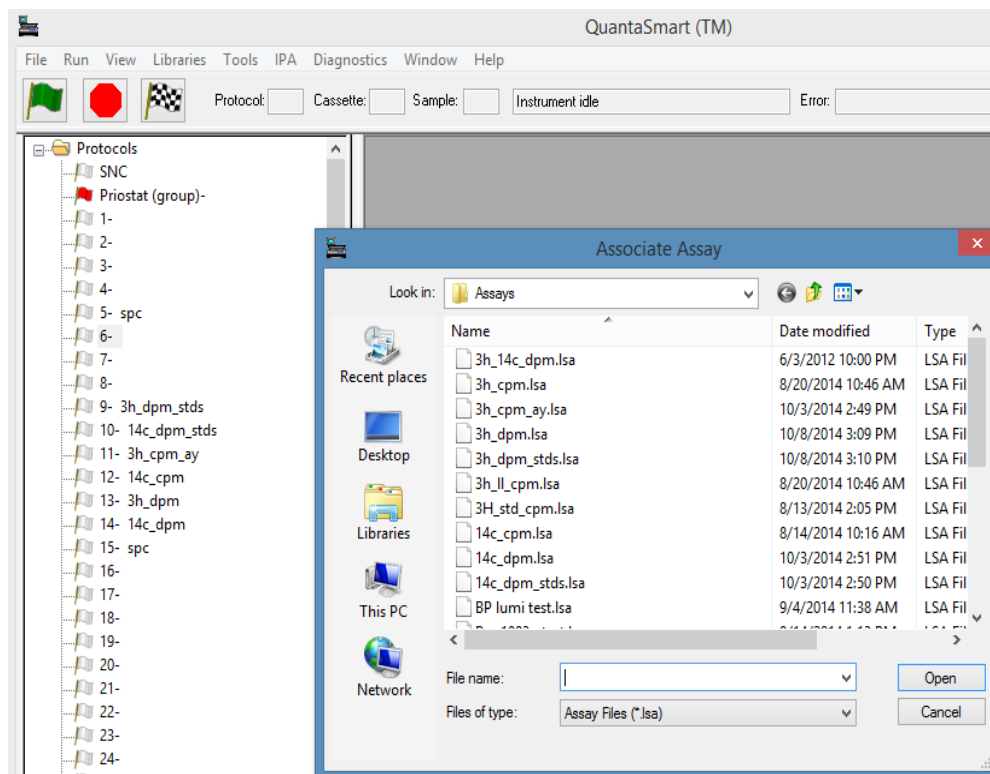


Figure 2-11. Protocols Tree (with Associate Assay Window).

- 1.0.2 When the *Data Paths* window appears (Figure 2-12), do the following:
- Select a **User** for the assay from the drop-down menu.
  - Type an **Additional Report Header**, if necessary.
  - Type an **Assay File Path**, if generating an RTF or Delimited Text file for the assay, and to save data in a directory other than the default. Select the **Use Default Output Data Path** checkbox to save the data in the default directory.

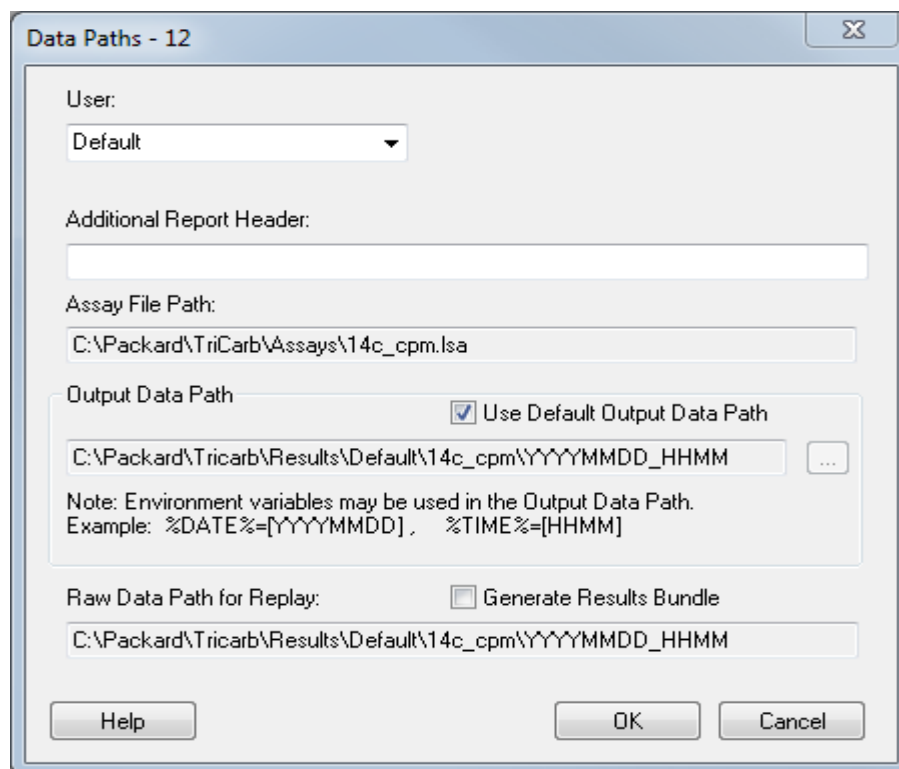
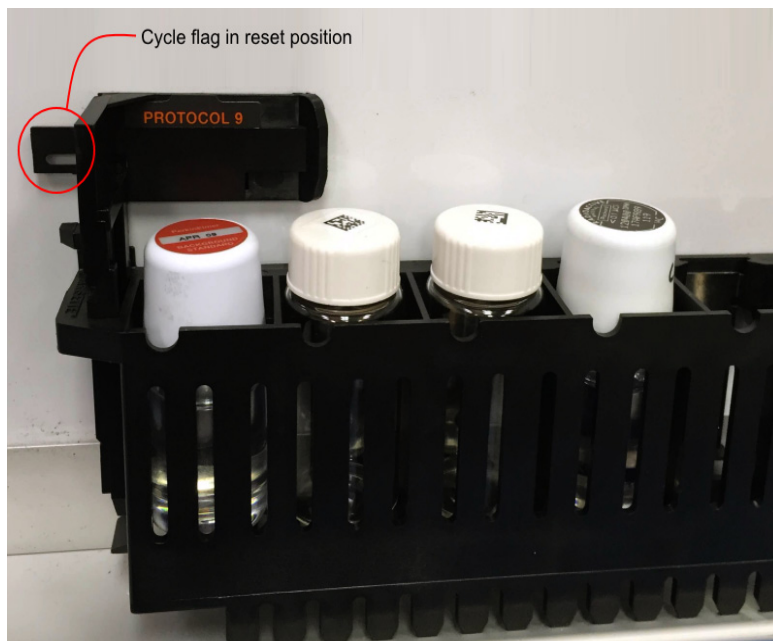



Figure 2-12. Data Paths Window.

## How to Count Samples

1. Attach the appropriate protocol flag to the cassette.
  - 1.0.1 Reset the protocol flag by moving the plastic arm to the far-left (Figure 2-13).

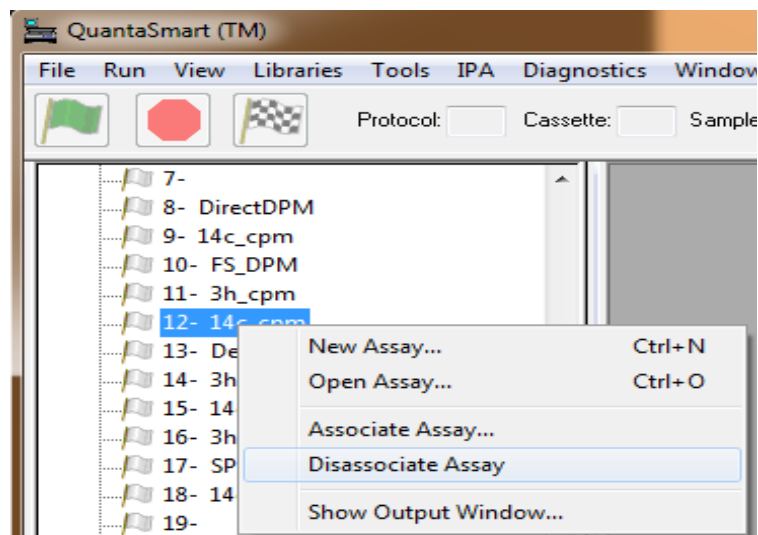


**Figure 2-13. Cassette with Protocol Flag in Reset Position.**

- 1.0.2 Place all background, reference, and sample vials into their appropriate vial positions.
  - 1.0.3 Place the cassette(s) in the sample changer deck so that the protocol number on the flag is facing front.
  - 1.0.4 Position the cassette on the right side, along the far wall of the sample changer deck (or after the last set of cassettes on the sample changer deck if the machine is in use).
2. Click the green flag start button  at the top of the main window to begin counting.

## How to Disassociate an Assay from a Protocol

1. In the **Protocols** tree of the main window, select an assay to disassociate from a protocol number.



**Figure 2-14. Disassociate Assay Option.**

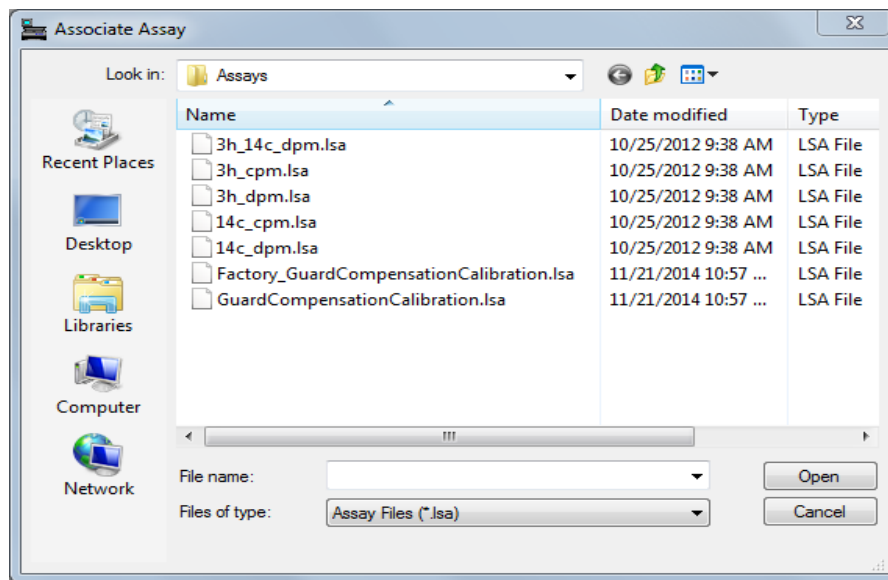
2. Right-click on the selected assay, and from the sub-menu displayed, select **Disassociate Assay**.



*Note:* Disassociate an assay from a flag by selecting the protocol flag, and then select **File | Disassociate Assay** from the menu bar.

## How to Edit an Assay

1. Select **File | Open Assay** from the menu bar.
  - 1.0.1 When the *Open Assay* window appears (Figure 2-15), select the assay to edit. Then click the **Open** button.



**Figure 2-15. Open Assay Window.**

- 1.0.2 When the *Assay Definition* window appears, edit the assay parameters (as needed) in each of the seven tabs. Refer to page 115 for more information about the *Assay Definition* window.
- 1.0.3 Save changes by doing one of the following:
  - To save an assay with the same name, click the **OK** button.

**OR**

  - To save an assay with a different name, click the **Save As** button. The *Save As* window is displayed. In the window, type an assay name, and then click the **Save** button.



## How to Print an Assay

1. Select **File | Print Assays** from the menu bar.
  - 1.0.1 When the *Select Assays to Print* window appears (Figure 2-16), select the assay to print, and then click the **Open** button.

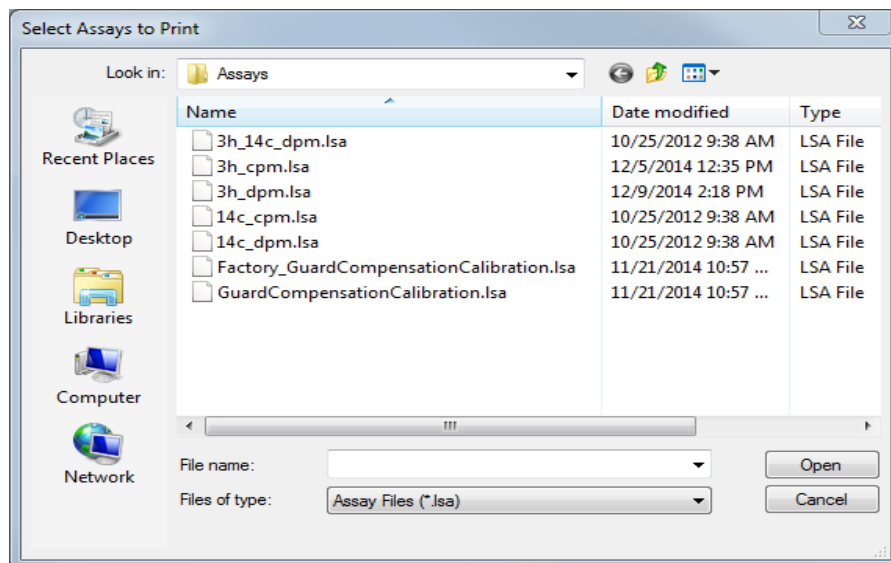





Figure 2-16. Select Assays to Print Window.

- 1.0.2 When the *Print* window appears, select the appropriate print parameters, and then click the **OK** button. A list of Assay Details, Count Conditions, Count Corrections, and Reports defined for the assay will print.

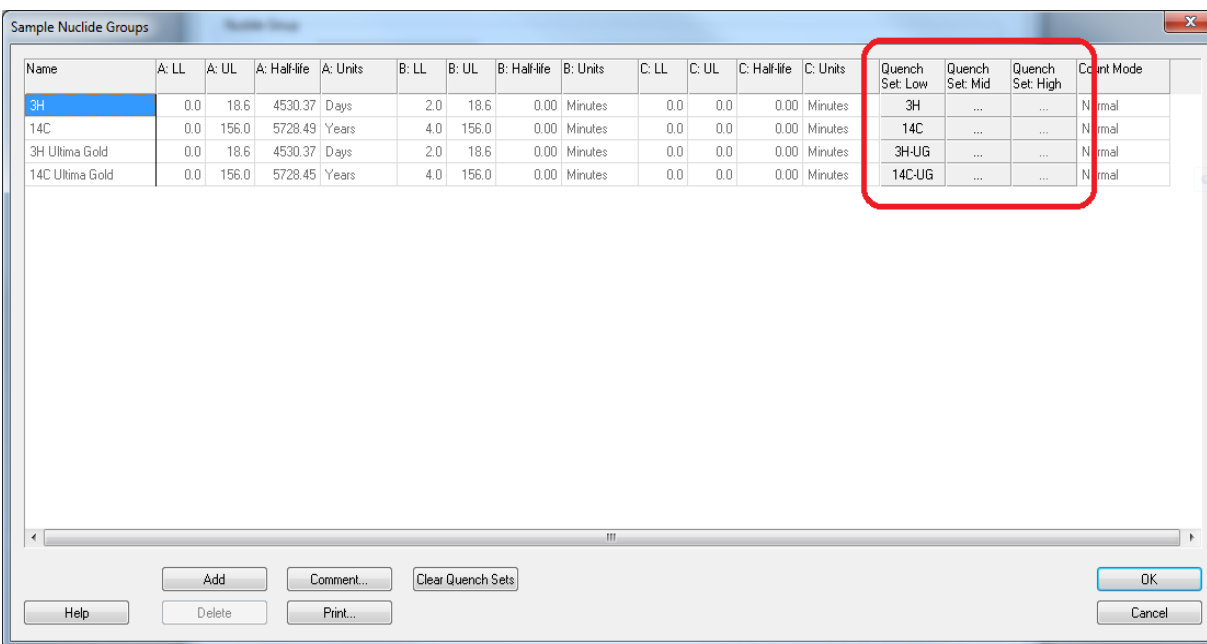
## How to Manually Print a Report

1. In the **Protocols** tree of the main window, select the report icon (  ) to print. The *Output* window is displayed.
2. In the *Output* window, select the print icon (  ). The report will print once the icon is selected.

## How to Link a Quench Set to a Sample Nuclide

 *Note:* For information on setting up a Quench Standards Assay, refer to page 36.

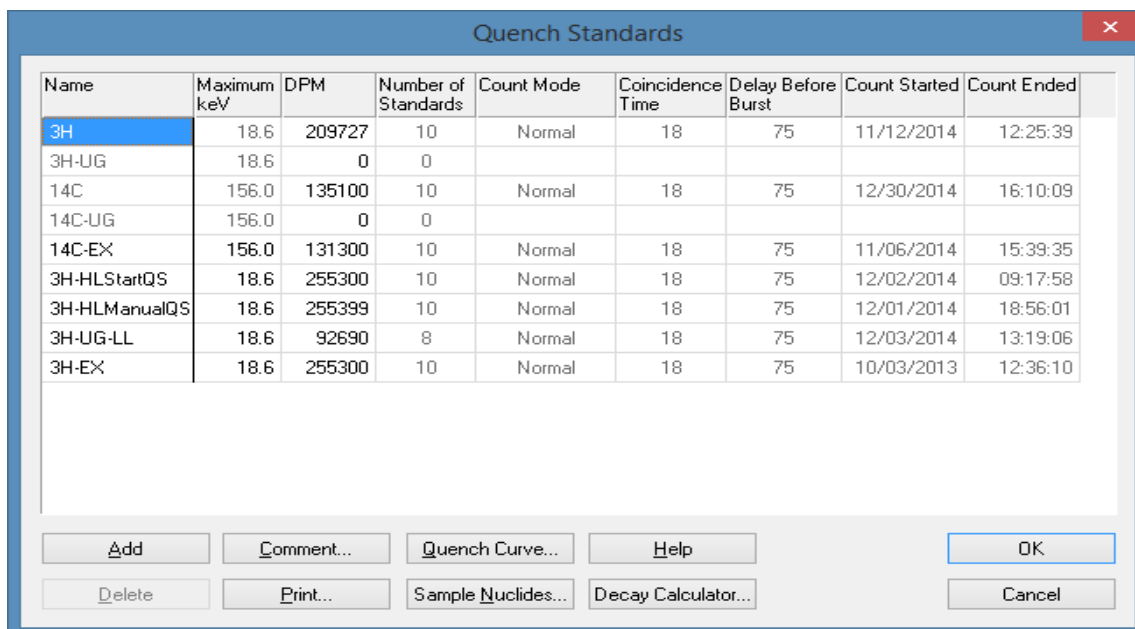
1. Select **Libraries | Sample Nuclides** from the menu bar.
  - 1.0.1 When the *Sample Nuclides* window appears (Figure 2-17), locate the sample nuclide in the list, and then click a Quench Set button for the nuclide.
    - Select the **Quench Set: Low** button if counting one nuclide in one counting region.
    - Select the **Quench Set: Mid** button if counting a second radionuclide in a separate region.
    - Select the **Quench Set: High** button if counting a third radionuclide in a third region.



**Figure 2-17. Sample Nuclides Window.**

- 1.0.2 After clicking the Quench Set button, the *Quench Standards* window will appear (Figure 2-18). In the window, select the quench set name to link to the sample nuclide, and then click **OK**.

The selected quench set name appears in the *Sample Nuclides Library* window (Figure 2-17, page 34) on the Quench Set button. Repeat steps 1 through 3 to link another quench set to the sample nuclide.



The screenshot shows a window titled "Quench Standards" with a table of data and a set of control buttons at the bottom. The table has the following columns: Name, Maximum keV, DPM, Number of Standards, Count Mode, Coincidence Time, Delay Before Burst, Count Started, and Count Ended. The "3H" row is highlighted in blue.

Name	Maximum keV	DPM	Number of Standards	Count Mode	Coincidence Time	Delay Before Burst	Count Started	Count Ended
3H	18.6	209727	10	Normal	18	75	11/12/2014	12:25:39
3H-UG	18.6	0	0					
14C	156.0	135100	10	Normal	18	75	12/30/2014	16:10:09
14C-UG	156.0	0	0					
14C-EX	156.0	131300	10	Normal	18	75	11/06/2014	15:39:35
3H-HLStartQS	18.6	255300	10	Normal	18	75	12/02/2014	09:17:58
3H-HLManualQS	18.6	255399	10	Normal	18	75	12/01/2014	18:56:01
3H-UG-LL	18.6	92690	8	Normal	18	75	12/03/2014	13:19:06
3H-EX	18.6	255300	10	Normal	18	75	10/03/2013	12:36:10

At the bottom of the window, there are two rows of buttons: Add, Comment..., Quench Curve..., Help, OK (top row); Delete, Print..., Sample Nuclides..., Decay Calculator..., Cancel (bottom row).


**Figure 2-18. Quench Standards Window.**

## How to Set Up a Quench Standards Assay

The following tasks are required when performing a Quench Standards assay:



*Note:* For 4810TR models, setting up a Quench Standards assay requires the single/dual color-corrected DPM option.


1. Normalize and calibrate the instrument, if needed. See Chapter 6 for more information.
  - 1.0.1 Do one of the following:
    - Create a new assay, selecting **Quench Standards** as the assay type (page 112). Then define the new assay parameters.
  - OR**
  - Open an existing Quench Standards assay and edit or review the assay, if necessary.
  - 1.0.2 When finished creating/editing the assay definition, save the assay in the Assays folder of the C:\Packard\TriCarb directory.
  - 1.0.3 Associate (link) the assay parameters with a protocol number in the **Protocols** tree, and attach the corresponding protocol flag to the first cassette to be counted.
  - 1.0.4 Load the cassette(s) with vial samples, and then load the instrument with cassettes.
2. Click the green flag start button  at the top of the main window to begin counting.



*Note:* When using the Low Level count mode (if available), do not use quench standards purged free of oxygen with an inert gas. Oxygen quenching in unpurged standards facilitates discrimination between background and true beta events. Unpurged standards are available from PerkinElmer.

---

## How to use Alpha/Beta Detection Mode

 *Note: This feature may be optional. Contact your PerkinElmer representative for details.*

### Overview

An Alpha/Beta assay is used to detect both Alpha and Beta decay events in a sample. Pulse Shape Analysis (PSA) is used to discriminate between alpha and beta events. When an event happens, the PSA value for the event is calculated and compared to the PSA discriminator. If the PSA is lower than the discriminator, the event is classified as a beta event; if it is higher it is classified as an alpha event. This method is very effective but not perfect. When events are misclassified, they are called Spillover which is represented as a percentage of total counts.

### Spillover Quantification

Spillover can be quantified by measuring a pure beta isotope and counting the alpha events. Since the pure beta isotope cannot generate alpha particles, any detection of alpha events is a misclassification. The same process is used for beta misclassification by measuring a pure alpha isotope and counting the beta events. The number of misclassified events is expressed as a fraction of total events using the term % Spillover. The % Spillover is calculated as part of an Alpha/Beta Standards assay. Alpha/Beta unknown assays may also be configured to calculate % Spillover. Once % Spillover is known, spill corrected CPM and DPM may be calculated.

## Spillover Reduction

Spillover can be reduced in a number of ways. One technique is to use two PSA discriminators to classify events. Events with a PSA less than the lower discriminator are added to the Beta spectrum. Events with a PSA greater than the upper discriminator are added to the Alpha spectrum. Events with a PSA between the discriminator values are unclassified, neither beta nor alpha. These unclassified events can be stored in the auxiliary spectrum as “Unclassified A/B”. Using dual discriminators results in a decrease in counting efficiency, but the measurement accuracy may be improved by the reduction in spillover.

Another technique for reducing spillover is to optimize energy windows. There are two reasons for optimizing energy windows:

1. When  $^{241}\text{Am}$  is used as the alpha standard, depending on the scintillator used, it produces low energy events that are not alpha decay events. However, because of their low energy, these events are incorrectly classified as beta events. As a result, the alpha to beta spillover percentage is artificially high. By setting appropriate alpha and beta energy windows, these incorrectly classified events can be minimized.
2. There is always some overlap in the energy of the alpha and beta decays, and selecting optimal energy regions for each type of decay can decrease the number of events that are misclassified.

As with dual discriminators, there is a decrease in counting efficiency, but the measurement accuracy may be improved by the reduction in spillover. These techniques can be combined to further improve performance.

The Sample PrioStat feature in QuantaSmart and the spectrum analysis software package, SpectraWorks2, can assist the user in optimizing regions based on visual inspection of the spectrum, or based on maximizing the Quality Metric.

## PSA Discriminators

After spillover has been quantified, PSA discriminator values are selected to minimize spill when counting unknown samples in an Alpha Beta Assay. These discriminator values are stored in the Alpha / Beta nuclides library, or in the Alpha / Beta Standards library, if the Alpha / Beta Nuclide has been linked an Alpha/Beta Standard.

---

## Steps for using Alpha/Beta detection mode

1. Prepare standards
  - 1.1 Determine the appropriate activity to use for the standards
    - 1.1.1 High activity standards (50, 000 DPM) are appropriate if the cocktail does not produce significant low energy events for the 241AM standard. Ultima Gold AB is one of the cocktails in this category.
    - 1.1.2 Lower activity standards are appropriate if the scintillator produces significant low energy events for the 241AM standard. Ultima Gold LLT is one of the cocktails in this category. The best activity to use can be determined empirically by measuring 241AM samples with varying activity in a CPM assay, and observing the fraction of low energy events in the "beta" spectrum compared to the alpha peak in that spectrum. The optimal activity is the highest activity that produces an acceptable fraction of low energy events. For Ultima Gold LLT, this will be well below 25,000 DPM.
    - 1.1.3 The lower the activity of the standards, the longer it will take to count them in order to determine spillover and the dual discriminators, and the larger the error in the spill factors caused by background.
  - 1.2 Prepare samples and background vial
    - 1.2.1 Prepare three vials with the same composition and sample preparation to produce a quench level that matches the quench level of the unknown samples.
    - 1.2.2 Add a pure alpha emitter such as 241Am to one vial, using the activity determined above.
    - 1.2.3 Add a pure beta emitter such as 90Sr to one of the other vials, using the activity determined above.
    - 1.2.4 Leave the third vial with no isotope added as the background
  - 1.3 Verify uniformity of Sample composition
    - 1.3.1 Measure each vial using a CPM assay with tSIE
    - 1.3.2 Each vial should be within +/- 20 tSIE units for best results
  - 1.4 Optional: Determine optimal energy regions by either of both of the following techniques.
    - 1.4.1 If low energy events were not completely eliminated by using low activity for your standards, measure the 241AM standard in a CPM assay, inspect the resulting spectrum, and estimate which region contains the most low-energy events (below the alpha peak). You can use this as the low beta energy limit.
    - 1.4.2 Use Sample Priostat: Optimize Region

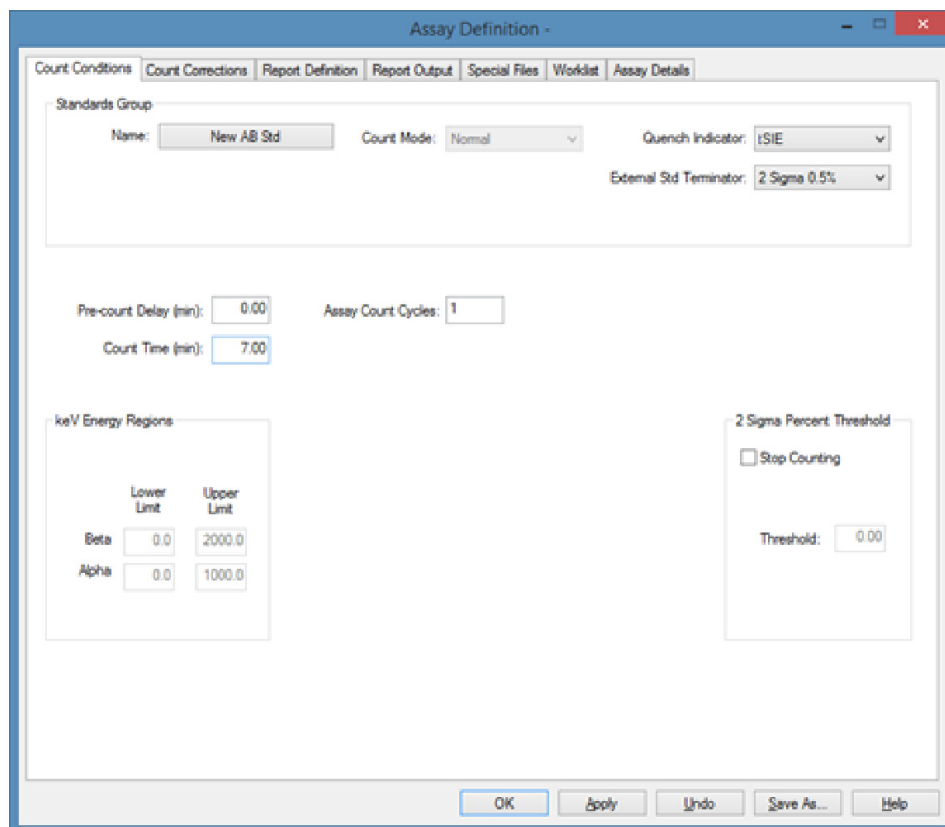
- 1.4.3 Beta and Background vial
- 1.4.4 Alpha and Background vial
- 1.5 Allow standards to temperature stabilize for 30 minutes by placing them on the instrument counting deck with the lid closed.
- 1.6 After standards have temperature stabilized, visually check the samples for signs of phase separation. If any standard appears milky, it will need to be reformulated.
- 2 Define an alpha/beta standard
  - 2.1 Under the Libraries menu, select Alpha Beta Standards

Name	Beta LL	Beta UL	Alpha LL	Alpha UL	Measurement Method	Starting Discriminator	Ending Discriminator	Number of Points	Lower Discriminator Computed	Lower Discriminator In Use	Upper Discriminator Computed	Upper Discriminator In Use	Count Started	Count Ended	Alpha Standard DPM	Beta Standard DPM
Legacy	0.0	2000.0	0.0	1000.0	Manual	1	255	10	52	52			11/03/2016	15:45:26	0	0
New AB Std	0.0	2000.0	0.0	1000.0	PSA Histogram										48000	52000
Sr90 / Am241	0.0	2000.0	0.0	1000.0	PSA Histogram										46500	51000

**Figure 2-19 Alpha Beta Standards**

- 2.2 Click Add
- 2.3 Enter the name for your nuclide pair of pure Beta and pure Alpha emitter. Consider including the cocktail type and information regarding quench levels if multiple formulations are used for these nuclides.
- 2.4 If regions have been optimized, enter the energy regions for the beta and alpha standards.
- 2.5 Under Measurement Method, select PSA Histogram. This is the fastest way to obtain the best discriminator and spillover values.
- 2.6 If you want DPM calculated for your unknown samples, scroll horizontally and enter the current activity of the Alpha and Beta standards.
- 2.7 Click OK
- 3 Create an alpha/beta standard assay
  - 3.1 Under the File menu, select new Assay
  - 3.2 Select Alpha/Beta Standards and click OK

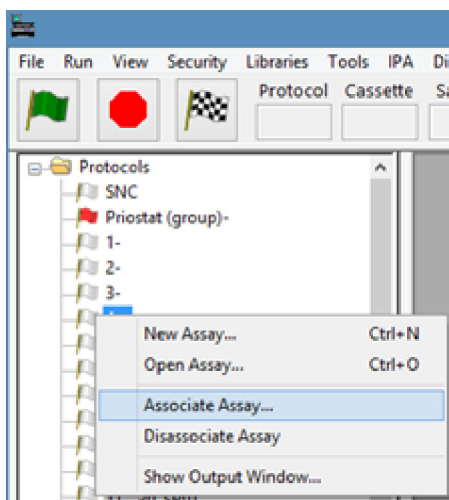




**Figure 2-20 - Assay Definition.**

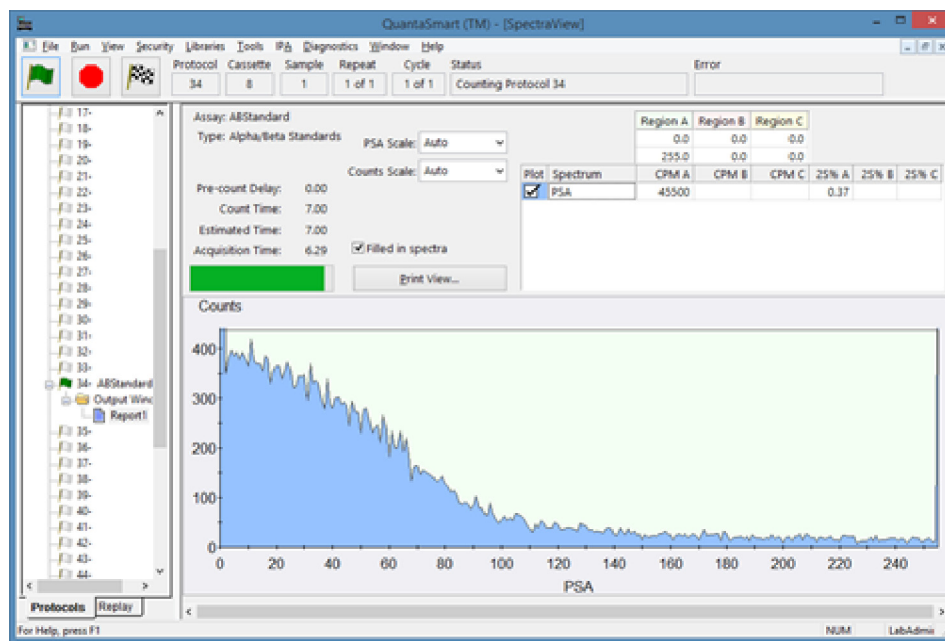
- 3.3 Click the Name button under the Standards Group. Select the name of the alpha/beta standard used in step 1.
- 3.4 Enter a Count Time long enough to give sufficient statistics. For example, a 50K DPM standard can be counted for 7 minutes using wide open windows. The less activity that is present, the longer the sample should be counted.
- 3.5 Change the Quench Indicator to tSIE. For good results, the quench level of the alpha and beta standard as well as the unknowns using the standard are approximately the same. If you are confident that quench is not changing between standards and unknowns, SIS may be selected to reduce counting time.
- 3.6 Click OK
  - 3.6.1 Enter a name for the Alpha/Beta Standards assay.
- 4 Measure the alpha/beta standard
  - 4.1 Select a protocol clip and put it on an empty cassette
  - 4.2 Put your pure beta standard in position 1 of the cassette

- 4.3 Put your pure alpha standard in position 2 of the cassette
- 4.4 Make sure the cycle tab of the protocol flag is pushed left
- 4.5 Place the cassette in the right lane of the instrument
- 4.6 Associate the number on that protocol clip with an assay in the protocol tree
  - 4.6.1 Right click on the protocol number in the tree and select "Associate Assay..."



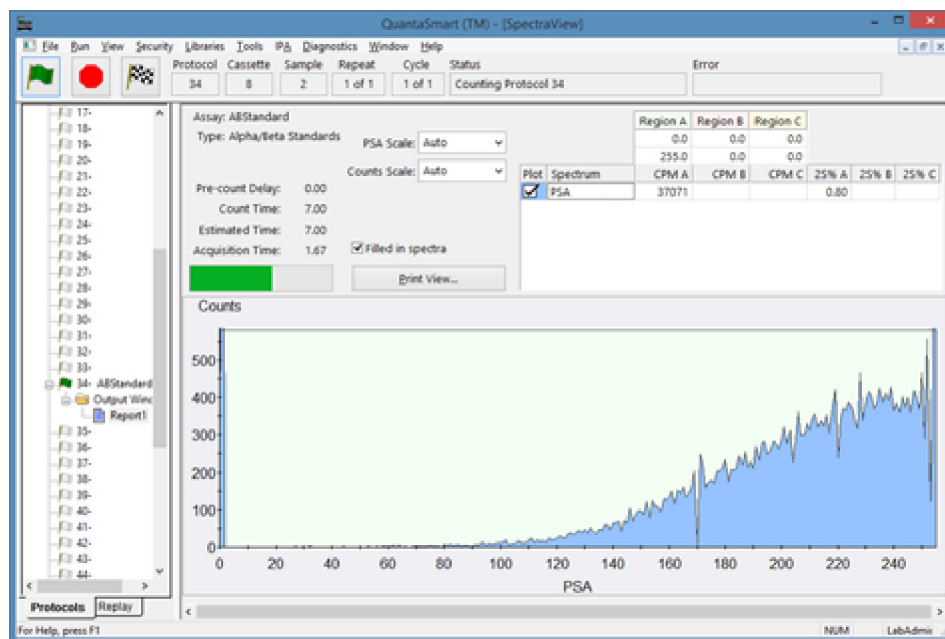
**Figure 2-21- Associate Assay**

- 4.6.2 Select the assay created in step 2
- 4.6.3 Select the data path settings and click OK
- 4.7 Allow the vials to temperature stabilize inside the instrument. Instruments with a chiller pack will temperature stabilize vials in approximately 30 minutes.
- 4.8 Click the Start button on the main screen
  - 4.8.1 The PSA histogram for beta isotopes have greater counts at the lower end. The shape of the histogram will change based on the isotope, cocktail and quench level. Figure 2-24 shows an example of a PSA histogram using  $^{90}\text{Sr}$  with Ultima Gold LLT.



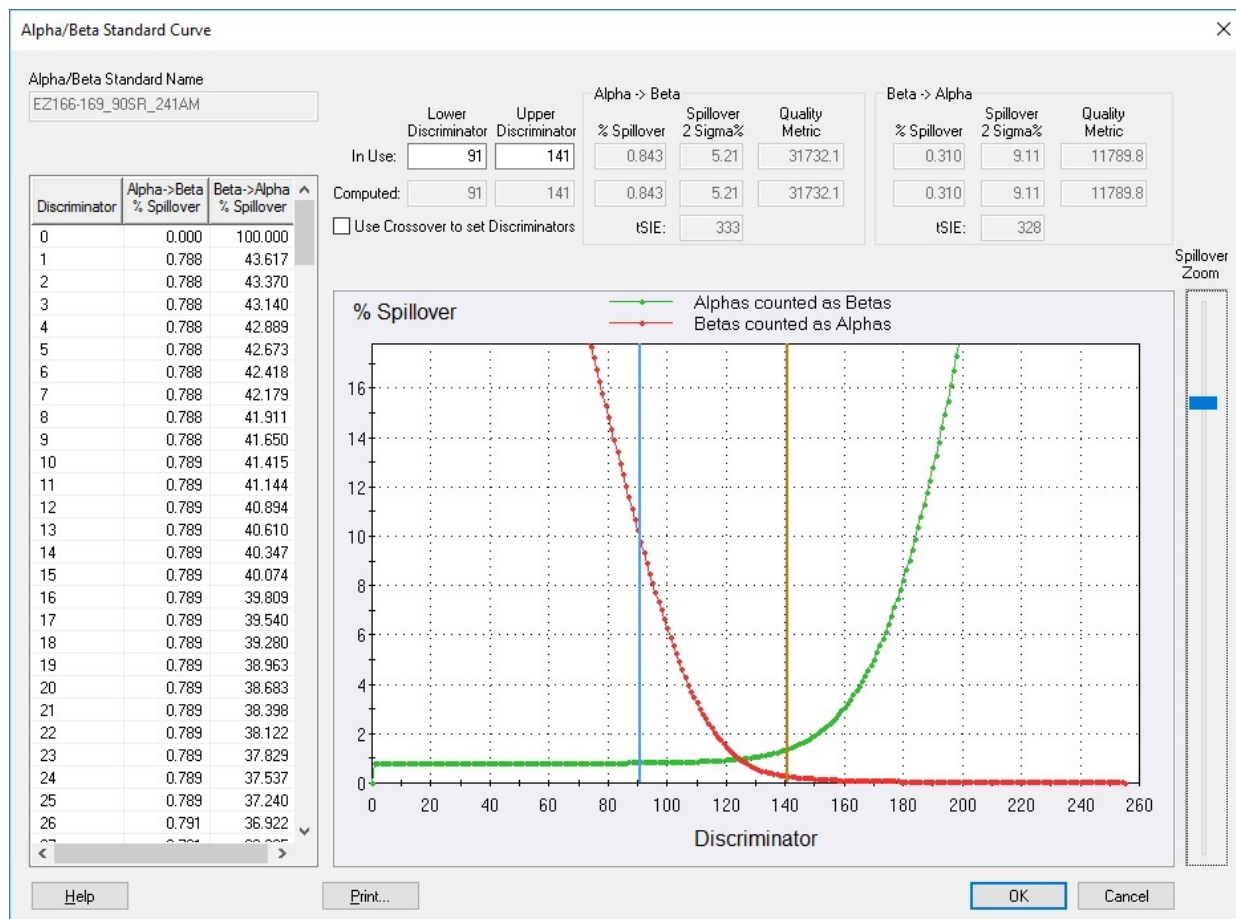
**Figure 2-22 - Typical Beta Standard Display**

- 4.8.2 The PSA histogram for alpha isotopes have greater counts at the upper end. The shape of the histogram will change based on the isotope, cocktail and quench level. Figure 2-24 shows an example of a PSA histogram using  $^{241}\text{Am}$  with Ultima Gold LLT.



**Figure 2-23 - Typical Alpha Standard Display**

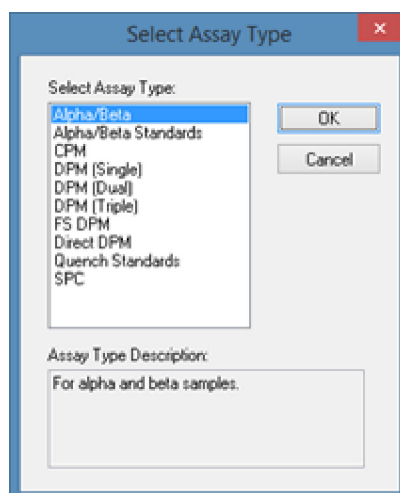
- 4.9 After the run completes, a report is generated with the calculated discriminator values. These values are automatically associated with the entry in the alpha/beta standards library.
- 5 Optional: Evaluate Standard Curve results
- 5.1 Under the Libraries menu, select Alpha Beta Standards
- 5.2 Select the standard created in step 2
- 5.3 Click on the AB Curve button



**Figure 2-24 - Alpha Beta Standard Curve**

- 5.4 Evaluate if the computed discriminators are acceptable by considering the spillover percentages and Quality Metric.
- 5.5 If sufficient counting statistics are available, the software will use dual discriminators to minimize spillover. In order to ensure reproducibility of measurement, dual discriminators are used when the Spillover 2 Sigma is below 10%. If the value is higher, consider increasing the assay count time.
- 5.6 Discriminators may be manually changed. The spillover and Quality Metric values will be recalculated to reflect the new discriminator values.
- 6 Create an alpha/beta nuclide
  - 6.1 Under the Libraries menu, select Alpha Beta Nuclides
  - 6.2 Click on the Add button

- 6.3 Enter a name for your alpha/beta nuclide pair
- 6.4 Click on the Standard Set button for the new entry. Select the Standard Set created in step 2
- 6.5 Click on OK
- 7 Create an alpha/beta assay
- 7.1 Under the File menu, Select new Assay
- 7.2 Select Alpha/Beta and click OK



**Figure 2-25 - Select Assay Type**

- 7.3 Click the Name button and select the Alpha/Beta Nuclide created in step 4.
- 7.4 Change the Quench Indicator to "tSIE"
- 7.5 Enter a Count Time to give you sufficient statistics for your unknown samples
- 7.6 If the error related to instrument background is significant compared to the activity you expect from your unknowns, you should measure a background vial with your unknown samples.
  - 7.6.1 Check the box Subtract Background
  - 7.6.2 Select 1st Vial
- 7.7 If you plan on using Replay to adjust regions
  - 7.7.1 Check the box Count Alpha/Beta Standards. This will measure the standards and calculate the spillover values as part of the assay instead of using values from the Alpha Beta Standard library.
- 7.8 Click on the Report Definition tab to select which fields to include
  - 7.8.1 Scroll to the bottom of the report fields list

Use	Name	Description	Format	Equation
<input type="checkbox"/>	SD:CPMa	Standard deviation - alpha region	00000.00	
<input type="checkbox"/>	SD:DPM1	Standard deviation - nuclide 1	00000.00	
<input type="checkbox"/>	SD:DPM2	Standard deviation - nuclide 2	00000.00	
<input type="checkbox"/>	SD:DPM3	Standard deviation - nuclide 3	00000.00	
<input checked="" type="checkbox"/>	% Alpha Spill	% alpha spill into to beta region	000.00	
<input checked="" type="checkbox"/>	% Beta Spill	% beta spill into alpha region	000.00	
<input checked="" type="checkbox"/>	CPMA Corrected	Spill corrected CPM - Region A	0000000	
<input checked="" type="checkbox"/>	CPMa Corrected	Spill corrected CPM - alpha region	0000000	
<input checked="" type="checkbox"/>	DPM Alpha	Alpha DPM from Alpha/Beta Assay	0000000	
<input checked="" type="checkbox"/>	DPM Beta	Beta DPM from Alpha/Beta Assay	0000000	
<input type="checkbox"/>	Eff Alpha in Beta	Efficiency of Alpha in Beta Region	0000.00	
<input type="checkbox"/>	Eff Alpha in Alpha	Efficiency of Alpha in Alpha Region	0000.00	
<input type="checkbox"/>	Eff Beta in Alpha	Efficiency of Beta in Alpha Region	0000.00	
<input type="checkbox"/>	Eff Beta in Beta	Efficiency of Beta in Beta Region	0000.00	
<input type="checkbox"/>	CPMA G	Counts / minute - Region A - Guard	0000000	
<input type="checkbox"/>	CPMB G	Counts / minute - Region B - Guard	0000000	
<input type="checkbox"/>	CPMC G	Counts / minute - Region C - Guard	0000000	
<input type="checkbox"/>	CPMA X	Counts / minute - Region A - Auxiliary	0000000	

**Figure 2-26 - Report Fields List**

- 7.8.2 Check the boxes for the fields to be included in the report
- 7.9 Click on OK
- 7.10 Enter a name for your Assay
- 8 Measure your unknown samples
- 8.1 Select a protocol clip and put it on an empty cassette
- 8.2 Fill the cassette with your unknown samples. Fill additional cassettes if necessary
- 8.3 If first vial background subtraction was checked for the assay, the first vial must be the background sample.
- 8.4 If Count Alpha/Beta Standards was checked for the assay, the next two vials in the first cassette must be beta standard and alpha standard.
- 8.4.1 First vial Background ON, Count Alpha/Beta Standards ON. The vial order is  
1: Background, 2:Beta Standard, 3:Alpha Standard
- 8.4.2 First vial Background OFF, Count Alpha/Beta Standards ON. The vial order is  
1: Beta Standard, 2:Alpha Standard
- 8.5 Make sure the cycle tab of the protocol flag is pushed left
- 8.6 Place the cassette in the right lane of the instrument
- 8.7 Associate the number on that protocol clip with an assay in the protocol tree
- 8.7.1 Right click on the protocol number in the tree and select "Associate




---

Assay"


- 8.7.2 Select the assay created in step 5
- 8.7.3 Select the data path settings and click OK
- 8.8 Click the Start button on the main screen
- 8.9 After the run completes, the flag next to the protocol number changes to a checkered flag and the report for the assay is printed.
- 9 Evaluate the results
  - 9.1 If the spill corrected values (CPMA Corrected, CPMa Corrected) are less than zero, this can be caused by a mismatch between the quench level of the background and the quench level of the sample
    - 9.1.1 Inspect the alpha and beta spectra of the sample and the corresponding spectra of the background sample using SpectraWorks2. If the background spectrum is higher than that of the corresponding sample spectrum, this will produce spill-corrected CPM values that are too low.
    - 9.1.2 If Count Alpha/Beta Standards was checked for the assay, and you suspect that the energy regions used for the measurement were incorrect, use Replay to adjust the energy regions, and observe whether this improves the measurement results

## How to Use the Replay Feature


 *Note:* This feature may be optional. Contact your PerkinElmer representative for details.


1. In the main window, click on the **Replay** tab. The **Replay** tree is displayed in the tab.
  - 1.0.1 In the **Replay** tree, select the results file to be analyzed. A listing of results files displays in the **Replay** tree using file names with the following syntax:

```
User id \ assay_name \ yyyyymmdd_militarytime
```

 *Tip:* To verify that you have the latest view of the Replay files, select **View | Refresh** from the menu bar.

- 1.0.2 Right-click on the selected file name, and select **Open for Replay**.
- 1.0.3 When the *Replay* window appears (Figure 2-27, page 51), do the following:
  - In the **Replay Conditions** tab, define the parameters (as needed) for reanalysis of sample data.
  - In the **Report Definition** tab, define any printed or electronic reports to generate for reanalysis of sample data.
  - Click the **Replay** button. Any defined reports are generated after data reanalysis occurs.

 *Note:* Data processed with the *Replay* feature does not change the original data. All *Replay* changes are temporary.

 *Note:* Please refer to chapter 7 *Advanced Features* for details on how to use *Replay*.

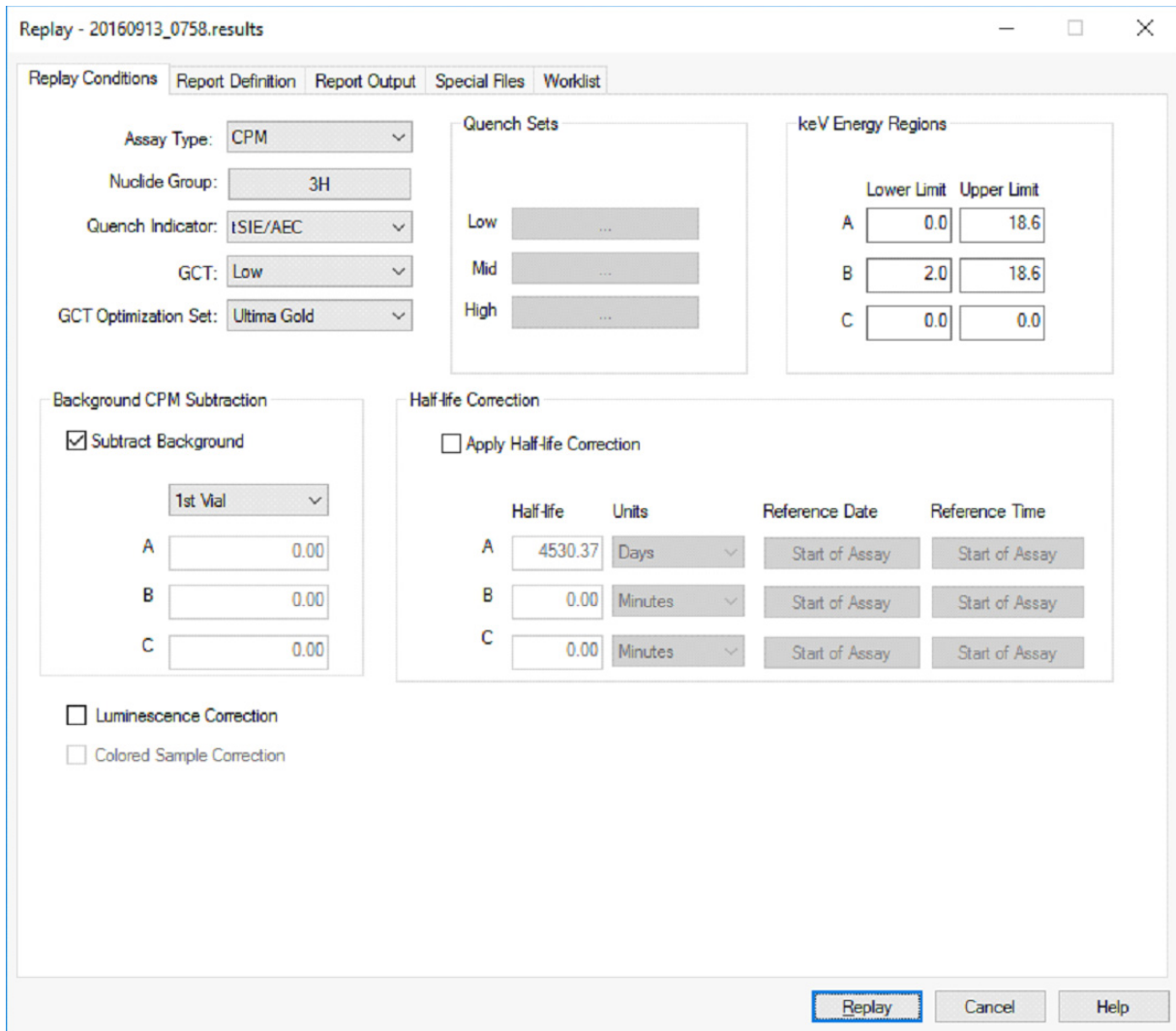


Figure 2-27. Replay Conditions Tab (Replay Window).

## How to Calculate Radioactive Decay

1. Select **Tools | Nuclide Decay** from the menu bar. The *Radionuclide Decay* window appears (Figure 2-28).

The screenshot shows a software window titled "Nuclide Decay" with a close button (X) in the top right corner. The window contains several input fields and buttons:

- Nuclide:** A drop-down menu showing "210Po".
- Half-Life:** A text input field containing "138.35".
- Half-Life Units:** A drop-down menu showing "Days".
- DPM Activity:** A text input field containing "40000".
- Reference Date:** A date picker showing "2 July 2016".
- Reference Time:** A time picker showing "09:14:23".
- Current DPM Activity:** A text input field containing "27470.67".

Buttons are located on the right side of the window:

- Close** (top right)
- Help** (middle right)
- Start Decay** (bottom right, highlighted with a blue border)
- Copy Activity** (bottom right)

**Figure 2-28. Nuclide Decay Window.**

- 1.0.1 From the **Nuclide** drop-down list, select a nuclide of interest. If the desired nuclide does not appear in the list, select **Manual** to manually enter nuclide half-life information in the **Half-Life** and **Half-Life Units** fields.
- 1.0.2 Type the appropriate information in the **Reference DPM Activity**, **Reference Date**, and **Reference Time** fields.
2. When finished, click the **Start Decay** button. The current DPM nuclide appears in the **Current DPM Activity** field.
3. For convenience, the calculated DPM can be copied to the clipboard by clicking on the **Copy Activity** button.

## Chapter 3

# System Software

The QuantaSmart program is the Windows interface for the Tri-Carb Liquid Scintillation Analyzer series of instruments. This tool allows users to access all instrument features via a main software window using standard Windows conventions, and grants easy access to all system capabilities. QuantaSmart also provides graphic representations of existing assay associations in the **Protocols** tree and data analyses in the *Output Report* and *SpectraView*<sup>™</sup> windows. Collected assay data may be reanalyzed without sample recounts via the system's optional Replay feature.

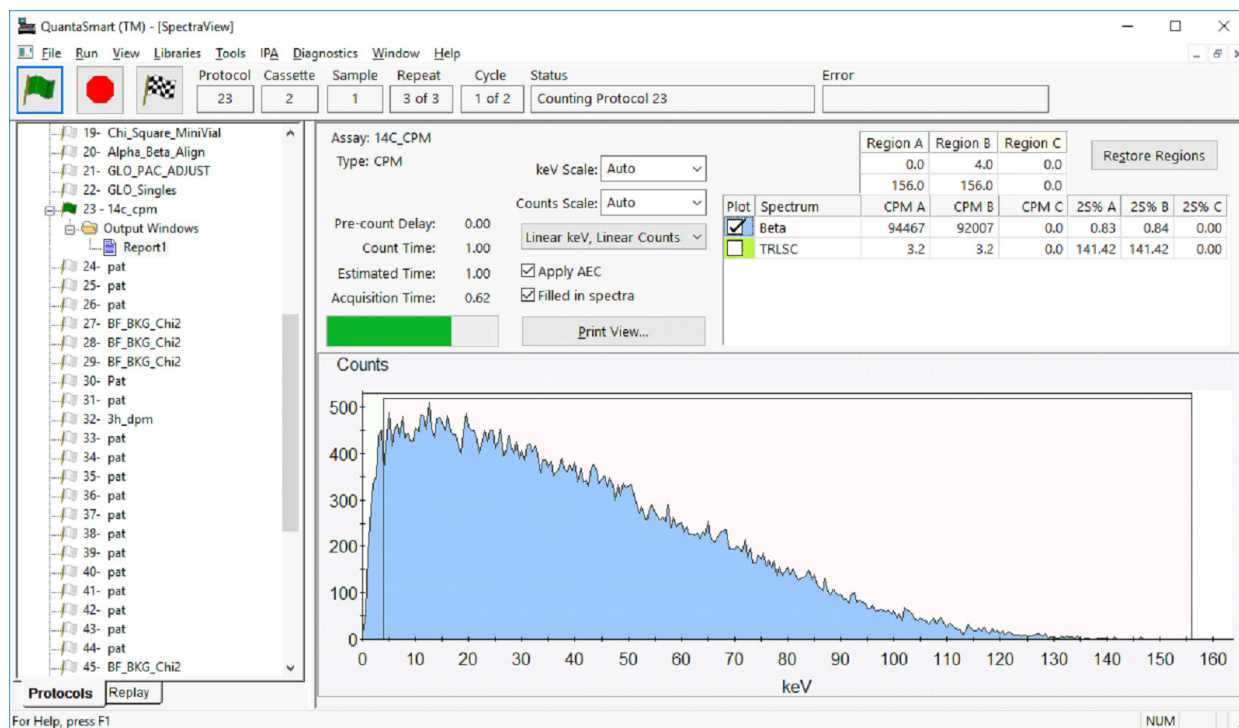
The system utilizes a set of Libraries to store standard and sample information. For systems equipped with the single/dual label DPM feature, the Sample Nuclides Library allows the flexibility of selecting and using the same standards sets in various assays, plus creates a convenient way of saving and reusing specific nuclide parameters and sample counting regions.

### **Software Security**

Security is built into the QuantaSmart software; the same software cannot be loaded on multiple systems due to this feature.

## Main Window

The main software window (Figure 3-1) is made up of functional elements that allow users to access all instrument features.



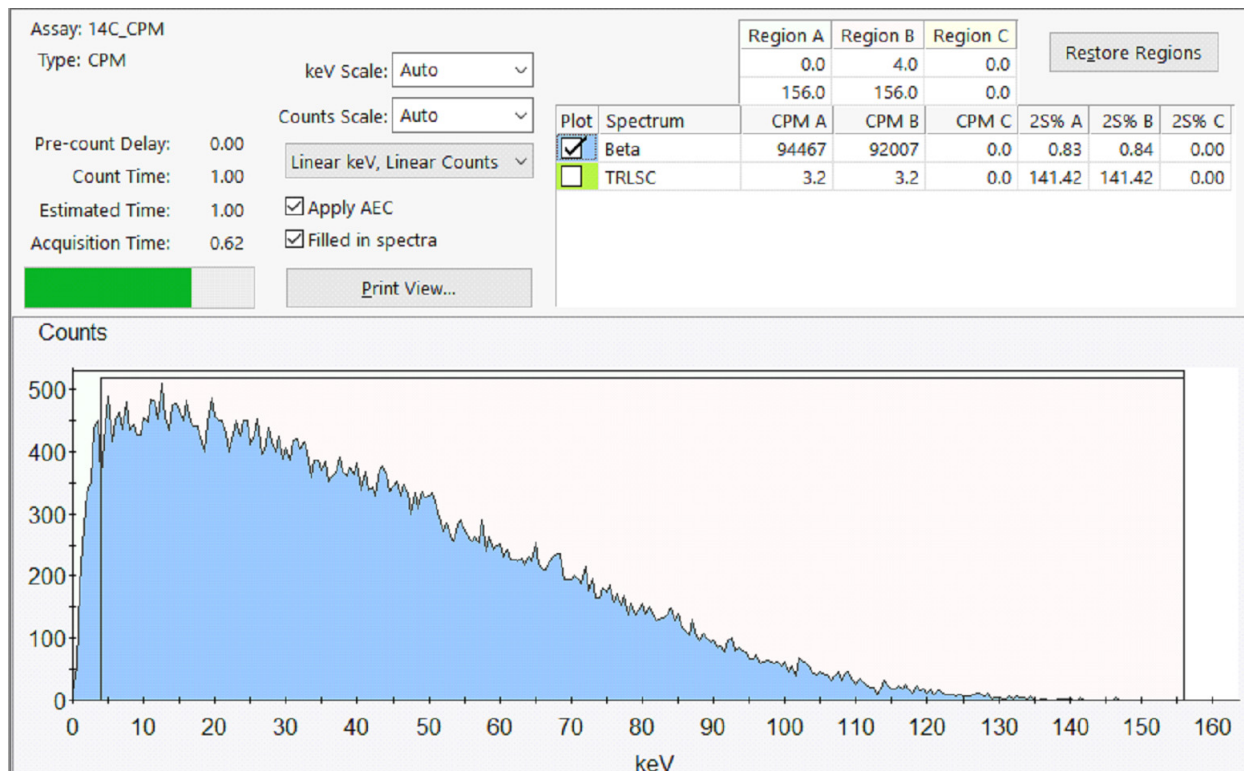
**Figure 3-1. Main Window.**

The following information discusses the elements of the main window:

- SpectraView Window (page 55)
- Instrument Status Bar (page 58)
- Protocols Tree (page 60)
- Replay Tree (page 62)
- Output Window (page 63)
- Menu Bar (page 63)

## SpectraView Window

The *SpectraView* window (Figure 3-2) is part of the main window. The *SpectraView* window displays a two-dimensional, real-time view of the spectrum for a current sample. The spectrum is updated every six seconds, and can be displayed using linear or logarithmic axes. It provides information about a sample count status, and region settings used in the counting procedure. Several display options are available for the spectrum, and other defined elements in this window.



**Figure 3-2. SpectraView Window.**

The *SpectraView* window is typically used for:

- Monitoring sample counting
- Detecting spectral distortions or compressions resulting from sample quench
- Observing the effect of altering counting region settings
- Viewing the spectrum in a linear or logarithmic scale

The X-axis of the spectral display represents energy (in keV) for each counting channel up to the defined endpoint of the sample spectrum. The Y-axis represents the gross counts for the current sample. Regions settings are graphically displayed using solid line boxes.

The following information describes the fields in the *SpectraView* window:

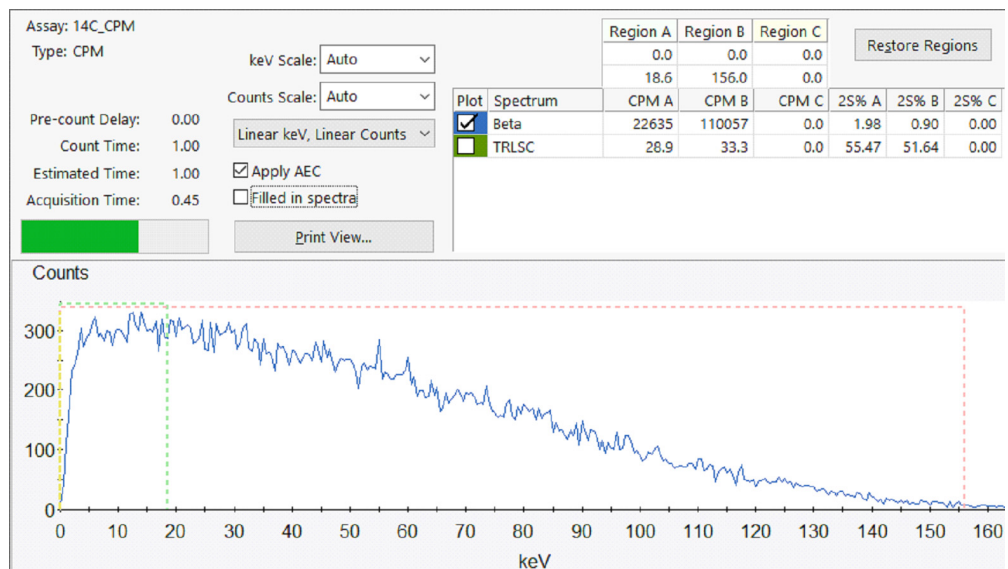
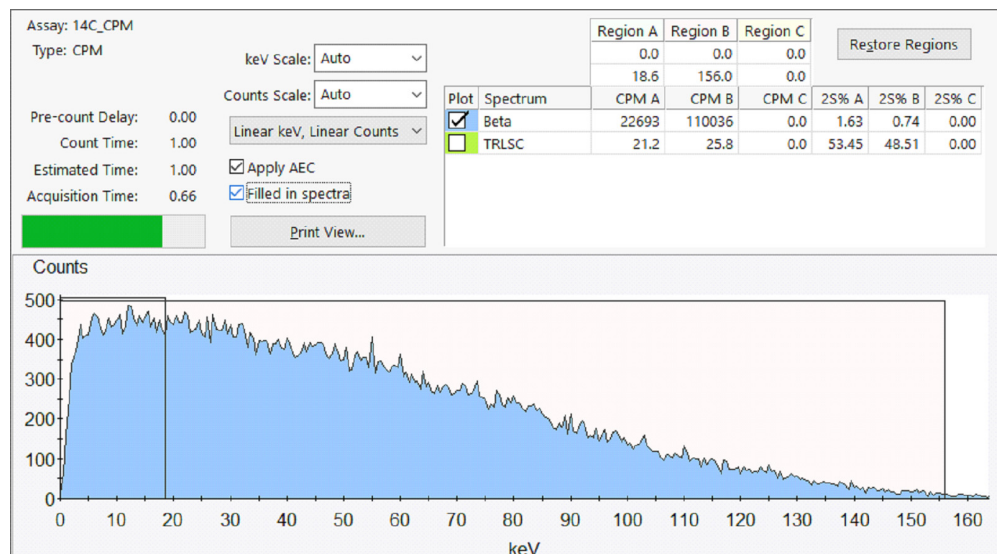
- **Assay** – The name of the assay being counted
- **Type** – The type of assay as selected from the New Assay dialog
- **Pre-count Delay** – This field indicates the time which each sample will remain in the instrument's detection chamber prior to counting.



*Note: This process is dark adaption. It allows luminescence emanating from a vial to dissipate prior to counting. Luminescence can distort the count statistics of the sample and is particularly problematic with low count rate samples.*

- **Count Time** – This field indicates the time which each sample is counted, as defined in the assay. When the external standard is being counted, this changes to “ES Count Time” and shows the time requested for counting the external standard. If the count is sigma terminated, the maximum count time is 10 minutes.
- **Estimated Time** – This shows how long the count will last to reach the requested sigma count statistics. If sigma termination is not being used, this value will match the count time.
- **Acquisition Time** – This is the length of time which the current sample has been counting.
- **Progress bar** – This shows the progress towards finishing the current count for a sample including measurement of the external standard and the sample.
- **keV Scale** – This value sets the ending energy range used for the graph. Select **Auto** to scale from 0 to the largest energy region. Select a region to scale the graph to both the lower and upper energy range. Use **Auto** to reset the lower energy range.
- **Counts Full Scale** – This value sets the maximum Y value used for the graph. Select **% Max** to scale each of multiple spectra to the proportion of their highest value. This allows easy visual comparison of peaks between spectra.
- **Linear keV Scale** – Displays the X-axis using a linear scale. This is the default setting for the X-axis scale.





- **Log keV Scale** – Displays the X-axis using a logarithmic keV scale. The default setting plots the X-axis using a linear scale.
- **Log keV/Log Counts Scale** – Displays keV and counts using a logarithmic scale. This setting is for visual representation only.
- **Apply AEC** – If tSIE/AEC is selected as the quench indicating parameter for the assay, the sample spectrum can be displayed with or without Automatic Efficiency Correction (AEC). Activating this feature will adjust the region settings to account for sample quench. Select this checkbox to display the sample spectrum using AEC.

- **Filled in spectra** – Check to draw spectra and regions in solid colors. Uncheck to draw as lines.
- **Print View** – Print View - Click this button to print the current SpectraView display.
- **Regions Grid** – This shows the energy ranges used to calculate CPM in the spectrum grid. If an invalid energy range is entered, the background changes to red. Adjust the values so that the first row is less than or equal to the second row. Region color is indicated by the background color of the column header. When Filled in spectra is checked, regions will be drawn on the graph as a rectangle behind the data. If not checked, regions are drawn as a dotted line.
- **Spectrum Grid** – This shows the spectra from the counted sample.
  - **Plot** - Check to show the spectrum in the graph. The background color of this checkbox matches the color in the graph.
  - **CPM** – Within the energy regions, background corrected counts divided by the count time
  - **2S%** - Gross uncertainty in a count value with 95% confidence limits.

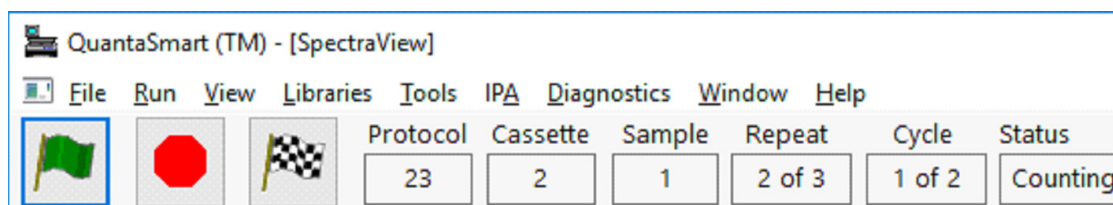


*Note:* When using Filled in spectra to display multiple spectra smaller spectra maybe covered by larger ones. Click on a spectrum in the Spectrum Grid to bring it to the front.

## Instrument Status Bar

This (Figure 3-3) contains a series of GUI buttons to start and stop the instrument, and end a current protocol. The status bar also provides information regarding current protocol status, and displays instrument messages.

The status bar is located at the top of the main window.



**Figure 3-3. Instrument Status Bar.**

**Start/Resume Counting Button**

Click this button to begin a counting protocol.



**Figure 3-4. Start/Resume Counting Button.**

**Pause/Stop Counting Button**

Click this button to end the current protocol and stop the instrument.



**Figure 3-5. Pause/Stop Counting Button.**

**End Protocol Button**

Click this button to end a counting protocol and continue counting the next protocol.



**Figure 3-6. End Protocol Button.**

## Protocols Tree

The **Protocols** tree, displayed in the **Protocols** tab (Figure 3-7), displays 15 - 60 available protocol flag numbers (depending on the Tri-Carb model and configuration) and assay names associated with the flag numbers. Existing reports are also shown in this view.

During protocol execution, this window uses various symbols to provide a visual indication of which protocol is being executed, which have remaining cycles, and which are completed.

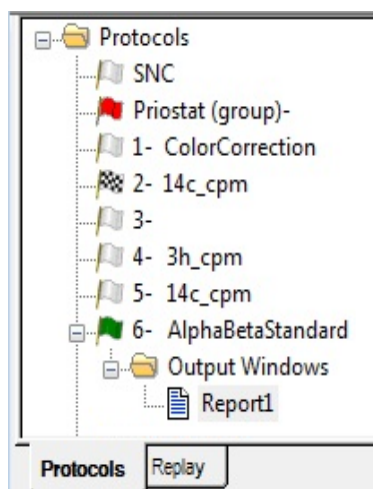




Figure 3-7. Protocols Tree.


## Protocol Tree Symbols


When a sample counting cycle begins, the protocol flag associated with this assay will change from white or yellow to green.


These protocol flags are listed below:


The Priostat flag  is the only flag in the **Protocols** tree that is normally red. It will turn from red to green when Priostat protocol begins.


A yellow flag  in the **Protocols** tree indicates that at least one count cycle for this assay has been completed, but that the protocol has remaining count cycles. This yellow flag will also appear if the protocol for a Priostat operation is interrupted.

A checkered flag  is displayed when all count cycles for the assay are completed.

A red prohibitory symbol  indicates that a protocol cannot be counted. Typically, this will result when no assay is associated with a protocol flag number that the instrument has detected. This symbol could also indicate that an assay file has been deleted.


A yellow prohibitory symbol  indicates that data analysis cannot be performed. Typically, this results when an appropriate standard set is missing from the Nuclides Library, or has been modified in the Library, but not recounted after changes were made.

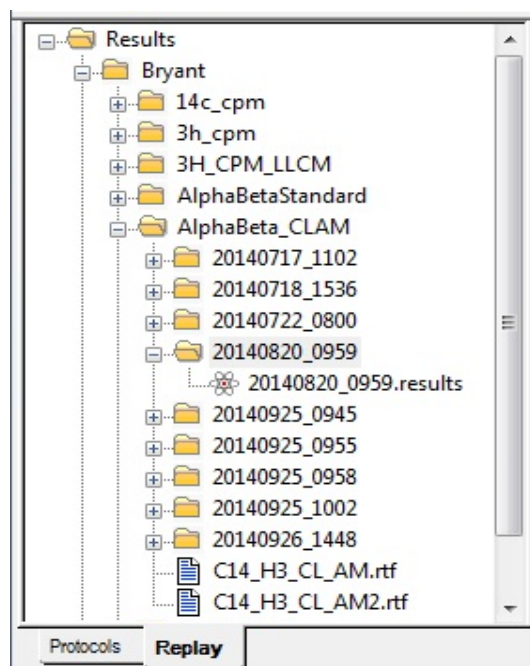
The page symbol  indicates that a report has been defined for this assay. The report name appears beside this symbol in the **Protocols** tree.

A white flag  indicates an inactive protocol. If no assay name appears adjacent to this flag, it is available to be associated to an assay.

## Replay Tree

The **Replay** tree, displayed in the **Replay** tab (Figure 3-8), displays a directory of folders containing previously collected data reanalyzed using different data reduction conditions without recounting samples.

 *Note: This feature may be optional. Contact your PerkinElmer representative for details.*



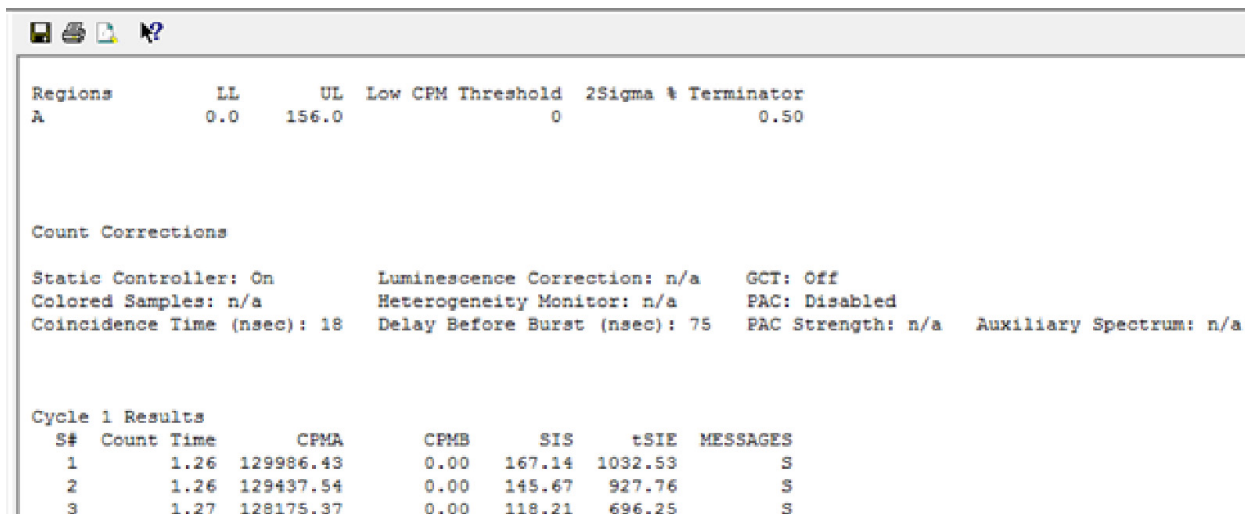
**Figure 3-8. Replay Tree.**

The Replay files have a fixed data storage path, but data can be exported to user-defined paths.

## Output Window

This window (Figure 3-9) is a multi-purpose window displaying various data items and assay parameters, and is a copy of the printer report (if selected). The output is defined in the **Report Definition** (page 125) and the **Report Output** tabs (page 134) of the *Assay Definition* window.

Figure 3-9 shows a typical *Output* window display.



Regions	LL	UL	Low CPM Threshold	2Sigma	% Terminator
A	0.0	156.0	0		0.50

Count Corrections						
Static Controller: On	Luminescence Correction: n/a	GCT: Off				
Colored Samples: n/a	Heterogeneity Monitor: n/a	PAC: Disabled				
Coincidence Time (nsec): 18	Delay Before Burst (nsec): 75	PAC Strength: n/a	Auxiliary Spectrum: n/a			


  

Cycle 1 Results							
S#	Count	Time	CPMA	CPMB	SIS	tSIE	MESSAGES
1	1.26	129986.43	0.00	167.14	1032.53		S
2	1.26	129437.54	0.00	145.67	927.76		S
3	1.27	128175.37	0.00	118.21	696.25		S

Figure 3-9. Output Window (Report Output Tab).

## Menu Bar

Located at the top of the QuantaSmart main window (Figure 3-10), the menu bar includes the **File**, **Run**, **View**, **Libraries**, **Tools**, **IPA**, **Diagnostics**, **Window**, and **Help** menus, each offering various selections and commands.

 *Note:* Some menu items include optional features. If your instrument is not equipped with these options, the corresponding menu items will be disabled.

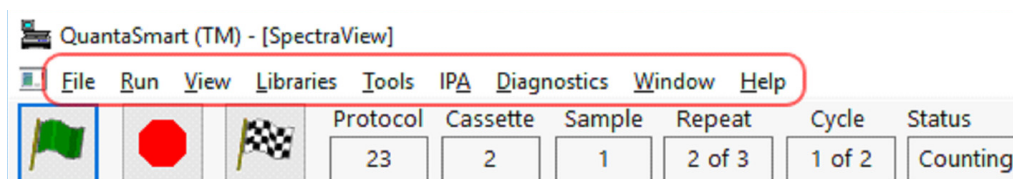


Figure 3-10. Menu Bar.

## File Menu

To display the **File** menu (Figure 3-11), select **File** from the menu bar.

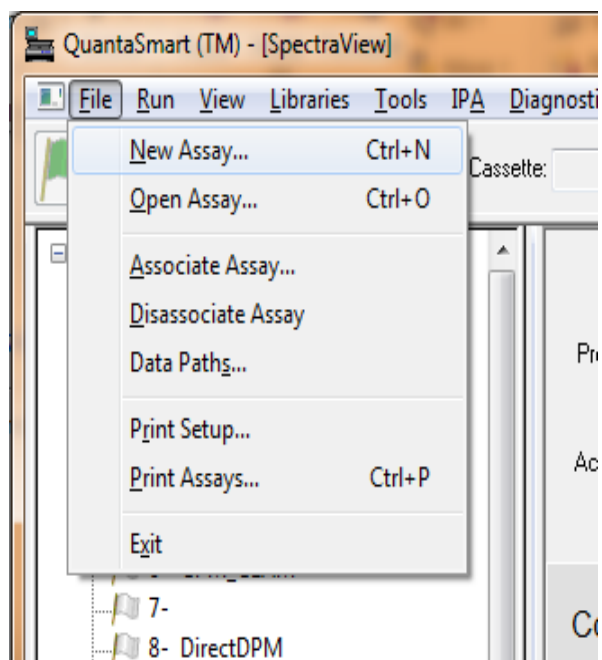


Figure 3-11. File Menu.



## New Assay

This menu item allows users to define a new assay. Select **New Assay** to open the *Select Assay Type* window (Figure 3-12). Refer to page 97 for information on assay types.

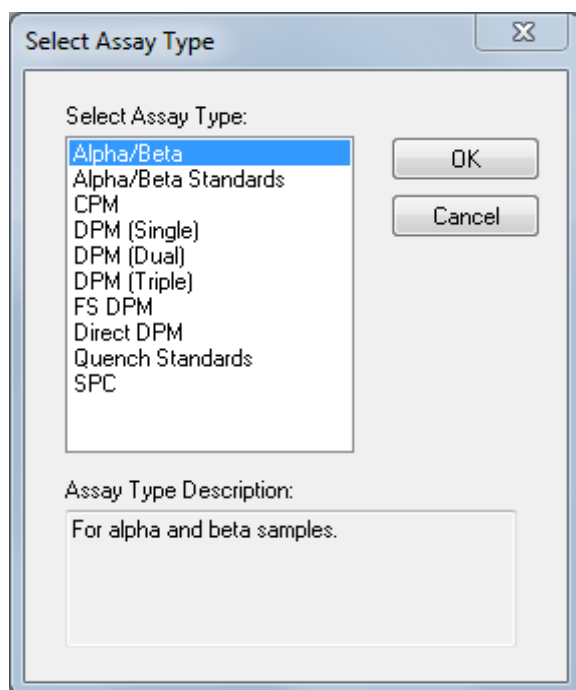


Figure 3-12. Select Assay Type.

Select an assay type and click **OK** to open the *Assay Definition* window (page 115) to define parameters for a new assay.

## Open Assay

Select to open the *Open Assay* window. From this window, select and open an existing assay.

## Associate Assay

Before selecting this function, select a protocol flag from the **Protocols** tree. Once done, select **File | Associate Assay** to open the *Associate Assay* window to select an assay to associate (link) with the protocol flag number.

Alternatively, associate an assay by right-clicking on a protocol flag number and selecting **Associate Assay** from the menu displayed.

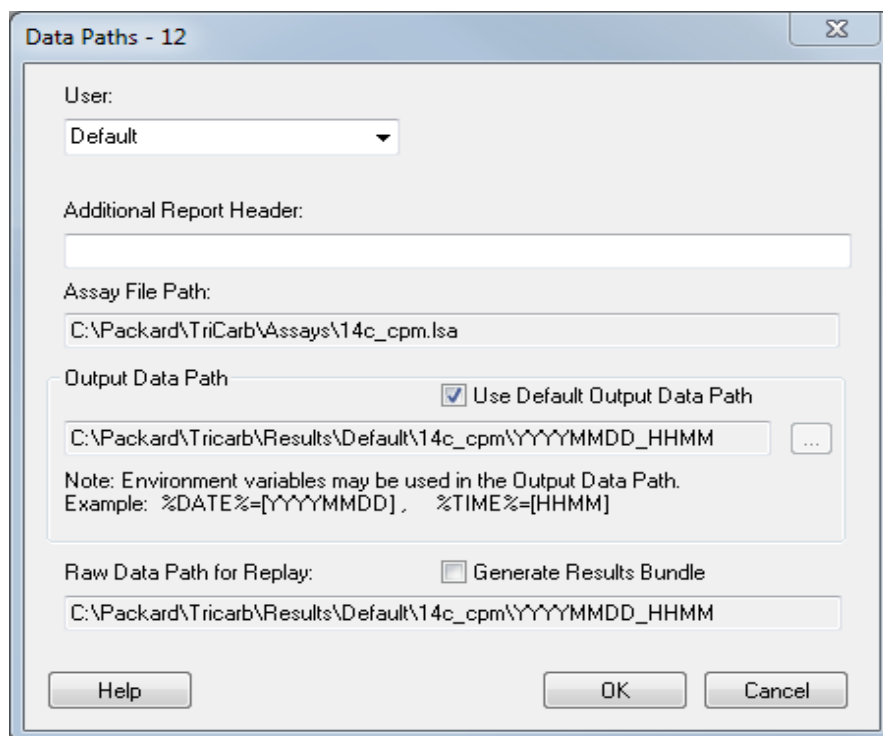
### Disassociate Assay

Before selecting this function, select a protocol flag from the **Protocols** tree. Once done, disassociate the assay linked to the protocol flag number by selecting **File | Disassociate Assay**. The assay name will disappear from the **Protocols** tree.


Alternatively, users may disassociate an assay by right-clicking on a protocol flag number, and selecting **Disassociate Assay** from the menu displayed.

### Data Paths

Select this function to open the *Data Paths* window (Figure 3-13). From this window, specify a location for storing data files generated by an assay. Users may also select this location based on additional applications used to process data, or comply with data storage strategy in a facility. Users may also save data to the default directory by selecting the **Use Default Output Data Path** checkbox.



**Figure 3-13. Data Paths Window.**

 *Note:* This information is stored on a per protocol basis, as indicated in the title bar of the Data Paths window (Figure 3-13).

### Print Setup

Select this function to open the *Print Setup* window. From this window, users can define print parameters.

## Print Assays

Select this function to open the *Select Assays to Print* window. From this window, select an assay, and then print a list of parameters defined for that assay.

## Exit

Select to close the QuantaSmart program.

## Run Menu

To display this menu (Figure 3-14), select **Run** from the menu bar.

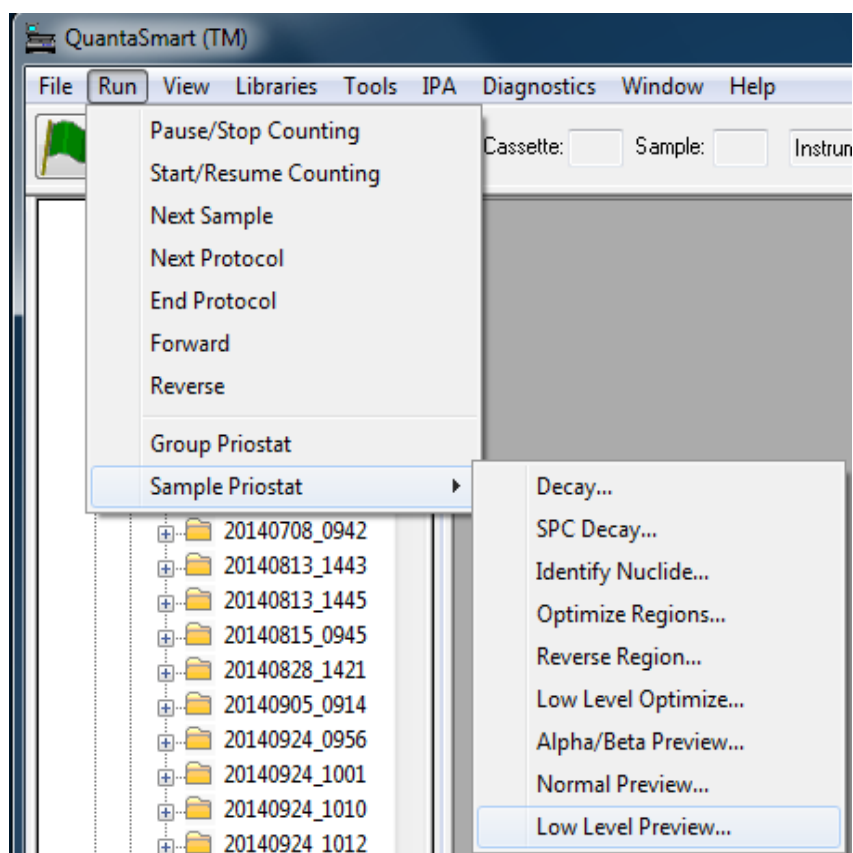


Figure 3-14. Run Menu with Priostat Sub-menu.

## Start/Resume Counting

Select this function to have the instrument load a sample currently at the detector position, and then begin counting. This command is also available when clicking the green flag icon button (Figure 3-4) on the Instrument Status Bar.

## Next Sample

Select this function to have the instrument unload any sample in the detector, move the next sample into the detector, and start counting.

### **Next Protocol**

Select this function to have the instrument unload any sample in the detector, and abort the current protocol. The instrument searches for the next cassette with an active protocol flag, and then begins running that protocol.

### **Pause/Stop Counting**

Select this function to end the current protocol, and stop the instrument. This command is also available when clicking the red flag icon button (Figure 3-5) on the Instrument Status Bar.

### **End Protocol**

Select this function to have the instrument unload any sample in the detector and end the protocol; data reduction continues until data from the last counted sample is reported. The system then begins counting the next protocol. This command is also available when clicking the checkered flag icon button (Figure 3-6) on the Instrument Status Bar.

### **Forward**

Select this function to have the instrument unload any sample in the detector, and move the sample changer in a counterclockwise direction.

### **Reverse**

Select this function to have the instrument unload any sample in the detector, and move the sample changer in a clockwise direction.

### **Group Priostat**

This menu item allows users to count a set of high priority samples immediately, while temporarily interrupting a current protocol. Refer to page 192 for more information.

### **End Group Priostat**

This menu item stops counting of the Priostat (priority) samples, and resumes counting interrupted samples.

## Sample Priostat



*Note: This feature may be optional. Contact your PerkinElmer representative for details.*

Sample Priostat (page 193) is a special interrupt mode that allows users to:

- preview sample count rates
- determine optimal counting conditions for variable and constant quench samples
- identify an unknown nuclide in a sample
- determine the duration of luminescence

The **Sample Priostat** menu item has the following options:

### Decay

This allows users to assess the duration of luminescence (light) in a radioactive sample via a decay histogram.

### SPC Decay

This allows users to assess the duration of luminescence in a non-radioactive, luminescent sample via a decay histogram.

### Identify Nuclide

This allows users to identify an unknown nuclide in a sample using the Quench Indicating Parameters SIS and tSIE.

### Optimize Regions

This allows users to optimize sample counting regions to provide the highest figure of merit for Normal count mode.

### Reverse Region

This allows users to re-optimize sample counting region settings for a sample, and determine equivalent unquenched region settings for variable quench samples.

### Low Level Optimize

This allows users to optimize sample counting regions to provide the highest figure of merit for Low Level count mode.

### Alpha/Beta Preview

This allows users to view a sample spectrum in the Alpha/Beta mode, and approximate activity for a sample containing both an Alpha and a Beta emitting nuclide.

### Normal Preview

This allows users to view the sample spectrum, and approximate activity for a sample using Normal count mode.

### Low Level Preview

This allows users to view the sample spectrum, and approximate activity for a sample using Low Level count mode.

## View Menu

To display the **View** menu (Figure 3-15), select **View** from the menu bar.

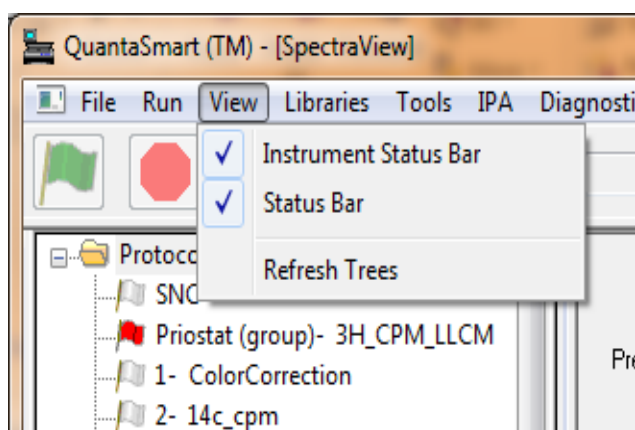


Figure 3-15. View Menu.

The **View** menu includes the following options:

### **Instrument Status Bar**

Select to view or hide the Instrument Status Bar and its buttons (Figure 3-3). The Instrument Status Bar is located beneath the menu bar in the main window.

### **Status Bar**

Select to view or hide the Status Bar located at the bottom of the main window.

### **Refresh Trees**

Select to update the **Protocols** and **Replay** trees in the main window. The Replay tree is automatically updated when a new assay is counted. The **Refresh Trees** command is only necessary to clear report entries from tree displays.

## Security Menu

The **Security** menu (Figure 3-16) is only present when the Enhanced Security option is installed. Please read the PDF “Tri-Carb Enhanced Security Option” for details about how to use Enhanced Security features.

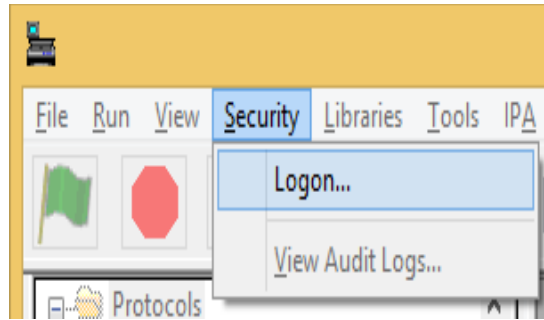


Figure 3-16. Security Menu.

The **Security** menu includes the following options:

### Logon

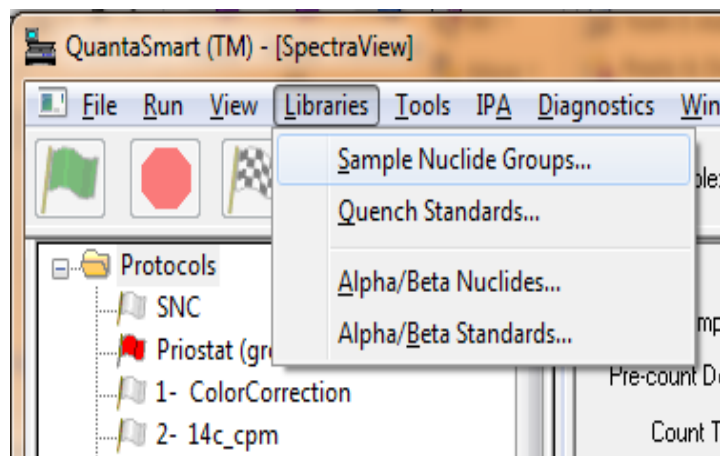
Select to access the **Security** option.

### View Audit Logs

Select to view security audit logs compiled by the system.

## Libraries Menu

To display this menu (Figure 3-17), select **Libraries** from the menu bar.



**Figure 3-17. Libraries Menu.**

Radionuclide information is stored and accessed in the Nuclide Library. The Nuclide Library consists of the Sample Nuclides and Quench Standards Libraries. If your instrument is equipped with an Alpha/Beta option, the Alpha/Beta Nuclides Library and Alpha/Beta Standards Library will also be included.

The Sample Nuclides Library allows users to specify and save nuclide names, counting region limits, and quench sets for sample nuclides. Up to three nuclides can be defined for each entry to support counting of multiple nuclides. These sample nuclide parameters are typically specified as part of the assay definition process, and may be edited (as needed).

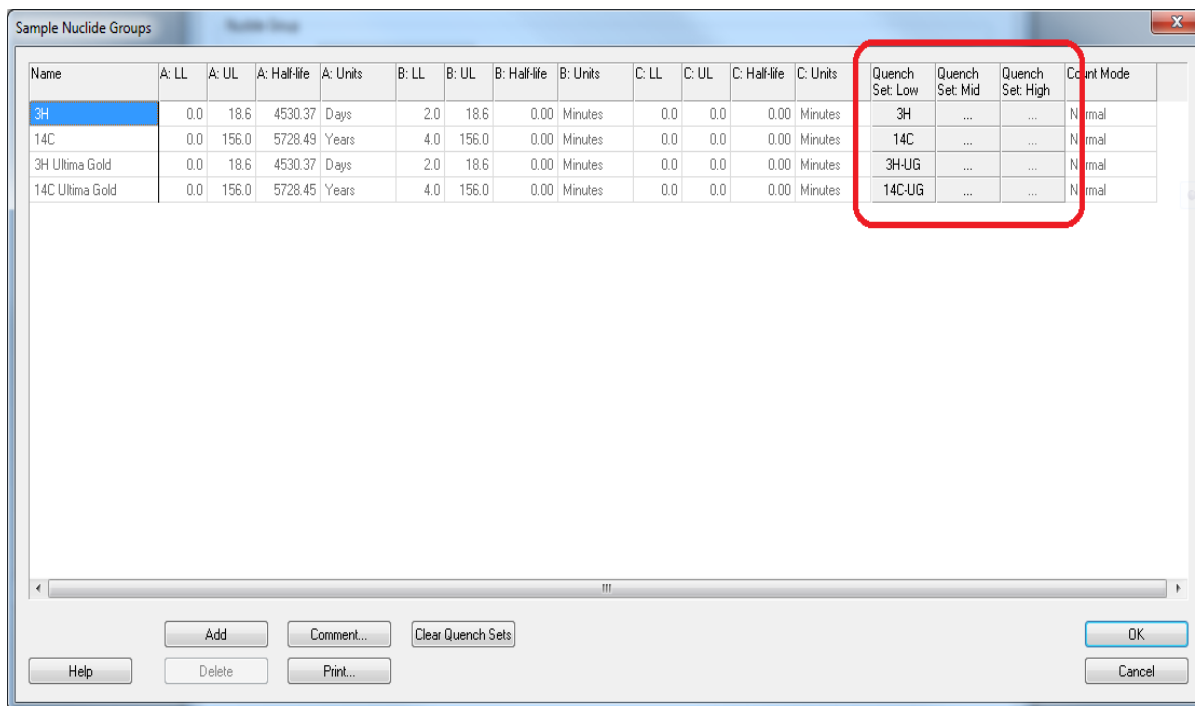
The Quench Standards Library is comprised of quench sets, with each quench set containing individual quench standards. Quench standard data is used to construct quench curves for calculating DPM in DPM assays. Quench Standards are counted once, and the entire spectrum for each quench standard stored independent of assay information. This enables users to select and use the same quench set in various assays, and construct a quench curve for each sample when counted.

The Alpha/Beta Standards and Alpha/Beta Nuclides Libraries (may be optional) are used in the same manner as Quench Standards and Sample Nuclides Libraries. Information stored in these libraries is relevant only when performing Alpha/Beta assays, where both an Alpha-emitting and a Beta-emitting radionuclides are quantified independently in the same sample vial.



## Sample Nuclides Groups

Select to display the *Sample Nuclides Groups* window (Figure 3-18) to enter information into (and retrieve information from) the Sample Nuclides Library. This Library is a repository of information on sample nuclides.



**Figure 3-18. Sample Nuclides Groups Window (Sample).**

For assays, use the Sample Nuclides Library to define and save nuclide names, and counting region limits for radionuclides. Users can also select a quench set for each sample nuclide with the Quench Set buttons in this window (Figure 3-18).


In Replay (page 209), use the Sample Nuclides Library to select a radionuclide for the purpose of reanalyzing sample data.



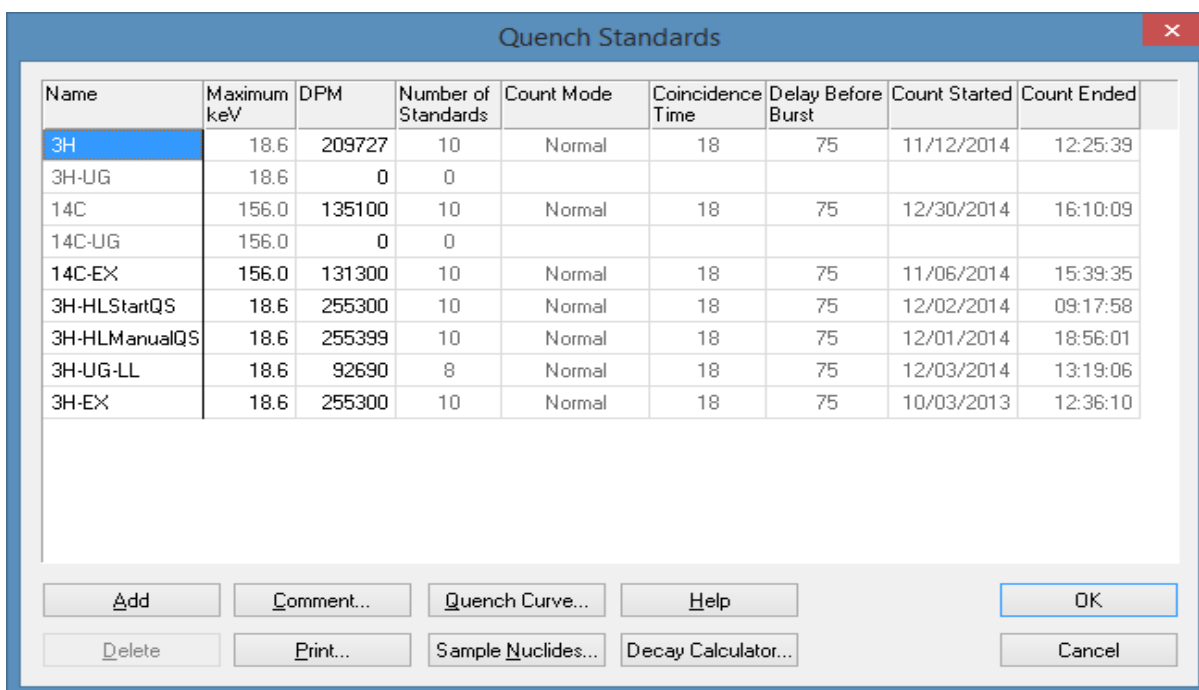
*Note:* Fields enabled in the Sample Nuclides Library will differ when accessed from various locations in QuantaSmart. The list of nuclides displayed are dependent on assay type, nuclide, and quench sets associated with the nuclide. See the Libraries chapter for information on adding a sample nuclide name.

### Quench Standards

Display the *Quench Standards* window (Figure 3-19) to define a new quench set to be stored, or select a quench standards set for DPM assays or data reanalysis in Replay. Quench sets data is used to construct quench curves for determining sample DPM.

 *Note:* The **Name**, **Max keV**, and **DPM** fields are the only entries required when entering a new quench set. Remaining parameters stored in the library are retrieved from assay parameters selected when defining an assay. The number of standards (up to 20) is determined automatically during counting.

For additional information, refer to the *Libraries* chapter (Chapter 5).



Name	Maximum keV	DPM	Number of Standards	Count Mode	Coincidence Time	Delay Before Burst	Count Started	Count Ended
3H	18.6	209727	10	Normal	18	75	11/12/2014	12:25:39
3H-UG	18.6	0	0					
14C	156.0	135100	10	Normal	18	75	12/30/2014	16:10:09
14C-UG	156.0	0	0					
14C-EX	156.0	131300	10	Normal	18	75	11/06/2014	15:39:35
3H-HLStartQS	18.6	255300	10	Normal	18	75	12/02/2014	09:17:58
3H-HLManualQS	18.6	255399	10	Normal	18	75	12/01/2014	18:56:01
3H-UG-LL	18.6	92690	8	Normal	18	75	12/03/2014	13:19:06
3H-EX	18.6	255300	10	Normal	18	75	10/03/2013	12:36:10

Buttons: Add, Comment..., Quench Curve..., Help, OK, Delete, Print..., Sample Nuclides..., Decay Calculator..., Cancel

**Figure 3-19. Quench Standards Window (Sample).**

## Alpha/Beta Nuclides



*Note:* This feature may be optional. Contact your PerkinElmer representative for details.

Display the *Alpha Beta Nuclides* window (Figure 3-20) to add information to or delete information from the Alpha/Beta Nuclides Library. This Library is a repository of information for previously defined Alpha and Beta emitting nuclides counted in Alpha/Beta assays.

For additional information, refer to the *Libraries* chapter (Chapter 5).

Name	Standard Set	Beta A: LL	Beta A: UL	Beta A: Half-Life	Beta A: HL-Units	Beta B: LL	Beta B: UL	Beta B: Half-Life	Beta B: HL-Units	Alpha: LL	Alpha: UL	Alpha: Half-Life	Alpha: HL-Units	Lower Discriminator	Upper Discriminator	Count Mode
GCT Calibration	...	0.0	7.0	0.00	Minutes	0.0	2000.0	0.00	Minutes	0.0	1000.0	0.00	Minutes	120	120	
AB Manual	...	0.0	2000.0	0.00	Minutes	0.0	0.0	0.00	Minutes	0.0	1000.0	0.00	Minutes	190	190	
AB Align	...	0.0	1000.0	0.00	Minutes	0.0	0.0	0.00	Minutes	0.0	1000.0	0.00	Minutes	1	1	
AB AMSR	AB AmSr	0.0	750.0	0.00	Minutes	0.0	0.0	0.00	Minutes	100.0	500.0	0.00	Minutes	141	141	Normal
AB SRAM	...	30.0	1000.0	0.00	Minutes	0.0	2000.0	0.00	Minutes	125.0	400.0	0.00	Minutes	106	106	
MWB-AB-histo	MWB-36CL-241AM	0.0	2000.0	0.00	Minutes	0.0	0.0	0.00	Minutes	0.0	1000.0	0.00	Minutes	116	116	Normal
MWB-test	...	0.0	2000.0	0.00	Minutes	0.0	1000.0	0.00	Minutes	0.0	1000.0	0.00	Minutes	50	50	

Buttons: Help, Add, Delete, Comment..., Print..., OK, Cancel

**Figure 3-20. Alpha Beta Nuclides Window (Sample).**

### Alpha/Beta Standards

Display the *Alpha Beta Standards* window (Figure 3-21) to add information to or delete information from the Alpha/Beta Standards Library. This Library is a repository of information for previously defined standards used in Alpha/Beta assays.

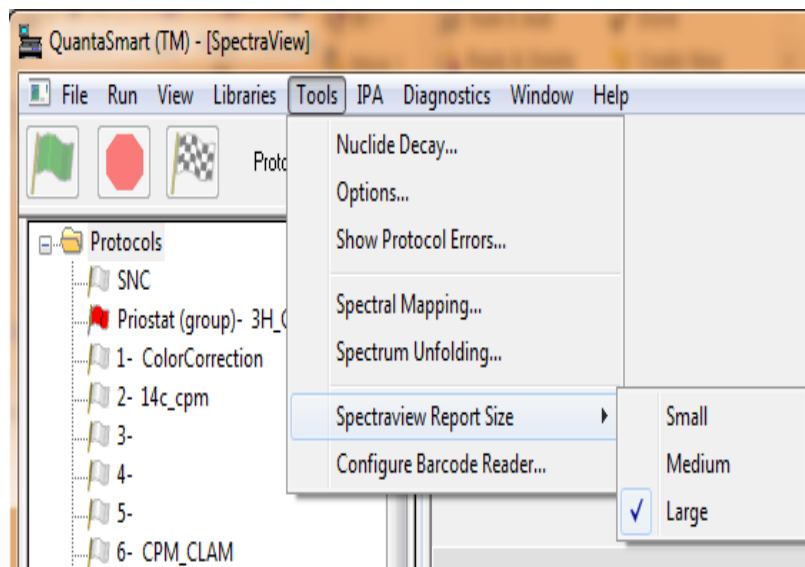
For additional information, refer to the *Libraries* chapter (Chapter 5).

Name	Beta LL	Beta UL	Alpha LL	Alpha UL	Measurement Method	Starting Discriminator	Ending Discriminator	Number of Points	Lower Discriminator Computed	Lower Discriminator In Use	Upper Discriminator Computed	Upper Discriminator In Use	Alpha Standard DPM	Beta Standard DPM	Count Mode	Coincidence Time	Delay Before Burst
A/B Test	0.0	2000.0	0.0	1000.0	Automatic	1	255	10	153	153			0	0	Normal	18	75
rhABtest	30.0	650.0	75.0	225.0	PSA Histogram				109	109	202	202	25068	25032		18	75
PSA Histogram Std	0.0	2000.0	0.0	1000.0	PSA Histogram				138	138	211	211	0	0		18	75
A/B Legacy	0.0	2000.0	0.0	1000.0	Automatic	1	255	10	153	153			0	0	Normal	18	75
PSA Time	0.0	2000.0	0.0	1000.0	PSA Histogram				153	153	153	153	0	0		18	75
A/B Test 2	0.0	2000.0	0.0	1000.0	Automatic	1	255	10	155	155			0	0	Normal	18	75
w17996	0.0	1900.0	0.0	1000.0	PSA Histogram				99	99	121	121	0	0		18	75
MwB-AB-test	50.0	600.0	200.0	600.0	PSA Histogram				139	139	139	139	0	0		18	75
MwB-AB-test2	110.0	200.0	4.0	250.0	PSA Histogram								0	0			
PSA Histogram 2	0.0	2000.0	0.0	1000.0	PSA Histogram				155	155	155	155	0	0		18	75
PSA Histogram 3	0.0	2000.0	0.0	1000.0	PSA Histogram				137	137	212	212	0	0		18	75
Histogram8054Test	0.0	2000.0	0.0	1000.0	PSA Histogram				138	5	211	250	49768	50109		18	75
PSA Histogram 4	0.0	2000.0	0.0	1000.0	PSA Histogram				139	139	211	211	0	0		18	75

Figure 3-21. Alpha Beta Standards Window (Sample).

## Tools Menu

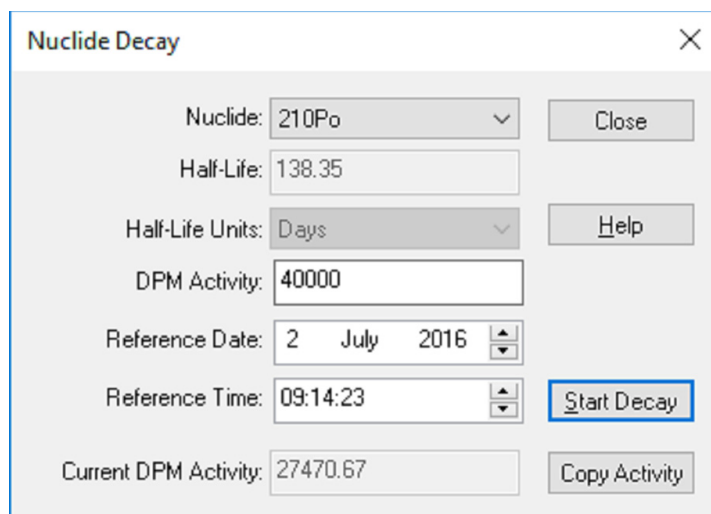
To display this menu (Figure 3-22), select **Tools** from the menu bar.



**Figure 3-22. Tools Menu.**

### Radionuclide Decay

Select to open the *Radionuclide Decay* window (Figure 3-23) to calculate DPM for radionuclides.



The screenshot shows a window titled "Nuclide Decay" with a close button (X) in the top right corner. The window contains the following fields and buttons:

- Nuclide:** A drop-down menu showing "210Po".
- Half-Life:** A text input field containing "138.35".
- Half-Life Units:** A drop-down menu showing "Days".
- DPM Activity:** A text input field containing "40000".
- Reference Date:** A date picker showing "2 July 2016".
- Reference Time:** A time picker showing "09:14:23".
- Current DPM Activity:** A text input field containing "27470.67".
- Buttons:** "Close", "Help", "Start Decay" (highlighted with a blue border), and "Copy Activity".

**Figure 3-23. Radionuclide Decay Window.**

The following information describes fields and buttons in the *Radionuclide Decay* window (Figure 3-23):

- **Radionuclide** – From this drop-down field, select a radionuclide for calculating decay. If a radionuclide is selected from this list, the half-life and half-life units are entered automatically in the corresponding fields. If **Manual** is selected from the **Radionuclide** field, enter the half-life and half-life units for the radionuclide.
- **Half-Life** – If a radionuclide is selected from the **Radionuclide** field, the half-life of that radionuclide is displayed in **Half-Life** field. If **Manual** was selected from the **Radionuclide** field, enter the half-life of the radionuclide.
- **Half-Life Units** – If a radionuclide was selected from the **Radionuclide** field, the half-life units of that radionuclide is displayed in this field. If **Manual** was selected from the **Radionuclide** field, enter the half-life units of the radionuclide.
- **Reference DPM Activity** – Enter the Reference DPM Activity for the radionuclide. This is the DPM of the radionuclide for the Reference Date.

- **Reference Date** – Enter the Reference Date of the radionuclide. This is the date on which the radionuclide has the specified amount of activity.
- **Reference Time** – Enter the Reference Time for the radionuclide. This is the time at which the radionuclide has the specified amount of activity.

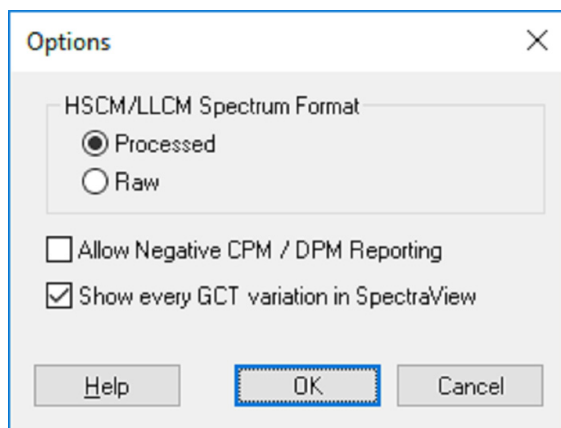


*Note: Typically, this parameter is defined only for radionuclides with very short half-lives.*

- **Current DPM Activity** – This field displays the current DPM activity of a radionuclide after the decay calculation has been performed. This value is displayed after all parameters are specified in the current window, and the **Start Decay** button has been clicked.
- **Start Decay** – Click this button after specifying all parameters in the current window. After clicking the **Start Decay** button, the decay calculation is performed, and current DPM activity is displayed in the **Current DPM Activity** field.
- **Copy Activity** – Click this button to copy the Reference DPM Activity, then paste the activity into the **DPM** field of the *Quench Standards* window.

## Options

Select to open the *Options* window (Figure 3-24). From this window, select a format for the Spectrum Files created in High Sensitivity and Low Level Count Modes, and activate the feature that allows negative CPM and DPM reporting.



**Figure 3-24. Options Menu.**

The options window is used to select various system level settings:

- HSCM/LLCM Spectrum Format – select the type of spectrum data to include for High Sensitivity Count Mode / Low Level Count Mode
- Allow Negative CPM / DPM Reporting – When this is unchecked, all negative values are displayed as zero. Check this box to determine if GCT may be overcorrecting.
- Show every GCT variation in SpectraView – Check this box to show all three flavors of Beta values (GCT off, GCT low and GCT High) to help visualize how GCT is affecting data. Note that GCT correction must not be off in the assay for variations to be displayed.

## Show Protocol Errors

Select to display certain error messages associated with an assay.



## Spectral Mapping

Select to view a three-dimensional spectral map for a sample and quench standards (Figure 3-25). This option is used for single-label DPM samples.

 *Note: Select a protocol flag before applying this command.*

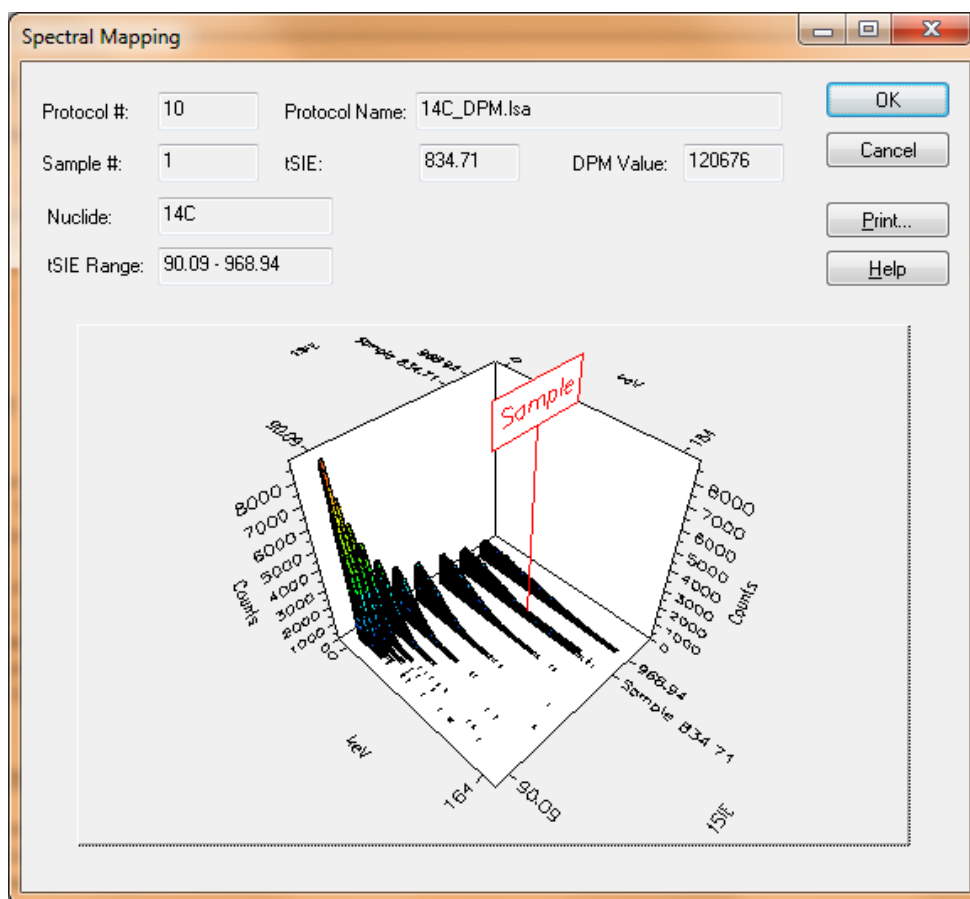


Figure 3-25. Spectral Mapping.

## Spectrum Unfolding

Select to view a three-dimensional display of separated, individual spectra for each nuclide in a Dual-label or Full Spectrum (FS) DPM sample counting procedure (Figure 3-26).

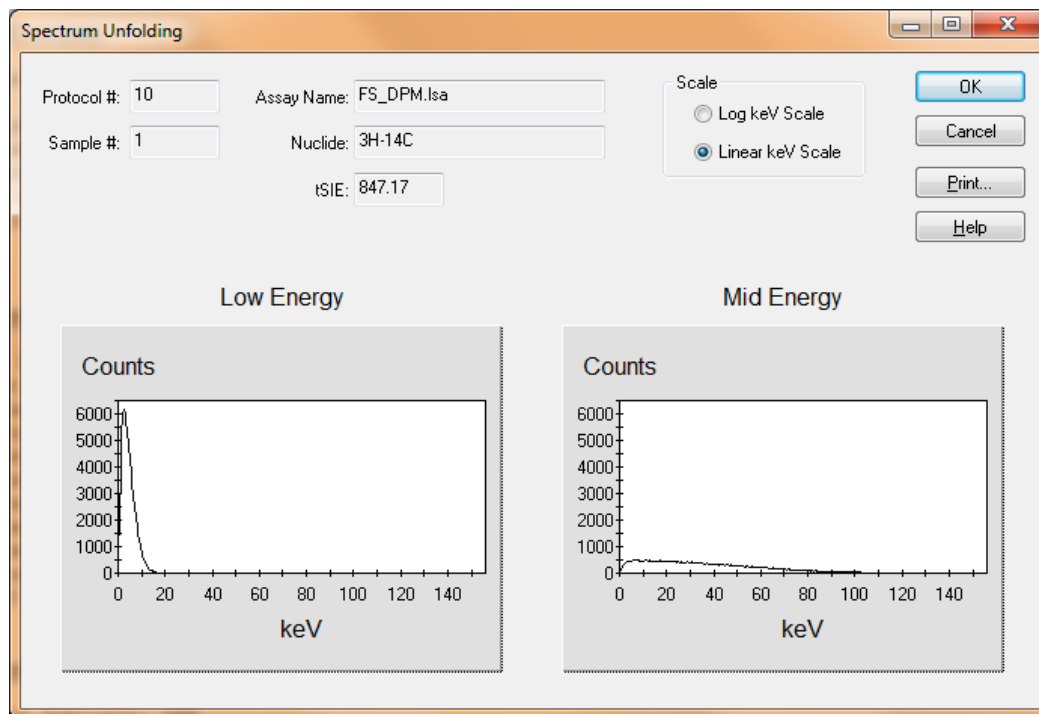



Figure 3-26. Spectrum Unfolding.

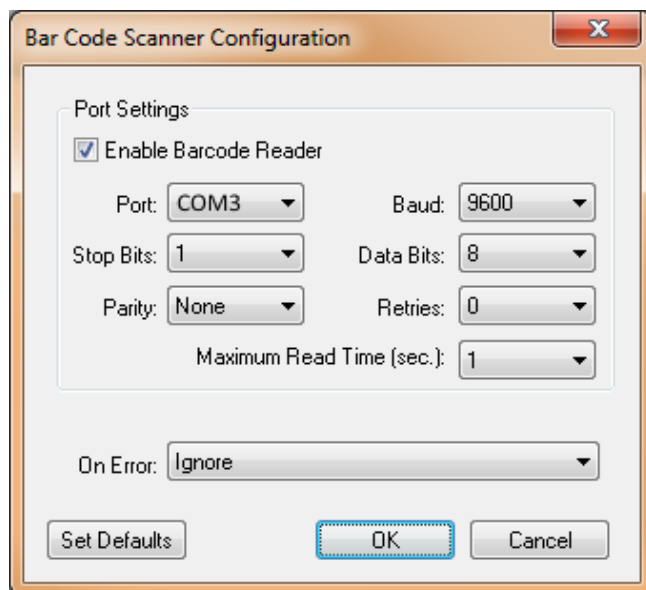
## Spectraview Report Size

Select from this option to choose the size of the spectrum graph in the report output file. This size selection is a global change, affecting all report output files; the size of spectrum graph on screen (in the *SpectraView* window) is unaffected.

## Configure Barcode Reader

 *Note:* This feature may be optional. Contact your PerkinElmer representative for details.

Select this function to open the *Bar Code Scanner Configuration* window (Figure 3-27).



**Figure 3-27. Bar Code Scanner Configuration Window.**

The following information describes fields and buttons in the *Bar Code Scanner Configuration* window:

- **Enable Barcode Reader** checkbox – Select to enable the bar code reader for all assays. When selected, the **Barcode Settings** area (page 150) of the **Assay Details** tab is available (not grayed out). Only select this checkbox if Bar Code Reader option is installed.
- **Port** field – Select the serial port that the bar code reader is using. If unsure which COM port the reader is using, locate the COM port number in Windows Device Manager. In the *Device Manager* window, locate the COM number for **ATEN USB to Serial Cable** (expand the **Ports** category).
- **Stop Bits, Parity, Baud, Data Bits** fields – The default selections in these fields match the settings in the bar code reader configuration file, and need not be modified.

- **Retries** field – Specify the maximum number of times the system should re-read a bar code label if the reader fails to read a label successfully. Once a bar code label is read successfully, the next sample is read.
- **Maximum Read Time (sec.)** field – Specify a maximum time (in seconds) the system must pause to read a bar code. Once the reader successfully reads a label, the next sample is read. The reader does not wait until the full time expires. For example, if the reader reads a label in 0.10 seconds, the next sample is immediately scanned; the reader will not wait the full one second before scanning the next sample.
- **On Error** field – Here, determine the system’s response to missing or unreadable bar codes.
  - ♦ Select **Ignore** to have the system continue processing the current assay, and bypass logging the error.
  - ♦ Select **Abort** to have the system stop processing the current assay when a bar code error occurs. The system then continues to the next assay.
  - ♦ Select **Log Error and Continue** to record the error condition in the report, and proceed with the assay.
- **Set Defaults** button – Click to populate fields with the recommended default settings.
- **OK** button – Click to save bar code configuration settings, and then close the window.
- **Cancel** button – Click to close without saving changes.

## IPA Menu

To display this menu (Figure 3-28), select **IPA** from the menu bar.

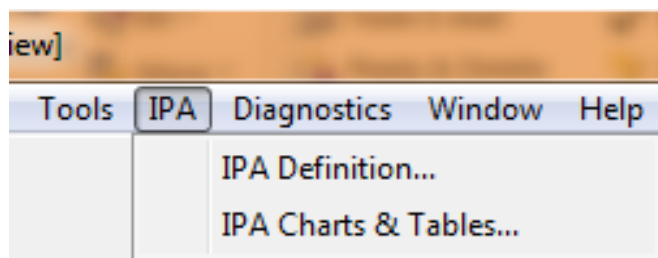


Figure 3-28. IPA Menu.

## IPA Definition

Select to open the *IPA Definition* window (Figure 3-29). From this window, define parameters used to assess instrument performance. For more information, see page 179.

The IPA Definition window is a software interface for configuring instrument performance parameters. It is divided into several sections:

- IPA Parameters:** Contains input fields for 3H Standard DPM (264300), 3H Reference Date (22 April 2009), 14C Standard DPM (132900), Background Count Time (min) (60.00), 3H FOM Threshold (180), and 14C FOM Threshold (380).
- Chi Square Tests:** Includes checkboxes for 3H and 14C, both of which are checked.
- RS-232:** Includes a checkbox for Transmit IPA Data, which is unchecked.
- IPA Data:** Includes a checkbox for Save copy of IPA data to a text file (unchecked) and a File Name field containing C:\Packard\TriCarb\IpaData.txt.
- Baselines:** Includes a field for Number of Datapoints to Establish Baselines (5) and a table for Mean and Limit values for 3H and 14C Background and Efficiency. All values are currently 'In Progress'.

Buttons for Help, OK, and Cancel are located at the bottom of the window.

Figure 3-29. IPA Definition Window.

### IPA Charts & Tables

Select this function to view, edit, and print all instrument performance assessment parameters in chart or tabular form. For more information, see page 183.

*Note:* This feature may be optional. Contact your PerkinElmer representative for details.

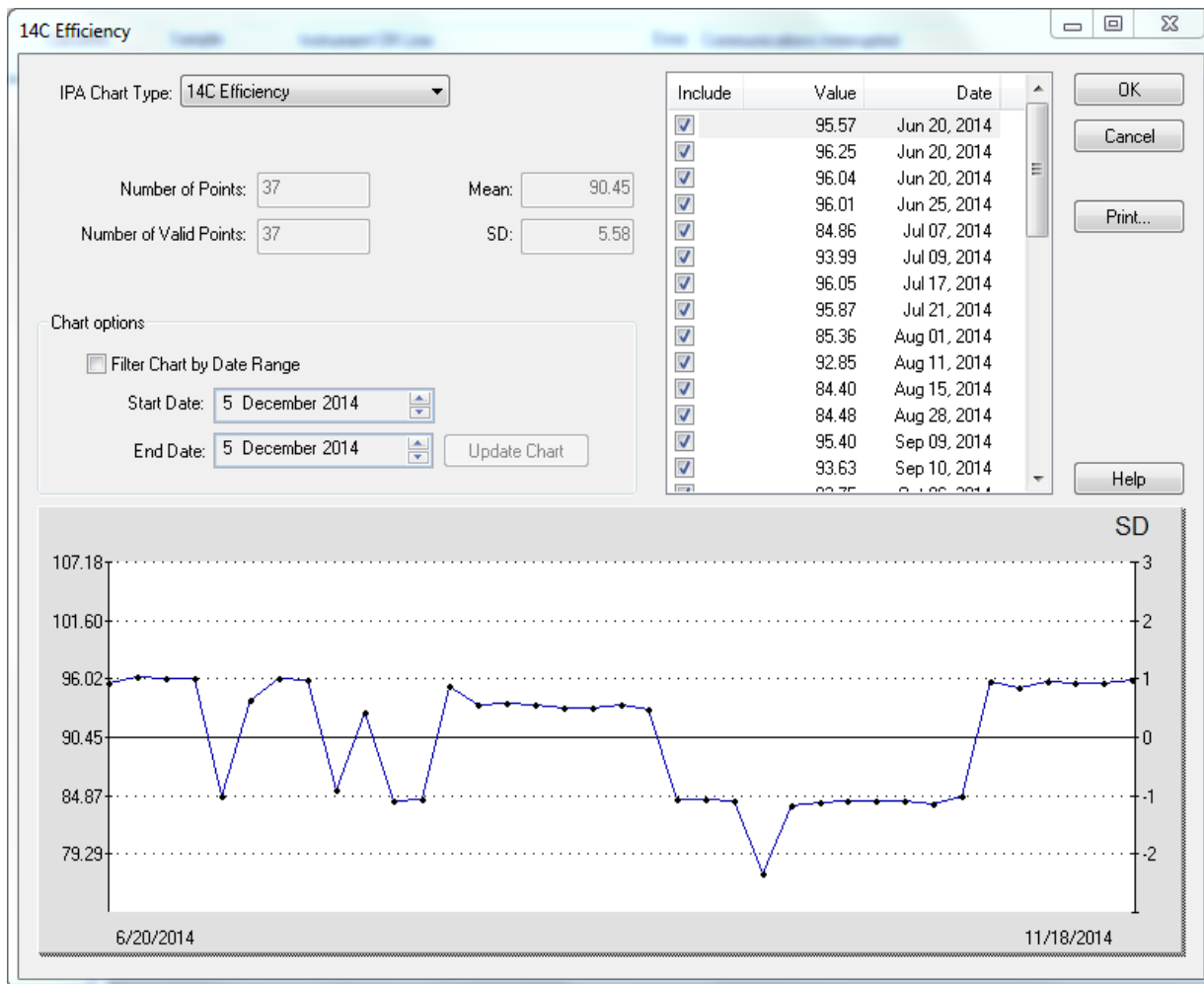
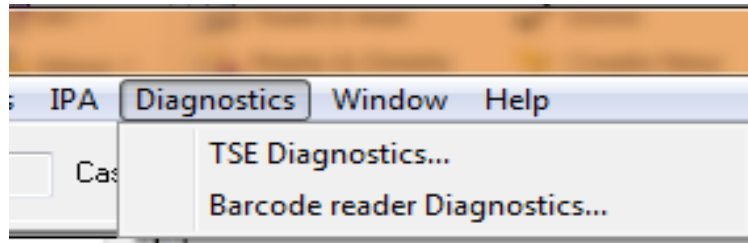


Figure 3-30. IPA Charts & Tables.

## Diagnostics Menu

To display this menu (Figure 3-31), select **Diagnostics** from the menu bar.



**Figure 3-31. Diagnostics Window.**

### TSE Diagnostics

This command in the **Diagnostics** menu is used by a PerkinElmer Service Engineer to view the system's diagnostic screens and assess the system's functional status. Unless logged in as a Technical Service Engineer (TSE), a password is required to access TSE Diagnostics.

### Barcode Reader Diagnostics

Select to display this window (Figure 3-32), and verify that the bar code reader is working properly. For example, testing that the correct COM port is selected in the *Bar Code Scanner Configuration* window (page 83).

Follow the instructions listed on the right-hand side of the *Barcode Diagnostics* window (Figure 3-32).

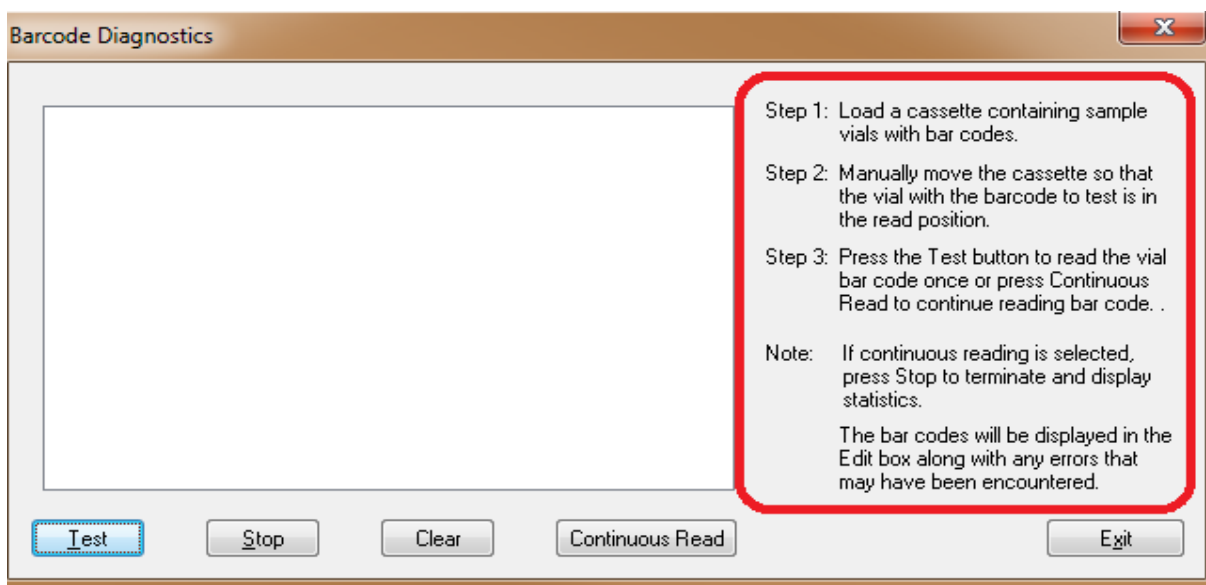


Figure 3-32. Barcode Diagnostics Window.

### Window Menu

To display this menu (Figure 3-33), select **Window** from the menu bar. The **Window** menu allows users to define a window display format, and restore the *SpectraView* window.

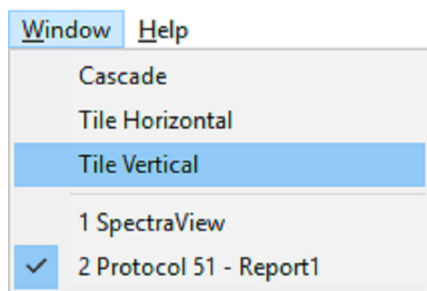


Figure 3-33. Window Menu.



### Cascade

Select to display the open windows in the format shown in Figure 3-34.

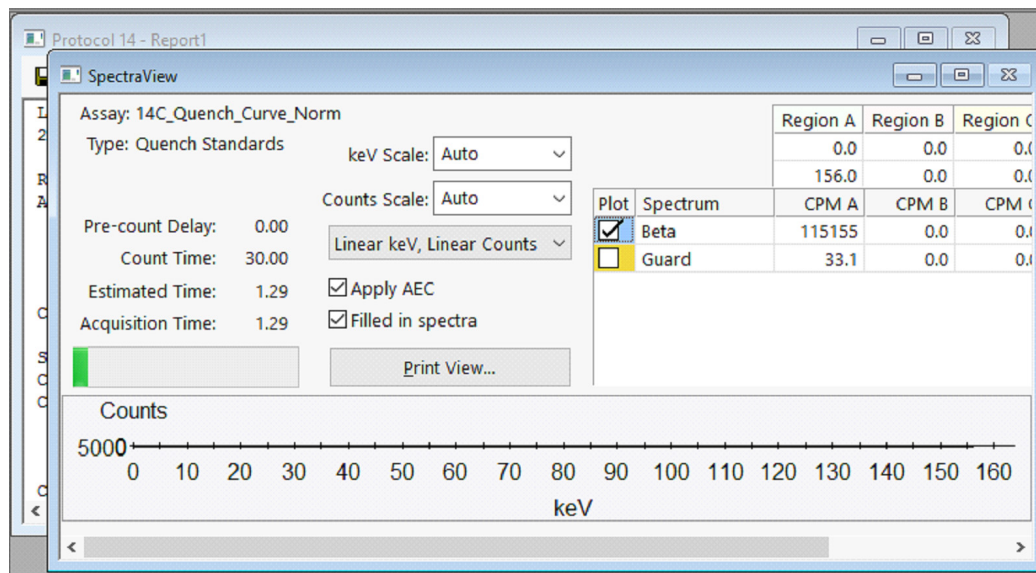


Figure 3-34. Cascaded Windows.

### Tile Horizontal

Select to display the open windows in the format shown in Figure 3-35.

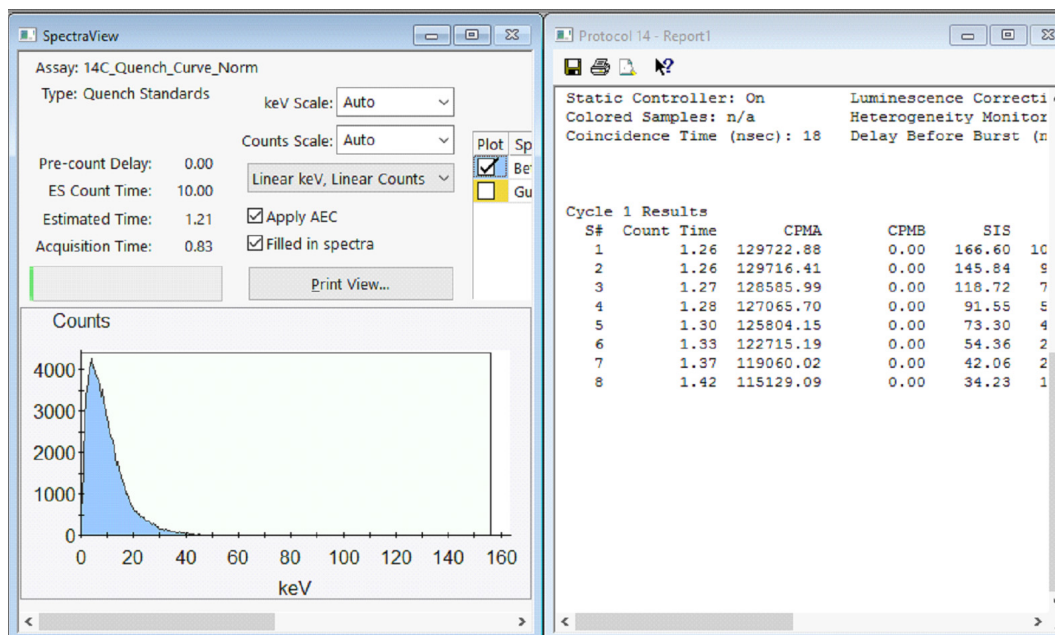


Figure 3-35. Horizontal Tiled Windows.

### Tile Vertical

Select to display the open windows in the format shown in Figure 3-36.

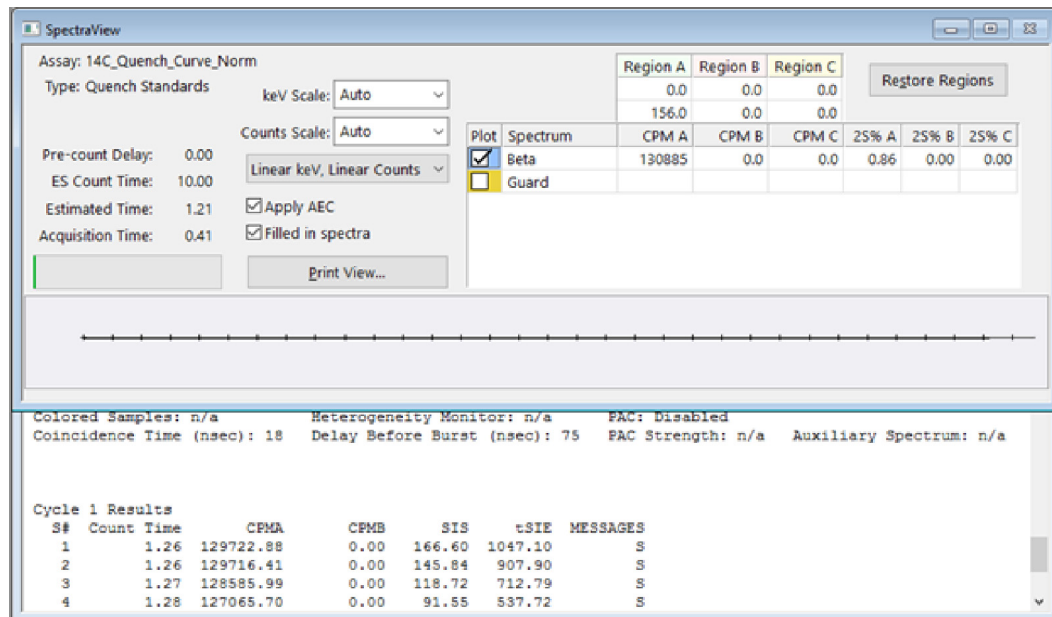


Figure 3-36. Vertical Tiled Windows.

### SpectraView

If the *SpectraView* window is minimized on the main screen, select **Window | SpectraView** to restore and view the *SpectraView* window (Figure 3-2, page 55). The *SpectraView* window displays a two-dimensional, real-time view of the spectrum for the current sample.

### Help Menu

To display this menu (Figure 3-37), select **Help** from the menu bar.

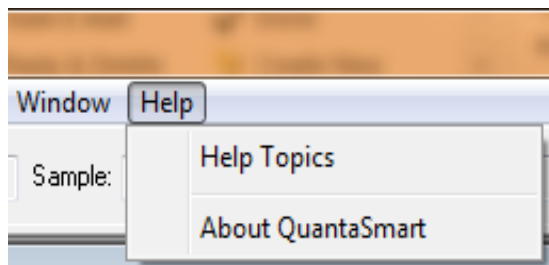


Figure 3-37. Help Menu.

### Help Topics

Select to launch the On-Line Help documentation.

### **About QuantaSmart**

Select to display a window that displays the following information:

- QuantaSmart software version and build number.
- QSIC software version.
- Firmware version.
- FPGA (firmware) version.

Also included in the window are the instrument's serial number, and a list of installed options.

### **Spectral Displays**

The QuantaSmart software provides resources for viewing graphic representations of spectra.

These resources include: *Spectral Mapping*, *Spectrum Unfolding* (page 93), and the *SpectraView* window (page 94).

## Spectral Mapping

During a single-label DPM sample count, the *Spectral Mapping* window (Figure 3-38) displays sample and quench standard spectra in a three-dimensional view:

- X-axis - Represents energy in keV.
- Y-axis - Represents counts.
- Z-axis - Represents quench indicating parameter (tSIE).

Use the spectral map for the following:

- Comparing a sample spectrum to the quench standard spectrum.
- Checking for spectral anomalies.

To display a spectral map, select **Tools | Spectral Mapping** from the menu bar.

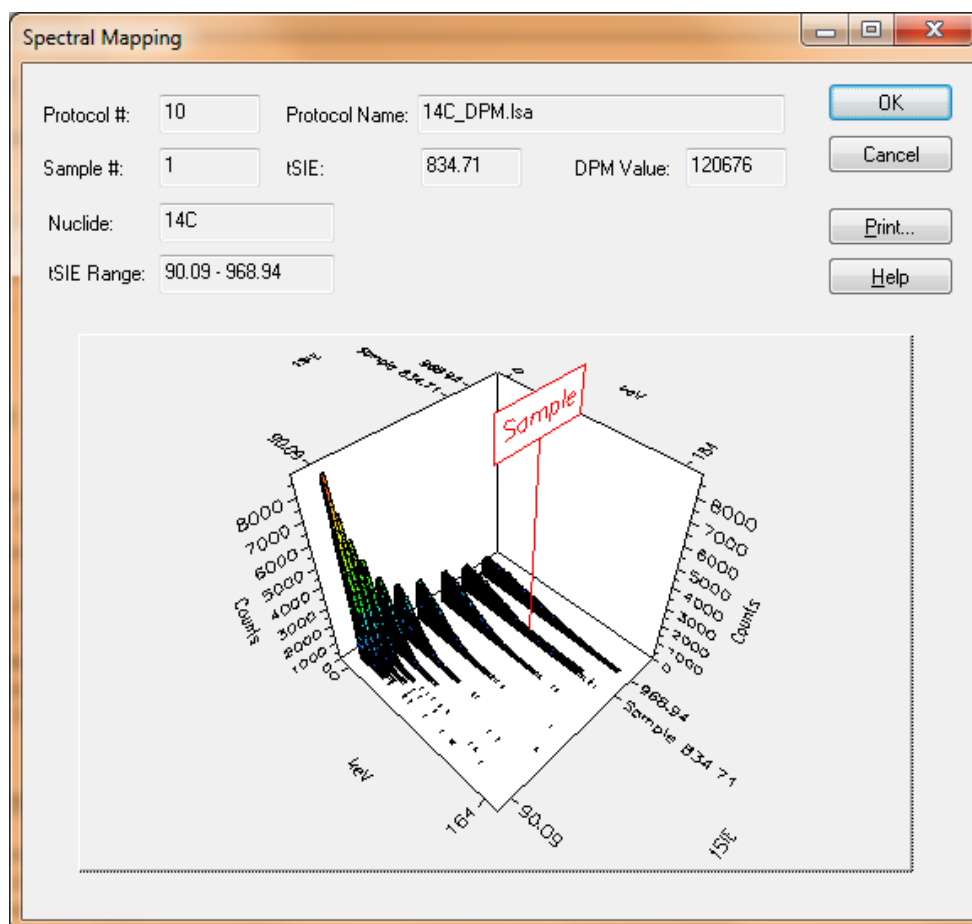


Figure 3-38. Spectral Mapping Window.

A sample with a quench level exceeding quench standard limits will have its map position determined by extrapolation. The lower limit of extrapolation is the tSIE plus 10% of the least quenched standard; the upper limit of extrapolation is the tSIE minus 10% of the most quenched standard.

## Spectrum Unfolding

During a Dual-label DPM or Full Spectrum DPM sample count, the *Spectrum Unfolding* window (Figure 3-39) can display, three dimensionally, the composite nuclide spectrum as individual, separate spectra for each nuclide.

The X-axis of the spectral displays represent energy (in keV) for each counting channel up to the defined endpoint of the sample spectrum. The Y-axis represents gross counts for a current sample.

Spectrum Unfolding is often useful for:

- Visualizing the relationship of individual nuclide spectra.
- Approximating the ratio of lower energy nuclide to higher energy nuclide.

To display the unfolded spectra, select **Tools | Spectrum Unfolding** from the menu bar.

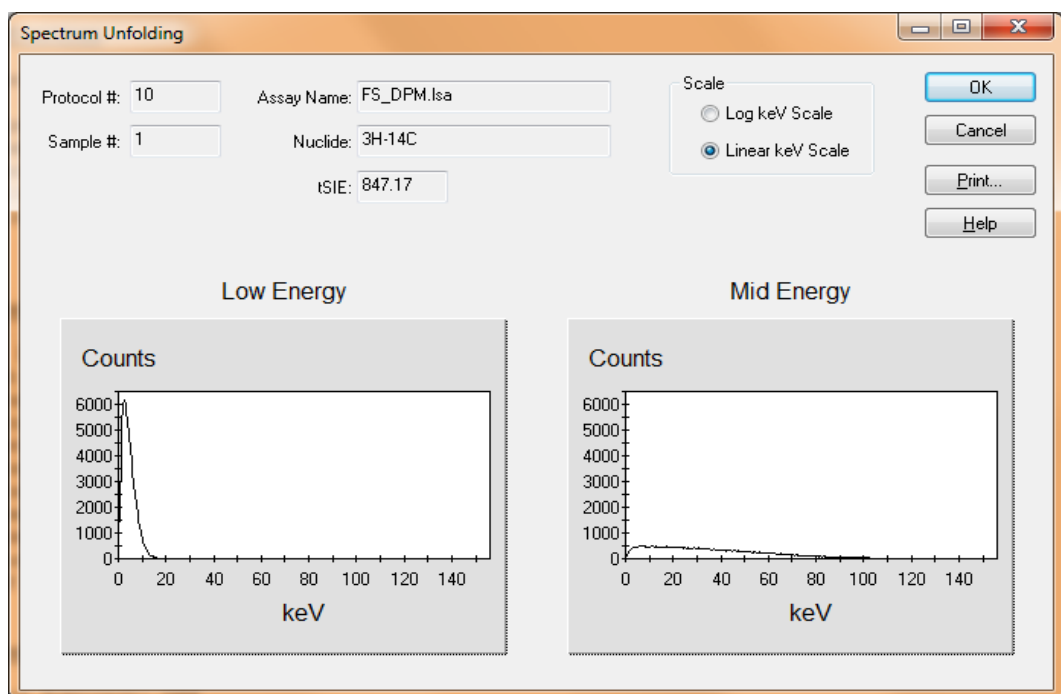


Figure 3-39. Spectrum Unfolding Window.

## SpectraView Window

The *SpectraView* window (Figure 3-2, page 55) is part of the main QuantaSmart window. Refer to page 55 for a description of the window and its features.

## Reports

Several reports may be generated using the QuantaSmart system: printed or electronic. On the **Report Definition** tab (page 125) of the *Assay Definition* window, first define the content and report name(s). After creating one or more named reports, go to the **Report Output** tab (page 134) to select how each is to be generated.

### Printed Reports

To obtain a printed report using the QuantaSmart system, on the **Report Definition** tab (page 125) of the *Assay Definition* window, define a named report with the desired information. Then, on the **Report Output** tab (page 134), select the named report, and the **Output to Printer** checkbox. If this checkbox is selected, the printed report(s) defined for an assay will automatically print after the assay is completed.

To print additional reports, select a report to print from the **Protocols** tree in the main QuantaSmart window. Then click the **Print** button to print the report when the *Output* window is displayed.

To print a list of parameters selected for an assay, select **File | Print Assays** from the menu bar. The *Select Assays to Print* window is displayed. In the window, select an assay to print and click **OK**.

## Electronic Reports

Various electronic reports can be generated using the QuantaSmart system. On the **Report Definition** tab (page 125) of the *Assay Definition* window, first define a named report with your desired information. Then, on the **Report Output** tab (page 134), select the named report, and indicate the type of electronic report to generate.

The electronic output formats include:

- Rich Text Format (RTF)
- Delimited Text (ASCII)
- RS-232 (cabled transmission, not a file format)

Other, predefined data sets can also be selected for output using the **Special Files** tab (page 139) of the *Assay Definition* window. These other sets of data include:

- Composite Spectra File
- Individual Spectrum Files
- IPA Data
- Protocol Data (PROT.DAT)
- Protocol Data (2000CA.DAT)

All data files are stored to the location defined for each protocol. When an assay is associated with a protocol flag for the first time, users are prompted for data path information. The *Data Paths* window (Figure 3-13, page 66) enables users to identify information specific to this protocol (not the assay) for data storage. Information for existing protocol associations may also be viewed or modified by selecting **Files | Data Paths** from the menu bar.





# Chapter 4

## Assays

This chapter describes assays performed when using QuantaSmart software. The process for defining an assay is also discussed (page 115), along with the *Assay Definition* window, where assay parameters may be selected.

### Assay Types

Depending on your instrument's configuration, the following assay types may be available in the QuantaSmart software:


- CPM Assays (page 97)
- DPM Assays (page 98)
- Full Spectrum (FS) DPM Assays (page 100)
- Direct DPM Assays (page 101)
- Alpha/Beta Assays (page 103)
- Alpha/Beta Standards Assays (page 109)
- Quench Standards Assays (page 112)
- Single Photon Counting (SPC) Assays (page 114)

### CPM Assays

A Counts Per Minute (CPM) assay provides information on total radioactivity within a sample in one, two, or three predefined counting regions. Data generated is expressed in CPM which only reflects activity detected without regard to counting efficiency or sample interference (e.g. quench).

### Performing a CPM Assay

To perform a CPM assay, do the following:

1. Normalize and calibrate the instrument (if necessary). See Chapter 6 for more information.
  2. Do one of the following:
    - Create a new assay, using **CPM** as assay type. Then, in the *Assay Definition* window, define the new assay parameters (see page 115).
- OR**
- Open an existing CPM assay, and edit or review it (if necessary).
  3. When finished creating or editing assay definitions, save the assay in the Assays folder of the C:\Packard\TriCarb directory.
  4. Associate (link) the assay parameters with a protocol number in the **Protocols** tree, and attach the corresponding protocol flag to the first cassette to be counted.
  5. Load the cassette(s) with vials and then load the instrument with cassettes.
  6. Click the green start button  at the top of the main window to begin counting.

### DPM Assays

A Disintegrations Per Minute (DPM) assay allows users to count one or more nuclides in a sample. Data is expressed as DPM, which (when calculated) must be sample-checked for quench. If not, incorrect DPM results may be reported.

For each sample in a DPM assay, the instrument:

- Measures activity in a sample vial as CPM.
- Determines quench level via Quench Indicating Parameters (QIPs).
- Interpolates counting efficiency from a quench curve (plots % Efficiency vs. QIP).
- Calculates DPM, where  $DPM = CPM / Efficiency$ .

Depending on Tri-Carb model, four DPM assays are available:


- Single, Dual, and Triple DPM assays allow users to count one, two, or three nuclides in a sample with one, two, and three defined counting regions.
- Full Spectrum DPM (FS DPM) assays allow users to count two nuclides in a sample with a full sample spectrum (no defined counting regions). See page 100 for more information about FS DPM assays.

## Performing a DPM Assay

To perform a DPM assay, do the following:

1. Normalize and calibrate the instrument (if needed). See Chapter 6 for more information.
2. Define and run a Quench Standards assay so counting efficiency and DPM can be determined for the samples (see page 112).
3. Do one of the following:
  - Create a new assay, choosing **DPM (Single)**, **DPM (Dual)**, or **DPM (Triple)** as the assay type. Then, in the *Assay Definition* window, define the new assay parameters (see page 115).

### OR

- Open an existing DPM assay, and edit or review the assay (if needed).
4. When finished creating or editing an assay definition, save the assay in the *Assays* folder of the C:\Packard\TriCarb directory.
  5. Select a quench standards set for use with the sample nuclide(s).
  6. Associate (link) the assay parameters with a protocol number in the **Protocols** tree, and attach the corresponding protocol flag to the first cassette to be counted.
  7. Load the cassette(s) with vials, and then load the instrument with cassettes.
  8. Click the green flag start button  at the top of the main window to begin counting.

## Quench Set

This field on the **Count Conditions** tab (page 116) is displayed only in DPM assays, and features the quench set selected for a Sample Nuclide in an assay. When using a quench set, counting efficiency is determined for each assay sample, reducing the time needed to count an assay. By selecting the **Constant Quench** option, count efficiency is determined only for the first assay sample. Count efficiency for this sample is used to calculate DPM for all assay samples.


## Full Spectrum (FS) DPM Assays

This method is used for regionless counting of dual label samples, and uses Quench Indicating Parameters, Spectral Index of the Sample (SIS), transformed Spectral Index of the External standard (tSIE), and spectral unfolding technique to separate a sample's composite spectrum.

A composite spectrum is separated into two component spectra, each the result of a different nuclide. Spectrum unfolding yields the actual CPM for each nuclide, and a quench correlation curve comparing SIS vs. tSIE; Efficiency vs. tSIE is used to determine the DPM of unknown samples. Maximum accuracy with this method occurs when sample nuclide concentration falls in the range of 50:1 to 1:8 (low to high energy nuclide). Quench standards used for FS DPM should match the chemistry, and geometry of any unknown sample.

### Performing an FS DPM Assay

To perform an FS DPM assay, do the following:

1. Normalize and calibrate the instrument (if needed). See Chapter 6 for more information.
  2. Define and run a Quench Standards assay to determine sample counting efficiency and DPM (see page 112).
  3. Do one of the following:
    - Create a new assay, selecting **FS DPM** as the assay type. Then, in the *Assay Definition* window, define the new assay parameters (see page 115).
- OR**
- Open an existing DPM assay, and edit or review the assay (if needed).
  4. When finished creating or editing the assay definition, save the assay in the *Assays* folder of the *C:\Packard\TriCarb* directory.
  5. Select a quench standards set for use with the sample nuclide(s).
  6. Associate (link) the assay parameters with a protocol number in the **Protocols** tree, and attach the corresponding protocol flag to the first cassette to be counted.
  7. Load the cassette(s) with vials, and then load the instrument with cassettes.
  8. Click the green flag start button  at the top of the main window to begin counting.

## Direct DPM Assays

This is a predefined assay that performs DPM calculations based on the Quench Indicating Parameter— Spectral Index of the Sample (SIS). As this assay is pre-installed, there is no need to define individual assay parameters. This assay will calculate DPM values for single label beta or beta/gamma nuclides (including Tritium). Single-label samples with different beta nuclides may be counted in the same cassette.

When using the Direct DPM method, samples are evaluated as follows:

- If the SIS value is greater than (or equal to) 40, DPM is reported with no message on the printout.
- If the SIS value is between 20 - 40, then DPM is reported, and the sample found Indeterminate (I) on the printout.
- If the SIS value is less than (or equal to) 20, and the sample is determined to contain Tritium, then DPM is reported with no message on the printout.
- If the SIS value is less than (or equal to) 20, and the sample is determined not to contain Tritium, then DPM is not reported, and the sample found Indeterminate (I) on the printout.



*Note: When a sample is listed as Indeterminate (I) on a printout, any DPM reported may be valid if the sample is not heavily quenched. Check the tSIE value to determine its quench level. If the tSIE exceeds 200, DPM reported is likely accurate and within statistical counting error. Accuracy is independent of cocktail density variation, vial size, vial type, sample volume, color and chemical quench. Direct DPM is not recommended for any background level samples counted for a short time.*


### Performing a Direct DPM Assay

To perform an Direct DPM assay, do the following:


1. Normalize and calibrate the instrument (if needed). See Chapter 6 for more information.
2. Define and run a Quench Standards assay so counting efficiency, and DPM can be determined for the samples (see page 112).
3. Create a new assay, using **Direct DPM** as the assay type.



*Note: If counting samples using PerkinElmer Ultima Gold™ scintillation cocktail, indicate this in the nuclide library. This will ensure that the appropriate quench curve is used to calculate DPM for Tritium.*

4. When finished creating the assay definition, save the assay in the Assays folder of the C:\Packard\TriCarb directory.
5. Select a quench standards set for use with the sample nuclide(s).
6. Associate (link) the assay parameters with a protocol number in the **Protocols** tree, and attach the corresponding protocol flag to the first cassette to be counted.
7. Load the cassette(s) with vials, and then load the instrument with cassettes.
8. Click the green flag start button  at the top of the main window to begin counting.

## Alpha/Beta Assays

 *Note: This feature may be optional. Contact your PerkinElmer representative for details.*

### Overview

An Alpha/Beta assay is similar to a CPM assay with the additional ability to detect both Alpha and Beta decay events in a sample. Pulse Shape Analysis (PSA) is used to discriminate between alpha and beta events. (See **Alpha/Beta Counting Theory**)

Alpha/Beta assays can also report spill corrected CPM and DPM. Spill correction depends on measuring an alpha and beta standard as well as a background. It is critical that these samples closely match the unknowns in composition, quench and use the same energy regions. In addition, the temperature of the sample may affect spillover for certain cocktails such as Ultima Gold LLT so it is recommended that the instrument have the Temperature Control option. Let the samples acclimate inside the instrument for at least 30 minutes for best results.

## Assay Definition dialog / Count Conditions

Assay Definition - C:\Packard\TriCarb\Assays\rhAB\_unks.lsa

Count Conditions | Count Corrections | Report Definition | Report Output | Special Files | Worklist | Assay Details

**Nuclide Group**

Name:  Count Mode:  Quench Indicator:   
 Alpha / Beta Standard Set:  External Std Terminator:

Pre-count Delay (min):  Assay Count Cycles:  Number of Vials per Sample:   
 Count Time (min):  Repeat Sample Count:   
 Calculate %Reference  
 Count Alpha/Beta Standards

**keV Energy Regions**

	Lower Limit	Upper Limit
Beta A	<input type="text" value="30.0"/>	<input type="text" value="650.0"/>
Beta B	<input type="text" value="0.0"/>	<input type="text" value="0.0"/>
Alpha	<input type="text" value="75.0"/>	<input type="text" value="225.0"/>

**Background CPM Subtraction**

Subtract Background

Beta A:   
 Beta B:   
 Alpha:

**Low CPM Threshold**

Stop Counting

Beta A:   
 Beta B:   
 Alpha:

**2 Sigma Percent Threshold**

Stop Counting  
 Regions:  Any Region  All Regions

Beta A:   
 Beta B:   
 Alpha:

OK Apply Undo Save As... Help

Figure 4-1 - AssayDefinition

### Nuclide Group

The nuclide group selected for the assay determines the energy ranges used. For Alpha/Beta assays there are two beta ranges (Beta A, Beta B) and one alpha range (Alpha). The nuclide group also specifies the discriminators used to separate alphas and betas. (See **Alpha/Beta Nuclide Library**) If a standard is associated with the nuclide group, it will be automatically selected in the Alpha/Beta Standard Set drop-list.

### Count Mode

If the selected nuclide uses a standard, the count mode is locked in Normal count mode since all standards are counted in that mode. If the nuclide has a manually entered discriminator, low level/high sensitivity count mode may be selected and the box for “Count Alpha/Beta Standards” must be checked for spillover to be calculated.



**Quench Indicator**

Spill correction depends on the quench level of the sample matching that of the standard. Turning on TSIE will report the quench level for each sample to help identify problems with mismatching quench. Do not use TSIE/AEC if performing spill correction since this will cause a region mismatch with the standard.

**Count Time**

Enter a count time that will provide sufficient counting statistics based on the activity of the samples being measured. Use a long count time and “2 Sigma Percent Threshold” to stop the count after reaching the desired level.

**Count Alpha/Beta Standards**

Check this box to measure the current spillover by counting the pure alpha and beta standard vials as part of the assay. This provides the ability to later change regions using Replay and automatically recalculated spillover. When Count Alpha/Beta Standards is checked, the first cassette must have a vials containing the pure Beta in position 1, and a vial containing a pure Alpha standard in position 2. If 1<sup>st</sup> Vial Background Subtraction is enabled as well, then the vial containing the pure Beta standard must be loaded in position 2, and the vial containing the pure Alpha standard must be loaded in position 3.

**Background CPM Subtraction**

For accurate spill correction, it is recommend enabling this feature and selecting 1<sup>st</sup> Vial. When enabled, the vial in position 1 of the first cassette must be a background vial with sample preparation matching the quench level of the unknown samples.

**2 Sigma Percent Threshold**

Use this feature to stop counting after acquiring a certain number of counts. For example, a 2 Sigma Percent of 0.5 means that counting would stop after acquiring 160,000 counts.

## Reporting

Alpha/Beta assays can include additional report fields. These can be selected on the Report Definition tab of the Assay Definition dialog. Beta counts per minute are represented as CPMA and CPMB for regions A and B. Alpha counts per minute are represented as CPMA. Additional results regarding spill correction and DPM are available towards the bottom of the Report Fields list:

Use	Name	Description	Format	Equalizer
<input type="checkbox"/>	SD:CPMA	Standard deviation - alpha region	00000.00	
<input type="checkbox"/>	SD:DPM1	Standard deviation - nuclide 1	00000.00	
<input type="checkbox"/>	SD:DPM2	Standard deviation - nuclide 2	00000.00	
<input type="checkbox"/>	SD:DPM3	Standard deviation - nuclide 3	00000.00	
<input checked="" type="checkbox"/>	% Alpha Spill	% alpha spill into to beta region	000.00	
<input checked="" type="checkbox"/>	% Beta Spill	% beta spill into alpha region	000.00	
<input checked="" type="checkbox"/>	CPMA Corrected	Spill corrected CPM - Region A	000000	
<input checked="" type="checkbox"/>	CPMA Corrected	Spill corrected CPM - alpha region	000000	
<input checked="" type="checkbox"/>	DPM Alpha	Alpha DPM from Alpha/Beta Assay	000000	
<input checked="" type="checkbox"/>	DPM Beta	Beta DPM from Alpha/Beta Assay	000000	
<input type="checkbox"/>	Eff Alpha in Beta	Efficiency of Alpha in Beta Region	0000.00	
<input type="checkbox"/>	Eff Alpha in Alpha	Efficiency of Alpha in Alpha Region	0000.00	
<input type="checkbox"/>	Eff Beta in Alpha	Efficiency of Beta in Alpha Region	0000.00	
<input type="checkbox"/>	Eff Beta in Beta	Efficiency of Beta in Beta Region	0000.00	
<input type="checkbox"/>	CPMA G	Counts / minute - Region A - Guard	000000	
<input type="checkbox"/>	CPMB G	Counts / minute - Region B - Guard	000000	
<input type="checkbox"/>	CPMC G	Counts / minute - Region C - Guard	000000	
<input type="checkbox"/>	CPMA X	Counts / minute - Region A - Auxiliary	000000	


Figure 4-2 - Report Fields

## Performing an Alpha/Beta Assay

To perform an Alpha/Beta Assay, do the following:

1. Normalize and calibrate the instrument (if needed). See Chapter 6 for more information.
2. Define and run an Alpha/Beta Standards assay (page 109) to establish a optimal PSA value.
3. Define an Alpha/Beta nuclide in the Alpha/Beta Nuclides Library (page 159).
4. Choose the Standards Set (second column in the table) from the Alpha/Beta Standards Library (page 164) to use the discriminator setting from the Standard Set. If a Standard Set is not chosen, manually enter a discriminator setting directly in the Alpha/Beta Nuclide Library.
5. Do one of the following:
  - Create a new assay, selecting **Alpha/Beta** as assay type. On the **Count Conditions** tab of the *Assay Definition* window, click the **Name** button to select the desired Alpha/Beta radionuclide name from the Alpha/Beta Nuclides Library. Define the other available parameters as desired (see page 115).

### OR

- Open an existing Alpha/Beta Assay, and edit or review the assay (if needed).
6. When finished creating/editing the assay definition, save the assay in the Assays folder of the C:\Packard\TriCarb directory.
  7. Associate (link) the assay parameters with a protocol number in the **Protocols** tree, and attach the corresponding protocol flag to the first cassette to be counted.
  8. Load the cassette(s) with vials, and then load the instrument with cassettes.
  9. Click the green flag start button  at the top of the main window to begin counting.

### Tips and Techniques for Performing Alpha/Beta Assays

- Quench should be minimized whenever possible, because Alpha/Beta Discrimination degrades in highly quenched samples. Be sure to match the quench level of your samples with your alpha and beta standards and with your background sample.
- By default, Alpha/Beta standards are counted with a wide open 0-2000 keV region for beta activity, and 0-1000 keV region for alpha activity. For the PSA Histogram measurement method, these regions can be changed to better optimize Alpha/Beta separation.



*Note: Using regions different from what was used to count the standard will affect spillover. If different regions are used, the alpha and beta standards should be re-measured with the unknown samples when those samples are measured in an Alpha/Beta assay. The software will re-calculate and report the correct spill if the standards are counted in the Alpha/Beta assay and the Count Alpha/Beta Standards checkbox is checked.*

- Repeat counting of your Alpha/Beta standards in your Alpha/Beta assay if you expect to replay the data with different energy regions. The software will re-calculate and report the correct spill if the standards are counted in the Alpha/Beta assay and the Count Alpha/Beta Standards checkbox is checked.




*Note: Only one region of interest (CPMA) is defined for Alpha activity. This field is included by default in Alpha/Beta assays. Beta activity can be reported in two regions: CPMA and CPMB. CPMA is always included by default in the report.*

- High Sensitivity Count Mode (HSCM) or Low Level Count Mode (LLCM) can be used in an Alpha/Beta assay. In this case, do not link an Alpha/Beta Standard Set name to an Alpha/Beta Nuclide name in the Alpha/Beta Nuclide Library. As Alpha/Beta standards are always counted with normal count mode by design, linking one to the Alpha/Beta Nuclide name will automatically select a Normal count mode.




*Note: High Sensitivity Count Mode or Low Level Count Mode is applied only to Beta counting, and not Alpha. Alpha background reduction is achieved with Alpha/Beta discrimination (Pulse Shape Analysis).*

- To use High Sensitivity Count Mode or Low Level Count Mode in an assay, define the Alpha/Beta Nuclide in the library. Do not link an Alpha/Beta Standard Set name. Alpha/Beta standards should be counted in the assay to determine Alpha/Beta misclassifications.

 *Note:* When counting high energy Beta emitters in a Low Level Count Mode, change the **Delay Before Burst** field value on the **Count Corrections** tab (default value is 75 nsec). By adjusting this value, background reduction is optimized for sensitivity. A value between 150 - 300 is typical. The optimum value must be empirically determined with a representative background and sample.

## Alpha/Beta Standards Assays

 *Note:* This feature may be optional. Contact your PerkinElmer representative for details.

## Overview

An Alpha/Beta Standards assay is used to determine the optimal PSA discriminators. (See **Alpha/Beta Counting Theory**) Using the discriminators, the alpha and beta spillover is calculated. The standard specifies the measurement method:

- Automatic/Manual  
A series of complete spectrum measurements are performed at different PSA settings for each vial. The number and range of measurements are defined by the standard in the Alpha/Beta Standards Library. (See **Alpha/Beta Standards Library**) The time required to complete will be the number PSA intervals times the count time times two. Example: 10 PSA intervals at 10 minutes count time will take at least 200 minutes.
- PSA Histogram  
All possible PSA values are measured at the same time in a single measurement.

When the standard is measured using PSA Histogram, Alpha/Beta assays using that standard can calculate spill corrected CPM and DPM.

## Assay Definition dialog / Count Conditions

### Standard Group

Select the standard group to be measured. (See **Alpha/Beta Standard Library**)

### **Quench Indicator**

This is set to SIS for standards using Automatic or Manual measurement methods. When PSA Histogram is used, the option to use TSIE is available. Spillover changes with quench. Measuring the standard with TSIE allows comparison of quench levels between the standard and unknowns.

### **Count Time**

Enter a count time that will provide sufficient counting statistics based on the activity of the samples being measured. There are several factors that can affect the count time so this may change after evaluating the results. A good starting point for a 50k DPM standard is 7 minutes.

### **2 Sigma Percent Threshold**

This allows the run to stop after acquiring a statistically significant number of counts. When using PSA Histogram, a single value is used for termination.

### **Evaluation**

See **Alpha/Beta Standards Library** for details on how to evaluate the results of an Alpha/Beta Standards assay.

The following tasks are required to run the Alpha/Beta Standards assay. Two standards are required—a pure Beta emitter and pure Alpha emitter.


1. Create a new Alpha/Beta Standard entry by selecting **Libraries | Alpha/Beta Standards** in the menu bar.
2. In the *Alpha Beta Standards* window, click the **Add** button to create a row for the new standard. In that new row, enter a name for the new Alpha/Beta Standard Set.


Name	Beta LL	Beta UL	Alpha LL	Alpha UL	Measurement Method	Manual PSA Start	Manual PSA Stop	Number of Points	Lower PSA Computed	Lower PSA In Use	Upper PSA Computed	Upper PSA In Use	Count Started	Count Ended	Count Mode	Coinc Time	Delay Before Burst
CL-AM	0.0	2000.0	0.0	1000.0	Automatic	0	255	10	116	116			02/05/2015	10:10:06	Normal	18	75
Test	0.0	2000.0	0.0	1000.0	Manual	80	120	5	90	90			07/21/2016	14:50:45	Normal	18	75
CLAM - hist	0.0	2000.0	0.0	1000.0	PSA Histogram				25	25	175	175	08/29/2016	15:53:23			
CLAM - longer	0.0	2000.0	0.0	1000.0	PSA Histogram				37	37	165	165	08/29/2016	16:06:35			
New Standard	0.0	2000.0	0.0	1000.0	PSA Histogram												

Buttons: AB Curve..., Add, Comment..., OK, Help, AB Nuclides..., Delete, Print..., Cancel

**Figure 4-3. Alpha Beta Standards window**

3. Select the type of measurement method to use to acquire the data for each vial:
  - PSA Histogram – Measure all possible PSA values at the same time using a single measurement. This is the recommended method since results can be acquired in significantly less time and allows Dual Discriminators to be used, to minimize spillover.
  - Automatic – Measure the standards to determine the best starting and stopping point for building table of 10 PSA values. After determining the range, perform a measurement for each PSA value. This method requires that standards have at least 50,000 CPM.
  - Manual – Manually enter the values for PSA Search Start, PSA Search Stop and Number of Points (5 to 15) for the table. Perform a measurement for each PSA value.


 *Note:* The Automatic and Manual methods do not allow PSA Histogram.

 *Note:* The remaining fields in the Alpha/Beta Standards window are for information only, and contain default values or values computed by the instrument.

4. Create a new assay, selecting **Alpha/Beta Standards** as the assay type. On the **Count Conditions** tab of the *Assay Definition* window, click the **Name** button to select the desired Alpha/Beta radionuclide name from the Alpha/Beta Standards Library. Define the other available parameters as desired (see page 115).



*Note: High Sensitivity or Low Level Count mode are not available when counting Alpha/Beta Standards. However, these modes are available when counting samples in an Alpha/Beta assay*

5. When finished creating the assay definition, save the assay in the Assays folder of the C:\Packard\TriCarb directory.
6. Associate (link) the assay parameters with a protocol number in the **Protocols** tree, and attach the corresponding protocol flag on a cassette.
7. Place the pure Beta emitter standard in the first vial position, and the pure Alpha emitter standard in the second vial position.
8. Load the cassette onto the instrument.
9. Click the green flag start button  at the top of the main window.
10. After counting is complete, the misclassification (or spillover) curve and optimum PSA discriminator value is stored for the Standard Set. Review the curve and PSA discriminator setting (if desired) from the Alpha/Beta Standards Library.

## Quench Standards Assays

This assay set is composed of several vials, each containing the same nuclide amount with varying degrees of quenching agent. Using quench standard data, a quench curve is generated to determine sample counting efficiency, and calculate DPM where  $DPM = CPM / Efficiency$ . The system stores each standard spectrum in the Quench Standards Set which is counted only once; whereas quench data is available for use with any protocol.

To accurately measure sample quench, the nature and composition of quench standards should reflect the matrix and environment of samples counted.



## Performing a Quench Standards Assay


The following tasks are required when performing a Quench Standards assay:



*Note: For 4810TR models, setting up a Quench Standards assay requires the single/dual color-corrected DPM option.*

1. Normalize and calibrate the instrument, if necessary. See Chapter 6 for more information.
2. Do one of the following:
  - Create a new assay, choosing **Quench Standards** as the assay type. Then define the new assay parameters (see page 115).

### OR

- Open an existing Quench Standards assay, and then edit or review the assay (if necessary).
3. When finished creating/editing the assay definition, save the assay in the Assays folder of the C:\Packard\TriCarb directory.
4. Associate (link) the assay parameters with a protocol number in the **Protocols** tree, and attach the corresponding protocol flag to the first cassette to be counted.
5. Load the cassette(s) with vials, and then load the instrument with cassettes.
6. Click the green flag start button  at the top of the main window to begin counting.



*Note: When using the Low Level count mode (if available), do not use quench standards that are purged free of oxygen with an inert gas. Oxygen quenching in unpurged standards creates discrimination between background and true Beta events. Unpurged standards are available from PerkinElmer.*

## Single Photon Counting (SPC) Assays

This assay measures photons emitted from non-radioactive, luminescent samples. To detect scintillation, Liquid Scintillation Counters use two Photomultiplier Tubes (PMTs) to collect virtually all light produced in a sample vial. Each pulse that occurs during sample counting time is registered and expressed as CPM. Sample events are considered true decay if they occur within a specified coincidence time. If not, the events are considered random (background) and not counted.


In an SPC assay, only one PMT is used. As a result, coincidence cannot be used to exclude background. Therefore, instrument background must be reduced to its lowest possible level. Lowering high voltage supplied to the PMT typically decreases background, and increases sensitivity in SPC assays.

### Performing an SPC Assay

The following tasks are required when performing an SPC assay:

1. Normalize and calibrate the instrument (if needed). See Chapter 6 for more information.
2. Do one of the following:
  - Create a new assay, select **SPC** as the assay type. Then define the new assay parameters (see page 115).

#### OR

- Open an existing SPC assay and edit or review the assay (if needed).
3. When finished creating/editing the assay definition, save the assay in the Assays folder of the C:\Packard\TriCarb directory.
4. Associate (link) assay parameters with a protocol number in the **Protocols** tree, and then attach the corresponding protocol flag to the first cassette to be counted.
5. Load the cassette(s) with vials, and then load the instrument with cassettes.
6. Click the green flag start button  at the top of the main window to begin counting.

#### Single Photon HV DAC %

This field is displayed only in SPC assays on the **Count Conditions** tab in the **Nuclide Group** section. High voltage supplied to the instrument's PMT is adjustable; lowering high voltage supplied to the PMT typically decreases background counts and increases sensitivity. The default setting for this device is 70%. The optimum setting must be determined empirically.

## Defining an Assay

Assay definition (via the system's seven tabs) is essential to the use of QuantaSmart software.

With these tabs, users can:

- Define a sample nuclide in the sample nuclides library (if one does not already exist).
- Link an nuclide to an assay.
- Link standards to an assay (if necessary).
- Specify appropriate count conditions and count correction factors that the instrument will use to analyze samples.
- Define reports for the system to generate.
- Output desired report options.
- Define an optional Worklist to designate Positive ID numbers, and sample names corresponding to sample numbers on a printout, if desired.
- Enter descriptive information about an assay's nature and author.


Parameters defined within the seven tabs can be saved, used, or edited. However, all assay information defined and saved becomes a functional entity only after being associated to a protocol number. These protocols are recognized by the instrument via a protocol flag (see page 7) containing an encoded, reflective metal used to identify protocol numbers and defined sample counting parameters. QuantaSmart enables users to define an unlimited number of assays, and associate them with a range of 15-60 protocols (depending on Tri-Carb model) by enabling the Lock Assay feature (page 150).

The following sections discuss each of the seven *Assay Definition* tabs:

- Count Conditions (page 116)
- Count Corrections (page 121)
- Report Definition (page 125)
- Report Output (page 134)
- Special Files (page 139)
- Worklist (page 144)
- Assay Details (page 149)

## Count Conditions

This tab (Figure 4-4) in the *Assay Definition* window allows users to define counting parameters for an assay.

 *Note:* Fields in the **Count Conditions** tab vary depending on assay type selected. Information in this section describes fields and buttons for managing CPM and DPM assay types. For details on other assay types, refer to page 97.

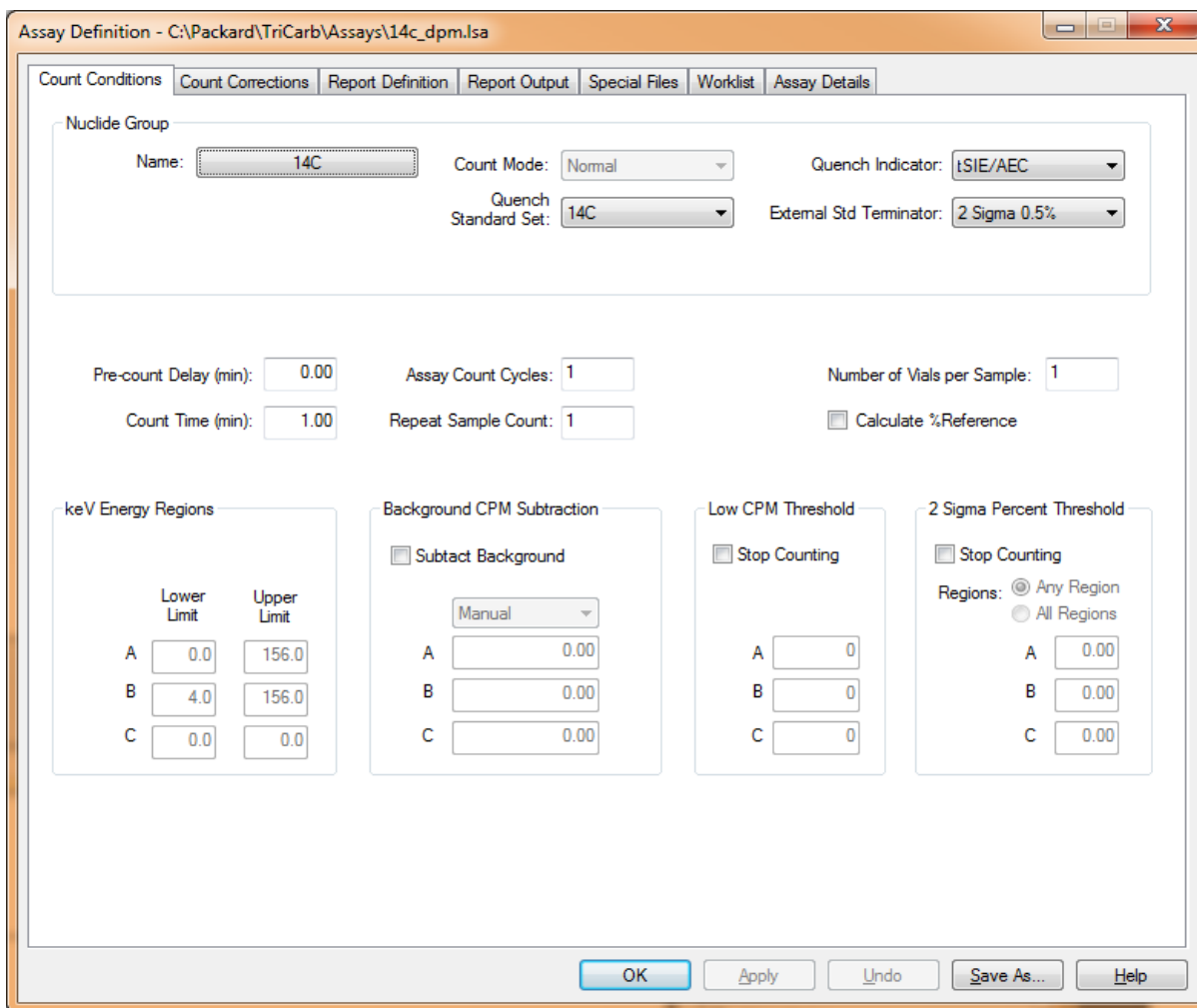


Figure 4-4. Count Conditions Tab (Assay Definition Window).

## Nuclide Group

This area of the **Count Conditions** tab contains the following:

- **Name** button – Opens the *Sample Nuclides* window; allows users to select the sample nuclides to use for this assay (see Sample Nuclides Library on page 141).
- **Count Mode** – Selections here depend on the Tri-Carb model used.
  - **Normal** mode (default) is desirable for most samples; background reduction via Guard Compensation Technology (GCT) may only be used with Normal mode (see page 108).
  - **High Sensitivity** provides higher sensitivity for strict criteria used to exclude background interference.
  - **Low Level** provides the highest sensitivity counting for low activity samples due to stricter criteria for excluding background interference (with minimal compromise in counting efficiency).
- **Quench Indicator** – Select **tSIE**, **tSIE/AEC**, or **SIS** to measure chemical quenching in a sample:
  - **tSIE** (transformed Spectral Index of the External Standard) – Using an external Barium-133 standard source, this method assigns a numeric value to a quench associated with a sample. This determination is independent of radioactivity quantity in a sample, and its count rate. The lower a tSIE value, the more the sample is quenched. A tSIE value of 1000 represents a fully unquenched sample. Accurate DPM values can be determined for samples with tSIE values as low as 10. To ensure accurate count statistics, the external standard is typically counted to a 0.5% 2 Sigma counting error, where the gross counts equal 160,000. tSIE is the most accurate quench indicator option, and is typically used for low count rate, variable quench, single label samples.
  - **tSIE/AEC** (transformed Spectral Index of External standards coupled to Automatic Efficiency Correction) – tSIE assigns a numeric value to a quench associated with a sample. As quench varies, the AEC automatically monitors and adjusts the counting region to exclude unwanted background. This setting is typically used for dual and triple label experiments with variable quench samples where optimal region settings are desired.
  - **SIS** (Spectral Index of the Sample) – SIS assigns a numeric value to the quench associated with a sample. SIS is determined from the spectral shape of a sample, and based on actual sample counts. The SIS setting is typically used to monitor quench level in single label, high count rate samples for CPM assays, or in single label Cherenkov counting.
  - **Quench Set** – This field appears in the **Count Condition** tab for DPM assays. For more information, refer to page 99.
- **External Std Terminator** – From this field, select a length of time the external standard is counted for calculating the quench index. Selecting **0.5 2s%** instead of a fixed time allows counting to occur until gross counts of 160,000 are measured. This provides statistical accuracy of 0.5% (at

95% confidence) for the tSIE parameter. The **External Std Terminator** field is only available when **tSIE** or **tSIE/AEC** is selected as the quench indicator; the field is grayed out if **SIS** is selected as the quench indicator.

### **Pre-count Delay**

In this field, enter the time (in minutes) for samples to sit in the closed detection chamber before counting begins. This process is *dark adaption*, and reduces any luminescence (light) originating from samples. Luminescence can distort sample count statistics, and is problematic with low count rate samples and long count times.

### **Count Time**

In this field, enter the maximum time (in minutes) that samples will be counted. For low activity samples, longer count times provide better count statistics and more accurate sample results. Count times can be changed during a run to a longer or shorter amount of time.

### **Assay Count Cycles**

In this field, enter the number of times which an assay will be counted. The assay is recounted after it has moved one complete cycle around the sample changer deck. Any samples currently on the sample changer deck will be counted before a sample recount.

### **Repeat Sample Count**

In this field, enter the number of times each sample is counted while in the counting chamber. This differs from the **Assay Count Cycles** field where samples are unloaded from the detector, and make a complete cycle around the sample changer deck before a recount.

### **Calculate % Reference**

Select this checkbox to activate the percent reference calculation. The instrument reports each sample value as a percentage of a reference vial. The reference vial should be the first non-background vial loaded in a cassette.

### **#Vials/Sample**

In this field, enter the number of replicates for each sample counted. The data output will report the average value of the replicates.

### **keV Energy Regions**

This area contains fields for the **Lower Limit** and **Upper Limit**. These fields represent lower and upper counting limits for regions A, B, and C—measured in keV.

### Background CPM Subtraction (Subtract Background)

Select this checkbox on the **Count Conditions** tab to subtract background CPM from all samples.

The background value is established in one of three ways, and selected from the following:

- **1st Vial** – The instrument counts the first vial in a cassette for ten minutes, or a defined protocol count time (whichever is greater) to establish a CPM value for each region. These are background values subtracted from each sample in each assay region.
- **IPA** – The instrument subtracts background values established during the Calibration and Instrument Performance Assessment (IPA) procedures from an entire spectrum of samples. The background spectra are stored during these procedures, and are available for any counting region.



*Note:* *GCT is not applied to IPA background.*

- **Manual** – Here, enter CPM values for the instrument to subtract from an entire spectrum of samples.



*Note:* *In Quench Standards assays, the **1st Vial** background subtraction option is not available. Background subtraction is only applied to the reported data for quench standards, and has no impact on a spectrum for each standard. Any background subtraction in DPM assays will apply to quench standards used for recalculating quench curve in the DPM assay.*

### Low CPM Threshold

Select this checkbox to stop counting early if sample activity is below a specified threshold. Enter CPM values for each counting region to halt counting if these values are not reached. The sample count is stopped if any region does not meet specified minimum CPM thresholds within the first 30 seconds of counting.

## 2 Sigma % Terminator

Select this checkbox to stop counting after acquiring enough counts to meet a statistical accuracy.

Two radio button options are available:

- **Any Region** – Select to enter the statistical accuracy level for each region (as a percent value) to achieve before counting terminates. Counting terminates when the Sigma value of any one region is reached. Using this feature, counting may stop before the specified count time elapses.
- **All Regions** – Select to enter the statistical accuracy level for each region (as a percent value) to achieve before counting terminates. Counting terminates when the Sigma value for each region is reached. Using this feature, counting may stop before the specified count time elapses.

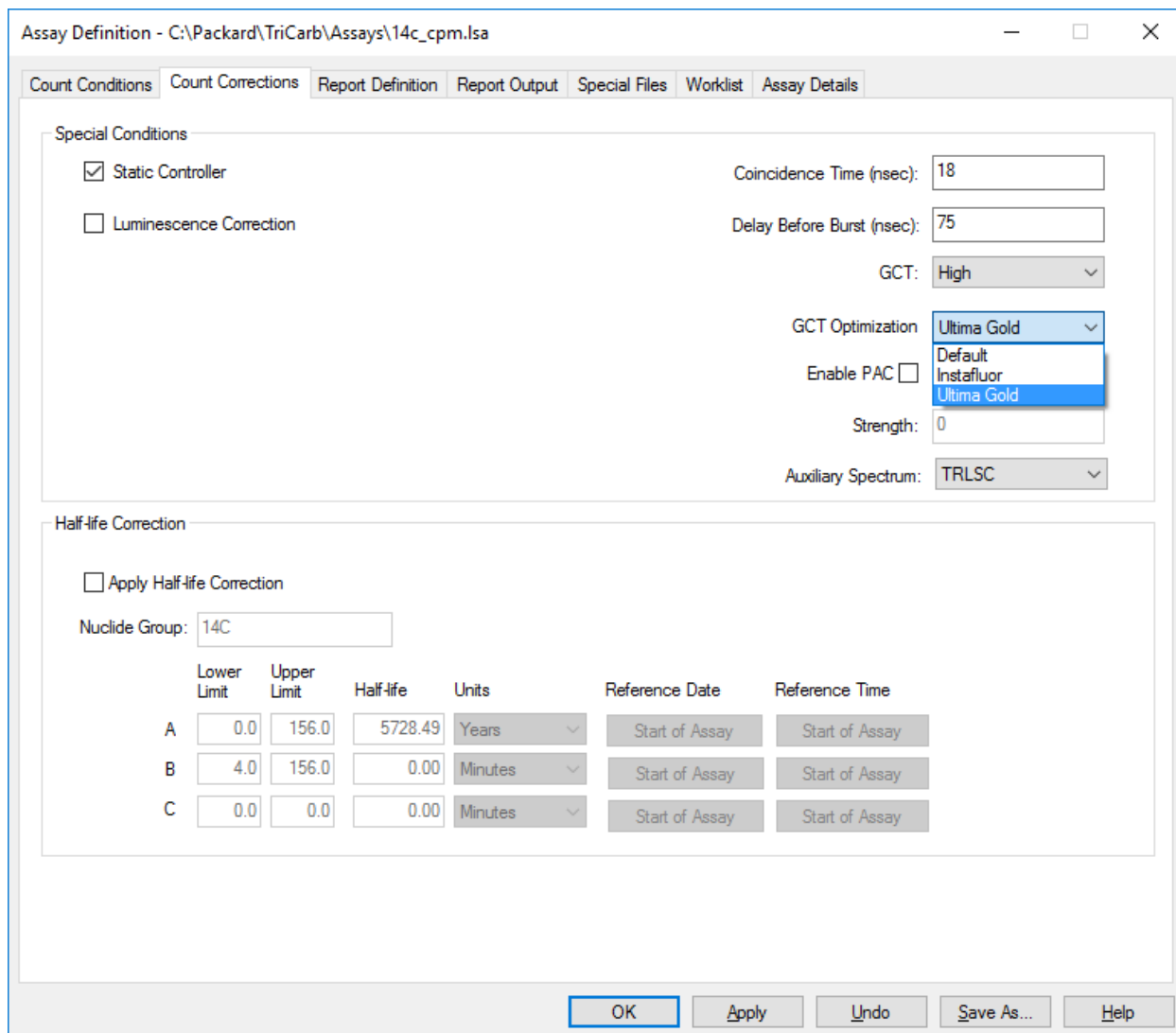
Changes made to the **2 Sigma % Terminator** parameter for an active assay will be implemented immediately.



## Count Corrections

This tab (Figure 4-5) in the *Assay Definition* window allows users to define specific count correction parameters for an assay.

 *Note:* The fields in the **Count Corrections** tab vary depending on the assay type defined.



Assay Definition - C:\Packard\TriCarb\Assays\14c\_cpm.lsa

Count Conditions | **Count Corrections** | Report Definition | Report Output | Special Files | Worklist | Assay Details

Special Conditions

Static Controller      Coincidence Time (nsec): 18

Luminescence Correction      Delay Before Burst (nsec): 75

GCT: High

GCT Optimization: Ultima Gold

Enable PAC       Default

Strength: 0      Instafluor

Auxiliary Spectrum: TRLSC      Ultima Gold

Half-life Correction

Apply Half-life Correction

Nuclide Group: 14C

	Lower Limit	Upper Limit	Half-life	Units	Reference Date	Reference Time
A	0.0	156.0	5728.49	Years	Start of Assay	Start of Assay
B	4.0	156.0	0.00	Minutes	Start of Assay	Start of Assay
C	0.0	0.0	0.00	Minutes	Start of Assay	Start of Assay

OK    Apply    Undo    Save As...    Help


**Figure 4-5. Count Corrections Tab (Assay Definition Window).**

### Static Controller

Select this checkbox to activate the instrument's static-controlling device, designed to reduce static originating on the sample vial. Static discharge can falsely elevate sample counts by producing non-beta pulses. This device should be active in most cases; its default value is ON. It is especially important in low humidity conditions (winter) when using plastic vials, and handling vials with latex gloves.

To further reduce the odds of generating static:

- Maintain a relative humidity level above 40%.
- Wipe latex gloves with anti-static wipes before handling vials.
- Use the **Pre-count Delay** timer (page 118) to delay counting of each sample, allowing time for static-induced pulses to dissipate.


 *Note: The Static Controller may decrease signal-to-noise ratio in SPC assays. Therefore, the Static Controller is typically not used. It is important in SPC assays to employ the above-mentioned techniques to minimize static.*

### Luminescence Correction

Select this checkbox to activate luminescence (light) correction. The instrument corrects data for counts resulting from sample luminescence. This is feature may be optional; contact your PerkinElmer representative for details.


### Colored Samples

Select this checkbox to activate color correction. The instrument will correct data for color quench. Typically, this is only required if samples are highly colored.

 *Note: This checkbox is available only for DPM Assays using tSIE/AEC for assays using Normal count mode, and for assays using one of the following nuclide groups:  $^3\text{H}$ ,  $^{14}\text{C}$ , or  $^3\text{H}$ - $^{14}\text{C}$ . In addition, the Colored Samples checkbox is unavailable on the Quantulus GCT model equipment.*

### Heterogeneity Monitor


Select this checkbox to activate a device that monitors and flags heterogeneous samples (e.g. samples with phase separation). This feature may be optional; contact your PerkinElmer representative for details.

 *Note: This checkbox is only available for Single Label DPM assays, where tSIE is selected as the Quench Indicating Parameter. The system uses tSIE and sample spectrum endpoint to determine sample heterogeneity.*

### Coincidence Time


In this field, specify the length of time (10–200 nanoseconds) that both PMTs must detect scintillation events.

- If the events occur in coincidence (and in the specified coincidence time), they are considered true sample decay events.
- If the events do not occur in coincidence, they are considered random (background) and not counted.

 *Note:* When using solid scintillators, coincidence time may need to be extended. The optimal setting must be determined empirically.

### Delay Before Burst


In this field, specify the length of time (75–800 nanoseconds) after the initial pulse (prompt pulse) which the detector will look for additional pulses (afterpulses). Afterpulses (which occur after a prompt pulse and delay time interval) indicate that a scintillation event is due to background. Some scintillators, such as PerkinElmer Ultima Gold, produce slower decaying pulses that may require longer delay times. When using these scintillators, lengthen delay time to retain high counting efficiencies. This is important when counting high energy beta-emitting nuclides. The default setting for this parameter is 75.

 *Note:* This parameter is only accessible with high sensitivity and low level count modes.

### GCT (Guard Compensation Technology)

This is a technique used to reduce backgrounds in the beta spectrum via efficiency calculations applied to events detected in the Guard via the following settings:

- **High** - Best suited for removing a maximum number of background events in the lowest energy channels, i.e. - 3H region.
- **Low** (default) - A less aggressive setting for background reductions over a wider range of energy channels.
- **Off** - No GCT background correction.

 *Note:* To detect GCT overcorrection, open the Options dialog under the Tools menu and check the box "Allow Negative CPM/DPM Reporting". When GCT overcorrection is present, the letter "O" will appear in the MESSAGES column of the printed report. If overcorrection is present, consider creating a GCT optimization set (see appendix D).

### **GCT Optimization**

Select the GCT Optimization set to use for GCT correction. Please refer to the document “Sample Type-Specific GCT Optimization Sets” for details about creating a custom GCT Optimization set.



*Note - Normal count mode must be selected when GCT is in use.*

### **Enable PAC (Pulse Amplitude Comparison)**

Select this checkbox to enable PAC. This is used to reduce background by comparing the amplitude of event pulses produced by each PMT, rejecting the event when the amplitudes differ. Strength values from 0 - 255 adjust how much the amplitudes can differ before the event pulses are removed.

### **Auxiliary Spectrum**

The auxiliary spectrum shows counts that have been rejected from the beta spectrum. Select the type of rejected events to be included in this spectrum: TRLS, PAC or Moat. Note that PAC is only available if PAC has been enabled. Moat is only available for Alpha/Beta assays. The selected auxiliary spectrum is available in the SpectraView spectrum list.

### **Half-life Correction (Apply Half-life Correction)**

This feature is typically used when working with short half-life nuclides; the instrument corrects sample counts for half-life decay of nuclide(s) counted. The **Reference Date** and **Reference Time** are used to make a decay calculation, with default settings corresponding to the start of an assay.



*Note: In Quench Standards assays, activate the half-life correction feature only if a DPM value entered into the Quench Standards Library for the nuclide is not corrected for decay. If the DPM value entered in the library for standards is decay-corrected, the half-life correction feature should not be used.*

## Report Definition

This tab (Figure 4-6) in the *Assay Definition* window allows users to design custom reports.

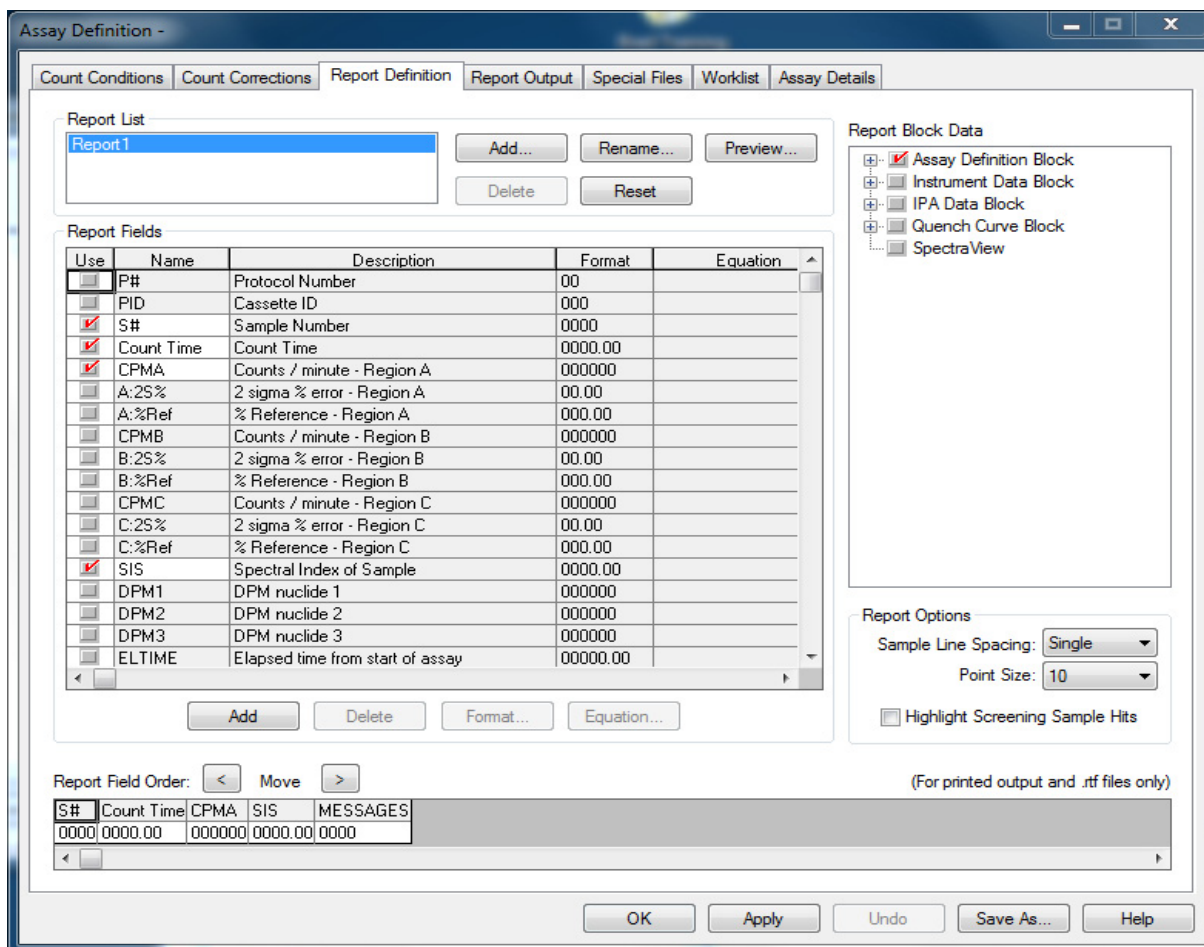


Figure 4-6. Report Definition Tab (Assay Definition Window).

### Report List

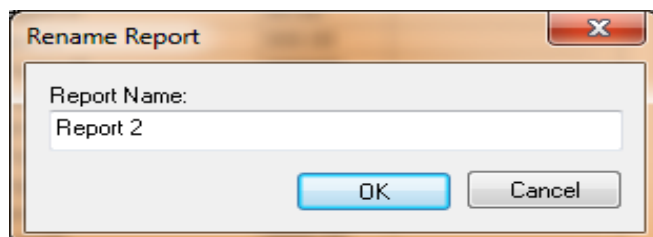
This area allows users to add, rename, preview, delete, or reset a report. The following information describes the buttons contained in this area:

#### Add

Click this button to define a new assay report. Use any named report formats in the list for output types identified on the **Report Output** tab (page 134). Different report formats may be used for each output type (Printer, Data File, RS-232, or Rich Text Format), if desired.


### Rename

Click this button to rename a report. First, select a report name, and then click **Rename**. After clicking the **Rename** button, the *Rename Report* window appears (Figure 4-7):



**Figure 4-7. Rename Report Window.**

In the **Report Name** dialog box, enter a new report name, and then click **OK**.

 *Note:* If an existing name is entered, or one with invalid characters (/ \ ? " | < >), a warning prompt will appear.

### Preview

Click on this button to view an on-screen version of a report. First, select a report name from the list in the **Report Name** box, and then click **Preview**. The fields selected in the **Use** column of the **Report Fields** area (page 126) will appear in the report with general information. Use the Preview feature as an interactive tool to refine report content (before starting a protocol).

### Delete

Click on this button to delete a report by selecting a report name from the list in the **Report Name** box, and then click **Delete**.

### Reset


Click this button to restore the default list of Report Fields for a selected report. First, select a report name from the list in the **Report Name** box, and then click **Reset**.

## **Report Fields**

This area allows users to select and edit fields to be included in a report. The following describes the fields/columns and buttons contained in this area:


### Use Column

Select the checkbox in the **Use** column to have the corresponding field appear on the report.

 *Note:* Any changes to the format or equation of custom fields will be saved when the Assay Definition window is closed - whether or not the **Use** field checkbox is selected.

### Data Field Column

This column provides predefined data fields for various report fields including typical result values (e.g. CPM, DPM, quench parameters, count time, statistical calculations, etc).

 *Tip:* If an instrument is configured with the Bar Code Reader option, add the **SMPL\_ID (Sample Name (from Worklist))** data field to a report to make bar code validation simpler. Selecting this field will print a bar code for each report sample.

In addition, users can define custom fields to report special calculations or formats for an application. These custom fields are added using the **Add** button (page 128), and are automatically titled **Custom1**, **Custom2**, etc., when created. These custom fields may be renamed. However, if a custom field is deleted, QuantaSmart will not reuse that title for an assay.

### Format Column

Each field in this column displays a sample format selected for an associated field. This sample is intended to show the number of digits and decimal places used to report this field. The zero character is used to represent a digit that can adopt any value appropriate for the field type (alpha and/or numeric). To define the format, click in a field to select it, and then click the **Format** button (page 129).

### Equation Column

Each field in this column displays an equation (if defined). To enter an equation or edit an existing one, select a field and click the **Equation** button (page 130), which displays the *Equation* window. In the window, define the information to appear in the selected field.

### Add Button

Click this button to add a new, custom field to the list of available output fields for a report. Users can define a name, format, and content of each custom field created. Custom field content can be defined to be a specific value, copy of a field for the same sample, or a formula using mathematical operands on other field values and/or constants.

Define only one operation per custom field.

For complex operations, create custom fields to generate intermediate values, which can be combined with other custom fields for the final result. Calculated custom fields need not be included in a final output, so intermediate results can be hidden (if desired). Custom fields are stored with individually named reports. However, custom fields used in one report are not available in other reports, even when used in the same assay.

### Delete Button

Click this button to omit a custom field.

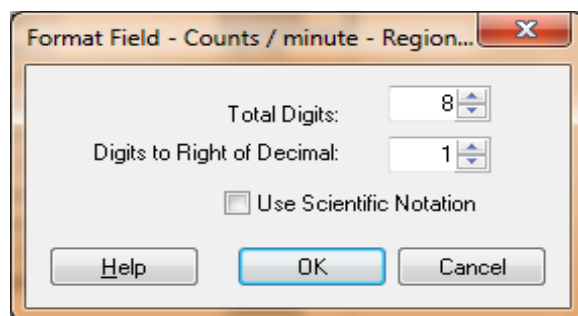


*Note: A custom field cannot be deleted if referenced by an equation in another field. Delete or modify any field(s) that reference another field to be deleted, and then delete the desired field.*



### Format Button

This button allows users to define a format for reporting a currently selected data field. To define a data format, select a field marked for use in a report (**Use** checkbox is selected), and then click the **Format** button. The *Format Field* window opens (Figure 4-8).



**Figure 4-8. Format Field Window.**

In the **Total Digits** field, specify the total number of digits for a field, representing the overall width, decimal space, integer space, and padding (spaces inserted before the value) necessary to fill any unused space. The decimal point (if appropriate) is not counted as a digit for this purpose.

In the **Digits to Right of Decimal** field, define the number of digits to the right of the decimal point.

For fields that may result in very large or very small numbers, select the **Scientific Notation** checkbox to report the numbers in Scientific Notation (see the following examples):

**Examples:**                    3.123e + 006 is equivalent to  $3.123 \times 10^6$  (3,123,000)

                                      3.123e - 003 is equivalent to  $3.123 \times 10^{-3}$  (0.003123)

Once finished defining a field's format, click **OK** to save changes. Click **Cancel** to exit the *Format Field* window without saving changes.

### Equation Button

Click this button to enter an equation defining a value reported by the selected custom field. After clicking the **Equation** button, the *Equation* window appears (Figure 4-9).

**Figure 4-9. Equation Window.**


The information below describes the buttons and fields in the *Equation* window (Figure 4-9).

- **Reference** – Select this radio button to select a single value for this custom field. The value may be a constant value, or entered from another defined field in the **Field** drop-down list.
- **One Operand** – Select this radio button to enable the **Operator** and **Operand** fields.
  - The **Operator** field contains the following operators: **log** (common logarithm), **exp** (inverse natural logarithm), and **sqrt** (square root).
  - The **Operand** field contains a list of defined report fields yielding a numeric value. Type a numeric constant (integer or a floating point number) in this field, or select an entry from the drop-down list.
- **Two Operands** – Select this radio button to select two data fields (operands) from drop-down lists of defined report fields, and a binary operator to perform the desired calculation.
  - The **Operand 1** field contains defined report fields yielding a numeric value. No alphabetic standard or blank custom fields are available. Type a numeric constant (integer or floating point number) in this field, or select from the drop-down list.

- The **Operator** field contains a list of binary operators:
  - + addition
  - subtraction
  - / division
  - \* multiplication
- Like **Operand 1**, the **Operand 2** field contains defined report data fields that yield a numeric value. No alphabetic standard or blank custom fields are available. Type a numeric constant (integer or floating point number) into this field, or select from the entries in the drop-down box.
- **Screening** – Click this radio button to enable the screening fields. Select a value from the **Field** field; this value will be compared with a second value to select or enter at the **Field or Value** field at far right. The calculated values meeting a selected criteria (**Less Than**, **Greater Than**, or **Between**) will appear in the subsequent report.
  - From the **Comparison** field, select a comparison criteria: **Greater Than**, **Less Than**, or **Between**. The calculated value (or values being sought) will appear in the subsequent report.
  - Value types in the **Bkg** field depend on the selection made in the **Background Subtract** field (page 119) on the **Count Conditions** tab (select **1st Vial**, **IPA**, or **Manual**). In the **Bkg** field(s) of the *Equation* window, select the Region(s) from which the background values must be subtracted. The difference is multiplied by the number entered in the adjacent box at right. The total is then added to the selected **Field or Value**.
  - In the **Field or Value** field, enter a value or select one from the drop-down list. The product of the preceding calculation (Region Background x manually entered value) is added to the selected field or value.
  - From the **Hit Indicator** field, select a hit indicator from the list (**Low**, **High**, or **In Range**), or type a custom hit indicator. A hit indicator is a report heading used to classify the screened value range.

## Report Block Data

These items contain predetermined data sets about the system, assay or samples. These block data items are included in printed reports and Rich Text Files (RTF). The other output types—Data Files and RS-232—will NOT include the selected block data items.

 *Note: Some information in block data items may also be included in the RS-232 output by marking appropriate checkboxes when choosing the RS-232 output type. This is not controlled via the use of block data item mechanism described here.*

When defining reports for an assay, include block data items and individual fields related to a specific block data item. For example, when expanding the **Assay Definition Block** tree, a list of related data items appears. Select the entire data block, or include/exclude individual items within the tree. When clicking on the main data block, all data items in the expanded tree (or trees) are automatically selected, and included in the report.

To exclude an item in the tree, expand the data block tree, and de-select each item to exclude. A data block item in the report is identified in the tree with a red check mark.

Available block data items include:

- Assay Definition Block (page 132)
- Instrument Data Block (page 133)
- IPA Data Block (page 133)
- Quench Curve Block (page 133)
- SpectraView (page 133)

Block data items can also be used to send files to an external device via the RS-232 communications port in an ASCII format. IPA data can be transmitted through the RS-232 communications port by selecting the **Transmit IPA Data** checkbox in the *IPA Definitions* window (page 179).

### Assay Definition Block

Select this block data item to include information on parameters used to count an assay in a printed (or RTF) report. These parameters include those defined on the **Assay Details** tab (page 116), **Count Conditions** tab (page 116), and **Count Corrections** tab (page 121).

### Instrument Data Block

Select this block data item to include instrument-related data in printed (or RTF file) reports. This block data contains information on instruments and software.

The following keywords and values are contained in the **Instrument Data Block**:

### IPA Data Block

Select this block data item to include information from the last set of acquired IPA data in printed (and RTF file) reports. This block data item contains information on efficiency, backgrounds, figures of merit, and Chi-squares for Tritium and <sup>14</sup>C system performance.

### Quench Curve Block

Select this block data item to include a graphic display of a quench curve associated with a DPM assay.

### SpectraView

Select this block data item to print a graphic display of a spectrum for each sample.

## **Report Field Order**


This area displays the order/format in which report fields are output. Fields highlighted in yellow will not fit on a single sample line when printing a report; these fields are wrapped to a second line for printed and RTF reports. The data output window does not wrap on-screen. This highlight is the only indication of how sample lines in printed reports will be formatted.


## **Report Options**

This area offers selections enabling users to modify the appearance of a printed report:

- **Sample Line Spacing** – Select the spacing required between each report lines: **Single** spacing, **1.5 Lines** of spacing, or **Double** spacing.
- **Point Size** – Select a point size for each printed character in a report: **10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20**.
- **Highlight screening sample hits** – Select this checkbox to print a report's screening sample hits in bold characters.

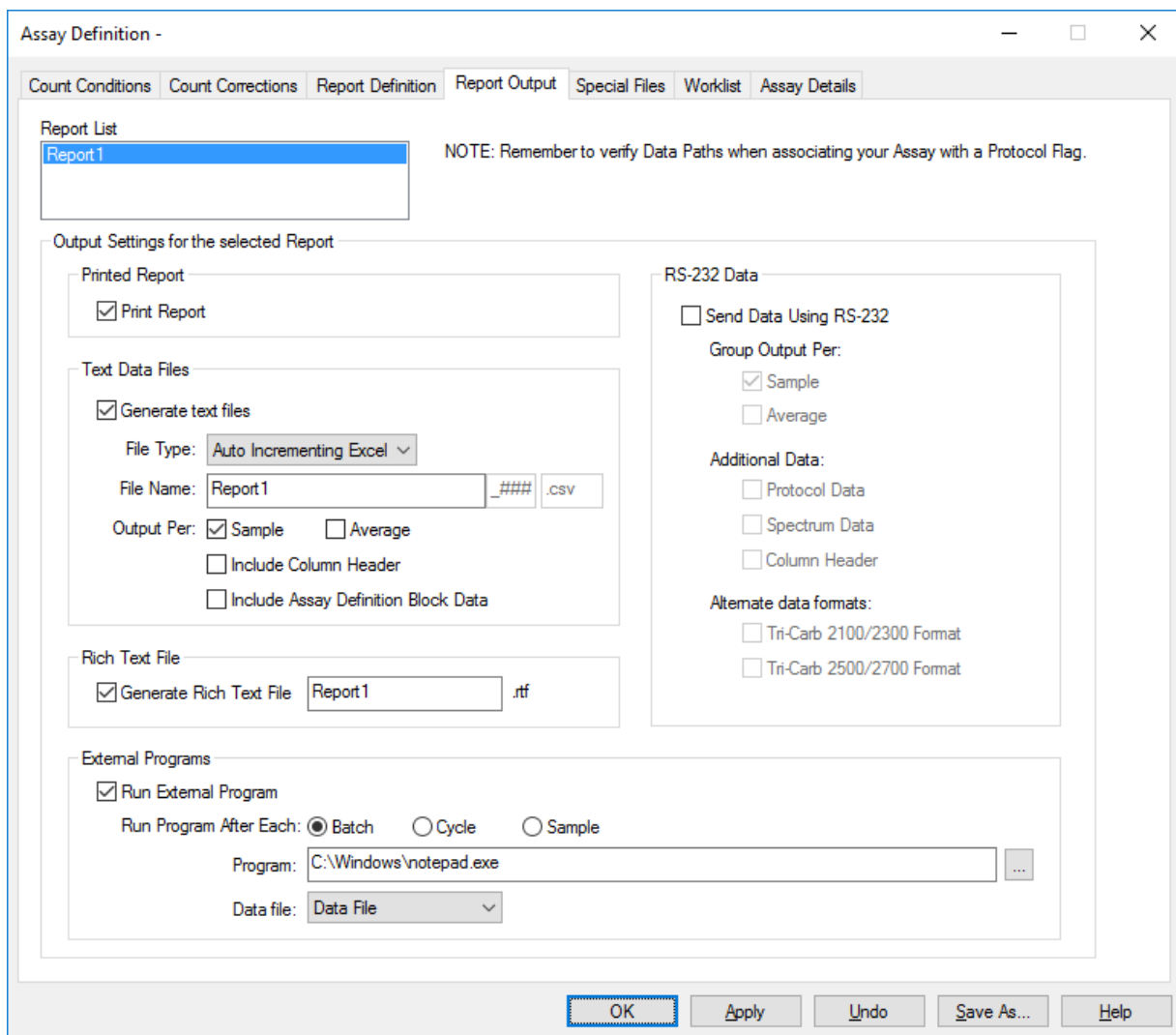
## **Report Field Order**

Use the  button to move a selected field to the left.

Use the  button to move a selected field to the right.

## Report Output

This tab (Figure 4-10) in the *Assay Definition* window allows users to customize a report's output.



**Figure 4-10. Report Output Tab (Assay Definition Window).**

### Report List

This region allows users to select a named report for output.

### Printed Report (Print Report)

Select this checkbox to send the selected report to a printer. Assay data will automatically print once an assay count cycle is completed.

### Text Data Files (Generate Text Files)

Select this checkbox to enable fields allowing users to output data to a specified file type. Specify the file type and other file settings using the following fields:

#### File Type

QuantaSmart automatically saves data for internal use and Replay (if available) as dated Results files. These files are separate from data files defined in the **Report Output** tab. The data file in the **Report Output** tab provides count data to other programs or archival facilities. Select the ASCII file type for this auxiliary data file using the **File Type** drop-down list. Data fields included in the file are defined by selections made in the **Report Definition** tab (page 125).

The following list describes the selections available in the **File Type** field:

- **Auto Incrementing Excel** – Select this to generate Excel format files with unique filenames.
- **Auto Incrementing** – With this option, QuantaSmart names the file by automatically incrementing a numerical extension each time that a file is generated. This prevents data from being overwritten from one run to the next.
- **Delimited Text** – With this option, QuantaSmart generates data as delimited ASCII text. If a numerical extension is entered, this selection is identical to the **Auto Incrementing** selection described above.
- **Excel** – With this option, QuantaSmart generates data compatible with Microsoft® Excel.
- **Lotus** – With this option, QuantaSmart generates data compatible with Lotus® 1-2-3.



*Note: The field delimiter is defined by the Microsoft® Windows O/S using the Regional and Language Options window accessed from Windows Control Panel. Once the Regional and Language Options window is opened, click the **Customize** button and access the **List Separator** field on the **Numbers** tab.*

#### File Name

In this field, a data file is named. If selecting a **Delimited Text** type, enter any file extension as the name. All other file types use predefined extensions based on conventions.

These predefined extensions are as follows:

- **Auto Incrementing** – **###** (incrementing numeric)
- **Delimited Text** – **.txt** (default, user-selectable)
- **Excel** – **.csv**
- **Lotus** – **.wks**

### Output Per Sample and/or Average

Select these checkboxes to indicate a data type to be included in an output:

- **Average** allows a data file to contain one line of data for each average data line in the output window.
- **Sample** allows a data file to contain one line of data for each sample data line in the output window.
- Checking both **Sample** and **Average** allows a data file to contain one line of data for each average data line, and one line of data for each sample data line.

### Include Column Header

Select this checkbox for headers to be included at the beginning of a data file for each data field.

### Include Assay Definition Block Data

Select this checkbox to include the Block Data information in a data file output.

## **RS-232 Data**

### Send Data Using RS-232

Select this checkbox to enable fields located in the **RS-232** area of the **Report Output** tab. These fields allow users to transmit lines of sample data via the RS-232 port. See RS-232 in Appendix B for serial port configurations. Specify the data to include settings for RS-232 data transmission with the following fields:

### Group Output Per Sample and/or Average

Select this checkbox to allow QuantaSmart to transmit one line of data for each average data line in the output window. Select **Output Per Sample** to allow QuantaSmart to transmit one line of data for each sample data line in an output window; the default selection is **Sample**.

### Additional Data

Select an appropriate checkbox to include additional information in the RS-232 output. Select any combination of the following three data items as desired:

- **Protocol Data** – Select this checkbox to transmit protocol information with the data. This information, if selected, is sent immediately before the report of first sample data.
- **Spectrum Data** – Select this checkbox to transmit spectrum information with the data. This information, if selected, is sent immediately after the last sample data reported for an assay.
- **Column Header** – Select this checkbox to transmit column headers with the data. Column headers, if selected, appear immediately before the first sample data of an assay to identify the transmitted data's field order.



### Alternate Data Formats

Select a checkbox for an alternate RS-232 format. Users may emulate the format from a model 2100/2300 Tri-Carb, or a model 2500/2700 Tri-Carb instrument. If neither of these alternate formats are emulated, RS-232 data will appear in a format defined by the selected Report Definition. Users may not emulate both alternate data formats simultaneously.

### **Rich Text File (RTF)**

Select this checkbox to have QuantaSmart generate an RTF containing the contents of the output window. If the **RTF** checkbox, enter a descriptive filename in the **File Name** field. QuantaSmart automatically assigns an extension of `.rtf`; the RTF file is essentially a copy of the output window.



*Note: Any name entered into the **File Name** field will remain unless changed. It is “grayed out” if the **Rich Text File** checkbox is not selected.*

### **Run Application**

Select this checkbox to use the Tandem Processing feature allowing the instrument to analyze samples, perform data reduction, and automatically pass data to an application program.

Enabling this feature will cause an external program to further process data. If information is entered in any fields in the **Run Application** area of the window, but the **Run Application** checkbox is not selected, the information is retained but “grayed out.”

The following information describes the fields in the **Run Application** area of the window:

#### Application

When you select this checkbox, enter a name and location of a Tandem Processing application to run. If necessary, use the button next to the field to browse for the application.

#### Data File

From this field, select a data file type for the Tandem Processing application to process. The appropriate file name is passed to the application as a command line parameter: the following options are available in the **Data File** field:

- **Data File** – Select this option to use the file defined in the **Data File** area.
- **None** – Select this option when no specific data file is identified for use.
- **RTF File** – Select this option to use the file defined in the **Rich Text File** area.

### Run After Each Batch, Cycle, or Sample

Select one of the radio buttons to specify when the application should run:

- **Batch** – Select this radio button to run the application program once at the end of the protocol.
- **Cycle** – Select this radio button to run the application program at the end of each cycle.



*Note: This option does not apply to Tandem Processing in Replay.*

- **Sample** – Select this radio button to run the application program after each sample.



*Note: Each time the application program is run, it must be loaded into memory. Whenever possible, run the application program after a batch or cycle, as it is more efficient than running the program after each sample.*

## Special Files

This tab (Figure 4-11) in the *Assay Definition* window allows users to select and configure information regarding files pertinent to an assay.

The screenshot shows the 'Special Files' tab in the 'Assay Definition' window. The window title is 'Assay Definition - C:\Packard\TriCarb\Assays\GCT Optimization Ultima Gold.Isa'. The 'Special Files' tab is selected, and the 'GCT Optimization' sub-tab is active. The 'GCT Optimization' section has a checked 'Create Optimization Set' checkbox, with the name 'Ultima Gold' entered in the 'Name' field. The 'Existing Sets' list contains 'Instafluor'. The 'Composite Spectra File' section has an unchecked 'Generate Spectra File' checkbox and an empty 'File Name' field. The 'Individual Sample Spectrum Files' section has an unchecked 'Generate Sample Spectrum Files' checkbox and a 'File Name' field containing the template 'Assay\_S####\_R##\_YYYYMMDD\_HHMM.Spectrum'. Below this field are definitions: 'S#### = sample number', 'R## = repeat count number', 'YYYYMMDD = Date', and 'HHMM = Time'. The 'IPA Data File' section has an unchecked 'Generate IPA File' checkbox and an empty 'File Name' field. The 'Additional Files' section has two unchecked checkboxes: 'Generate Prot.dat File' and 'Generate 2000CA.dat File'. A note at the bottom states: 'Note: These files will be created in the folder set in the Data Paths window.' The bottom of the window features buttons for 'OK', 'Apply', 'Undo', 'Save As...', and 'Help'.

Figure 4-11. Special Files Tab (Assay Definition Window).

### **Composite Spectra File (Generate Spectra File)**

Select this checkbox to have QuantaSmart generate a single, composite, ASCII spectra file containing all samples counted in the assay. Each individual sample spectrum is appended to the end of this composite file as it is counted to provide all sample data.

The data file format is similar to that created for individual spectrum files (discussed below), with count parameters for a single sample in a header and the channel data listed serially after it. The protocol number, sample number, and sample repeat value precede each parameter header to identify the individual sample spectra within a file.

In the **File Name** field, enter a file name. The composite spectra file will be created in the **Output Data Path (Raw Data Path for Replay** if used from Replay) identified in the *Data Paths* window (page 66).

### Individual Sample Spectrum Files (Generate Sample Spectrum Files)

If performing a Tandem Processing application that requires spectrum files, select this checkbox to create individual sample spectrum data files in the **Output Data Path** directory for the assay. A Spectrum file is an ASCII text file with spectral data for a single sample (a separate file is created for each sample). The spectral data is reported in 0.5 keV increments—up to the highest endpoint of the defined regions being counted (one channel is reported per line).

If GCT is set to Low or High, the Beta spectrum counts will have the GCT background reduction algorithm applied.

The **File Name** field displays the file name structure of data files as follows:

Assay\_S####\_R##\_YYYYMMDD\_HHMM.Spectrum

Spectrum data files are created with a file name that corresponds to the following structures:

#### Beta Spectrum Files

Example: 3HCPM\_20040511\_1024\_S0001\_R01.Spectrum

- 3HCPM = assay name
- 20040511 = year/month/day
- 1024 = hour/minute
- S0001 = sample number
- R01= sample repeat count number
- .Spectrum = file extension

#### Alpha Spectrum Files (Alpha/Beta Assay)

Example: 3HCPM\_20040511\_1024\_S0001\_R01\_A.Spectrum

- Same convention as Beta with \_A suffix.

#### Guard Spectrum Files (Quantulus GCT Only)

Example: 3HCPM\_20040511\_1024\_S0001\_R01\_G.Spectrum

- Same convention as Beta with \_G suffix.

The following keywords and values are contained in the Spectrum Data file.

Keywords	Values
CTIME	Sample count time defined in protocol

Keywords	Values
<b>TSIE</b>	Quench Indicating Parameter defined in protocol
<b>LLA</b>	Lower counting limit for Region A
<b>ULA</b>	Upper counting limit for Region A
<b>LLB</b>	Lower counting limit for Region B
<b>ULB</b>	Upper counting limit for Region B
<b>LLC</b>	Lower counting limit for Region C
<b>ULC</b>	Upper counting limit for Region C
<b>COIN_TIME</b>	Coincidence Time defined in protocol
<b>DELAY_BEFORE_BURST</b>	Delay Before Burst defined in protocol
<b>COUNT_MODE</b>	Count Mode defined in protocol
<b>COMMENTS</b>	Comments
<b>COUNTS</b>	List of counts/channel (one channel per line)

#### IPA Data File (Generate IRA Data File)

Select this checkbox to have QuantaSmart generate an IPA data file containing the most recent IPA parameter values. In the **File Name** field, enter a file name.

#### Additional Files (Prot.dat File)

Select this checkbox to have QuantaSmart generate a Prot.dat file containing information regarding the protocol. The Prot.dat file is an ASCII text file containing information for a protocol. The following keywords and values are contained in the Prot.dat file.

Keywords	Values
<b>P#</b>	Protocol number
<b>DATE</b>	Date the protocol was performed
<b>TIME</b>	Time the protocol was performed
<b>COUNTFILE</b>	Filename containing count data in ASCII format
<b>FILEPATH</b>	Drive and directory containing count data file
<b>PROTNAME</b>	Protocol name

Keywords	Values
SN1UNK	Sample number of the first unknown
CTIME	Count time defined in protocol
DATAMODE	Data mode defined in protocol
AVG/SMPL	Individual sample data or replicate averages
NUCA	Nuclide selected for Region A
NUCB	Nuclide selected for Region B
LLA	Lower counting limit for Region A
ULA	Upper counting limit for Region A
LLB	Lower counting limit for Region B
ULB	Upper counting limit for Region B
LLC	Lower counting limit for Region C
ULC	Upper counting limit for Region C
#/VIAL	Number of times a sample is counted in the detector
#/SMPL	Number of replicates per sample
ULD	User ID entered in protocol
ADDLHEAD	Additional heading entered in protocol
\EOF	End-of-File

### Additional Files (2000CA.dat File)


Select this checkbox to have QuantaSmart generate a 2000CA.dat file - an ASCII, comma-delimited text file including information about a protocol.


### GCT Optimization

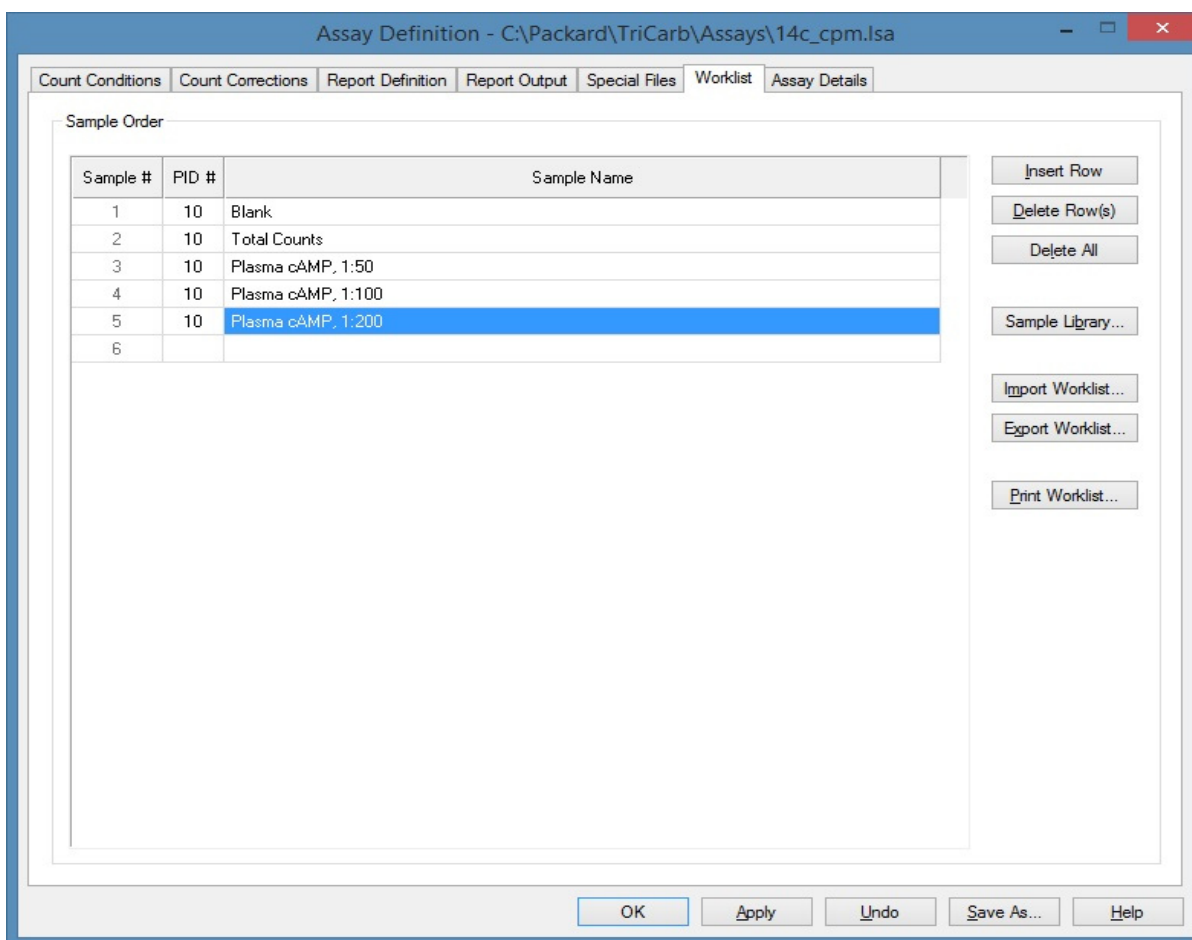
Check the box if this assay will be used to create a GCT optimization set. Enter the name for this set. If the name entered already exists, the Optimization Set will be replaced when this assay is counted. Please refer to "Sample Type-Specific GCT Optimization Sets" (*see appendix D*) for more details.

## Worklist

This tab (Figure 4-12) in the *Assay Definition* window allows users to designate Positive Identification numbers (PID #) and sample names corresponding to sample numbers on a printout or electronic report. Users may also create a Sample List Library of frequently used sample names.

 **Note:** *In the Worklist, every vial has a unique name to ensure that every vial in a sample group has a unique ID.*

 **Note:** *This feature may be optional. Contact your PerkinElmer representative for details.*



**Figure 4-12. Worklist Tab (Assay Definition Window).**




### Sample #

The number listed in this field represents the sample number on a printout or electronic report. The **Sample #** is the physical location of a sample vial in a cassette. For example, Position 1 in a cassette corresponds to **Sample #1** in the Worklist.

### PID#

This field contains the Positive (Sample) Identification Number (PID#). In this field, enter the cassette number (located on the end of each cassette) used to hold each sample. Position 1 in the cassette corresponds to **Sample #1** in the Worklist.


 *Note:*      *If any empty cassette positions exist, the corresponding sample in the Worklist should be left blank.*

### Sample Name

In this field, enter a name for each sample number (maximum characters = 25).

If your Tri-Carb instrument is equipped with the Bar Code Reader option, you may do the following:

- Enter a sample bar code in the **Sample Name** field of the **Worklist** tab. Then, if **Validate Bar Code against worklist** is selected in the **Assay Details** tab (page 150), the software will cross-check the bar codes read with those manually entered into the Worklist.
- Add a sample's bar code to the Worklist. Select the **Add Bar Code to worklist** radio button in the **Assay Details** tab (page 150) to have the bar codes added to the Worklist as they are scanned. With the Replay feature, the scanned bar code will override the name in the **Sample Name** field, if a sample name was entered.

 *Tip:*      *To simplify bar code validation, add the **SMPL\_ID (Sample Name (from Worklist))** data field in the **Report Definition** tab to a report. Selecting this field will print the bar code for each sample listed on the report.*

### Insert Row

Click this button to add a blank row to the **Sample Order** table.

### Delete Row

Click this button to delete selected rows from the **Sample Order** table.

### Delete All

Click this button to delete all rows from the **Sample Order** table.

### Sample Library

Click this button to display the *Sample Library* window. This window is used to create lists of frequently used sample names for the Sample List Library.

### Import Worklist

Sample ID names saved in ASCII format can be imported into the **Worklist** tab. Click the **Import Worklist** button to import a Worklist; the *Import Worklist* window is displayed. Select the file to import as a Worklist, and then click **Open**.

#### About the Imported File

The file must have the exact header with the exact case and punctuation as shown in Figure 4-13. This is the format used by the Export Worklist function.

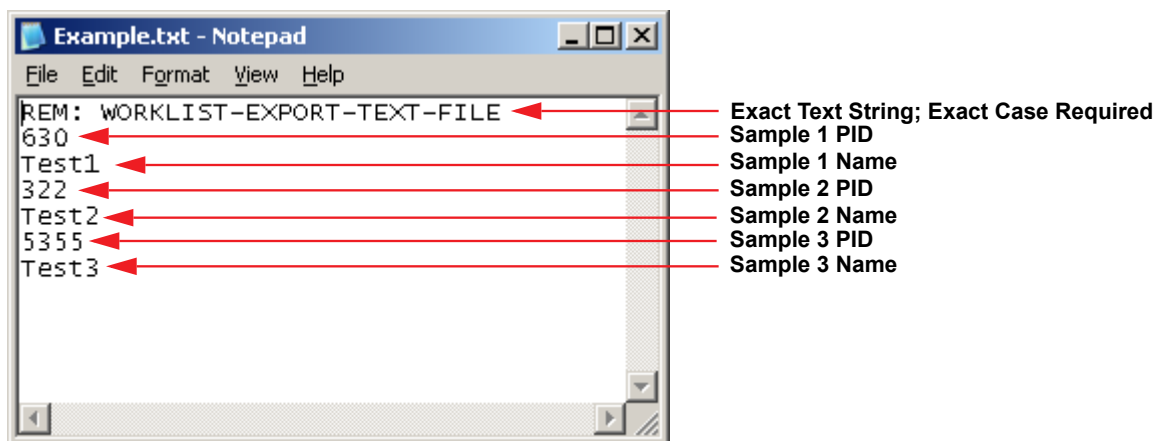
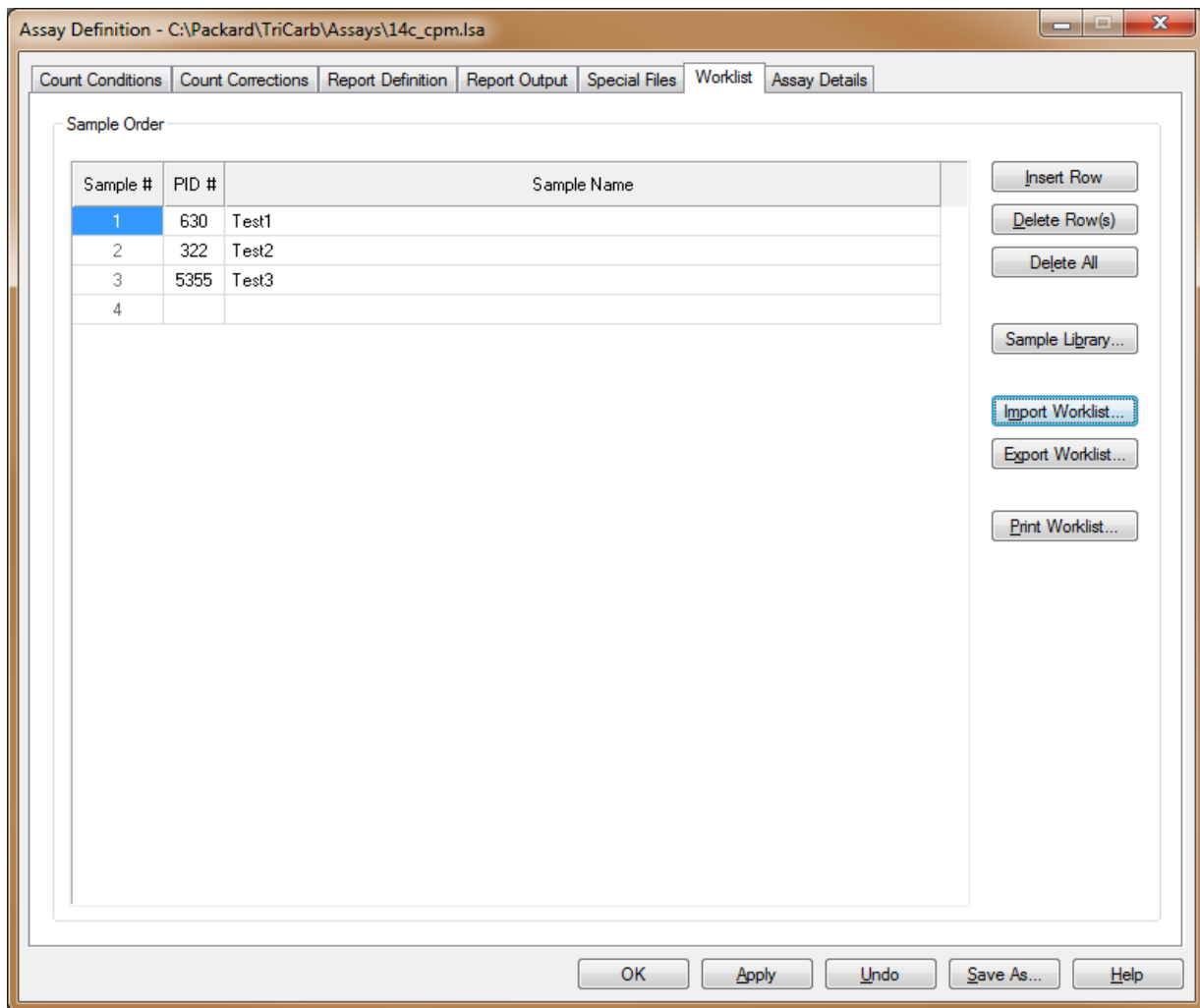


Figure 4-13. Example of an Imported Worklist File.

The file shown in Figure 4-13 would appear like Figure 4-14 when imported into the **Worklist** tab.



**Figure 4-14. Imported Worklist (Sample).**

### Export Worklist

Sample ID names can be exported from the **Worklist** tab for future use. Any exported files will be saved in ASCII format. Click the **Export Worklist** button to export a Worklist; the *Export Worklist* window is displayed. Enter a name for the Worklist, and then click **Save**.

The exported Worklist file is saved in the required format shown in Figure 4-13 for later use the Import Worklist function to reuse the exported Worklist (if desired).



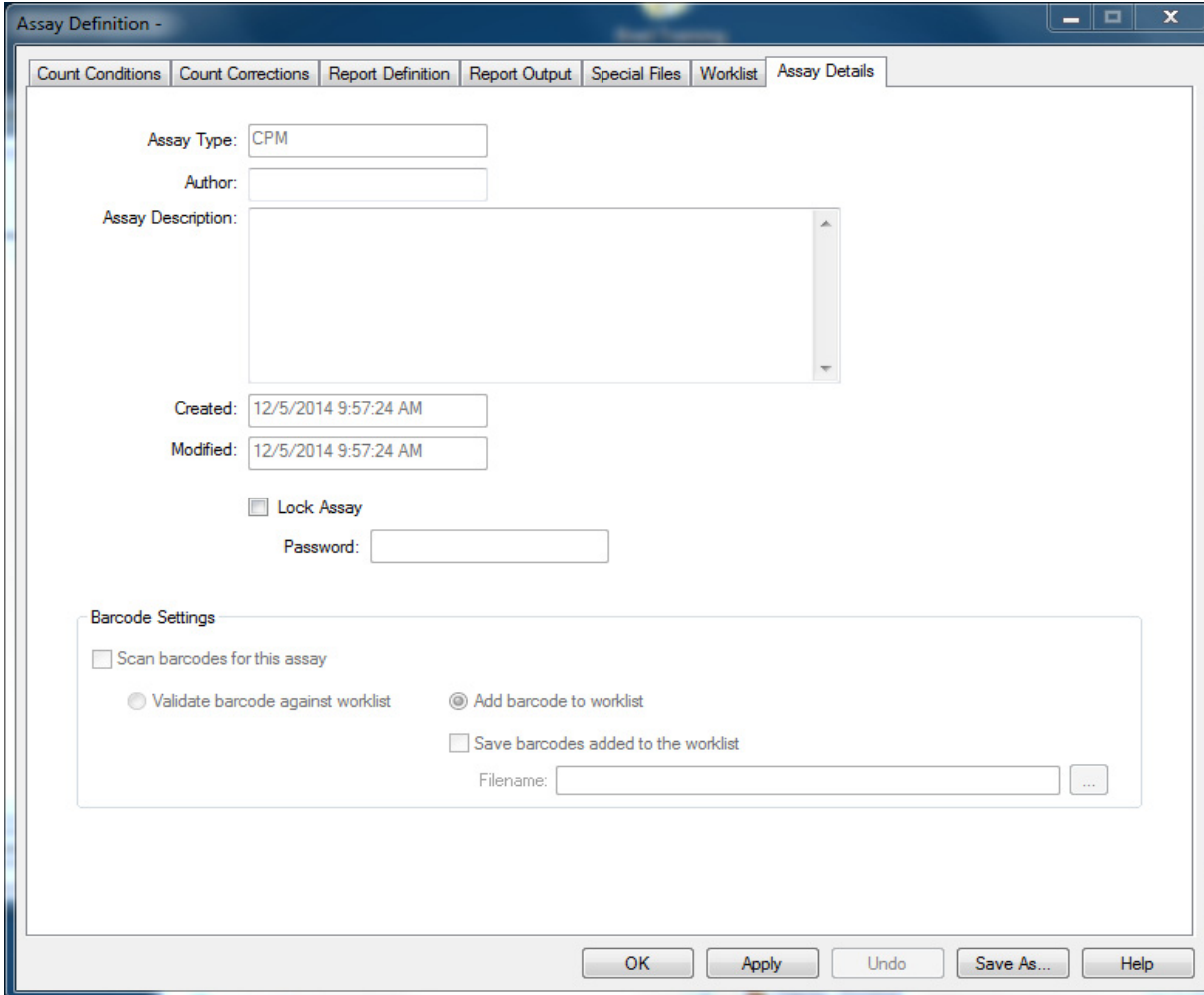
*Note:*        *The default folder for exporting Worklists is the Libraries folder. Worklists may be saved to other folders, as necessary.*

### Print Worklist

Click this button to print a Worklist.

## Assay Details

This tab Figure 4-15 in the *Assay Definition* window allows users to define specific detail parameters for an assay.



The screenshot shows the 'Assay Definition' window with the 'Assay Details' tab selected. The window has a title bar with standard minimize, maximize, and close buttons. Below the title bar is a tabbed interface with the following tabs: 'Count Conditions', 'Count Corrections', 'Report Definition', 'Report Output', 'Special Files', 'Worklist', and 'Assay Details'. The 'Assay Details' tab contains the following fields and controls:

- Assay Type:** A text box containing 'CPM'.
- Author:** An empty text box.
- Assay Description:** A large text area with a vertical scrollbar.
- Created:** A text box containing '12/5/2014 9:57:24 AM'.
- Modified:** A text box containing '12/5/2014 9:57:24 AM'.
- Lock Assay:** A checkbox that is currently unchecked.
- Password:** An empty text box.
- Barcode Settings:** A group box containing:
  - Scan barcodes for this assay
  - Validate barcode against worklist
  - Add barcode to worklist
  - Save barcodes added to the worklist
  - Filename:  ...

At the bottom of the window are five buttons: 'OK', 'Apply', 'Undo', 'Save As...', and 'Help'.

**Figure 4-15 Assay Details Tab (Assay Definition Window).**

### Assay Type

This field displays the assay type selected from the *Select Assay Type* window (Figure 3-12, page 65). Refer to page 97 for information on the different assay types.

### Author

In this field, enter a name or other identification as the assay author. This is an optional entry.

**Assay Description**

In this field, enter descriptive information about the assay. This is an optional entry.

**Date Created**

This field displays the date on which the assay was created.

**Date Modified**

This field displays the date on which the assay was last modified.

**Lock Assay**

Select this checkbox to restrict editing functions for an assay; type a password in the **Password** field.

**Password**

In the **Password** field, enter a password to restrict editing functions for the assay. Select the **Lock Assay** checkbox before entering a password in this field.

**Barcode Settings**

This region contains parameters for the bar code reader. For these fields to be active (not grayed out), the bar code reader must first be enabled in the *Bar Code Scanner Configuration* window (page 83). The following settings are in the **Barcode Settings** area:



*Note:*      *This feature may be optional. Contact your PerkinElmer representative for details.*

- **Scan Bar Codes for this assay** – Select this checkbox to scan bar codes when the assay runs. If not, bar codes will not scan for this assay. If this checkbox is grayed out (unavailable), the bar code reader is not enabled in the *Bar Code Scanner Configuration* window (page 83).
- **Add Bar Code to worklist** – Select this radio button to have bar code(s) automatically added to the Worklist. When selecting this option, the **Save Bar Code to file** checkbox is available (not grayed out) for selection.
- **Validate Bar Code against worklist** – Select this radio button to have the bar codes read cross-checked with those manually entered into the Worklist. All bar codes read must match those entered into the Worklist.
- **Save Bar Code to file** – This checkbox is available when selecting the **Add Bar Code to worklist** radio button. When clicking this checkbox, also specify the file to which the bar code(s) will be saved. Click on the **Browse** button to navigate to the specified file.

## Chapter 5

### Libraries

Radionuclide information is stored in the Nuclide Library - consisting of Quench Standards and Sample Nuclides Libraries. If an instrument is equipped with the optional Alpha/Beta Discrimination feature, an Alpha/Beta Standards Library and Alpha/Beta Nuclides Library will also be included.

The Quench Standards Library is comprised of quench sets, each containing individual quench standards. Data from quench standards is used to build quench curves for calculating in assays. Quench Standards are counted once, and the entire spectrum for each is stored independent of assay information. This allows users to select and use the same quench set in various assays, and build a quench curve for each sample when counted.

The Sample Nuclides Library allows users to specify and save nuclide names, counting region limits, and quench sets for sample nuclides. Up to three nuclides can be defined for each entry to support the counting of multiple nuclides. These sample nuclide parameters are typically specified as part of the assay definition process, and may be edited.

The Alpha/Beta Standards and Alpha/Beta Nuclides Libraries are used in the same way as Quench Standards and Sample Nuclides Libraries. Information stored in these libraries is relevant only when performing Alpha/Beta assays, where both Alpha-emitting and a Beta-emitting radionuclides are quantified independently within the same sample vial.

## Sample Nuclides Library

This window (Figure 5-1) allows users to enter information into (and retrieve information from) the Sample Nuclides Library. To access this library, select **Libraries | Sample Nuclides** from the menu bar.

Name	A: LL	A: UL	A: Half-life	A: Units	B: LL	B: UL	B: Half-life	B: Units	C: LL	C: UL	C: Half-life	C: Units	Quench Set: Low	Quench Set: Mid	Quench Set: High	Count Mode
3H	0.0	18.6	4530.37	Days	2.0	18.6	0.00	Minutes	0.0	0.0	0.00	Minutes	3H	...	...	Normal
14C	0.0	156.0	5728.49	Years	4.0	156.0	0.00	Minutes	0.0	0.0	0.00	Minutes	14C	...	...	Normal
3H-14C	0.0	12.0	4530.37	Days	12.0	156.0	5728.45	Years	0.0	0.0	0.00	Minutes	3H	14C	...	Normal
32P	5.0	1700.0	14.29	Days	50.0	1700.0	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
125I	0.0	70.0	59.24	Days	6.0	70.0	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
3H-125I	0.0	12.0	4530.37	Days	12.0	70.0	59.24	Days	0.0	0.0	0.00	Minutes	...	...	...	
3H-32P	0.0	16.0	4530.37	Days	16.0	1700.0	14.29	Days	0.0	0.0	0.00	Minutes	...	...	...	
3H-14C-32P	0.0	12.0	4530.37	Days	12.0	156.0	5728.45	Years	156.0	1700.0	14.29	Days	...	...	...	
3H Ultima Gold	0.0	18.6	4530.37	Days	2.0	18.6	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
14C Ultima Gold	0.0	156.0	5728.45	Years	4.0	156.0	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
3H Low Level	0.0	18.6	4530.37	Days	2.0	18.6	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
Direct DPM 3H	0.0	2000.0	4530.37	Days	0.0	0.0	0.00	Minutes	0.0	0.0	0.00	Minutes	3H	...	...	Normal
Direct DPM 3H-UG	0.0	2000.0	4530.37	Days	0.0	0.0	0.00	Minutes	0.0	0.0	0.00	Minutes	3H-UG	...	...	Normal
GCT Calibration	0.0	2000.0	0.00	Minutes	0.0	7.0	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
Wide Window	0.0	2000.0	0.00	Minutes	0.0	0.0	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
Manual 3H	0.0	18.6	0.00	Minutes	1.0	18.6	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
Manual 14C	0.0	156.0	0.00	Minutes	4.0	156.0	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
Manual Hi Sens	1.0	12.5	0.00	Minutes	14.5	97.5	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
Manual 3H-14C	1.0	12.5	0.00	Minutes	14.5	97.5	0.00	Minutes	0.0	0.0	0.00	Minutes	...	...	...	
Manual BGO Bk	0.0	2000.0	0.00	Minutes	0.0	2000.0	0.00	Minutes	0.0	2000.0	0.00	Minutes	...	...	...	

Buttons: Add, Comment..., Clear Quench Sets, Help, Delete, Print..., OK, Cancel

**Figure 5-1. Sample Nuclides Window.**

For assays, use the Sample Nuclides Library to define and save nuclide names, and counting region limits for radionuclides. Select a quench set for each sample nuclide using the Quench Set buttons in this window (Figure 5-1).

In Replay (page 209), use the Sample Nuclide Library to select a radionuclide for reanalyzing sample data.



*Note:* Fields enabled in the Sample Nuclides window will differ when accessed from different locations in the software. The list of nuclides displayed is dependent on assay type, nuclide, and number of quench sets associated with the nuclide.



The following table describes columns/fields in the Sample Nuclides table (Figure 5-1).

Column/Field	Description
<b>Nuclide Name</b>	In this column of the <i>Sample Nuclides</i> window (Figure 5-1), select the appropriate nuclide(s) for an assay, and click <b>OK</b> . To define a different nuclide, click the <b>Add</b> button, and type the name of the nuclide to count. Define the parameters in the fields displayed in the new row in the table, and then click <b>OK</b> . To delete a nuclide from the list, select that nuclide, click the <b>Delete</b> button, and then click <b>OK</b> .
<b>A: LL</b>	This field represents the lower counting limit for Region A, measured in keV.
<b>A: UL</b>	This field represents the upper counting limit for Region A, measured in keV.
<b>A: Half-life</b>	This field represents the half-life of Nuclide A.
<b>A: Units</b>	This field represents the units for the half-life of Nuclide A.
<b>B: LL</b>	This field represents the lower counting limit for Region B, measured in keV.
<b>B: UL</b>	This field represents the upper counting limit for Region B, measured in keV.
<b>B: Half-life</b>	This field represents the half-life of Nuclide B.
<b>B: Units</b>	This field represents the units for the half-life of Nuclide B.
<b>C: LL</b>	This field represents the lower counting limit for Region C, measured in keV.
<b>C: UL</b>	This field represents the upper counting limit for Region C, measured in keV.
<b>C: Half-life</b>	This field represents the half-life of Nuclide C.
<b>C: Units</b>	This field represents the units for the half-life of Nuclide C.

Column/Field	Description
<b>Quench Set: Low, Mid, High</b>	<p>Select a quench set by clicking one or more quench set button. Select <b>Quench Set: Low</b> if counting one nuclide in one counting region; select <b>Quench Set: Mid</b> if counting two nuclides in two counting regions; and select <b>Quench Set: High</b> if counting three nuclides in three counting regions.</p> <p>After clicking a Quench Set button, the <i>Quench Standards</i> window opens. In this window, select a quench standards name to use for calculating DPM values. The selected quench set names appear on the Quench Set buttons in the <i>Sample Nuclides</i> window.</p> <p><i>Note: Depending on the DPM options installed, users may not have access to all three quench sets.</i></p>
<b>Count Mode</b>	<p>The fields in this column are for display purposes only. Each field represents the count mode used for quench standards defined in the Quench Standards assay. The count modes are Normal, High Sensitivity, Low Level, and Ultra Low Level.</p> <p><i>Note: The count mode is associated with Quench standards used in DPM assays when linking the Quench set(s) to sample nuclides.</i></p>

The following information describes the buttons found in the *Sample Nuclides* window (Figure 5-1).

### Add

Click this button to add a line to the table, and enter the new nuclide name. Manually enter regions A, B, and C.

### Delete

Click this button to delete a selected entry from the table.

### Clear Quench Sets

Click this button to unlink all quench sets linked to a selected sample nuclide. To unlink individual quench sets from a sample nuclide, right-click on the corresponding Quench Set button in the Sample Nuclides table (Figure 5-1), and click **Clear Quench Sets**.

### Comment

Click this button to enter descriptive comments.

## Quench Standards Library

This window (Figure 5-2) allows users to enter information into, and retrieve information from, the Quench Standards Library. To access this Library, select **Libraries | Quench Standards** from the menu bar.

The screenshot shows a window titled "Quench Standards" with a table of standards and a set of control buttons at the bottom. The table has the following data:

Name	Maximum keV	DPM	Number of Standards	Count Mode	Coincidence Time	Delay Before Burst	Count Started	Count Ended
3H	18.6	209727	10	Normal	18	75	11/12/2014	12:25:39
3H-UG	18.6	0	0					
14C	156.0	135100	10	Normal	18	75	12/30/2014	16:10:09
14C-UG	156.0	0	0					
14C-EX	156.0	131300	10	Normal	18	75	11/06/2014	15:39:35
3H-HLStartQS	18.6	255300	10	Normal	18	75	12/02/2014	09:17:58
3H-HLManualQS	18.6	255399	10	Normal	18	75	12/01/2014	18:56:01
3H-UG-LL	18.6	92690	8	Normal	18	75	12/03/2014	13:19:06
3H-EX	18.6	255300	10	Normal	18	75	10/03/2013	12:36:10

Below the table are several buttons: Add, Comment..., Quench Curve..., Help, Delete, Print..., Sample Nuclides..., Decay Calculator..., OK, and Cancel.

**Figure 5-2. Quench Standards Window.**

Quench set data is used to build quench curves for determining DPM in DPM assays. Use the Quench Standards Library to define and save a name, maximum energy value, and number of standards for each quench set for Quench Standards assays. Quench standards are counted once, and the entire spectrum for each quench standard stored in the Quench Standards Library, which allows users to select and use the same quench set in various assays.

In Replay (page 209), the *Quench Standards* window allows users to select a quench standards set to reanalyze sample data. Data from these quench sets is used to construct quench curves for determining sample DPM.



*Note:* Fields enabled in the Quench Standards window will be different when accessed from different locations within the software.

To count a new quench curve, the following fields must be completed in the Quench Standards table:

- **Name**
- **Max keV**
- **DPM**

The remaining fields—**# of Standards**, **Count Mode**, **Coincidence Time**, **Delay Before Burst**, **Date Counted**, and **Time Counted**—will be filled in after the quench standards are counted.

The following table describes the columns/fields in the Quench Standards table (Figure 5-2).

Column/Field	Description
<b>Name</b>	This is the name of the Quench Standards Set. To add a new standards set to the library, click the <b>Add</b> button. A blank row appears in the table; type the appropriate information in the fields provided.
<b>Max keV</b>	Enter the maximum energy in keV of the nuclide in quench standards.
<b>DPM</b>	Enter the DPM value of quench standards. If the Quench Standards Set was purchased from PerkinElmer, the DPM value and reference date are printed on the vial label.  <i>Note: DPM value entered can be the value at the reference date, or value corrected for nuclide decay. If the uncorrected value is entered, activate the half-life correction feature before counting standards. To enter a corrected DPM, the half-life correction feature should not be activated. The Radionuclide Decay feature (page 157) in the QuantaSmart program can be used to perform decay calculation.</i>
<b># of Standards</b>	This field displays the number of standard vials contained within the Quench Standards Set.  <i>Note: This field is for information only.</i>
<b>Count Mode</b>	This field displays the Count Mode used for counting a Quench Standards Set.  <i>Note: This field is for information only.</i>

Column/Field	Description
<b>Coincidence Time</b>	This field displays the Coincidence Time used for counting a Quench Standards Set. <i>Note: This field is for information only.</i>
<b>Delay Before Burst</b>	This field displays the Delay Before Burst used for counting a Quench Standards Set. <i>Note: This field is for information only.</i>
<b>Date Counted</b>	This field displays the date on which the Quench Standards Set was counted. <i>Note: This field is for information only.</i>
<b>Time Count Ended</b>	This field displays the time the counting of the Quench Standards Set was completed. <i>Note: This field is for information only.</i>

The following information describes the buttons found in the *Quench Standards* window (Figure 5-2).

### **Add**

Click this button to add a line to the table, and enter a new quench standards set.

### **Delete**

Click this button to delete a selected entry from the table.

### **Comment**

Click this button to enter descriptive comments.

### **Decay Calculator**

Click on this button to display the *Radionuclide Decay* calculator. Refer to page 78 for more information.

### Quench Curve

Click this button to display the *Quench Curve* window (Figure 5-3) for a selected Quench Standards Set.

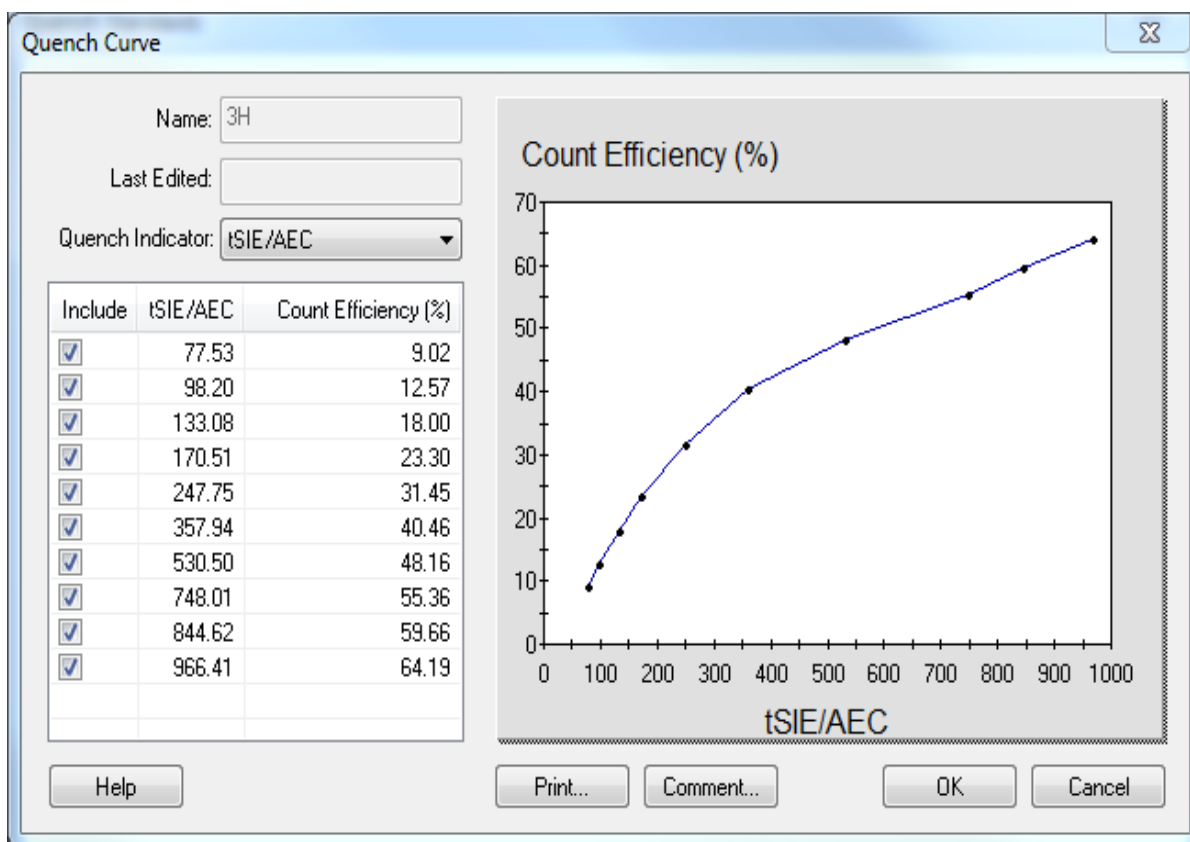


Figure 5-3. Quench Curve Window.

The following information describes the fields and buttons in the *Quench Curve* window (Figure 5-3).

- **Name** – This field displays the quench standards set name used to generate the quench curve.
- **Last Date Edited** – This field displays the last date on which the quench curve was edited.
- **Quench Indicator** – From this field, select a Quench Indicating Parameter (QIP) for use in plotting a quench curve.
- **Comment** – Click this button to enter free-form comments; the *Comment* window is displayed.
- **Quench Curve Table** – This table displays values for the Quench Indicating Parameter, and percentage count efficiency for each quench standard used to generate a quench curve. A checkmark beside each data point indicates that this point is used to plot a quench curve. To exclude points from the curve, de-select the checkboxes for the corresponding points.

### Sample Nuclides

Click this button, in the *Quench Standards* window, to display the *Sample Nuclides* window (Figure 5-1).

## Alpha/Beta Nuclides Library



*Note: This feature may be optional. Contact your PerkinElmer representative for details.*

### Overview

The *Alpha Beta Nuclides* library contains a list of alpha/beta nuclides. These nuclides contain information used to detect and discriminate between alpha and beta isotopes.

The *Alpha Beta Nuclides* window (Figure 5-4) allows users to define and save Alpha/Beta nuclide names, their associated counting regions, and the instrument's discriminator setting (this allows discrimination between Alpha and Beta events) in the Alpha/Beta Nuclides Library. Using the **Standard Set** button in Column 2 of this library, reference parameters for an existing Standard Set.

## Alpha/Beta Nuclides dialog

To access the Alpha/Beta Nuclides Library, select **Libraries | Alpha/Beta Nuclides** from the menu bar.

Alpha Beta Nuclides ×

Name	Standard Set	Beta A: LL	Beta A: UL	Beta A: Half-Life	Beta A: HL-Units	Beta B: LL	Beta B: UL	Beta B: Half-Life	Beta B: HL-Units	Alpha: LL	Alpha: UL	Alpha: Half-Life	Alpha: HL-Units	Lower PSA	Upper PSA	Count Mode
GCT Calibration	...	0.0	7.0	0.00	Minutes	0.0	2000.0	0.00	Minutes	0.0	1000.0	0.00	Minutes	120	120	
Wide Window	...	0.0	2000.0	0.00	Minutes	0.0	0.0	0.00	Minutes	0.0	1000.0	0.00	Minutes	120	120	
AB Manual	MWB-AB	0.0	2000.0	0.00	Minutes	0.0	0.0	0.00	Minutes	0.0	1000.0	0.00	Minutes	89	89	Normal
AB Align	A/B Test	0.0	2000.0	0.00	Minutes	0.0	0.0	0.00	Minutes	0.0	1000.0	0.00	Minutes	151	151	Normal
CLAM	...	0.0	0.0	0.00	Minutes	0.0	0.0	0.00	Minutes	0.0	0.0	0.00	Minutes	0	0	

**Figure 5-4. Alpha Beta Nuclides Window (Sample).**



The following table describes the columns/fields in the Alpha/Beta Nuclides table (Figure 5-4).

Column/Field	Description
<b>Name</b>	This field lists the name of the Alpha/Beta nuclide. To enter a name, click the <b>Add</b> button, which displays an additional row to define a new nuclide.
<b>Standard Set</b>	The field (if one is showing) lists the name of the Alpha/Beta standard set linked (associated) with the Alpha/Beta nuclide name. Click on the <b>Standard Set</b> field/button to display the entire Alpha/Beta Standards Library (page 164).  In the <i>Alpha Beta Standards</i> window (Figure 5-5), highlight the desired standard linked to the nuclide, and then click <b>OK</b> . The standard set name selected appears beside the Alpha/Beta nuclide name in the <i>Alpha Beta Nuclides</i> window.
<b>Beta A: LL</b>	This is the counting region's lower limit for the Beta nuclide in Region A, measured in keV.  <i>Note: This value cannot exceed 2000.</i>
<b>Beta A: UL</b>	This is the counting region's upper limit for the Beta nuclide in Region A, measured in keV.  <i>Note: This value cannot exceed 2000.</i>
<b>Beta A: Half Life</b>	For Region A, enter the numeric value for half-life correction, if desired. See the next entry.
<b>Beta A: Half Life Units</b>	For Region A, select the appropriate units to apply to the numeric half-life value. Click on the field to display a drop-down list of available units: <b>Minutes, Hours, Days, Weeks, or Years</b> . Select the appropriate unit from the list.
<b>Beta B: LL</b>	This is the counting region's lower limit for the Beta nuclide in Region B, measured in keV.  <i>Note: This value cannot exceed 2000.</i>
<b>Beta B: UL</b>	This is the counting region's upper limit for the Beta nuclide in Region B, measured in keV.  <i>Note: This value cannot exceed 2000.</i>
<b>Beta B: Half Life</b>	For Region B, enter the numeric value for half-life correction, if desired. See the next entry.

Column/Field	Description
<b>Beta B: Half Life Units</b>	For Region B, select the appropriate units to apply to the numeric half-life value. Clicking on the field displays a drop-down list of available units: <b>Minutes, Hours, Days, Weeks, or Years</b> . Select the appropriate unit from the list.
<b>Alpha: LL</b>	This is the counting region's lower limit for the Alpha nuclide, measured in keV. <i>Note: This value cannot exceed 1000.</i>
<b>Alpha: UL</b>	This is the counting region's upper limit for the Alpha nuclide, measured in keV. <i>Note: This value cannot exceed 1000.</i>
<b>Alpha: Half Life</b>	In this field, enter the numeric half-life value (see the next entry).
<b>Alpha: Half Life Units</b>	Click on this field to display a drop-down list of available units: <b>Minutes, Hours, Days, Weeks, or Years</b> . Select the appropriate unit from the list.
<b>Upper Discriminator</b>	This is the upper discriminator value to use with this nuclide. If a Standard Set is associated with the nuclide, this value will come from it; otherwise this value may be manually entered.
<b>Lower Discriminator</b>	This is the lower discriminator value to use with this nuclide. If a Standard Set is associated with the nuclide, this value will come from it; otherwise this value may be manually entered.
<b>Count Mode</b>	If an Alpha/Beta Standard Set is referenced by the nuclide, then <b>Normal</b> (Count Mode) is displayed. If no Alpha/Beta Standard Set is linked, this field remains blank.

If standard set is associated with a nuclide, the energy regions for Beta A and Alpha must match those used in the standard set for accurate spill correction. If these do not match, configure the alpha/beta assay to enable "Count Alpha/Beta Standards". (See Alpha/Beta Assay)

The following information describes the buttons found in the *Alpha Beta Nuclides* window (Figure 5-4).

### Add

Click this button to add a line to the Alpha/Beta Nuclides table, and enter the new nuclide name.

**Delete**

Click this button to delete a selected entry from the Alpha/Beta Nuclides table.

**Comment**

Click this button to enter descriptive comments.

## Alpha/Beta Standards Library

*Note:* This is feature may be optional. Contact your PerkinElmer representative for details.

### Overview

The Alpha/Beta Standards library is used to configure and store the results for an Alpha/Beta Standards measurement.

This window (Figure 5-5) allows users to define an Alpha/Beta Standard Set for use with Alpha/Beta assays. Once the information is entered in the Alpha/Beta Standards Library, an Alpha/Beta Standards assay can be run to establish the instrument's optimum pulse discriminator value. This value is used to discriminate between Alpha and Beta nuclides in Alpha/Beta assays.

### Alpha/Beta Standards dialog

To access the Alpha/Beta Standards Library, select **Libraries | Alpha/Beta Standards** from the menu bar.

Name	Beta LL	Beta UL	Alpha LL	Alpha UL	Measurement Method	Starting Discriminator	Ending Discriminator	Number of Points	Lower Discriminator Computed	Lower Discriminator In Use	Upper Discriminator Computed	Upper Discriminator In Use	Count Started	Count Ended	Alpha Standard DPM
CLAM	0.0	2000.0	0.0	1000.0	Automatic	1	255	10	116	116			02/05/2015	10:10:06	0
Test	0.0	2000.0	0.0	1000.0	Manual	20	120	10	90	90			07/21/2016	14:50:45	0
CLAM - hist	0.0	2000.0	0.0	1000.0	PSA Histogram				112	25	112	175	08/29/2016	15:53:23	0
CLAM - longer	0.0	2000.0	0.0	1000.0	PSA Histogram				97	37	134	165	08/29/2016	16:06:35	0
Legacy Alpha/Beta Standard	0.0	2000.0	0.0	1000.0	Manual	1	255	10	1	2			11/03/2016	13:33:04	0
Si/SO / Am241	20.0	200.0	30.0	300.0	PSA Histogram				5	5	64	64	11/03/2016	13:42:36	0
PSA Test	0.0	2000.0	0.0	1000.0	PSA Histogram										0

Buttons: Help, Add, Delete, AR Curve..., AB Nuclides..., Comment..., Print..., Decay Calculator..., OK, Cancel

Figure 5-5. Alpha Beta Standards Window (Sample).

The following table describes the columns/fields in the Alpha/Beta Standards table (Figure 5-5).

Column/Field	Description
<b>Name</b>	This is the name of the Alpha/Beta Standard Set. To add a new standard set to the library, click the <b>Add</b> button. A blank row appears in the table. Type in the desired name for the Alpha/Beta Standard Set in the <b>Name</b> field.
<b>Beta: LL</b>	This is the counting region's lower limit for the Beta nuclide, measured in keV. <i>Note: This field is for information only in this library.</i>
<b>Beta: UL</b>	This is the counting region's upper limit for the Beta nuclide, measured in keV. <i>Note: This field is for information only in this library.</i>
<b>Alpha: LL</b>	This is the counting region's lower limit for the Alpha nuclide, measured in keV. <i>Note: This field is for information only in this library.</i>
<b>Alpha: UL</b>	This is the counting region's upper limit for the Alpha nuclide, measured in keV. <i>Note: This field is for information only in this library.</i>

Column/Field	Description
<b>Measurement Method</b>	<ul style="list-style-type: none"> <li>■ PSA Histogram – This method measures all possible PSA values using a single measurement. This method allows advanced techniques for spillover reduction such as dual discriminators and use of optimized regions. This is the recommended method for best results.</li> <li style="text-align: center;">■</li> <li>These legacy methods measure a limited number of discriminator values with wide energy windows to generate a spillover curve. They are limited to a single discriminator.</li> <li>■ Automatic – This method performs measurements to determine the best PSA value for the start of the spillover curve. It then performs ten measurements using a PSA discriminator of increasing values. These ten measurements are used to build the spillover curve. This method requires that standards have at least 50,000 CPM of activity. There may be cases where automatic mode fails to determine a starting point. If this happens, use the Manual or PSA Histogram method.</li> <li>■ Manual – This method uses manually entered values for Starting Discriminator (1-255), Ending Discriminator (1-255) and Number of Points (5 to 15). Using the Number of Points, a number of measurements are performed using the starting discriminator. These measurements are used to build the spillover curve.</li> </ul> <p><i>Note: When using <b>Automatic</b> mode, each pure standard source must generate a minimum of 50,000 CPM. A minimum of 10,000 counts (total combined Alpha + Beta) when using <b>Manual</b> mode.</i></p>
<b>Starting Discriminator</b>	Enter the first PSA value to use for the standard curve in <b>manual</b> mode.
<b>Ending Discriminator</b>	Enter the last PSA value to use for the standard curve in <b>manual</b> mode.
<b>Number of Points</b>	In this field, enter the number of points used to manually generate Alpha and Beta misclassification curves. This is not required if <b>Automatic</b> was selected in the <b>Discriminator Type</b> field. If <b>Automatic</b> was selected, <b>10</b> is displayed in the <b>Number of Points</b> field. If <b>Manual</b> was selected, up to <b>15</b> points can be entered.
<b>Lower Discriminator Computed</b>	This is the lower PSA value calculated by the alpha/beta standards assay to minimize spillover

Column/Field	Description
<b>Lower Discriminator in Use</b>	Enter a different PSA value to override the calculated value
<b>Upper Discriminator Computed</b>	This is the upper PSA value calculated by the alpha/beta standards assay to minimize spillover
<b>Upper Discriminator In Use</b>	Enter a different PSA value to override the calculated value
<b>Count Started</b>	This field represents the date on which the Alpha/Beta Standards assay was counted. <i>Note: This field is for information only.</i>
<b>Count Ended</b>	This field represents the time at which the Alpha/Beta Standards assay was completed. <i>Note: This field is for information only.</i>
<b>Alpha Standard DPM</b>	Activity of the pure Alpha standard. This is required to calculate the Alpha DPM of the unknown.
<b>Beta Standard DPM</b>	Activity of the pure Beta standard. This is required to calculate the Beta DPM of the unknown.
<b>Count Mode</b>	<b>Normal</b> is the Count Mode used to count the Alpha and Beta Standards. <i>Note: This field is for information only.</i>
<b>Coincidence Time</b>	This field represents the Coincidence Time of 18 ns used when counting the Alpha/Beta Standards assay. <i>Note: This field is for information only.</i>
<b>Delay Before Burst</b>	This field represents the Delay Before Burst time of 75 ns used when counting the Alpha/Beta Standards assay. <i>Note: This field is for information only.</i>

The following information describes the buttons found in the *Alpha Beta Standards* window (Figure 5-5).

#### **Add**

Click this button to add a line to the table and enter a new Alpha/Beta Standard Set.

**Delete**

Click this button to delete a selected entry from the Alpha/Beta Standards table.

**Comment**

Click this button to enter descriptive comments.

**AB Nuclides**

Click this button to display the Alpha/Beta Nuclides Library (page 159).

**AB Curve**

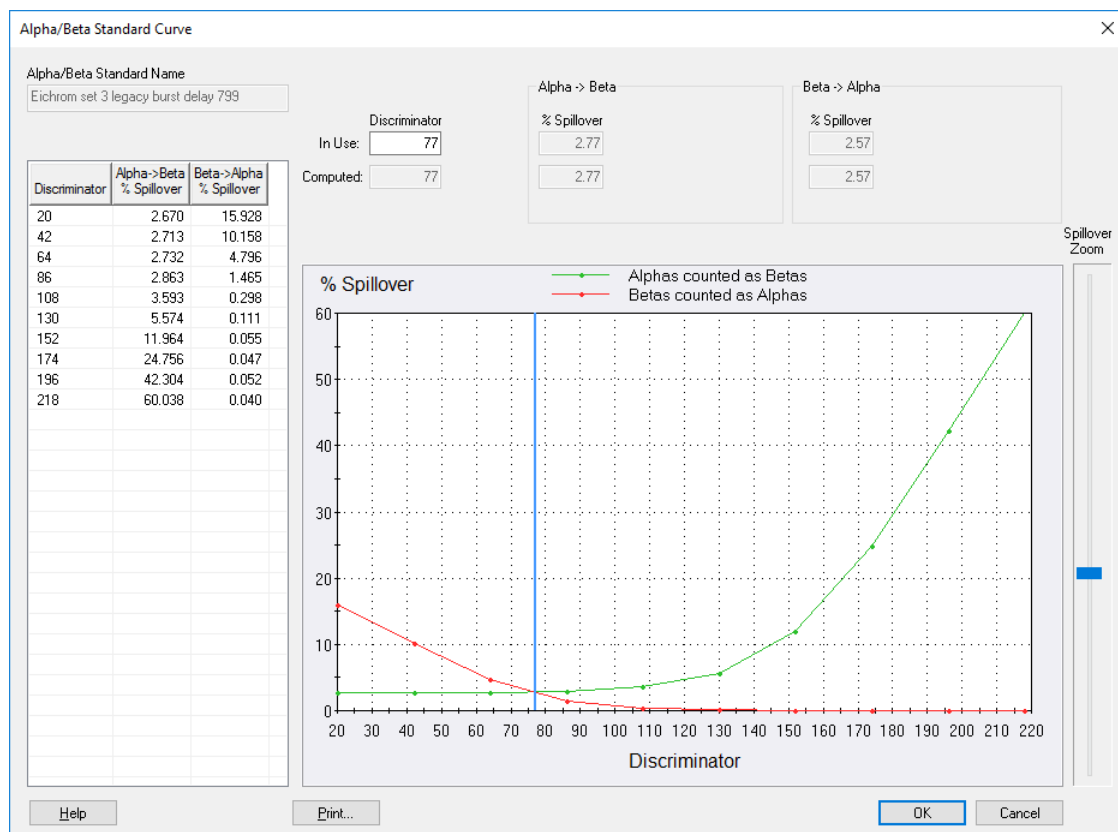
Click this button to display a stored Alpha/Beta Standard misclassification (spillover) curve for the Standard Set selected in the table.



## Alpha/Beta Standard Curve

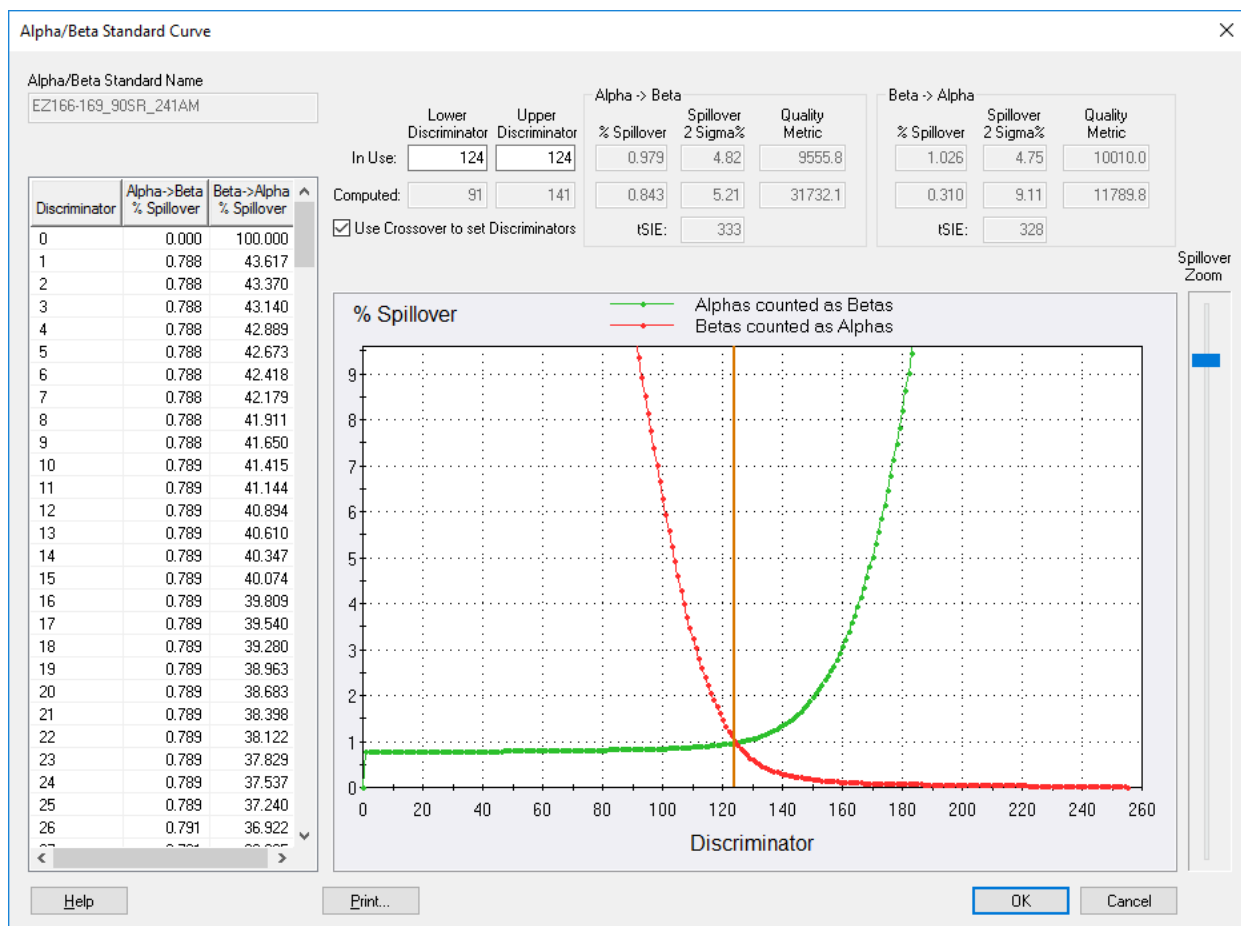
The standard curve dialog provides a way evaluate how discriminator values change spillover. (See **Alpha/Beta Theory**)

When the standard measurement method is Manual or Automatic the dialog will appear as:



**Figure 5-6 - Alpha/Beta Standard Curve**

When the standard measurement method is PSA Histogram, the dialog appears with additional information:



**Figure 5-7 - Alpha/Beta Standard Curve**

- The list on the left side shows the spillover values for each PSA discriminator setting.
- The graph in the center shows a visual representation of the spillover values
- The slider control on the right side controls the Y scale of the graph

### Discriminator modes

- Single discriminator – This is when the lower and upper discriminator can have the same value. When the PSA value for an event is less than the discriminator, the event is classified as beta. When it is more, the event is classified as alpha. Standards that use automatic or manual measurement mode can only use a single discriminator
- Dual discriminators – This is when the lower and upper discriminators have different values. Events with a PSA less than the lower discriminator are classified as beta. Events with a PSA higher than the upper discriminator are classified as alpha. Events between the discriminators are *unclassified*. Note that the Auxiliary spectrum can be configured to show unclassified events. (See **Count Corrections**)

### Discriminator sets

- Computed – These are the optimal discriminator values recommended by QuantaSmart
- In Use – These are the actual discriminator values that will be used with the standard. These values can be changed and the associated spillover values will be calculated.

### Spillover values

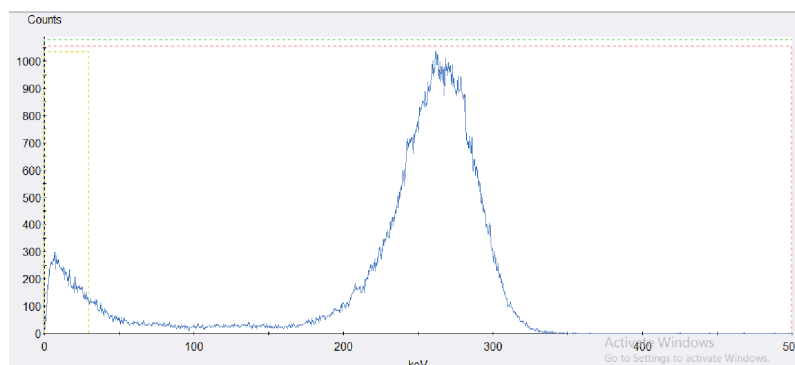
When the Alpha/Beta Standard is acquired, the software computes the discriminators which yield the lowest spillover / highest Quality Metric. The top of the dialog shows spillover results based on different discriminators for Alpha into Beta and Beta into Alpha spill.

- % Spillover – the percentage of counts misclassified
- Spillover 2 Sigma% - the statistical significance of spillover counts. When this is more than 10 there are not sufficient statistics for reproducible results using dual discriminators so Crossover will be selected.
- Quality Metric – a representation of the quality of the discriminator weighing spillover reduction versus efficiency loss.
- tSIE – quench indicator if the standard was measured using tSIE
- Use Crossover to set Discriminators – Check this box to use a single discriminator value at the crossover point. This will be automatically checked if the Spillover 2 Sigma% is more than 10 indicating that there are not sufficient statistics for reproducible results.

### Evaluation of discriminators

The discriminator values may be changed and the new spillover using those values is displayed. Click the checkbox to use a single discriminator set at the crossover point. In the example above, the In Use value is using a single discriminator with spillover values of 0.98 and 1.02. When dual discriminators are used, spillover is reduced to 0.84 and 0.866.

The example spillover curve above shows an issue to investigate. The spillover curves are not symmetrical. The alpha curve has a higher overall level. The first step for investigation is to check the shape of the spectrum by running a CPM assay using the alpha standard. The following figure shows the spectrum of the  $^{241}\text{Am}$  standard.



**Figure 5-8 - AM241 Spectrum**

The counts between 150 and 250 keV are expected while the counts below 50 keV are not. These extra events are increasing the spillover. By adjusting the regions to exclude this area we can reduce spillover. The standard is edited to change the energy range and the Alpha/Beta Standard assay is re-run. The spill curve decreased in magnitude when the energy regions were used. This resulted in a reduction of spill over at the cross over point from 0.979/1.026 in Figure 5-6 to 0.241/0.238 in Figure 5-6.

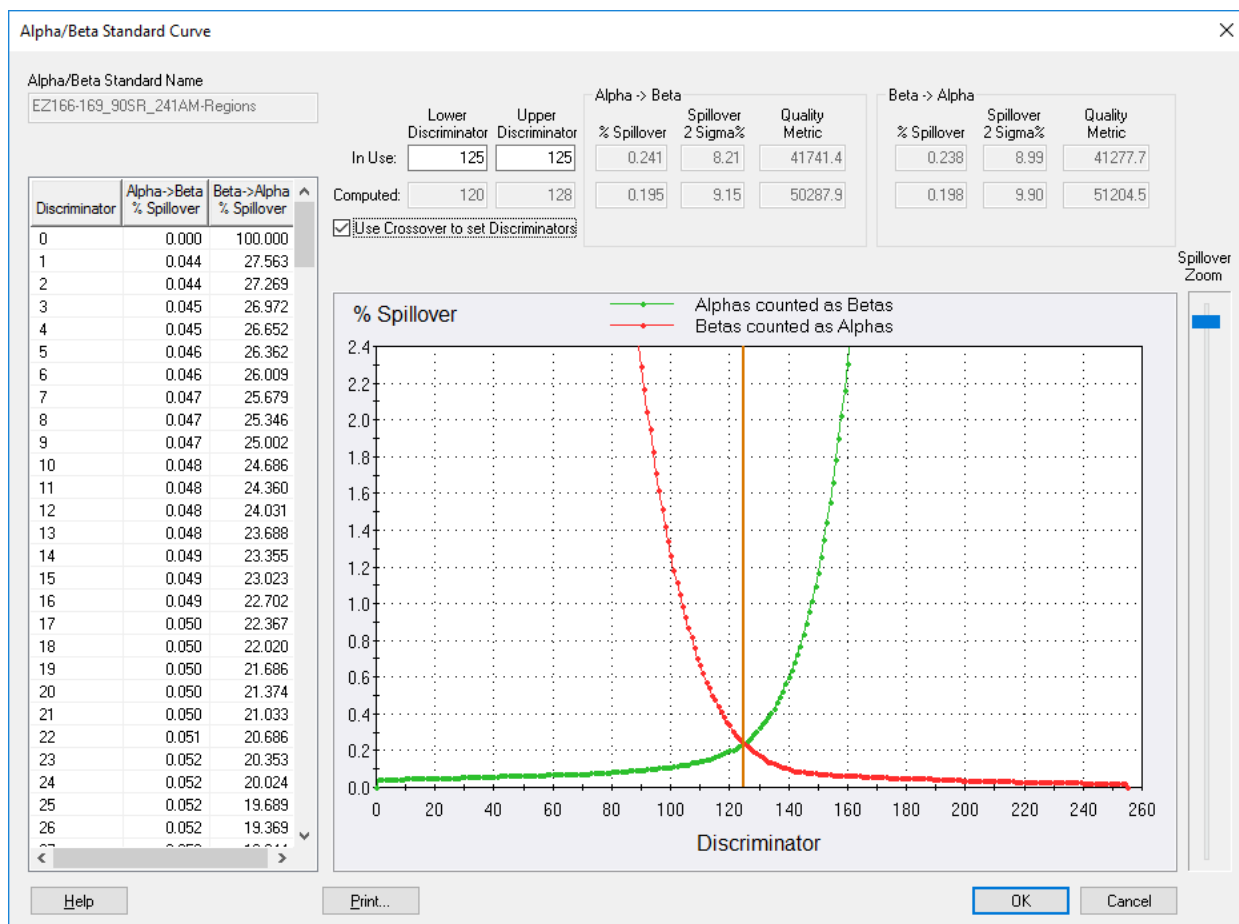


Figure 5-9 - Alpha/Beta Standard Curve

### Temperature influence on spillover

Temperature of the sample may affect spillover for certain cocktails such as Ultima Gold LLT. The following figures show how the spillover curves shift with temperature for the same standard measured at 75F/24C and at 55F/13C when using Ultima Gold LLT.

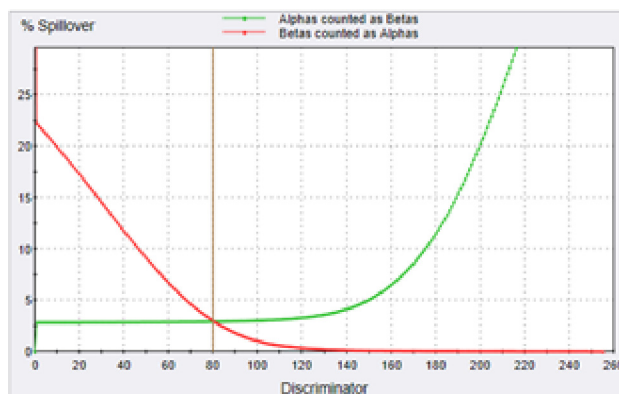


Figure 5-10 - Spillover Curve at 24C

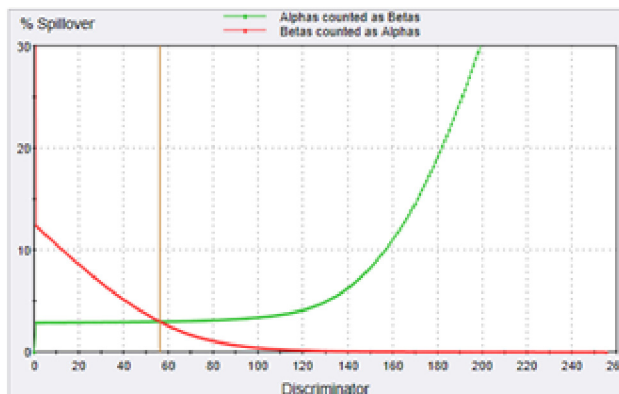


Figure 5-11 - Spillover Curve at 13C

For reproducible results, always let samples temperature stabilize before acquisition.

### Quench influence on spillover

The amount of quench present in a sample can significantly shift discriminators and change spillover values. The figures below are spillover curves for  $^{90}\text{Sr}/^{241}\text{Am}$  nuclides that were prepared with the same sample to scintillator ratio, but quenched to different levels:

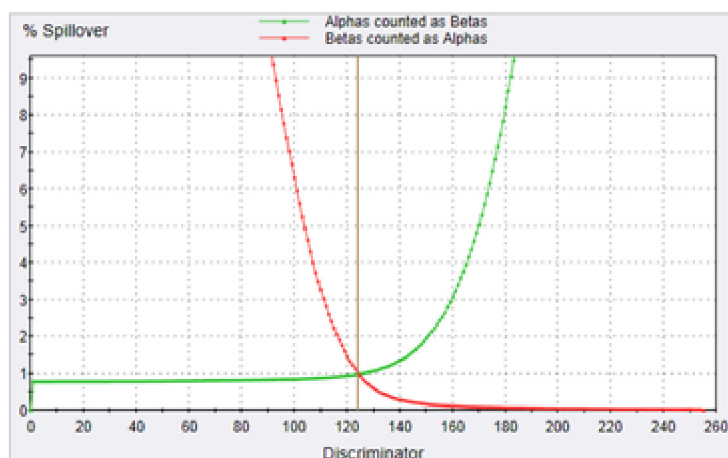


Figure 5-12 - Spillover Curve at Lower Quench

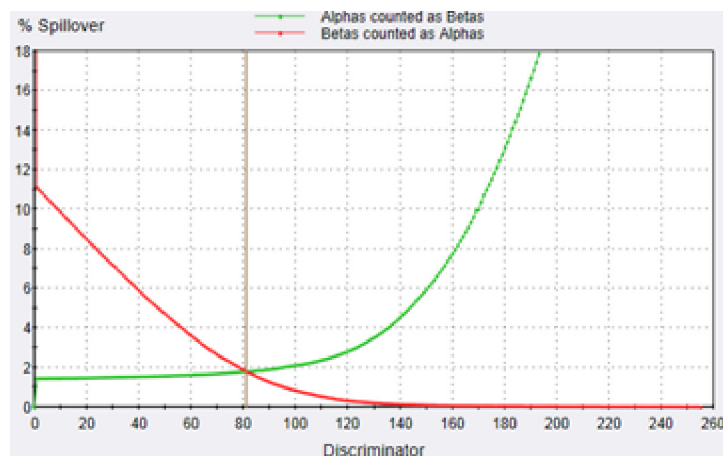


Figure 5-13 - Spillover Curve at Higher Quench

This is why it is critical to prepare standard and unknown samples so that they have the same quench levels. Enable tSIE for the standard and unknown assays so that quench levels can be compared.

The algorithm for generating computed discriminators uses the curve to determine what values generate the highest Quality Metric while maintaining reproducibility of the spill and limiting the efficiency loss. If the lower and upper PSA discriminator

values are the same, this is because the spillover CPM was not significant enough. Consider increasing the count time for the alpha/beta standards.

The discriminators may be manually changed by changing the values In Use. Lower values will increase Beta, higher values will increase Alpha. As these values are changed, the corresponding spillover, sigma and Quality Metric values will change. Note that a wider range of discriminator settings will reduce counting efficiency.

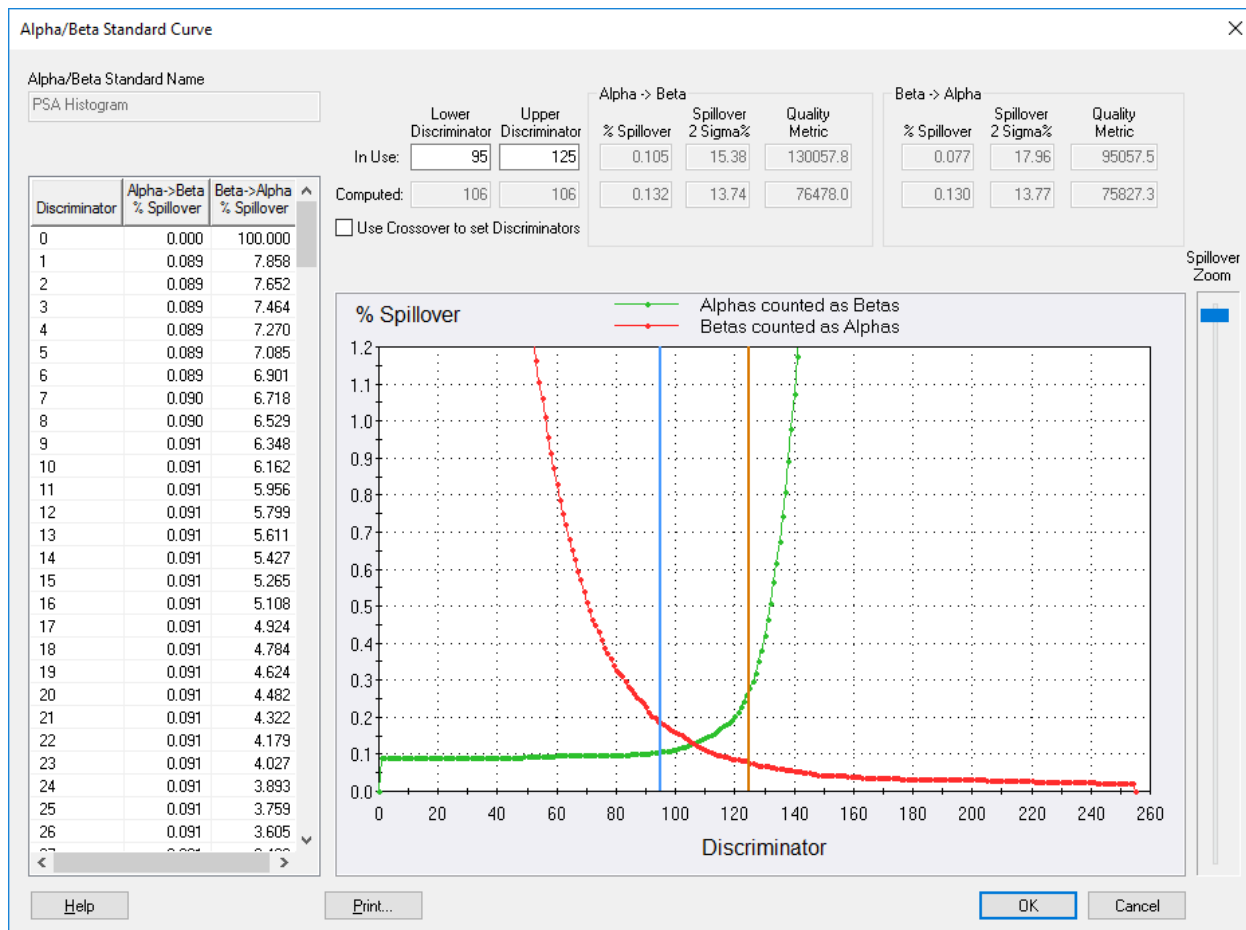


Figure 5-14. Alpha/Beta Standard Curve Window.



## Chapter 6

### Normalization, Calibration, and IPA

Before any samples are counted, the system must be normalized and calibrated using Self Normalization and Calibration (SNC), then instrument performance assessed using Instrument Performance Assessment (IPA). The SNC/IPA protocol requires a special protocol flag and cassette loading step that depends on instrument model.

During the normalization and calibration portion of SNC, voltage applied to the two Photomultiplier Tubes (PMTs) is adjusted until synchronized in their response to a  $^{14}\text{C}$  standard. Then, the voltage to both PMTs is adjusted simultaneously until the  $^{14}\text{C}$  spectrum endpoint falls at the appropriate position in the Spectralyzer (on-board 4000 channel) multi-channel analyzer. This process is designed to ensure that the instrument accurately quantifies energy from all Beta-particle emissions.

During IPA, the instrument measures background, counting efficiency, sensitivity (Figure-of-Merit), and the reproducibility of sample counting (Chi-Square test). Refer to page 179 for more information about IPA.

The remainder of this chapter discusses the following topics:

- When to Perform These Procedures (page 178)
- Defining an Instrument Performance Assessment (page 179)
- Performing Self-Normalization and Calibration (SNC) (page 187)

## When to Perform These Procedures

Normalization, calibration, and IPA occurs automatically by leaving the Self-Normalization and Calibration (SNC) and IPA cassette (containing the  $^{14}\text{C}$  calibration standard, unquenched Tritium standard, and background standard) on the instrument counting deck at all times. Whenever the SNC protocol flag is read by the instrument, a 23-hour timer is checked.

- If 23 hours have passed since the previous normalization and calibration, the instrument will perform the SNC/IPA procedure.
- If 23 hours have not passed since the previous calibration and normalization, the SNC/IPA cassette is bypassed, and the SNC/IPA procedure is not performed.

Ideally, the instrument normalization, calibration, and IPA should be performed on this timed, 23-hour (daily) cycle. SNC is only initiated if the sample changer is moving. It will not start at the 23-hour mode. Certain IPA parameters must be defined prior to the machine performing assessment procedures. Instrument normalization, calibration, and IPA may be performed manually (not using the 23-hour timer) by “resetting” the cycle flag on the cassette.

An IPA report is generated after each IPA procedure is completed. To access data generated from all IPA runs, select **IPA | IPA Charts & Tables**.



*Note: This feature may be optional. Contact your PerkinElmer representative for details.*

## Defining an Instrument Performance Assessment

Before performing IPA, first define the parameters that the instrument will use during the assessment process by selecting **IPA | IPA Definition** from the menu bar.

The IPA Definition window is divided into several sections:

- IPA Parameters:**
  - 3H Standard DPM: 269900
  - 3H Reference Date: 22 July 2014
  - 14C Standard DPM: 132900
  - Background Count Time (min): 60.00
  - 3H FOM Threshold: 180
  - 14C FOM Threshold: 380
- Chi Square Tests:**
  - 3H
  - 14C
- RS-232:**
  - Transmit IPA Data
- IPA Data:**
  - Save copy of IPA data to a text file
  - File Name: C:\Packard\TriCarb\IpaData.txt
- Baselines:**
  - Number of Datapoints to Establish Baselines: 5

	Mean	Limit
3H Background:	15.40	31.10
3H Efficiency:	64.50	61.50
14C Background:	22.60	41.62
14C Efficiency:	95.96	92.96

  - Reset Baseline Values

Buttons at the bottom: Help, OK, Cancel.

**Figure 6-1 IPA Definition Window.**

The following information describes the fields in the *IPA Definition* window:

### **3H Standard DPM**

In this field, enter a DPM value for the unquenched, sealed Tritium standard (supplied). The DPM values for standards purchased from PerkinElmer are printed on the vial.

### **3H Reference Date**

In this field, enter the reference (calibration) date for the unquenched Tritium standard. This is the date on which the standard has the specified amount of activity. Enter this value for half-life correction to occur. The reference date for standards purchased from PerkinElmer are printed on the vial.

### **14C Standard DPM**

In this field, enter the DPM value for the unquenched, sealed <sup>14</sup>C standard (supplied). The DPM values for standards purchased from PerkinElmer are printed on the vial. A reference date is not required due to the long half-life of <sup>14</sup>C.

### **Background Count Time**

In this field, enter the length of time (in minutes) the instrument will measure the background counts. The background for both <sup>14</sup>C and Tritium are collected simultaneously. Typically, a 60-minute count time is used to assess background.

### **3H FOM Threshold**

This is the lower limit for the calculated Tritium Figure of Merit value (FOM = Efficiency<sup>2</sup>/Background). If the FOM value falls below the defined threshold, a message is displayed in the main window. The message will indicate an increase in background, or a decrease in efficiency. Typically, the default threshold can be used until sufficient IPA data for this parameter is collected, and an alternate threshold is established.

### **14C FOM Threshold**

This is the lower limit for the calculated <sup>14</sup>C Figure of Merit value. If the FOM value falls below the defined threshold, a message is displayed in the main window. The message will indicate an increase in background, or decrease in efficiency. Typically, the default threshold can be used until sufficient IPA data for this parameter is collected, and an alternate threshold is established.

### **Chi-Square Tests (3H)**

Select this checkbox to enable a test measuring reproducibility for Tritium sample counts. If the Chi-Square value for a Tritium standard counted 20 times falls within an acceptable range of values, the variation in individual sample counts is a result of sample count statistics, as opposed to an instrument problem.

### Chi-Square Tests (14C)

Select this checkbox to enable a test measuring reproducibility for  $^{14}\text{C}$  sample counts. If the Chi-Square value for a  $^{14}\text{C}$  standard counted 20 times falls within an acceptable range of values, the variation in individual sample counts is a result of Tritium count statistics, as opposed to an instrument problem.



*Note: The range of acceptable values for the Chi-Square test is based on a 95% confidence level. Therefore, statistically, one out of every 20 Chi-Square tests could fail.*

### RS-232 (Transmit IPA Data)

Select this checkbox to transmit IPA data to an external device via the RS-232 communications port. See RS-232 in Appendix B for serial port configurations.

### Save IPA Data to Text File

Select this checkbox and then type a filename in the dialog box below it to save IPA data to a file.

### # of Datapoints to Establish Baselines

In this field, enter the number of IPA runs to generate baselines for Tritium and  $^{14}\text{C}$  background and efficiency. The range for this value is between 5 - 99.

### 3H Background Mean and Limit

The instrument calculates the mean value for Tritium background from the number of IPA runs (datapoints) specified. The limit is calculated as the baseline + 4 standard deviations. When the limit is reached, a message is displayed in the main window.

### 14C Background Mean and Limit

The instrument calculates the mean value for  $^{14}\text{C}$  background from the number of IPA runs (datapoints) specified. The limit is calculated as the baseline + 4 standard deviations. When the limit is reached, a message is appears in the main window.

### 3H Efficiency Mean and Limit

The instrument calculates the mean value for Tritium efficiency from the number of IPA runs (data points) specified. The limit is calculated as 3% below the baseline, or less than 58% efficiency. When this limit is exceeded, a message is displayed in the main window.

### 14C Efficiency Mean and Limit

The instrument calculates the mean value for  $^{14}\text{C}$  efficiency from the number of IPA runs (data points) specified. The limit is calculated as 3% below the baseline. When this limit is exceeded, a message is displayed in the main window.

**Reset Baselines**

Click this button to delete the current baselines. The instrument will establish new baselines from the number of datapoints indicated in this window.

**Not Processed**

This message indicates that Chi-Square data has never been collected. To acquire Chi-Square data for Tritium or  $^{14}\text{C}$ , check the corresponding boxes in the *IPA Definition* window.

## IPA Charts & Tables


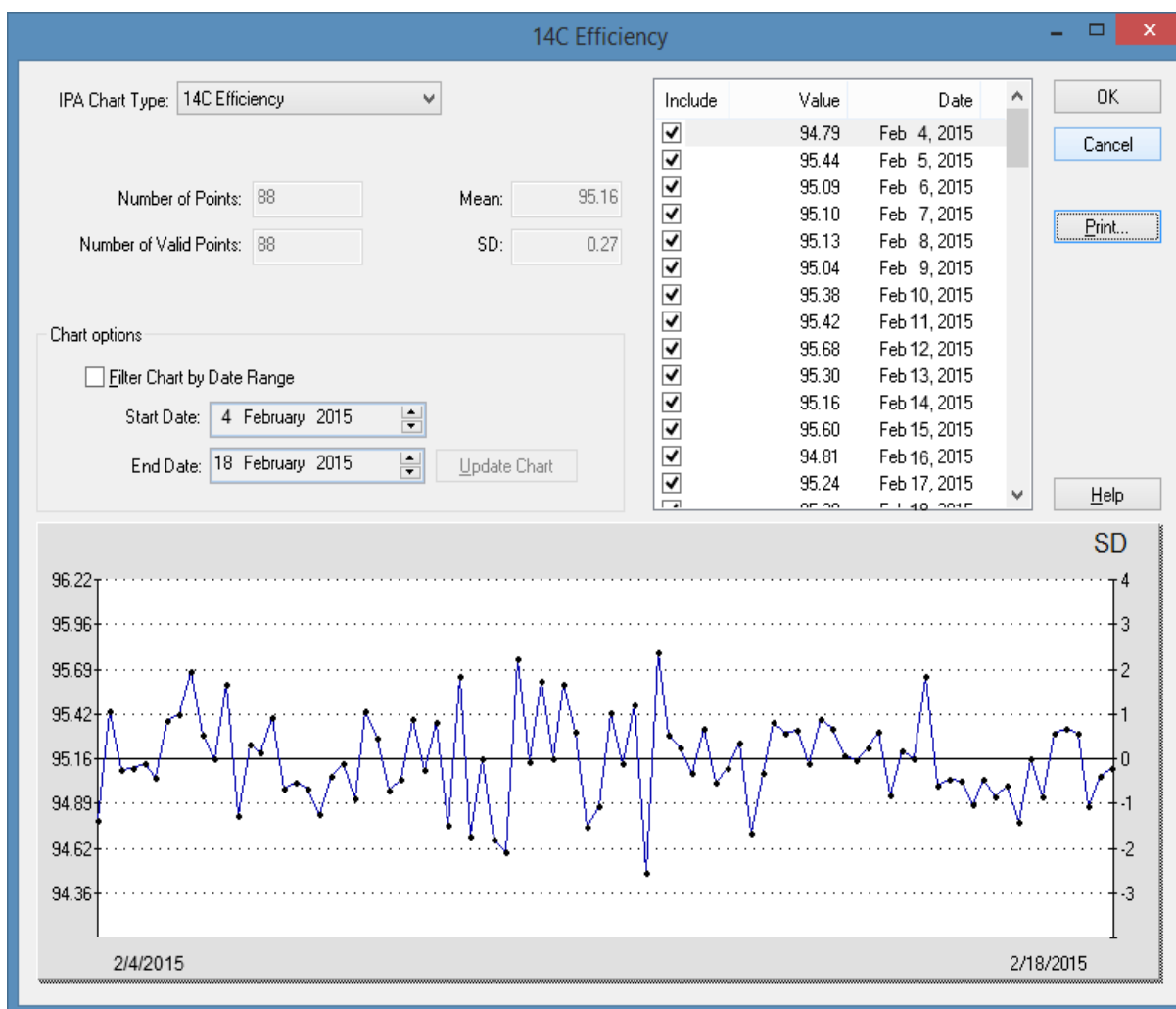
 *Note:* This feature may be optional. Contact your PerkinElmer representative for details.

Figure 6-2 is an example of a typical IPA chart and table for <sup>14</sup>C Efficiency.



**Figure 6-2. IPA Charts & Tables Window**

The *IPA Charts & Tables* window allows users to view, edit, and print data for individual IPA parameters in chart or tabular form. When data is displayed as a table, points can be included or excluded from a data set. To exclude a data point, uncheck the **Include** box beside the value in the list. The axis on the chart represents Mean and Standard Deviation values for a selected IPA parameter. Using the **Print** button, users can print an individual IPA chart or table (or all IPA charts and tables).

The following information describes the fields in the IPA Charts & Tables window. Note that all available IPA charts have similar graphic displays, and include the same data items.

### IPA Chart Type

In this drop-down field, select an IPA parameter to view in chart or tabular form.

The following IPA Charts are available:

- **14C Background** – This chart displays IPA test results for  $^{14}\text{C}$  background counts. This test checks for detector contamination or light leaks. The limit for this parameter is  $> \text{baseline} + 4 \text{ standard deviations}$ . The mean and SD for this parameter are recalculated as new IPA data is generated.
- **14C Background Baseline** – This chart displays the  $^{14}\text{C}$  background data based on a fixed baseline value. The number of values used to generate the baseline is defined in the *IPA Definition* window. The default for this setting is “5”.
- **14C Chi-Square** – This chart displays IPA test results measuring the reproducibility of  $^{14}\text{C}$  sample counting. The test is performed by counting a single sample in the detector 20 consecutive times with a count time of 30 seconds for each repeat measurement. The normal range for this value is 7.63 - 36.19 with 95% confidence. A properly performing instrument may generate Chi-Square values outside this range 2% of the time, due to the test’s statistical nature. The mean and standard deviations for this parameter are recalculated as new IPA data is generated.
- **14C FOM** – Figure of Merit (FOM) is a measure of the sensitivity of the instrument for  $^{14}\text{C}$  based on the  $^{14}\text{C}$  background, and instrument’s counting efficiency. The mean and standard deviations for this parameter are recalculated as new IPA data are generated.
- **14C Efficiency** – This chart displays the results of repeated  $^{14}\text{C}$  efficiency determinations. The mean and standard deviations for this parameter are recalculated as new IPA data is generated.
- **14C Efficiency Baseline** – This chart displays  $^{14}\text{C}$  efficiency data based on a fixed baseline value. The number of values used to generate a baseline is defined in the *IPA Definition* window. The default for this setting is “5”.
- **3H Background Baseline** – This chart displays the Tritium background data based on a fixed baseline value. The number of values used to generate the baseline is defined in the *IPA Definition* window. The default for this setting is “5”.



- **3H Chi-Square** – This chart displays IPA test results measuring the reproducibility of Tritium sample counting. The test is performed by counting a single sample in the detector 20 consecutive times with a count time of 30 seconds for each repeat measurement. The normal range for this value is 7.63 - 36.19 with 95% confidence. A properly performing instrument may generate Chi-Square values outside this range 2% of the time, due to the statistical nature of the test. The mean and standard deviation for this parameter are recalculated as new IPA data is generated.
- **3H Efficiency** – This chart displays the results of repeated Tritium efficiency determinations. The mean and standard deviation for this parameter are recalculated as new IPA data is generated. The limit for this parameter is  $< \text{baseline} - 3\%$ .
- **3H Efficiency Baseline** – This chart displays the Tritium efficiency data based on a fixed baseline value. The number of values used to generate the baseline is defined in the *IPA Definition* window. The default for this setting is “5”.
- **3H FOM** – Figure of Merit (FOM) is a measure of instrument sensitivity for Tritium based on the Tritium background, and the instrument’s counting efficiency. The mean and standard deviations for this parameter are recalculated as new IPA data is generated.
- **3H Background** – This chart displays the results of the IPA test for Tritium background counts. This test checks for detector contamination or light leaks. The limit for this parameter is  $> \text{baseline} + 4 \text{ standard deviations}$ . The mean and SD for this parameter are recalculated as new IPA data is generated.

**Total # of Points**

This field indicates the total data points available for the selected IPA parameter.

**Mean**

This field displays a Mean value of the selected IPA parameter calculated from all included data points. A deleted data point is not used to determine the mean value of the IPA parameter.

**Valid # of Points**

This field indicates the number of points used to generate the selected chart.

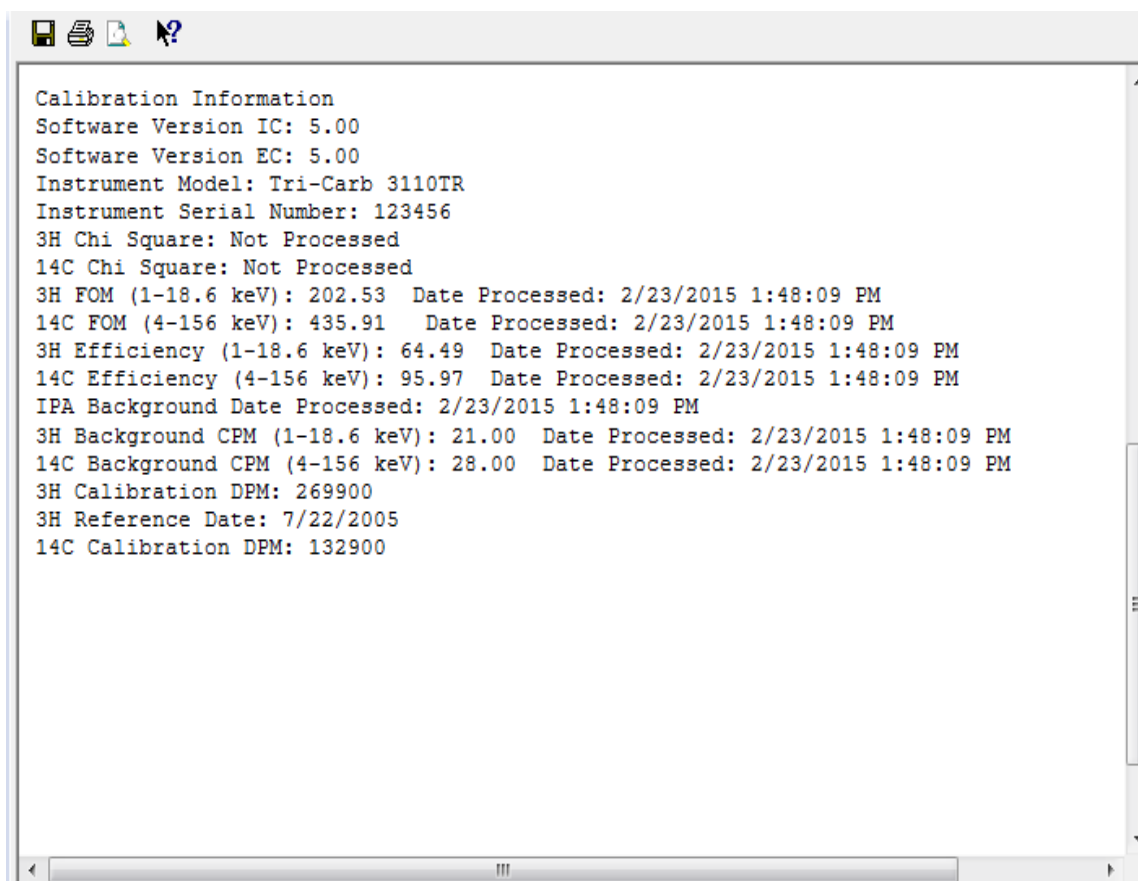
**Standard Deviation (SD)**

This field displays the SD of a selected IPA parameter calculated from all included data points. A deleted data point is not used to determine the SD of an IPA parameter.

## IPA Reports

Any IPA or calibration operation that fails to meet specifications will generate a warning message at the top of an IPA report. Errors or warnings listed at the bottom of this report represent the most recent status of any IPA parameter which generated messages during an IPA run.

Dates for errors or warnings may vary to reflect the most recent date on which data for individual IPA parameters were acquired; a report will also be printed after an IPA procedure is completed.



```
Calibration Information
Software Version IC: 5.00
Software Version EC: 5.00
Instrument Model: Tri-Carb 3110TR
Instrument Serial Number: 123456
3H Chi Square: Not Processed
14C Chi Square: Not Processed
3H FOM (1-18.6 keV): 202.53 Date Processed: 2/23/2015 1:48:09 PM
14C FOM (4-156 keV): 435.91 Date Processed: 2/23/2015 1:48:09 PM
3H Efficiency (1-18.6 keV): 64.49 Date Processed: 2/23/2015 1:48:09 PM
14C Efficiency (4-156 keV): 95.97 Date Processed: 2/23/2015 1:48:09 PM
IPA Background Date Processed: 2/23/2015 1:48:09 PM
3H Background CPM (1-18.6 keV): 21.00 Date Processed: 2/23/2015 1:48:09 PM
14C Background CPM (4-156 keV): 28.00 Date Processed: 2/23/2015 1:48:09 PM
3H Calibration DPM: 269900
3H Reference Date: 7/22/2005
14C Calibration DPM: 132900
```

Figure 6-3 IPA Report (Sample)

## Performing Self-Normalization and Calibration (SNC)

1. Select **IPA | IPA Definition** from the menu bar.
2. In the *IPA Definition* window (Figure 6-4), enter the date and activity of your standards (see page 179).

The screenshot shows the 'IPA Definition' dialog box with the following fields and options:

- IPA Parameters:**
  - 3H Standard DPM: 269900
  - 3H Reference Date: 22 July 2014
  - 14C Standard DPM: 132900
  - Background Count Time (min): 60.00
  - 3H FOM Threshold: 180
  - 14C FOM Threshold: 380
- Chi Square Tests:**
  - 3H
  - 14C
- RS-232:**
  - Transmit IPA Data
- IPA Data:**
  - Save copy of IPA data to a text file
  - File Name: C:\Packard\TriCarb\IpaData.txt
- Baselines:**
  - Number of Datapoints to Establish Baselines: 5

	Mean	Limit
3H Background:	15.40	31.10
3H Efficiency:	64.50	61.50
14C Background:	22.60	41.62
14C Efficiency:	95.96	92.96

  - Reset Baseline Values

Buttons at the bottom: Help, OK, Cancel.

**Figure 6-4. IPA Definition Window.**

3. Reset the SNC protocol flag to the reset position at far left when the plug is on the left end of the cassette.
4. Proceed to the following section (SNC Cassette Loading), and refer to the related procedures depending on your instrument type (Quantulus GCT or Other Tri-Carb Models).

## SNC Cassette Loading




**CAUTION:** Do not use unpurged, Low Level standards to calibrate the instrument, even if used in Low Level, High Sensitivity, or Super Low Level count mode.



*Note:* For the following steps, a background vial and Tritium vial may be excluded from a cassette for faster SNC processing. However, a  $^{14}\text{C}$  and empty vial must always be present.

### Quantulus GCT Instruments

1. Load the cassette with a purged, unquenched  $^{14}\text{C}$  standard.
2. Load the cassette with an empty vial in the second vial position. This vial must be of the same type and material (glass, plastic, Teflon) used to count low level samples.
3. Load the cassette with a purged, unquenched Tritium standard (optional).
4. Load the cassette with a purged background standard (optional).
5. Load the instrument with cassettes.
6. Click the green flag start button  at the top of the main window to begin counting.

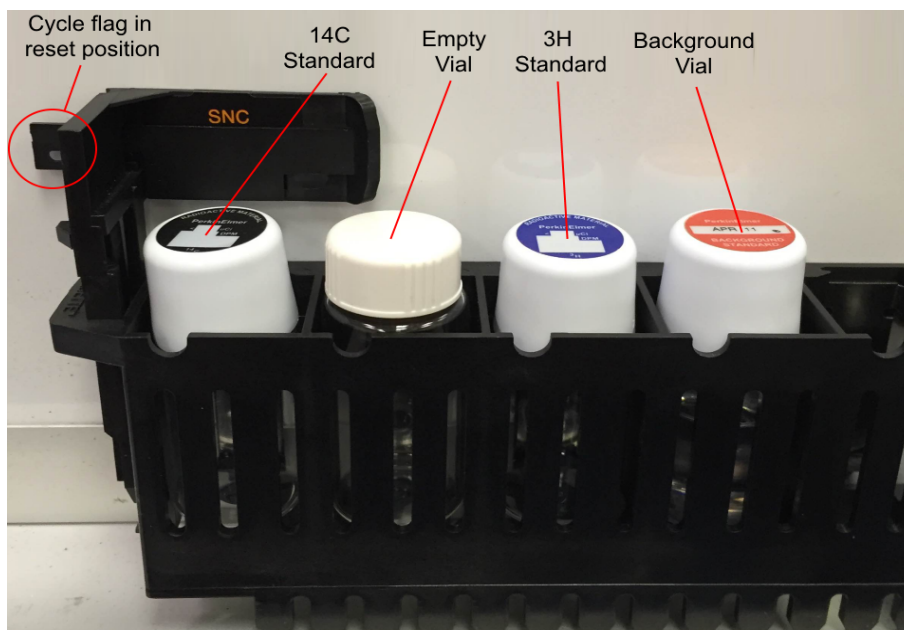

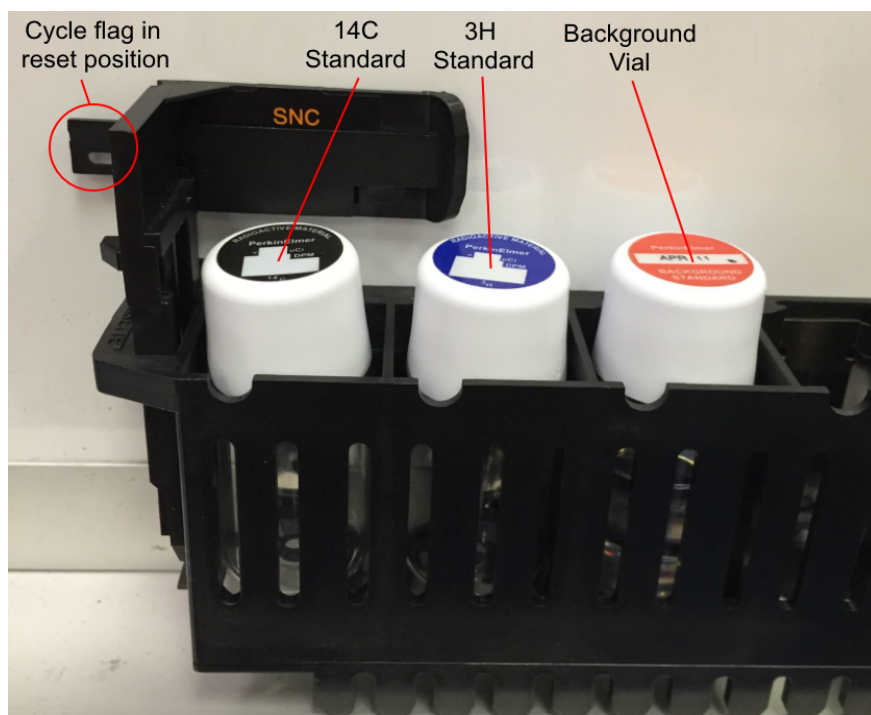


Figure 6-5 Quantulus GCT SNC Cassette Load (Sample).

**All Other Tri-Carb Models**

1. Load the cassette with a purged, unquenched  $^{14}\text{C}$  standard.
2. Load the cassette with a purged, unquenched Tritium standard (optional).
3. Load the cassette with a purged background standard (optional).
4. Load the instrument with cassettes.
5. Click the green flag start button  at the top of the main window to begin counting.



**Figure 6-6 General Tri-Carb SNC Cassette Load (Sample).**



## Chapter 7

### Advanced Features

This chapter discusses advanced features available with the Tri-Carb system:

- Priostat (page 192)
- Replay Feature (page 209)
- High Sensitivity and Low Level Counting (page 217)
- Alpha/Beta Counting (page 220)
- Tandem Processing (page 220)
- 2D Bar Code Reader Option (page 221)

## Priostat

Priostat allows direct control over sample analysis features between two count types: Group Priostat and Sample Priostat (page 193).

### Group Priostat

This method allows users to count a set of high priority samples while temporarily interrupting a current protocol. Select any existing assay for data reduction.

To use this feature, do the following:

1. Load the samples into cassettes, and then attach the Priostat flag to the first cassette to be counted.
2. Select **Run | Group Priostat** from menu bar. The *Associate Assay for Priostat* window appears.
3. In the window, select an assay used to count samples.



*Note:* The interrupted protocol number cannot be selected to count Group Priostat samples.

The instrument will search for the Priostat flag, and begin counting samples. Once completed, the instrument automatically resumes the interrupted protocol with the sample in place when Group Priostat counting began. Results of Group Priostat counts appear in the *Output* window.

4. Print the Group Priostat count results by selecting the print GUI icon in the *Output* window.



*Note:* To end Group Priostat protocol before counting all samples, from the **Run** menu, select **End Group Priostat**.




*Note:* Group Priostat does not support multiple cycles. If the selected protocol defines multiple cycles, only one cycle of the assay will be acquired.



## Sample Priostat

This method allows users to count individual samples by various analysis options without defining an assay. This is a high priority interrupt mode using a method similar to Group Priostat.

 *Note: This feature may be optional. Contact your PerkinElmer representative for details.*

The following items are available via the **Run | Sample Priostat** menu option:

- **Decay** (page 194) - Gauges the duration of luminescence (light) in a radioactive sample via a decay histogram.
- **SPC Decay** (page 195) - Gauges the duration of luminescence in a non-radioactive, luminescent sample via a decay histogram.
- **Identify Nuclide** (page 197) - Identifies an unknown nuclide in a sample using the Quench Indicating Parameters—SIS and tSIE.
- **Optimize Regions** (page 199) - Optimizes sample counting regions to provide the highest figure of merit in Normal count mode for samples with a constant quench.
- **Reverse Region** (page 201) - Optimizes sample counting region settings for a sample, and determine equivalent unquenched region settings for variable quench samples.
- **Low Level Optimize** (page 203) - Optimizes sample counting regions to provide the highest figure of merit for Low Level count mode.
- **Alpha/Beta Preview** (page 205) - Views the sample spectrum and approximates activity for samples with both Alpha and Beta-emitting nuclides.
- **Normal Preview** (page 207) - Views the sample spectrum and activity for samples using Normal count mode.
- **Low Level Preview** (page 208) - Views the sample spectrum and approximate sample activity using Low Level count mode.

Sample Priostat is a manual process:

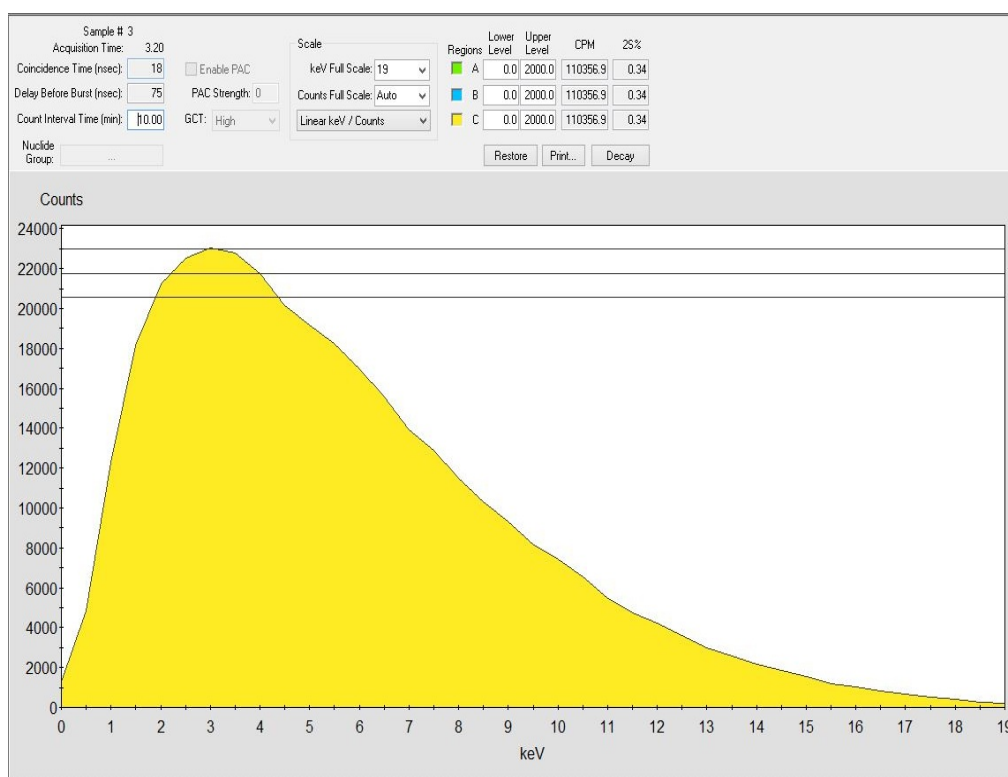
- From the **Run** menu, select **Count** to begin sample counting.
- To continue to the next cassette sample, from the **Run** menu, select **Next Sample**.
- To stop a sample count, from the **Run** menu, select **Stop**.
- To end a Sample Priostat counting session, select **End Sample Priostat** from the **Run** menu.

Data generated during a Sample Priostat option is not saved. To print data, click the **Print** button in the *Report* window.

## Decay

This feature allows users to confirm sample luminescence (light), and determine luminescence decay rates in a radioactive sample. With this mode, samples are recounted until a count is manually stopped. If the counts collected decrease with each successive count (assuming the nuclide half-life is long in relation to the total count time), the radioactive sample is confirmed as luminescent.

Users may view a sample spectrum or results plotted as a histogram with sample luminescence decay rates. This process is useful in establishing an appropriate Pre-Count Delay Time for assay samples.



**Figure 7-1. Decay (Sample Priostat Window).**

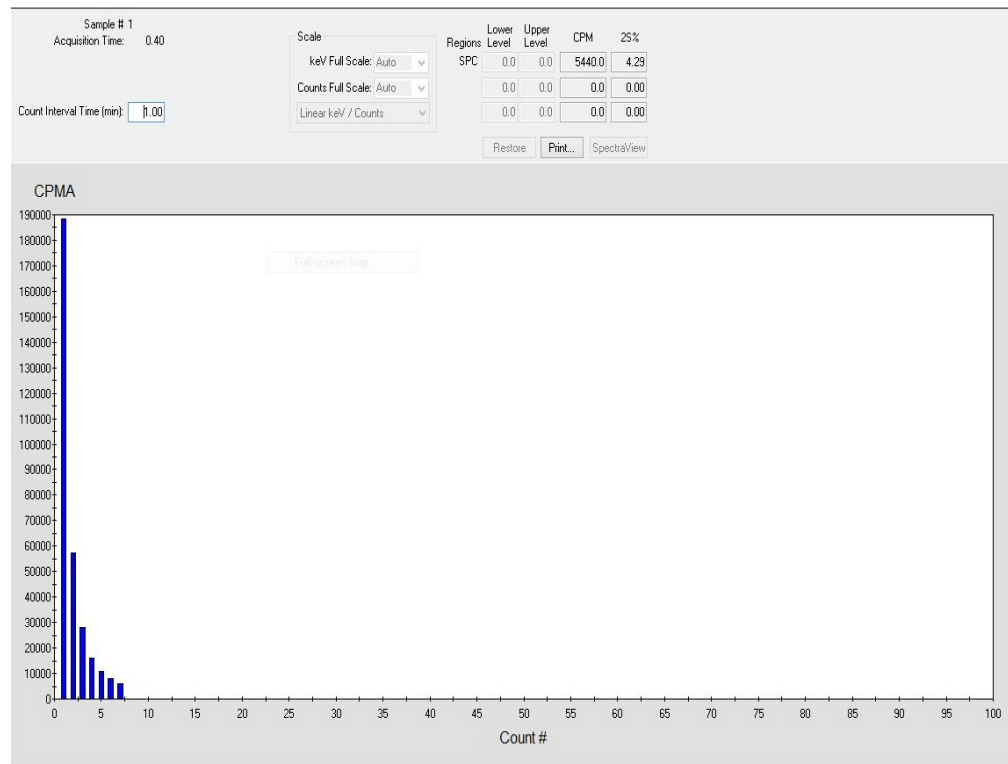
To count samples using Decay mode, do the following:

1. Load a sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette (Figure 1-3, page 7).
2. Select **Run | Decay** from the menu bar. The *Sample Priostat* window appears (Figure 7-1).

3. Select **Run | Count** from the menu bar. Sample counting will begin after the instrument identifies the Priostat flag.
4. Stop the sample count by selecting **Run | Stop** from the menu bar.
5. To count additional samples, select **Next | Sample Count** from the **Run** menu.
6. To stop the sample count, select **Run | End Sample Priostat**.

### Single Photon Counting (SPC) Decay

This feature allows users to measure luminescence decay rates (and view the results plotted) for non-radioactive samples as a histogram. In SPC counts, a single PMT is used to collect counts for non-radioactive, luminescent samples. Using SPC Decay mode, samples are recounted until the process is manually halted. The rate at which counts decrease with each successive recount then determines a sample's decay rate.



**Figure 7-2. SPC Decay (Sample Priostat Window).**

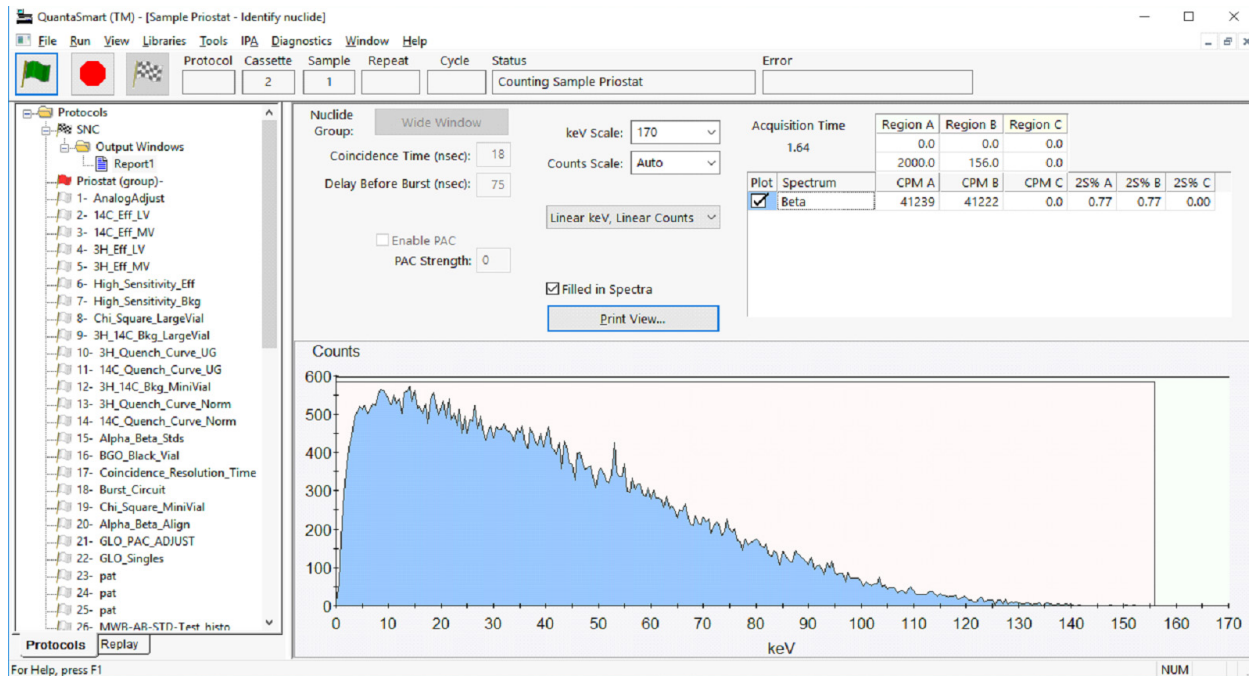
To count samples with SPC Decay mode, do the following:

1. Load your sample(s) into a cassette, attaching the Priostat flag in the reset position to the cassette (Figure 1-3, page 7).
2. Select **Run | SPC Decay** from the menu bar. The *Sample Priostat* window appears.
3. Select **Run | Count** from the menu bar. Sample counting begins immediately after the instrument identifies the Priostat flag.
4. To stop a sample count, select **Run | Stop**.
5. To count additional samples, select **Next Sample | Count** from the **Run** menu.
6. To stop the sample count procedure, select **Run | End Sample Priostat**.

## Identify Nuclide

Several nuclides display a characteristic relationship between their calculated SIS and tSIE Quench Indicating Parameters. As a result, the **Identify Nuclide** feature allows users to identify the following nuclides in a single-label sample:

- Carbon-14 ( $^{14}\text{C}$ ) or Sulphur-35 (these nuclides cannot be differentiated)
- Chlorine-36
- Iron-55
- Nickel-63
- Phosphorus-32
- Tritium ( $^3\text{H}$ )



**Figure 7-3. Identify Nuclide (Sample Priostat Window).**

To identify an unknown nuclide in a sample, do the following:

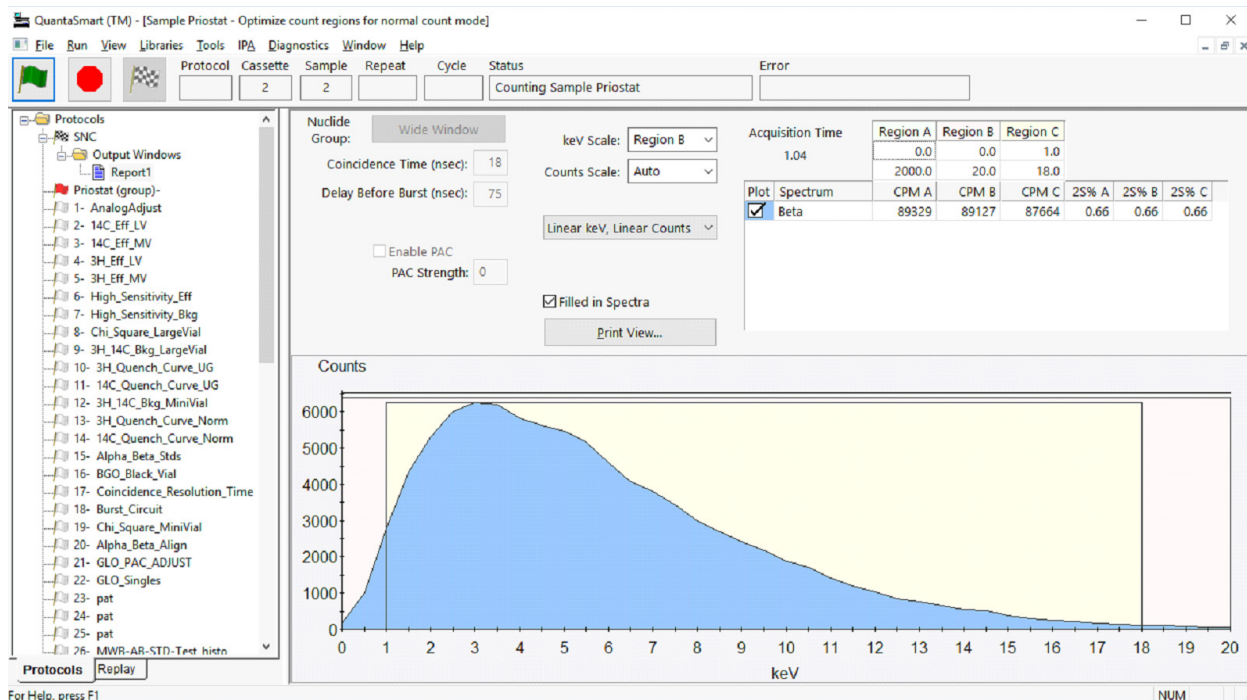
1. Load a sample(s) into a cassette, and attach the Priostat flag in the reset position to the cassette (Figure 1-3, page 7).
2. Select **Run | Identify Nuclide** from the menu bar. The *Sample Priostat* window appears.
3. Select **Run | Count** from the menu bar. Sample counting will begin after the instrument identifies the Priostat flag.
4. To stop a sample count, select **Run | Stop**.

5. To count additional samples, select **Next Sample | Count** from the **Run** menu.
6. To stop a sample count procedure, select **Run | End Sample Priostat**. An output window appears with the nuclide's identity.

## Optimize Regions

This function allows users to eliminate a portion of background counts, increasing the overall Figure of Merit for a counting procedure for samples with constant quench in a Normal count mode.

To automatically optimize sample counting regions for a sample's chemical environment, perform the Reverse Region compensation procedure (page 201) before region optimization. This feature is typically used for samples with variable quench; it allows the instrument to gauge the endpoint equivalent for a nuclide spectrum if a sample was not quenched.



**Figure 7-4. Optimize Regions (Sample Priostat Window).**

To establish the optimal region settings for a nuclide using the Optimize Regions feature, do the following tasks:

1. Load the background vial in odd numbered vial positions, and the sample vials in even numbered vial positions.



*Note:* A background vial must be counted for each sample vial. Attach the Priostat flag in the reset position to the cassette (Figure 1-3, page 7).

2. Select **Run | Optimize Regions** from the menu bar. The *Sample Priostat*

window appears.

3. Select **Run | Count** from the menu bar. Counting will begin after the instrument identifies the Priostat flag.
4. Allow the samples to count long enough to reach a statistical accuracy (2S%) of 2.00 (equivalent to 10,000 gross counts) before stopping. The recommended minimum count time for a background sample is 10 minutes.
5. To stop a sample count, select **Run | Stop**.
6. To count additional samples, select **Run | Next Sample**.
7. To stop the Optimize Region count procedure, select the **Run | End Sample Priostat** menu item. An output window displays providing the optimal region settings for the sample nuclide.
8. Add this nuclide with the optimized region settings into the Sample Nuclide Library (page 152) for later use in various assays. Any Quench Standards Sets defined for use with this nuclide will automatically use the new region settings. No new quench standards must be counted if the nuclide is the same.

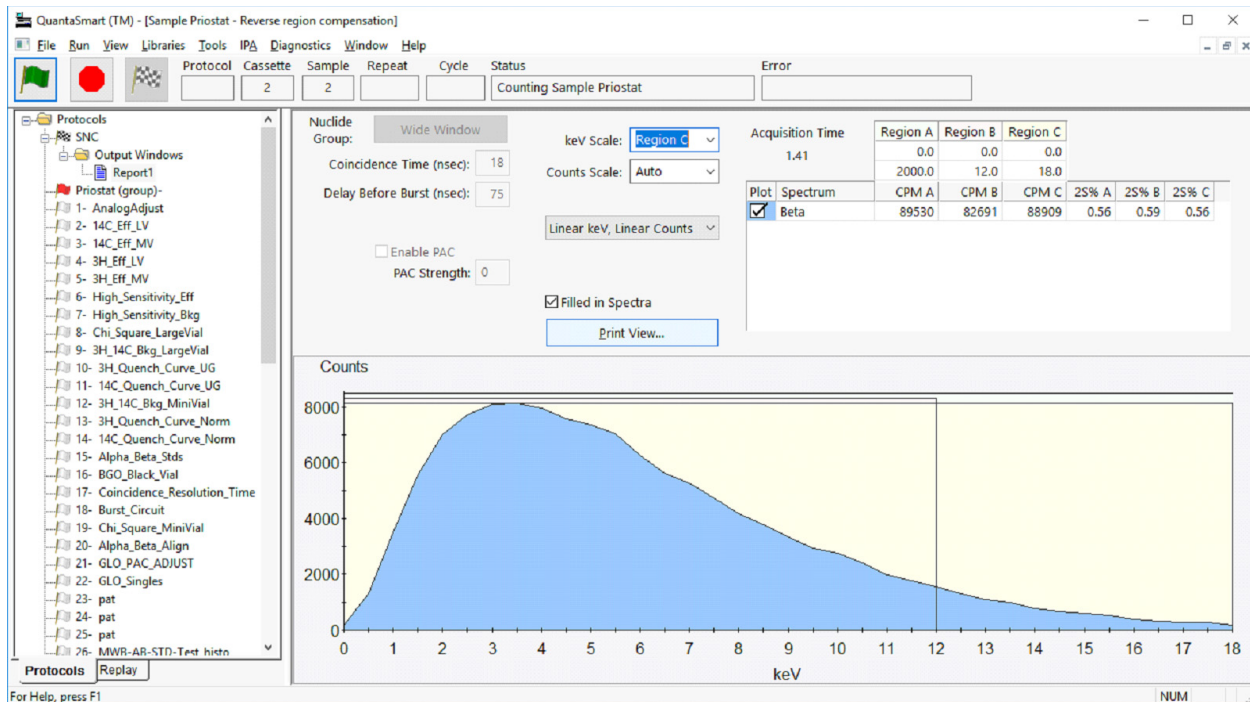


*Notes: Enter values in the **Regions** fields to change axis and counting regions for Regions A, B, and C. To restore counting region limits defined for a nuclide in the Nuclides Library, click the **Restore** button. If no nuclide exists (or one is not available), the region default setting for the Lower Level is 0.0, and the Upper Level is 2000.0*



## Reverse Region

Use this compensation feature to optimize counting region settings to gauge a sample's chemical environment. Reverse Region determines region settings using a factor based on the sample's tSIE and observed spectral endpoint.



**Figure 7-5. Reverse Region (Sample Priostat Window).**

To establish optimal region settings with the Reverse Region option, approximate these settings using the Sample Priostat Preview function:

1. Load your sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette (Figure 1-3, page 7).
2. Preview samples using one of the Sample Priostat Preview options (Normal, Alpha/Beta, or Low Level). The appropriate option corresponds to the count mode used to count samples; these options are available via the **Run | Sample Priostat** menu option.
3. Select **Run | Count**. Counting begins after the instrument identifies the Priostat flag.

4. Allow the samples to count to a statistical accuracy (2S%) of 1.0 (equivalent to 40,000 gross counts). While previewing the sample, determine lower level and upper level region settings by observing the sample spectrum.
5. To stop the Sample Priostat count, select **Run | Stop**.
6. To count additional samples, select **Run | Next Sample**
7. Select **Run | Reverse Region** from the menu bar. The *Sample Priostat* window appears. Enter the region settings established during the preview count.
8. Select **Run | Count**.
9. To stop the Reverse Region sample count, select **Run | Stop**.
10. To count additional samples, select **Next Sample | Count** from the **Run** menu.
11. To stop the Reverse Region sample count, select the **End Sample Priostat** menu item. An output window displays with the Equivalent Unquenched Settings for Regions A, B, and C of the sample nuclide.
12. Add this nuclide with the optimized region settings into the Sample Nuclide Library (page 152) for later use in various assays. Any Quench Standards Sets defined for use with this nuclide will automatically use the new region settings. No new quench standards must be counted if the nuclide is the same.

## Low Level Optimize

This function allows users to eliminate a portion of background counts, increasing the overall Figure of Merit for a counting procedure using the Low Level count mode.

To optimize sample counting regions for a chemical environment, perform the Reverse Region compensation procedure (page 201) prior to Low Level region optimization.

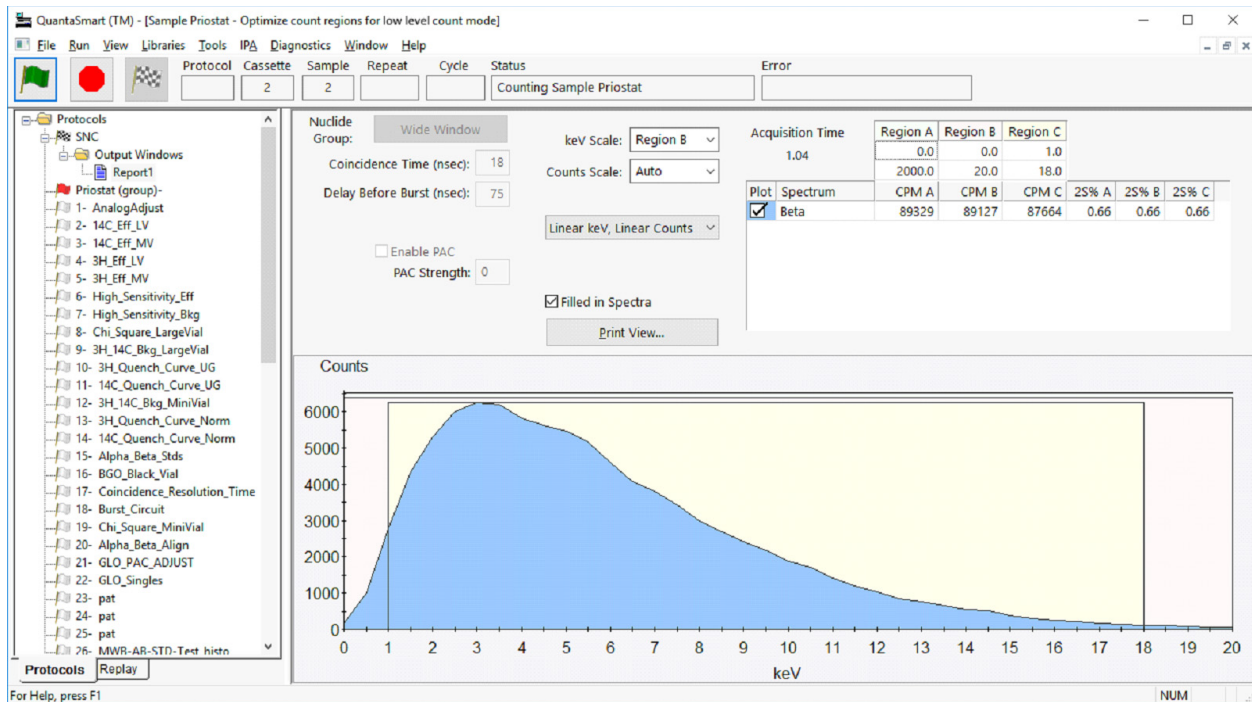


Figure 7-6. Low Level Optimize (Sample Priostat Window).

To establish optimal region settings for a nuclide, do the following tasks:

1. In the cassette, load the background vial in an odd numbered vial position, and the sample vials into even numbered positions.



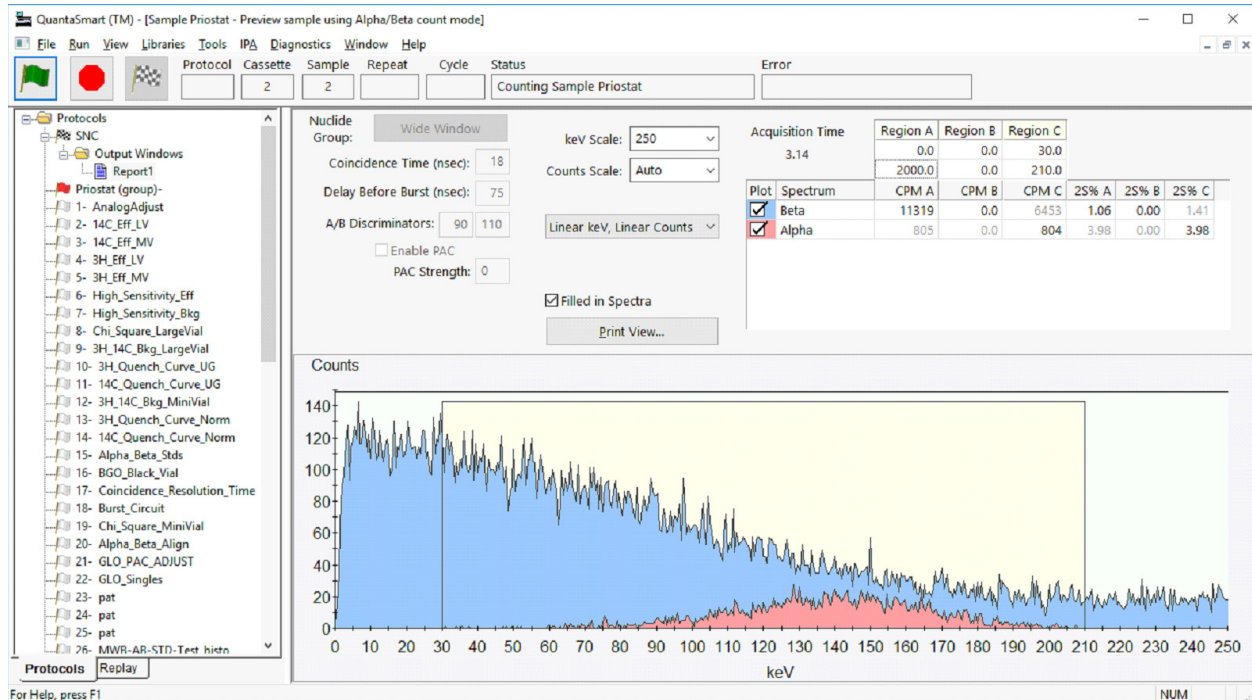
*Note:* A background vial must be counted for each sample vial. Attach the Priostat flag in the reset position to the cassette (Figure 1-3, page 7).

2. Select **Run | Low Level Optimize** from the menu bar. The *Sample Priostat* window appears.
3. Select **Run | Count**. Counting will begin after the instrument identifies the Priostat flag.

4. Allow the samples to count long enough to reach statistical accuracy (2S%) of 2.00 (equivalent to 10,000 gross counts) before ending the count procedure. The recommended minimum count time for a background sample is 10 minutes.
5. To stop the a sample count, select the **Run | Stop**.
6. To count additional samples, select **Next Sample** followed by **Count** from the **Run** menu.
7. To stop the Low Level Optimize counting procedure, select the **Run | End Sample Priostat** menu item. An output window displays provides the optimal region settings for the sample nuclide.
8. Add this nuclide with the optimized region settings into the Sample Nuclide Library (page 152) for later use in various assays. Any Quench Standards Sets defined for use with this nuclide will automatically use the new region settings. No new quench standards must be counted if the nuclide is the same.

## Alpha/Beta Preview

This function is a Sample Priostat option available via the **Run** menu which allows users to observe a sample spectrum, and approximate a sample count rate with Alpha and Beta emitting nuclides in the same vial.



**Figure 7-7. Alpha/Beta Preview (Sample Priostat Window).**

To preview sample counting using the Alpha/Beta Preview feature, do the following tasks:

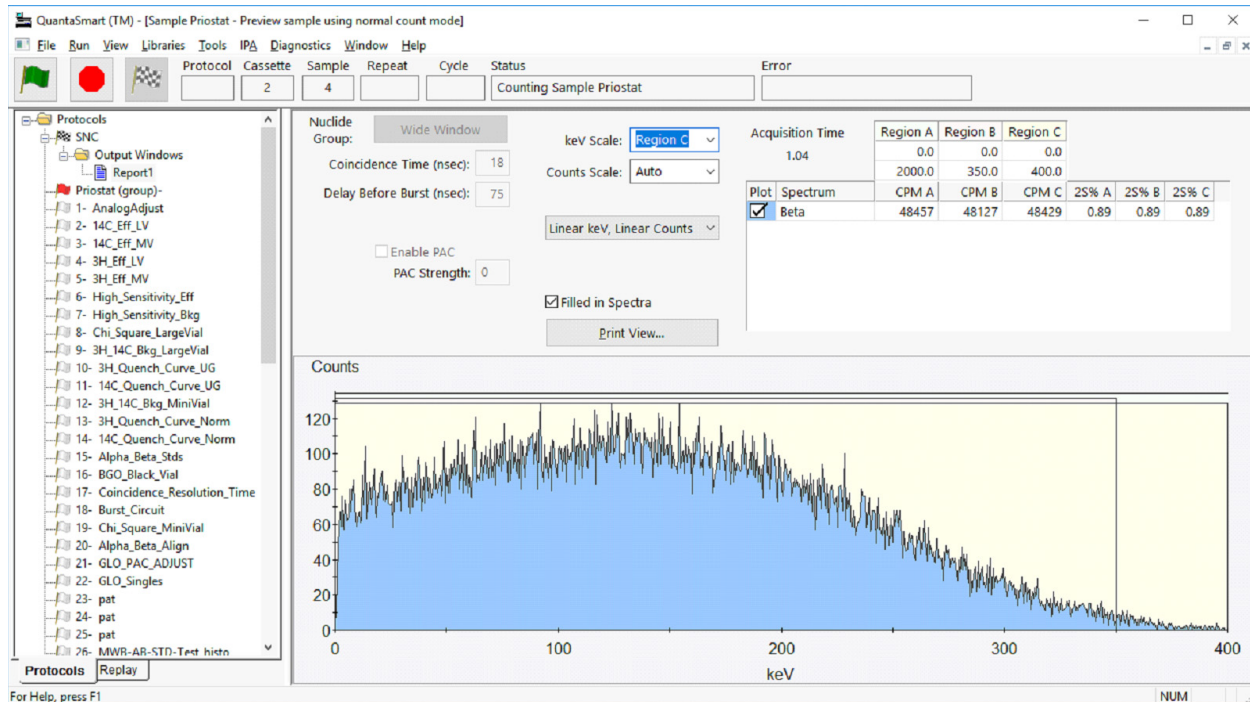
1. Load your sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette (Figure 1-3, page 7).
2. From the Menu bar select **Run | Sample Priostat | Alpha/Beta Preview** from the menu bar. The *Sample Priostat* window is displayed.
3. Select the Nuclide group which has the desired regions and discriminators.
4. Adjust the discriminator(s) as needed.
5. From the **Run | Count**. Sample counting will begin after the instrument identifies the Priostat flag.
6. To stop a sample count, select **Run | Stop**.
7. To count additional samples, select **Next Sample | Count** from the **Run**

menu.

8. To stop the sample counting procedure, select **Run | End Sample Priostat**.

## Normal Preview

This function is a Sample Priostat option available via the **Run** menu which allows users to observe a sample spectrum, and approximate a sample count rate using Normal count mode.



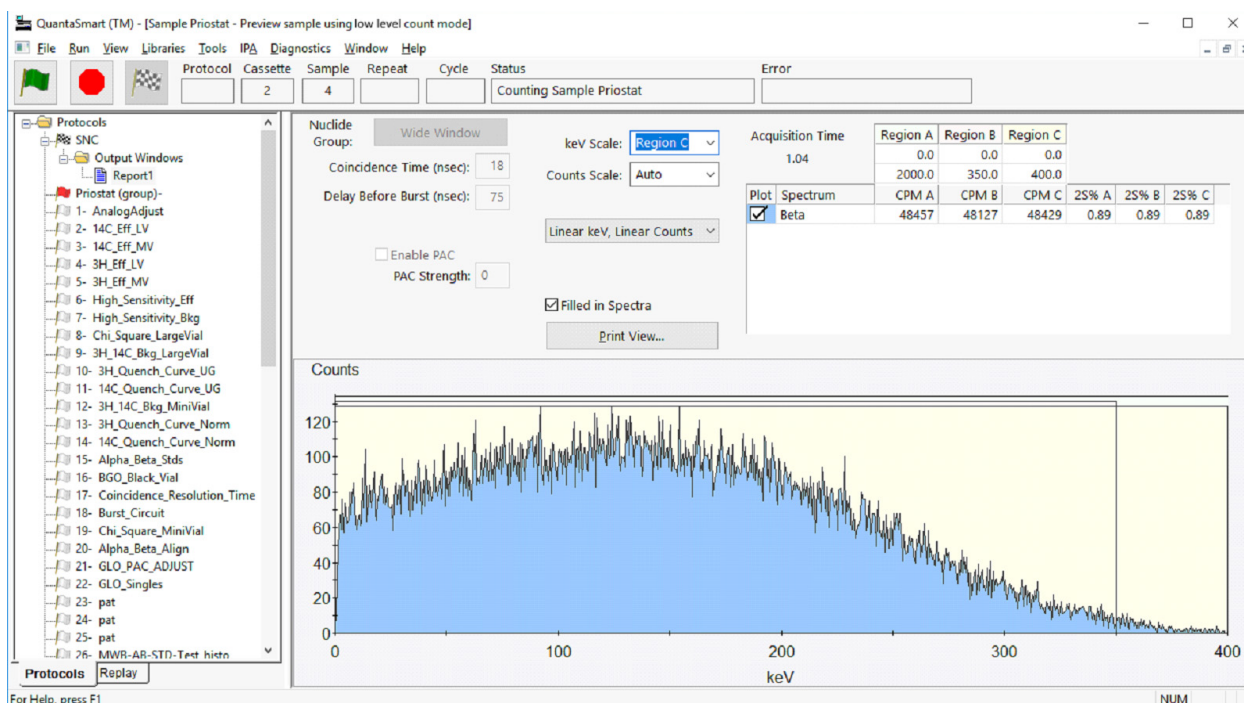
**Figure 7-8. Normal Preview (Sample Priostat Window).**

To preview sample counting using the Normal Preview feature, do the following tasks:

1. Load your sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette (Figure 1-3, page 7).
2. From the Menu bar select **Run | Sample Priostat | Normal Preview** from the menu bar. The *Sample Priostat* window is displayed.
3. Select **Run | Count**. The sample counting will begin after the instrument identifies the Priostat flag.
4. To stop sample counting, select **Run | Stop**.
5. To count additional samples, select **Run | Next Sample | Count**.
6. To stop the sample counting procedure, select **Run | End Sample Priostat**.

## Low Level Preview

This function is a Sample Priostat option available via the **Run** menu allowing users to observe the sample spectrum, and gauge sample count rates using a Low Level count mode.




**Figure 7-9. Low Level Preview (Sample Priostat Window).**

To preview sample counting using the Low Level Preview feature, do the following tasks:

1. Load your vial sample(s) into a cassette. Attach the Priostat flag in the reset position to the cassette (Figure 1-3, page 7).
2. From the menu bar, select **Run | Sample Priostat | Low Level Preview**. The *Sample Priostat* window is displayed.
3. Select **Run | Count**. The sample count will begin after the instrument identifies the Priostat flag.
4. To stop sample counting, select **Run | Stop**.
5. To count additional samples, select **Run | Next Sample | Count**.
6. To stop the sample counting procedure, select **Run | End Sample Priostat**.



## Replay Feature

 *Note: This feature may be optional. Contact your PerkinElmer representative for details.*

This feature (see Figure 7-10) allows users to analyze previously collected data under various data reduction conditions. As each sample spectrum is saved, data may be reanalyzed using various data reduction parameters without recounting samples. Data reduction protocols listed in the **Replay** tab of the main window match those listed in the **Protocols** tab. Any changes made to protocols during Replay do not affect the original acquisition parameters.

To access the Replay function, select the **Replay** tab in the main window, and then select the data file to be reanalyzed. Right-click on the data file, and select **Open for Replay**.

Replay - 20160913\_0758.results

Replay Conditions | Report Definition | Report Output | Special Files | Worklist

Assay Type: CPM

Nuclide Group: 3H

Quench Indicator: tSIE/AEC

GCT: Low

GCT Optimization Set: Ultima Gold

Quench Sets

Low ...

Mid ...

High ...

keV Energy Regions

	Lower Limit	Upper Limit
A	0.0	18.6
B	2.0	18.6
C	0.0	0.0

Background CPM Subtraction

Subtract Background

1st Vial

A	0.00
B	0.00
C	0.00

Half-life Correction

Apply Half-life Correction

	Half-life	Units	Reference Date	Reference Time
A	4530.37	Days	Start of Assay	Start of Assay
B	0.00	Minutes	Start of Assay	Start of Assay
C	0.00	Minutes	Start of Assay	Start of Assay

Luminescence Correction

Colored Sample Correction

Replay Cancel Help

Figure 7-10. Replay Window (Replay Conditions Tab).

## Replay Conditions Tab

The **Replay Conditions** tab of the *Replay Window* (Figure 7-10) contains the following fields:

### Assay Type

From this drop-down field, select the data type (CPM or DPM) for the instrument to calculate from the stored sample data and spectra.

### Nuclide Group

Click this button to display the Sample Nuclides Library (page 152) for informational purposes.

### Quench Indicator

From this drop-down field, select one of the following Quench Indicating Parameters (QIPs) used to calculate DPM with the instrument's Replay feature:

- **tSIE** (transformed Spectral Index of External standard) assigns a numeric value to a quench associated with a sample. This is independent of the sample's radioactivity amount and count rate. tSIE is the most accurate of the quench indicator options, and typically used for low count rate, variable quench, single label samples. Select this Quench Indicator only if samples were originally counted using tSIE.
- **tSIE/AEC** (transformed Spectral Index of External Standard coupled to Automatic Efficiency Correction). tSIE assigns a numeric value to the quench associated with a sample. As quench varies, the AEC automatically monitors and adjusts the counting region to exclude unwanted background. This setting is typically used for dual and triple label experiments with variable quench samples where optimal region settings are desired. Select this Quench Indicator only if the samples were originally counted using tSIE.
- **SIS** (Spectral Index of the Sample) assigns a numeric value to a quench associated with a sample. The SIS is determined from the spectral shape of a sample, and is based on actual sample counts. The SIS setting is typically used to monitor a quench level in single label, high count rate samples for CPM assays, or in single label Cherenkov counting.

### Guard Compensation Technology (GCT)

From this drop-down field, set a GCT for this sample (e.g. Off, High, Low).

### Luminescence/Colored Sample Correction

Select these checkboxes to activate luminescence (light) or colored sample correction. During Replay, the instrument corrects data for any counts involving luminescence or sample discoloration.

### Quench Sets

From these drop-down fields, specify a sample quench setting between Low, Mid and High ranges.

### keV Energy Regions

From this drop-down field, define background values for each of the three regions—A, B, and C.



*Note: This feature may be optional. Contact your PerkinElmer representative for details.*

### Background CPM Subtraction

When this feature is activated by selecting its checkbox (Subtract Background), the instrument subtracts background values from sample data before reanalysis in Replay. Select a background source from the drop-down list:

- **Manual** – Select this option to manually define background values for each of the three regions—A, B, and C.
- **IPA** – After selecting this option, the instrument subtracts background values established during the calibration and IPA procedures from the entire spectrum of samples.
- **1st Vial** – After selecting this option, the instrument counts the first vial in a cassette for 10 minutes, or the defined protocol count time (whichever is greater) and establishes a CPM value for each region. These values are the background values subtracted from each sample in each assay region.

### Apply Half-life Correction


When this feature is activated by selecting its checkbox (Apply Half-life Correction), the instrument corrects the sample data for half-life decay of the nuclide(s) being reanalyzed in Replay. The Reference Date and Time are used to make decay calculations; default settings correspond to the start of an assay.

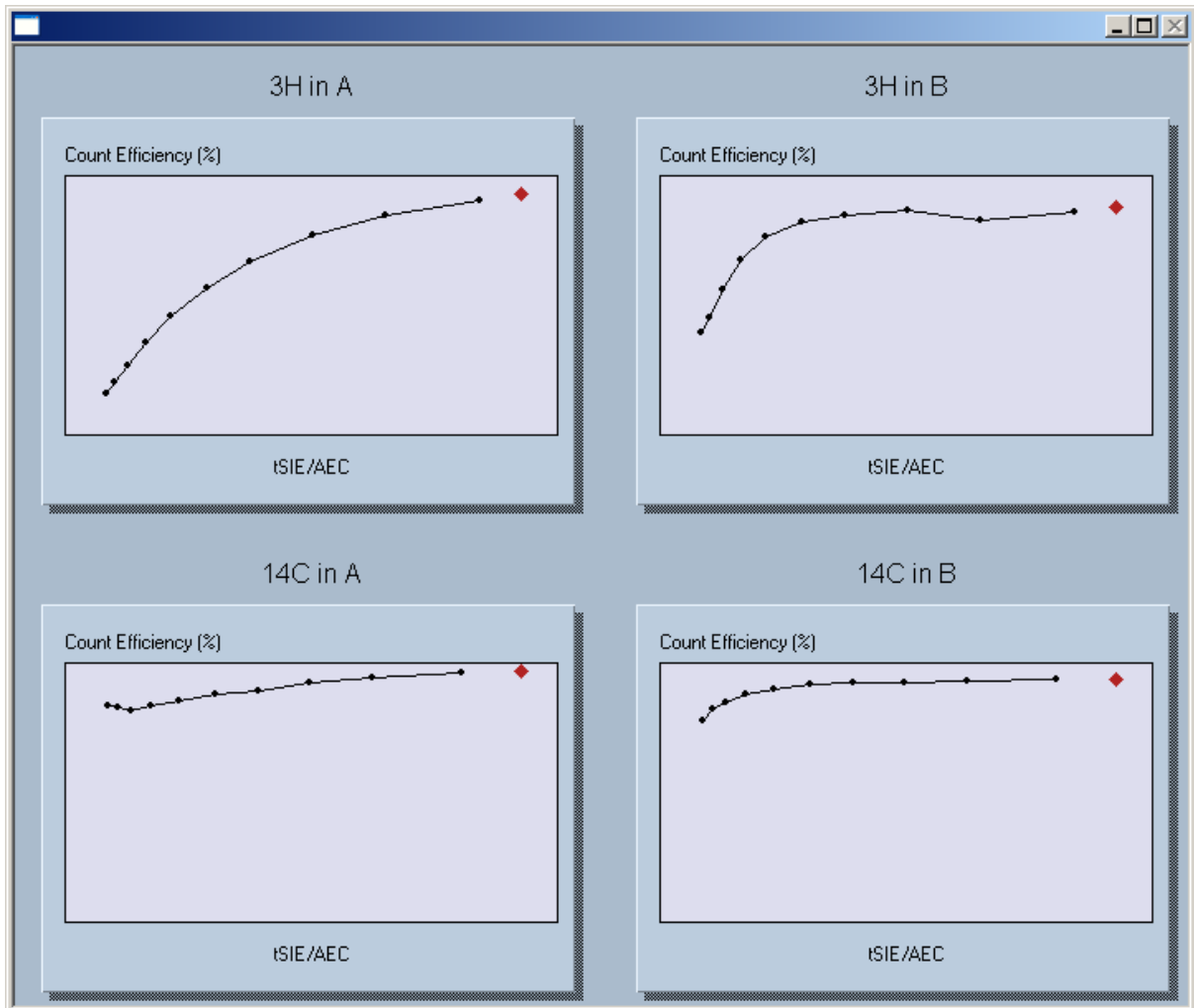
### Replay

When clicking this button, data is reanalyzed, and then the following Replay windows appear in the main window: *Replay Quench Curves* (page 213), *Replay SpectraView* (page 214), and *Replay Output* (page 215).

### Replay Quench Curves Window

Figure 7-11 is an example of a *Replay Quench Curves* window for a dual-label assay in Replay.

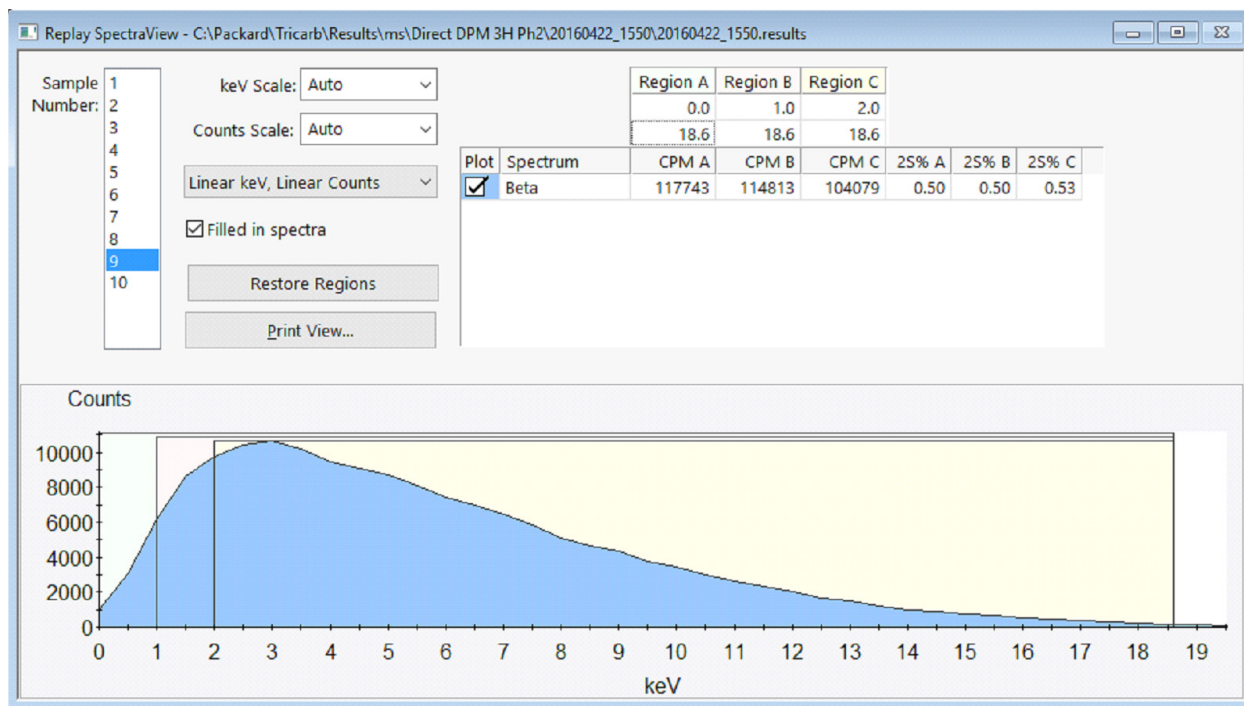
 *Note:* If the **Quench Curve Block** from the **Report Definition** tab of the *Replay* window is selected, only the curve is initially displayed. Double-click on the curve to view the **Expanded Quench Curve** window with standard points and efficiency displayed.



**Figure 7-11. Replay Quench Curves Window (Samples).**

**Replay SpectraView Window**

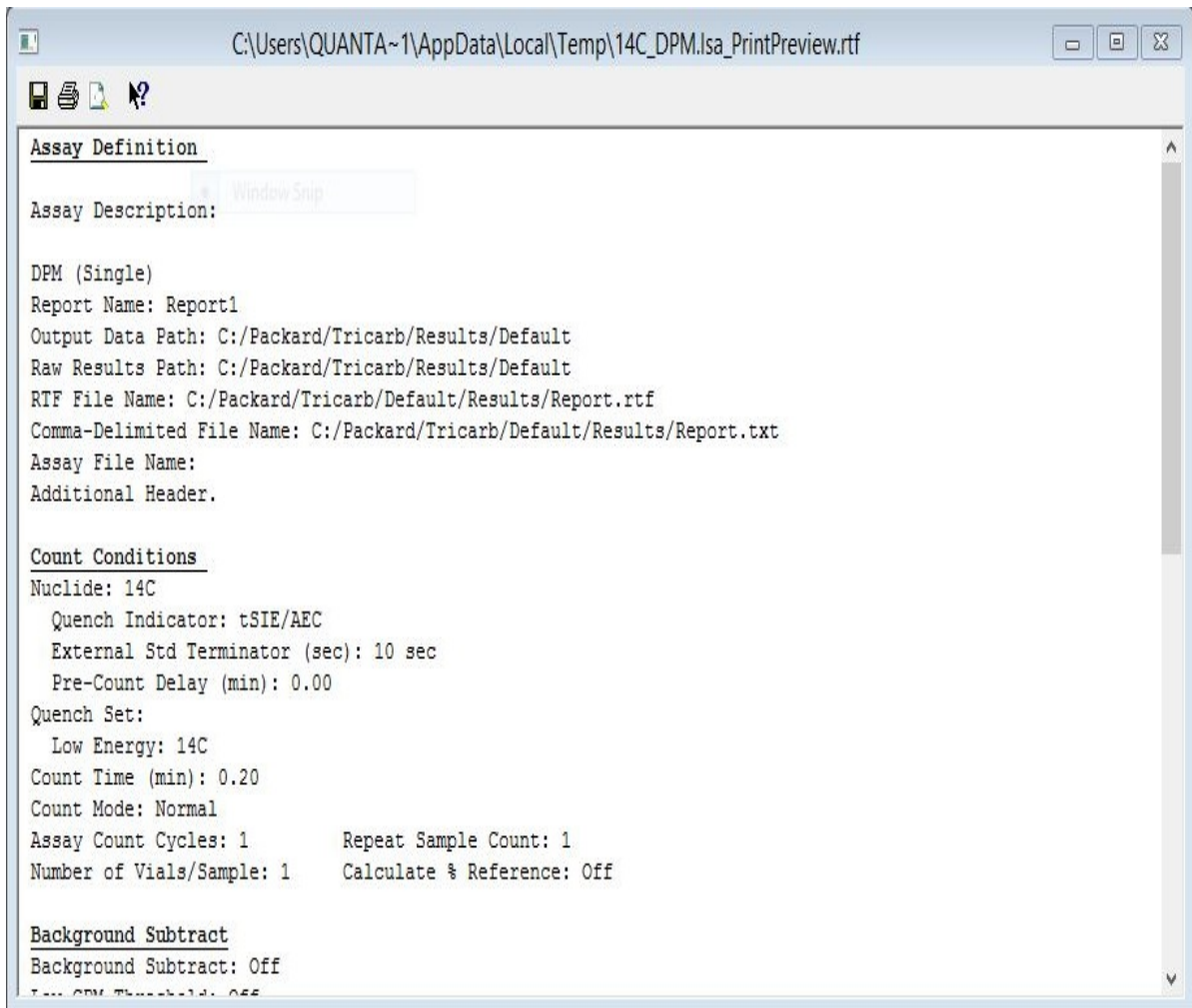
Figure 7-12 is an example of a *Replay SpectraView* window for a dual-label assay in Replay.



**Figure 7-12 Replay SpectraView Window (Sample).**

### Replay Output Window

This window (see Figure 7-13) displays various assay parameters and data items. Customize information shown in this window by defining the output window/printer report; this report is defined in the **Report Definition** and **Report Output** tabs of the *Replay* window.



**Figure 7-13. Replay Output Window (Sample).**

### Report Definition Tab

This tab of the *Replay Window* (Figure 7-10, page 210) contains the same fields as the **Report Definition** tab of the *Assay Definition* window. For information on the fields in this tab, refer to page 125.

### Report Output Tab

This tab of the *Replay Window* (Figure 7-10, page 210) contains the same fields as the **Report Output** tab of the *Assay Definition* window. For information on the fields in this tab, refer to page 134.

### Special Files Tab

This tab of the *Replay Window* (Figure 7-10, page 210) contains the same fields as the **Special Files** tab of the *Assay Definition* window. For information on the fields in this tab, refer to page 139.

### Worklist Tab

This tab of the *Replay Window* (Figure 7-10, page 210) contains the same fields as the **Worklist** tab of the *Assay Definition* window. For information on the fields in this tab, refer to page 144.




*Note:* This feature may be optional. Contact your PerkinElmer representative for details.




## High Sensitivity and Low Level Counting

In liquid scintillation counting, detection limits rely on an instrument's efficiency and ability to detect background counts. Tri-Carb instruments use Time Resolved Liquid Scintillation Counting (TR-LSC), an electronic background discrimination technique (burst counting circuitry) to enhance sensitivity.

 *Note: Sensitivity may be further enhanced via GCT on the Quantulus model.*

The following table describes the differences between counting modes available on Tri-Carb instruments. However, counting modes available on your specific instrument are dependent on your Tri-Carb model, and the options purchased.

Type of Counting	Background Discrimination	Instrument Count Mode	Typical Count Rate	Availability
Normal	Minimal	Normal	> 500 CPM	Standard
Low Activity	Intermediate	High Sensitivity	50–500 CPM	Optional
Ultra Low Level	High	Low Level	1–20 CPM above background	Optional
Super Low Level	Maximum	Low Level	1–20 CPM above background	Optional with BGO Detector Guard only

 *Note: Do not use High Sensitivity or Low Level Count Modes to count Alpha samples in normal CPM or DPM counting assays. These TR-LSC discrimination modes are not appropriate for counting Alpha samples. Extremely low Alpha count rates will be observed.*

An increase in sensitivity with various counting modes results from altering the amount of electronic background discrimination. For High Sensitivity and Low Level Count Modes, criteria employed for discriminating true Beta counts from background counts is more stringent. Loss of counting efficiency may occur as background discrimination increases. Background reduction, however, is usually far greater than any counting efficiency loss, resulting in greater counting efficiency as measured by  $E^2/B$  (Efficiency<sup>2</sup>/Background). Counting high energy beta emitters like <sup>90</sup>Sr or <sup>90</sup>Y in High Sensitivity or Low Level Count Mode requires optimization of TR-LSC parameters. This is accomplished by changing the **Delay Before Burst** value in the **Count Corrections** tab (page 121) of the *Assay Definition* window. The Delay Before

Burst feature works by delaying the time by which an afterpulse discrimination begins to preserve high beta count efficiency at the lowest possible background.

## Super Low Level Counting

This capability (for Tri-Carb Quantulus GCT 6220) uses a slow, scintillating BGO detector guard. The assembly replaces the conventional sample changer, and provides an increase in Figure of Merit performance compared to standard counting systems alone. With the exception of the normalization, calibration, and IPA procedures, the operation of Tri-Carb models equipped with a BGO detector is the same as standard Tri-Carb models.

The following information is relevant when performing Low Activity, Ultra Low Level, or Super Low Level Counting:

- Low potassium (K) glass vials are recommended when counting low levels of Tritium or  $^{14}\text{C}$  as these vials enhance discrimination between Beta pulses and background pulses. Certain plastic vials may be suitable for measuring Tritium in water.
- A water source used for making background determinations must be free of contamination by radionuclides. When counting very low levels of radionuclides (especially Tritium), even the smallest contamination will increase the count rate of a background sample. Therefore, it is necessary to secure a “dead” water source that is free of radioactivity.
- Samples must be free of extraneous sources of radionuclides, such as those found in scintillators, or any reagents used in preparation.
- Glass vials should be washed and rinsed with a dilute (0.1M) ethylene diamine tetraacetic acid (EDTA) solution, followed by a dead, deionized water rinse. This will reduce background and surface contaminants that could taint the detector guard or sample chamber.
- All vials used with this instrument should be sealed with Teflon<sup>®</sup> cap liners, and screw caps to prevent leakage.

- Maximum vial dimensions are as follows:
  - ◆ Small vials must not exceed 17.8 mm in diameter and 58.0 mm in height (including the cap).
  - ◆ Large vials must not exceed 28.1 mm in diameter and 63.0 mm in height (including the cap).
- The maximum sample activity is 100,000 CPM. If a sample exceeds this count rate, the system will automatically switch to the Normal Count Mode. This is vital when purchasing or preparing quench or reference standards for use in High Sensitivity or Low Level Count Mode.
- The luminescence correction feature is not typically used when counting very low CPM samples. It is preferable to dark adapt samples before counting. The instrument provides a protocol-specific, pre-count delay of up to 99.99 minutes where a sample is lowered into the detection chamber, and allowed to dark adapt for a specified delay time. This allows any light from a sample vial to dissipate.

### Cautions and Limitations

Note that background radiation varies throughout the world, and will be a factor in determining background. For example, higher elevations and geological areas where Uranium, and its decay products tend to concentrate will likely experience higher background levels. Exact instrument background and performance for a location must be determined at the installation site.




**Caution:** When using High Sensitivity or Low Level Count Modes, do not use quench standards that are purged free of oxygen with an inert gas. Oxygen quenching in unpurged standards creates discrimination between background and true beta events. Unpurged standards are available from PerkinElmer. For best DPM performance, quench standards should match your unknown samples as closely as possible for cocktail, vial type, and sample volume.



*Note:* Do not use Low Level (LL) standards to calibrate (SNC/IPA) the instrument. The Tri-Carb should always be calibrated with an unquenched, purged  $^{14}\text{C}$  standard.

## Alpha/Beta Counting

 *Note:*      *This feature may be optional. Contact your PerkinElmer representative for details.*

For Alpha/Beta assays see Alpha/Beta Assays (page 103)

For Alpha/Beta Standards Assay see Alpha/Beta Standards Assays (page 109)


For Alpha/Beta Counting Theory see Alpha/Beta Counting Theory (page 270)

## Tandem Processing

This allows the Tri-Carb instrument to pass data from an assay to an application program. Application programs can provide various features including data manipulation (data reduction, graphing, etc.). Suitable application programs are commercially available, or can be written and compiled by users. The instrument can store appropriate data from an assay to a disk file, where the application program can access it without user intervention.

These data files are generated if the following is done:



- Create a report that includes the desired data fields.
- Specify that a data file of the desired format be created.
- Select any appropriate, special files that may be required by your application. `Prot.dat` and `2000ca.dat` are special files necessary for certain PerkinElmer application programs, but additional data from spectrum files or IPA information may also be required.
- Select the **Run Application** checkbox in the **Report Output** tab (Figure 4-10, page 134). In the fields below the checkbox, specify the application program name, program type, and when the application should run for the assay.

 *Note:*      *Each time the application program is run, it must be loaded into memory. Whenever possible, run the application program after a batch or cycle, as it is more efficient and faster than running the program after each sample.*

- Specify a data file location in the *Data Paths* window (page 66) so the data files area is accessible to an application program.

## 2D Bar Code Reader Option

This is an optional feature providing automated sample tracking for the Tri-Carb system. Bar code data can be imported directly into a sample Worklist, saved to a file, or used to verify existing Worklists.

-  *Note:*      *This feature may be optional. Contact your PerkinElmer representative for details.*
-  *Note:*      *Linear 1D bar codes are also supported - if they fit onto the top of a vial cap. Use the bar code reader's software to accommodate linear 1D bar codes (see the software's help for instructions). Also disable all other bar codes not used for maximum speed and efficiency.*

When using the Bar Code Reader option:

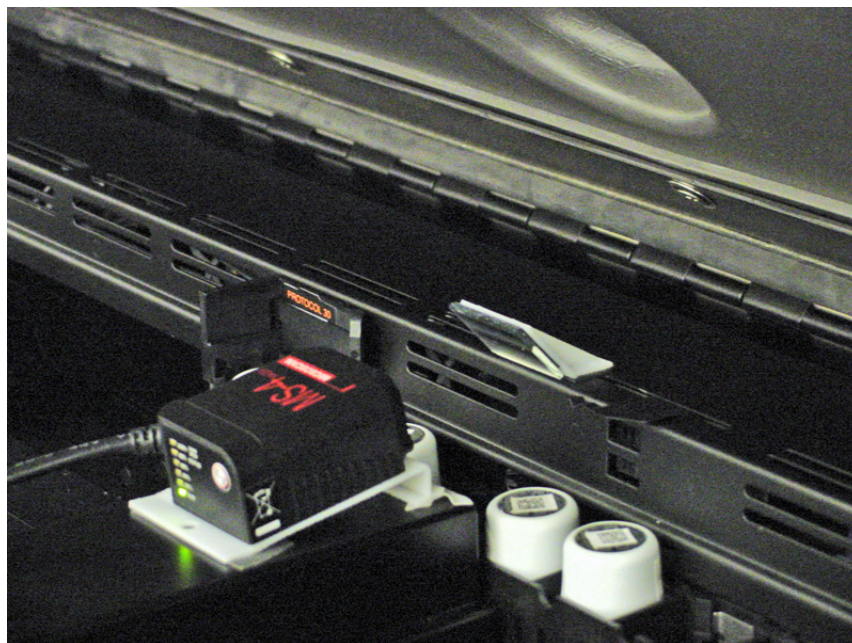
- On multiple cycles, bar codes are read and stored only during the first cycle. Bar codes are validated on subsequent cycles.
- On repeat counts, bar codes are only read on the first count; all other repeats will have the same bar code linked to them.
- Bar code parameters are set on a per assay basis, and are not parameters of a specific protocol flag being used. For information on setting bar code parameters, see page 150.

Refer to the following sections for more information on the bar code reader:

- *Configure Barcode Reader* on page 83 (explains how to enable the Bar Code Reader option, if installed).
- *Barcode Settings* on page 150 (discusses the bar code settings and parameters available through the **Assay Details** tab).
- *Sample Name* on page 145 (explains how bar code reading can be used with Worklists).

## Bar Code Size and Placement

The 2D Bar Code Reader option supports the following bar code sizes: 10 mil, 15 mil, and 20 mil 2D data matrix bar codes. The bar code reader is capable of handling alphanumeric data. The 2D bar codes are placed on the top of the sample vial caps.



**Figure 7-14. Bar Code Reader Option and Sample Vials with 2D Bar Codes on Vial Caps.**

## Chapter 8

### Maintenance and Troubleshooting

This chapter contains information about maintaining your Tri-Carb instrument, and troubleshooting any problems that may occur. The following information is discussed:

- Preventative Maintenance
- Storing Data (page 224)
- Power Failure Recovery (page 225)
- Troubleshooting Operational Errors (page 225)
- Troubleshooting IPA Errors (page 227)
- Troubleshooting Warnings and Messages (page 229)

#### Preventative Maintenance

With the exception of inspection and cleaning, there are no preventative maintenance steps to perform. Normal system preventative maintenance can be performed on a prescribed basis under a PerkinElmer Maintenance Agreement. Contact your PerkinElmer district office, or official PerkinElmer distributor for information on the availability of a maintenance agreement.

## Inspection

The following should be inspected on the Tri-Carb system at least once per week, or whenever a system malfunction occurs:

1. Verify that all cassettes and sample changer surfaces are free of dirt or oil.
2. Cassette movement should be smooth with no excessive vibration.
3. Check for loose electrical or mechanical connectors.



**CAUTION: Do not perform any disassembly.**

4. Ensure that all controls and indicators are working.

## Cleaning

Verify that the Tri-Carb instrument is unplugged before any cleaning, then clean outer surfaces with a soft cloth and mild detergent.

The sample changer lid should be cleaned using a soft cloth moistened with mild soap and water, and the system sample changer cleaned a soft cloth moistened with PicoClean-N, or an appropriate commercial cleaning agent.

If the Tri-Carb system has an optional refrigeration unit installed, check (monthly) that the filter is dust-free, and clean (rinse with water) as required.

## Storing Data

### Back Up Hard Drive

To safeguard against data loss due to hard drive failure, periodically back up all files in the `Packard` folder automatically created when QuantaSmart software is installed. This folder contains the **TriCarb** folder, including sub-folders for various program and data files.



## Folder Contents

### TriCarb

The TriCarb folder (located in the Packard folder) contains several sub-folders containing various program or data files.



*Note: Because the system requires certain program files to be located in specific folders, do not move files in the sub-folders.*

The **TriCarb** folder contains the following sub-folders:

- **Assays** – These files contain information on parameters specified during the assay definition process.
- **Bin** – These files contain information on the execution of QuantaSmart program.
- **Drivers** - These files contain information on the USB device driver.
- **Help** – These files contain information on the Help system for the QuantaSmart program.
- **IPA Results** – These files contain information on IPA data.
- **Libraries** – These files contain information on Libraries used in the QuantaSmart program.
- **QuenchStdResults** – These files contain information on Quench Standards.
- **Results** – These files contain sample data generated from assays.

## Power Failure Recovery

Tri-Carb allows the computer to continue to recover after the instrument experiences a power failure. Once power is restored, the instrument will resume counting the sample being processed at the time of the power failure. Rarely, if ever, will acquired data or replay data be lost during a power failure.

## Troubleshooting Operational Errors

The following problems may occur during normal system operation:

### Erratic Sample Changer Motion

- Verify that the instrument lid is closed. The sample changer optical sensors are affected by bright light.
- Verify that no obstructions exist in the sample changer.
- Confirm that the Varisette cassette is properly labeled with a protocol flag.

**No Display**

- Confirm that the monitor power switch is in the ON position, and the monitor cable is connected to the monitor port on the left side of the Tri-Carb instrument.
- Reboot the computer - press <Ctrl+Alt+Delete> on the keyboard.

**No Printout**

- Confirm that the printer power switch is on.
- Verify that the ON-LINE indicator light is on.
- Confirm that the printer has sufficient paper.
- Reset the printer by powering it off and on again.

**Protocol Flag Bypassed**

- Verify that an assay has been defined and associated with the protocol flag number.
- Verify that the protocol flag is active (Figure 1-3, page 7).
- Determine if all sample counting cycles have completed.

**Sample Changer Fails to Respond to Sample Changer Commands**

- Confirm that the Tri-Carb instrument power switch (Figure 1-6, page 15) is in the on position.
- Verify that the sample changer deck contains the appropriate number of cassettes. Push all cassettes on deck toward the detector chamber. If any cassettes remain in the "Clear Zone" (at the front of the deck), there are too many cassettes on the sample changer deck.
- Determine if the instrument has begun Priostat recovery.
- Check if an error message is displayed in the Status Bar of the main QuantaSmart window.
- Reset the Tri-Carb instrument by turning the power switch off for 10 seconds, and then turn the switch back on (Figure 1-6, page 15).

**Sample Changer Idle**

- Confirm that the Tri-Carb instrument power switch (Figure 1-6, page 15) is in the ON position.
- Determine if all sample counting cycles have completed.
- Check for an error message in the Status Bar of the main QuantaSmart window, and on the printout.
- Determine if a sample is counting.

### Samples Fail to Load

- Verify that an assay has been defined and associated with a protocol flag.
- Determine if all sample counting cycles have completed.
- Check the vial dimensions. See Specifications for sample vials (page 9).

### System Locks Up

- Reboot the computer by pressing <Ctrl+Alt+Delete> on the keyboard.
- Reset the Tri-Carb instrument by turning the power switch off for 10 seconds, and then turn the switch back on (Figure 1-6, page 15).

### Cannot Access Diagnostics

The *Diagnostics* windows are typically used by PerkinElmer Technical Service to assess the system's functional status. The **TSE Diagnostics** item in the **Diagnostics** menu are accessible only if you can log onto the system with TSE rights.

## Troubleshooting IPA Errors

The following problems occur when IPA parameters are outside specified limits:

### High Carbon-14 Background

- Check for a contaminated detector by counting an empty vial and displaying the spectrum via the *SpectraView* window. If contamination is found, call PerkinElmer Technical Service.
- Check for increased environmental radiation; determine if high energy sources are stored near the instrument.
- Check for electrostatic discharge with a static controller.
- If gamma sources are used in a lab, perform a wipe test to check for gamma nuclide contamination on a vial.
- Check for electronic noise; use a separate power line for the instrument, or call PerkinElmer Technical Service.

### High Chi-Square

This may be caused by a problem with the high voltage power supply, or Photomultiplier Tubes (PMTs). Call PerkinElmer Technical Service.



*Note: A properly performing instrument may exceed the 7.63 - 36.19% limit 2% of the time. This is a result of the Chi-Square test's statistical nature.*

**High Tritium Background**


- Check for a contaminated detector by counting an empty vial and displaying the spectrum in the *SpectraView* window. If a contamination is found, call PerkinElmer Technical Service.
- Check for increased environmental radiation; determine if high energy sources are stored near the instrument.
- Check for electrostatic discharge; use the static controller.
- If gamma sources are used in the lab, perform a wipe test check for gamma nuclide contamination on the vial.
- Check for electronic noise; use a separate power line for the instrument, or call PerkinElmer Technical Service.

**Low Carbon-14 Figure of Merit**

- Verify that the previous efficiency measurement is within  $\pm 2\%$  when using the same standard. If not, clean the outside of the vials and re-run.
- Check that  $^{14}\text{C}$  background and efficiency values are within specification (when using unquenched standards). If so, IPA standard integrity is suspect.

**Low Chi-Square**

- Check for electronic noise. This typically creates spurious pulses of uniform rate. Use a separate power line for the instrument, or call PerkinElmer Technical Services for assistance.

 *Note:* A properly performing instrument may exceed the 7.63 - 36.19% limit 2% of the time. This is a result of the Chi-Square test's statistical nature.

**Low Tritium Efficiency**

- Verify that the instrument is calibrated. If not, perform an SNC calibration (page 187).
- Confirm that the correct standard (unquenched and purged of oxygen) is being used.
- Confirm that the tSIE standard value is in a range of 950–1050. If not, check the standard expiration date.
- Confirm that the efficiency is  $\pm 2\%$  of the previous measurement using the same standard. If not, clean the vial exterior and re-run.

**Low Tritium Figure of Merit**

- ❑ Verify that the previous efficiency measurement is within  $\pm 2\%$  when using the same standard. If not, clean the vial exteriors and re-run.
- ❑ Check that Tritium background and efficiency values are within specification (when using unquenched standards). If so, the IPA standards integrity is suspect.

**Troubleshooting Warnings and Messages**

The following information describes Tri-Carb system messages (presented in alphabetical order) and provides troubleshooting tips.

**2000CA File Error**

The system encountered an error while writing the 2000CA.DAT file. This file is needed by PerkinElmer application programs. Re-run the assay. If the error reoccurs, call PerkinElmer Technical Service.

**? (Messages column)**

If this character appears in the **MESSAGES** column of a report, a math error has occurred when calculating a sample result.

**< (Messages column)**

If this character appears in the **MESSAGES** column of a report, the sample was rejected due to a low count rate within the first 30 seconds of a sample count.

**# (Messages column)**

If this character appears in the **MESSAGES** column of a report, the sample was determined to be heterogeneous. Typically, this is due to phase separation in the sample vial.

**\* (Messages column)**

If this character appears in the **MESSAGES** column of a report, the sample counts exceeds 100,000 in High Sensitivity or Low Level count mode. The instrument automatically switched to Normal count mode.

**A (Messages column)**

If this character appears in the **MESSAGES** column of a report, this data line represents an average value for replicate sample vials.

**A quench set associated with this assay's nuclide was modified after being run.**

Information for a quench set has changed in the Quench Standards Library (page 155), but the standard set has not been recounted after changes were made.

Recount the quench set.

**A quench set associated with this assay's nuclide was not counted with a sufficient number of samples.**

A sample nuclide has been defined in the Sample Nuclides Library (page 152), but the quench set selected for the nuclide has not been counted. A minimum of two quench standards must be counted for each quench set.

Count the appropriate quench standards.

**An active protocol is invalid for group Priostat.**

An active protocol was selected as a Group Priostat protocol (page 192).

Select a different protocol, or wait until the active protocol is completed.

**B (Messages column)**

If this character appears in the **MESSAGES** column of a report, this data line represents data about a background subtraction vial.

**BACK PIN JAM FWD**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.

**BACK PIN JAM REV**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.

**BAD ELEV/EXT STD**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.

**Bad shutter**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Service.

**BGO spectrum not present**

External standard counting was attempted on an instrument with a BGO detector guard before the SNC/IPA calibration was performed.

Perform the SNC/IPA calibration (page 187).

**C (Messages column)**

If this character appears in the **MESSAGES** column of a report, this indicates that a color quench correction for this sample is suspect ( $tSIE < 100$ ).

The reported sample results may be invalid.

**Cannot associate an assay with the Priostat flag while that assay is active.**

An assay cannot be associated with the Priostat flag while Priostat is active (page 192).

Allow the current set of Priostat samples to finish counting before changing the assay associated with the Priostat protocol flag.

**Cannot associate another assay to this flag while the current assay associated with this flag is active.**

Multiple assays cannot be associated to the same protocol flag number.

Allow the instrument to complete the current assay, disassociate the assay from the protocol flag, and associate a different assay to it.

**Cannot change Priostat flag association while Priostat is active. Stop priostat first.**

The assay associated with the Priostat flag cannot be changed while Priostat is active (page 192).

Allow the current set of Priostat samples to finish counting before changing the assay associated with the Priostat protocol flag.

**Cannot disassociate assay from this flag while the assay is active.**

The protocol flag for the assay that is currently counting cannot be disassociated from the assay while active.

Allow the instrument to complete the current assay before disassociating it from the protocol flag.

**Cannot find the protocol associations file.**

An assay file has been moved from the **Assays** folder, or an assay file has been deleted.

Call PerkinElmer Technical Services.

**Cannot open serial port. Make sure that it is configured and not in use by some other program.**

A multiple instance of the QuantaSmart program may be running.

Close any multiple instances of the program.

**Cannot read results file.**

A results file may have been moved from the **Results** folder or a results file has been deleted.

Call PerkinElmer Technical Services.

**Cannot replay assays.**

The assay type cannot be used in Replay.

Only CPM, Single, Dual, Triple, and FS DPM assays may be used in Replay.

**Can't drop vial.**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.

**Can't raise vial.**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.



**Check the assay file: either the assay file does not exist or the assay file format is corrupted.**

An assay file is corrupted, or a standard associated with an assay has been deleted.

Call PerkinElmer Technical Services.

**Communications Interrupted.**

An RS-232 failure has occurred.

Restart the QuantaSmart program.

**E (Message column)**

If this character appears in the **MESSAGES** column of a report, this indicates that the quench indicating parameter (SIS or tSIE) value was extrapolated from a portion of quench curve beyond an end data points.

Depending on how well the curve fits the standard data points, the extrapolated quench value for the sample may not be accurate.

**Elevator down.**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.

**Elevator up.**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.

**Error in BGO spectrum determination.**

An error was encountered during the acquisition of the BGO detector guard spectrum while counting the SNC/IPA protocol.

Re-run the SNC/IPA calibration procedure. If the problem persists, call PerkinElmer Technical Services.

**EXT STD IN.**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.

**EXT STD OUT.**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.

**Fatal SC error.**

An unrecoverable sample changer error has occurred.

Call PerkinElmer Technical Services.

**FRONT PIN JAM FWD**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.

**FRONT PIN JAM REV.**

A sample changer error has occurred.

No action is required unless a message is printed. If so, call PerkinElmer Technical Services.

**I (Messages column)**

If this character appears in the **MESSAGES** column of a report, this sample has been found to be *Indeterminate* in a Direct DPM assay. This means that the system could not reliably determine a DPM value for this sample.

When a sample is found *Indeterminate*, the DPM reported may be valid if the sample is not heavily quenched. Check the tSIE sample value to determine quench level. If the tSIE exceeds 200, the DPM reported is likely accurate within statistical counting error. Accuracy is independent of cocktail density variation, vial size or type, sample volume, color, and chemical quench.

**Internal error**

A system error (such as file mismatch) has occurred on the instrument.

Perform a cold start of the instrument. If the error message reappears, call PerkinElmer Technical Services.

**Instrument off line**

The instrument is not responding to the computer.

Verify that the instrument's power is on (Figure 1-6, page 15).

### **IPA error C-14 chi-square**

The Chi-Square test failed while counting the  $^{14}\text{C}$  source.

Re-run the Chi-Square test. If the test fails again, call PerkinElmer Technical Services.

### **IPA error C-14 LCR**

The  $^{14}\text{C}$  source does not contain enough activity.

Check that the correct source is being used. Use a new source, if necessary.

### **IPA error-H-3 chi-square**

The Chi-square test failed while counting the Tritium source.

Re-run the Chi-Square test. If the test fails again, call PerkinElmer Technical Services.

### **IPA error-H-3 LCR**

The Tritium source does not contain enough activity.

Verify that the correct source is being used. Use a new source, if necessary.

### **LOST PIN POS**

A sample changer error has occurred.

No action is required unless a message is printed. If not, call PerkinElmer Technical Services.

### **Missing Vial**

This message indicates that a vial is missing from the cassette.

### **No Quench sets specified**

No quench set has been selected for the assay.

Select the appropriate quench set from the Quench Standards Library (page 155). If an appropriate standard set does not exist, perform an appropriate Quench Standards assay.

### **No quench standard is defined for this assay**

A standard being used by a sample nuclide in an assay has been de-selected.

Re-select the assay standard.

**Normalization error-both tubes LCR**

The count rate in both PMTs is too low.

Verify that the unquenched  $^{14}\text{C}$  source is in the first vial position in the cassette. Call PerkinElmer Technical Services.

**Normalization error-both tubes SIS**

The count rate in both photomultiplier tubes is too low.

Verify that the unquenched  $^{14}\text{C}$  source is in the first vial position in the cassette. Call PerkinElmer Technical Services.

**Normalization error-EXT STD**

The external standard is not loading properly.

Call PerkinElmer Technical Services.

**Normalization error-left PMT LCR**

The count rate in the left PMT is too low.

Check that the unquenched  $^{14}\text{C}$  source is in the first vial position in the cassette. Call PerkinElmer Technical Services.

**Normalization error-left PMT SIS**

The left photomultiplier tube has detected inappropriate beta energy.

Check that the unquenched  $^{14}\text{C}$  source is in the first vial position in the cassette. Call PerkinElmer Technical Services.

**Normalization error-right PMT LCR**

The right photomultiplier tube detected inappropriate beta energy.

Check that the unquenched  $^{14}\text{C}$  source is in the first vial position in the cassette. Call PerkinElmer Technical Services.

**Normalization error-right PMT SIS**

The right photomultiplier tube detected inappropriate beta energy.

Check that the unquenched  $^{14}\text{C}$  source is in the first vial position in the cassette. Call PerkinElmer Technical Services.

**Not normalized**

The instrument has not been normalized.

Perform the calibration procedure (page 187) before counting any samples.

**O (Messages column)**

If this character appears in the MESSAGES column of a report, this sample is overcorrected by GCT. If GCT High was used, use Replay to change the value to GCT Low and review the results. Consider creating a GCT optimization set to refine the correction factors for these samples (see appendix D).

**Power fail**

The system has recovered from a power failure.

Check your sample results for missing data.

**Power recovery**

Power to the instrument was lost.

The instrument should resume the function it had been performing when the power failure occurred.

**Priostat ready to count**

A Priostat sample has been loaded into the detection chamber. Sample counting has not begun.

To start sample counting, click the green start button on the toolbar.

**Priostat SC NO ACK**

The selected sample changer control command was not accepted by the instrument during Priostat counting mode.

Check the instrument **State** field in the main window for an INSTRUMENT OFF-LINE message. If this message appears intermittently, shut down Windows, and then turn the instrument power off and back on. If this message does not appear, wait and periodically retry the sample changer commands.

**Priostat search**

The instrument is searching the sample changer deck for the Priostat cassette.

Verify that the Priostat cassette is on the sample changer deck.

**R (Messages column)**

If this character appears in the **MESSAGES** column of a report, this report line represents data about a reference standard vial, used for calculating % Ref.

**S (Messages column)**

If this character appears in the **MESSAGES** column of a report, this report line represents data about a quench standard vial, used for generating quench curves.

**Shutter close**

A sample changer error has occurred.

No action is required unless a message is printed. If this message appears on a printout, call PerkinElmer Technical Services.

**Shutter open**

A sample changer error has occurred.

No action is required unless a message is printed. If this message appears on a printout, call PerkinElmer Technical Services.

**Skipped cassette with no label**

A cassette on the sample changer deck is without an ID label.

Attach an ID label to the cassette.

**The instrument encountered a protocol flag for which there is no assay associated. This protocol was not counted.**

There is a cassette on the instrument's sample changer deck with a protocol flag to which no assay has been associated.

Remove the cassette from the sample changer deck, or associate an assay to the protocol flag number.

**The nuclide associated with this assay has an incorrect number of Quench sets.**

One or more quench sets associated with a multiple label sample nuclide has been deselected from the assay, or deleted from the library.

Re-select the appropriate quench sets for the sample nuclides. Recount the quench set, if necessary.

**The nuclide associated with this assay was not found in the nuclide library. Unable to retrieve nuclide information.**

The sample nuclide defined for the assay was deleted from the Sample Nuclides Library (page 152).

Re-enter the sample nuclide information in the Sample Nuclides Library.

**The quench standard associated with this assay's nuclide was not found in the Quench standard library.**

A quench set associated with a sample nuclide in an assay has been deleted from the library.

Re-enter the standard information in the library and recount the standards.

**The standard associated with this assay has not been counted.**

The standard selected for the assay has not been counted before performing the assay.

Count the standards and restart the assay.

**Vial release close**

A sample changer error has occurred.

No action is required unless a message is printed. If this message appears on a printout, call PerkinElmer Technical Services.

**Vial release open**

A sample changer error has occurred.

No action is required unless a message is printed. If this message appears on a printout, call PerkinElmer Technical Services.

**W (Messages column)**

If this character appears in the **MESSAGES** column of a report, this indicates that the Positive ID (PID) entered in the Worklist does not match the PID read from the cassette.

Verify that the PID number used in the Worklist matches the number found on the appropriate cassette.

**Warning: C-14 Normalization DPM not defined.**

The  $^{14}\text{C}$  Normalization DPM has not been defined.

In the *IPA Definition* window (page 179), enter a DPM value for the  $^{14}\text{C}$  Standard.

**Warning: H-3 Normalization DPM not defined.**

The Tritium Normalization DPM has not been defined.

In the *IPA Definition* window (page 179), enter a DPM value for the Tritium Standard.

**Warning: IPA background data not available.**

No IPA background values are available for background subtraction.

Perform the IPA procedures (page 179).

**Warning: Questionable C-14 background value-please view historic data.**

The background source failed the IPA check in the  $^{14}\text{C}$  region.

If  $^{14}\text{C}$  background is high (and Tritium background is normal) there may be an increase in environmental radiation due to detector contamination, or light is leaking into the chamber. Check the background spectrum via the *SpectraView* window, and review historic IPA data. Call PerkinElmer Technical Services.

**Warning: Questionable C-14 chi-square value-please view historic data.**

The Chi-Square result is outside the range of 7.63 - 36.19.

Verify the integrity of the  $^{14}\text{C}$  spectrum via the *SpectraView* window. Repeat the Chi-Square test. If the result falls outside the range on the repeat test, call PerkinElmer Technical Services.

**Warning: Questionable C-14 figure of merit value-please view historic data.**

Check the Figure-of-Merit threshold value. Clean the  $^{14}\text{C}$  and background sources, and repeat the test. Check the efficiency and background values for  $^{14}\text{C}$ . If these values are within specifications, call PerkinElmer Technical Services.

**Warning: Questionable H-3 background value-please view historic data.**

Check that the correct background sample is in vial position number 3. The detector may be contaminated, or light is leaking into the detector. Review the historic IPA data, and call PerkinElmer Technical Services.

**Warning: Questionable H-3 chi-square value-please view historic data.**

The Chi-Square result is outside the range of 7.63 - 36.19.

Verify the  $^{14}\text{C}$  spectrum integrity via the *SpectraView* window. Repeat the Chi-Square test. If the result falls outside the range on the repeat test, call PerkinElmer Technical Services.



**Warning: Questionable H-3 efficiency value-please rerun quench curves and view historic data.**

The Tritium source failed the IPA check, and the tSIE value for the source is less than 950.

Check that the correct source is being used in the second vial position of the SNC/IPA cassette. Check for dirt or oil on the Tritium standard. Check the DPM value entered in the *IPA Definitions* window (page 179). Review the historic IPA data, and re-run the quench curve. Call PerkinElmer Technical Services.

**Warning: Questionable H-3 efficiency value-please view historic data.**

The Tritium source failed the IPA check.

Check that the correct source is being used in the second vial position of the SNC/IPA cassette. Check for dirt or oil on the Tritium standard. Check the DPM value entered in the *IPA Definitions* window (page 179), and review historic IPA data. Call PerkinElmer Technical Services.

**Warning: Questionable H-3 figure of merit value-please view historic data.**

The Figure-of-Merit value for Tritium is below the threshold entered in the *IPA Definitions* window (page 179).

Check the Figure-of-Merit threshold value, and efficiency/background values for Tritium. If these values are within specifications, call PerkinElmer Technical Services.

**Warning: System not normalized.**

The instrument is not normalized.

Perform the instrument Calibration and Normalization procedures (page 187).

**Warning: User Has Modified Count Conditions**

Changes have been made to the assay currently being counted.

Allow the current assay to finish counting before making changes.

**You cannot exit the application because the instrument is counting a protocol.**

The QuantaSmart program cannot be closed while the instrument is counting samples.

Allow the instrument to finish counting before closing the program.

**You cannot exit the application because the instrument is counting group priostat.**

The QuantaSmart program cannot be closed while the instrument is counting samples.

Allow the instrument to finish counting before closing the program.

**You cannot exit the application because the instrument is engaged in a sample priostat activity.**

The QuantaSmart program cannot be closed while the instrument is counting samples.

Allow the instrument to finish counting before closing the program.

# Appendix A

## Calculations

This appendix describes calculations performed by the Tri-Carb instrument including:

- Background Correction
- Background Threshold (page 244)
- Chi-Square Calculation (page 244)
- Disintegrations Per Minute (DPM) (page 244)
- Efficiency (page 245)
- Figure of Merit (FOM) Calculation (page 245)
- Half-life Correction (page 245)
- IPA Background (page 245)
- Low Count Reject (LCR) (page 246)
- LUM (% Luminescence) (page 246)
- Radioactivity Units (page 246)
- 2 Sigma % (%2s) (page 247)
- Radionuclide Decay Calculator (page 248)
- % Reference (% Ref) (page 248)

### Background Correction

This process subtracts backgrounds from sample nuclide activity. The background correction is performed before any other calculations (e.g. half-life corrections) are performed. The correction of the sample count for background is calculated as:

$$\text{CPM}_{\text{corrected}} = \text{CPM}_{\text{sample}} - \text{CPM}_{\text{background}}$$

## Background Threshold

This value is expressed as Counts Per Minute (CPM) and calculated from the Instrument Performance Assessment (IPA) background value.

$$\text{BKG}_{\text{threshold}} = \overline{\text{BKG}}_{\text{IPA}} + \frac{4 \times \sqrt{\text{BKG}_{\text{IPA}} \times \text{CT}}}{\text{CT}}$$

where:

$\text{BKG}_{\text{threshold}}$  = Background threshold in CPM

$\overline{\text{BKG}}_{\text{IPA}}$  = Mean of first five IPA background values in CPM

CT = Background count time for IPA

## Chi-Square Calculation

This test is a measure of reproducibility of sample counting, and is performed by counting a single sample in the detector 20 consecutive times with a count time of 30 seconds for each repeat measurement.

$$\chi^2 = \frac{\sum (\text{CNT}_i - \overline{\text{CNT}})^2}{\overline{\text{CNT}}}$$

where :

$\overline{\text{CNT}}$  = mean of the repeat measurements

$\text{CNT}_i$  = gross count of each repeat measure

This test is not a measure of detector accuracy.

## Disintegrations Per Minute (DPM)

This is an expression of radionuclide activity, and calculated as follows:

$$\text{DPM} = \frac{\text{Counts Per Minute}}{\text{Efficiency}}$$

## Efficiency

This is a measurement of the instrument's ability to quantify radionuclide activity. This value is calculated as follows:

$$\text{Efficiency} = \frac{\text{Counts Per Minute}}{\text{Disintegrations Per Minute}}$$

## Figure of Merit (FOM) Calculation

This is a measure of instrument sensitivity based on counting efficiency. This value is calculated as follows:

$$\text{FOM} = \frac{(\text{Efficiency})^2}{\text{Background}}$$

## Half-life Correction

This process recalculates sample CPM or DPM, and accounts for the half-life decay of a sample nuclide. This calculation is performed as follows:

$$\text{Activity}_{\text{current}} = \text{Activity}_{\text{initial}} \times e^{-0.693t/T(\text{hl})}$$

where :

Activity<sub>current</sub> = the current remaining activity

Activity<sub>initial</sub> = the starting activity of the nuclide

T(HL) = the half - life of the radionuclide, in hours

e = 2.71828 (base of natural logarithmic scale)

t = time interval in hours, from the reference date to the current date

The half-life correction is performed after a background correction.

## IPA Background

This function may be subtracted from all samples. The value is established as the mean of the first five background values collected via the Self-Normalization and Calibration (SNC) protocol.

$$\overline{\text{BKG}}_{\text{IPA}} = \sum_1^5 \text{BKG}_i$$

## Low Count Reject (LCR)

This is a means of rejecting and flagging samples if nuclide activity does not meet a minimum specified criterion within the first 30 seconds of a sample count.

## LUM (% Luminescence)

This value represents the % luminescence of a sample and is calculated as follows:

$$\text{LUM} = \frac{\text{chance coincidence events}}{\text{true coincidence events}} \times 100$$

## Radioactivity Units

The Curie and the Becquerel represent different units of measure for radioactivity. The Becquerel is the International System (SI) unit of activity.

One Becquerel = One Disintegration Per Second (DPS)

One Curie =  $3.7 \times 10^{10}$  Becquerels

## 2 Sigma % (%2s)

This value represents the percent of uncertainty in a gross count value (with 95% confidence limits). It is calculated as:

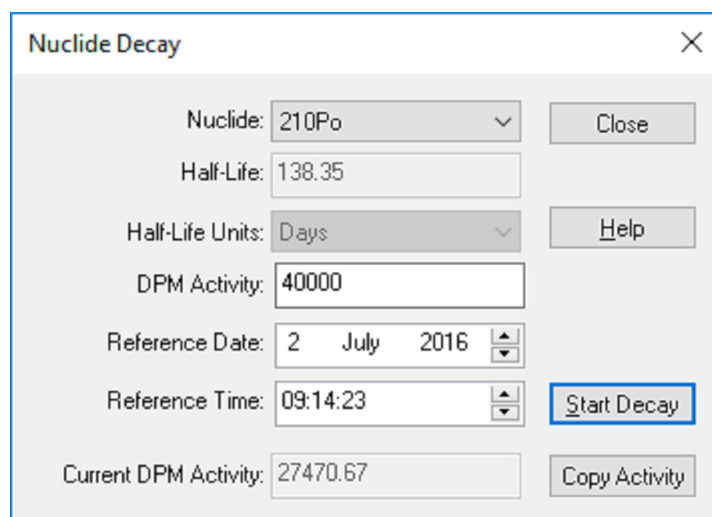
$$\%2s = \frac{200}{\sqrt{\text{accumulated counts}}}$$

The following table indicates the total accumulated counts necessary to achieve the corresponding 2% Sigma:

<b>Uncertainty 2 Sigma %</b>	<b>Total Accumulated Counts</b>
0.4	250,000
0.5	160,000
0.8	62,500
1.0	40,000
1.5	17,778
2.0	10,000
2.5	6400

## Radionuclide Decay Calculator

This calculator (Figure A-1) allows users to calculate the Current DPM Activity for common nuclides. Refer to page 78 for more information about the Radionuclide Decay calculator.



The screenshot shows a software window titled "Nuclide Decay" with a close button (X) in the top right corner. The interface includes several input fields and buttons:

- Nuclide: 210Po (dropdown menu)
- Half-Life: 138.35 (text input)
- Half-Life Units: Days (dropdown menu)
- DPM Activity: 40000 (text input)
- Reference Date: 2 July 2016 (date picker)
- Reference Time: 09:14:23 (time picker)
- Current DPM Activity: 27470.67 (text input)

Buttons include "Close", "Help", "Start Decay" (highlighted with a blue border), and "Copy Activity".

Figure A-1. Radionuclide Decay Calculator.

## % Reference (% Ref)

This value represents the percent of a reference standard, and is calculated using the CPM of the unknown sample and reference standard. The reference standard is typically the first vial counted in the assay, unless used to measure background. In this case, the second vial is used as the reference standard.

$$\% \text{Ref} = \frac{\text{CPM}_{\text{sample}}}{\text{CPM}_{\text{reference}}} \times 100$$



## Appendix B

### Glossary

#### **2S%**

This value represents the percent of uncertainty in a gross count value.

#### **Acquisition Time**

This represents the amount of time a sample has been counting.

#### **Automatic Efficiency Correction (AEC)**

Used to adjust counting region settings to compensate for the effect of quenching on a sample spectrum.

#### **Background Radiation**

This includes environmental radiation (e.g. cosmic rays from space), and radionuclides present in metals, glasses, ceramics and concrete.

#### **Becquerel (Bq)**

An International System of Units basic unit of radioactivity.

- One Becquerel = One Disintegration Per Second
- One Curie =  $3.7 \times 10^{10}$  Becquerels

The calculation for Bq is (DPM for nuclide 1, 2, or 3)/(60DPM/Bq).

- For uCi =  $\text{DPM}(\text{nuclide 1, 2, or 3}) / (2.22 \times 10^6 \text{ DPM/ uCi})$
- For pCi =  $\text{DPM}(\text{nuclide 1, 2, or 3}) / (2.22 \text{ DPM/pCi})$

### **Block Data Items**

Comprised of several data items, these are used to define reports - typically, in printing reports. By selecting certain Block Data items, the instrument can create reports including instrument, protocol, spectrum, or performance (IPA) information. For more information, refer to page 132.

### **Calibration**

This a process by which voltage applied to each Photomultiplier Tube (PMT) in a liquid scintillation counter is adjusted until the tubes are synchronized in their standard response. This is designed to assure that the instrument accurately quantifies the energy from all beta-particle emissions. For more information, refer to Chapter 6.

### **Cassettes**

These are plastic racks that hold sample vials, and allow them to be moved on the sample changer deck.

### **Chemical Quenching**

This is the reduction in scintillation intensity detected by PMTs of a liquid scintillation counter due to materials present in the scintillation solution that interfere with processes leading to light production. The result is fewer photons per keV of beta particle energy, and usually a reduction in counting efficiency.

### **Chemiluminescence**

This involves random single photon events generated as a result of chemical interaction of sample components. The coincidence circuit used in the Tri-Carb instrument excludes most chemiluminescent events, except when they occur at high rates.

### **Chi-Square Test**

This is a general procedure for determining a probability that two different distributions are samples of the same population. In scintillation counting, this test is often used to compare observed variations in repeat counts of a radioactive sample with variations predicted by statistical theory.

### **Cocktail**

This is a solution in which samples are placed for measurement in a liquid scintillation counter. Solvents and scintillators are the major components of a scintillation cocktail.

**Coincidence**

This refers to a system using a special circuit which rejects pulses not received from the scintillation counter's two PMTs within a specified coincidence time. If scintillation events occur "in coincidence" (both events must occur within the specified coincidence time), these events are considered true decay events from the sample. If not, they are considered random (background) and are not counted.

**Coincidence Time**

This is the time (10–200 nanoseconds) during which both PMTs must detect scintillation events. If scintillation events occur in coincidence (both events must occur within the specified coincidence time), these events are considered true decay events from a sample. If not, they are considered random (background) and not counted. Use the default of 18 for most cases. When using solid scintillators, this value may be increased to an empirically determined value.

**Color Quenching**

This is the reduction in scintillation intensity seen by PMTs of a liquid scintillation counter due to colored materials in a scintillation solution that interfere with light detection. The result is fewer photons per keV of beta particle energy, and usually a reduction in counting efficiency.

**Counts Per Minute (CPM)**

This is an expression of radionuclide activity. The gross counts *per channel* cumulatively equal the counts per region; the gross counts *per counting region* are divided by the count time to calculate CPM for each region.

**Curie (Ci)**

This is a basic unit of radioactivity named for Marie and Pierre Curie, who co-discovered Radium in 1898.

- One Curie =  $3.7 \times 10^{10}$  Becquerels
- One Becquerel = One Disintegration Per Second

**Decay, radioactive**

This is the spontaneous transformation of one nuclide into another, or into a different energy state of the same nuclide. This process results in a decrease over time of the number of original radioactive atoms in a sample, and the emission from a nucleus of alpha/beta particles, gamma rays, or the nuclear capture or ejection of orbital electrons (fission). Also called radioactive disintegration.

**Delay Before Burst**

This is the length of time (75–800 nanoseconds) after an initial pulse (prompt pulse) that the detector looks for additional pulses (afterpulses). Afterpulses, which occur after the prompt pulse and delay time interval, indicate that a scintillation event is due to background. Some scintillators, such as PerkinElmer Ultima Gold, produce slower decaying pulses that may require longer delay times. When using these scintillators, it is advisable to lengthen delay times to retain high counting efficiencies. This is vital when counting high energy beta-emitting nuclides. The default setting for this parameter is 75.

**Delimited Text File**

This checkbox is located on the **Report Output** tab (page 134) of the *Assay Definition* window. Select this checkbox to create a delimited text; delimited text is a file format in which each data item is separated by a defined delimiting character. This is a common format for transferring data between applications as database systems can import and export this file type.



*Note: The field delimiter is defined by the Windows O/S using the Regional and Language Options window accessed from Windows Control Panel. Once the Regional and Language Options window is opened, click the **Customize** button and access the **List Separator** field on the **Numbers** tab.*

**Detector**

This is a device sensitive to radiation, and can produce a response signal suitable for measurement or analysis. In a liquid scintillation counter, this device measures the light emitted from the interaction between a scintillation cocktail, and an alpha-emitting or beta-emitting nuclide.

**Discriminator**

This is an electronic circuit that distinguishes signal pulses by pulse height or voltage. A discriminator is used to exclude extraneous radiation counts or background radiation, and is the basis for pulse height analysis.

**Disintegrations per Minute (DPM)**

An expression of radionuclide activity. DPM are calculated as follows:

$$\text{DPM} = \frac{\text{Counts Per Minute}}{\text{Efficiency}}$$

**Dual Label**

This refers to a sample that contains two different radionuclides.

**Efficiency**

This is the ratio of measured counts to the number of decay events that occur during a measurement interval. Efficiency is usually expressed as a percentage.

**External Standard**

This is a radioactive source placed next to a sample to produce scintillation to monitor the sample's quench level. The Tri-Carb instrument uses a Barium-133 source for this purpose.

**Figure of Merit**

This is a term applied to a numerical value used to characterize the performance of a system.

**Flags, protocol**

These are numbered, plastic devices with encoded, reflective metal that the instrument uses to identify appropriate assay counting parameters for a set of samples. Physically place an appropriately numbered flag on the first vial cassette of a group to identify the protocol that associates the desired assay parameters. See Figure 1-3 on page 7 for an example of a protocol flag placed on a cassette.

**GCT (Guard Compensation Technology)**

This is a technique used to reduce backgrounds in the beta spectrum via efficiency calculations applied to events detected in the Guard via the following settings:

- “High” - Best suited for removing a maximum number of background events in the lowest energy channels, i.e. - 3H region
- “Low” (default) - A less aggressive setting for background reductions over a wider range of energy channels.
- “Off” - no GCT background correction.

“Normal” count mode must be selected when GCT is applied.

**Half-Life**

This is the time in which one-half (50%) of the atoms in a radioactive substance disintegrate to another nuclear form.

**IPA (Instrument Performance Assessment)**

This is a process by which a Tri-Carb instrument measures background, counting efficiency, sensitivity (Figure of Merit), and the reproducibility of sample counting (Chi-Square test). For more information, refer to Chapter 6.

**Isotope**

This refers to atoms of the same element with the same atomic number, but different atomic weights.

**keV (kiloelectron Volt)**

One thousand electron volts; used to express energy associated with radioactive decay.

**Library**

In the QuantaSmart program, this is a repository of data regarding sample nuclides or standards. For more information, refer to Chapter 5.

**Luminescence**

This is a general term applied to light emissions (in photons) that cannot be attributed to sample radioactivity. Luminescence is typically due to a chemical reaction between the sample and emulsifier (detergent) containing cocktails, and often caused by alkaline pH and peroxides in a sample.

**Normalization**

This is a process used to establish a lower limit of quench measurement. For more information, refer to Chapter 6.

**Nuclide**

A general term applicable to all isotopes (stable and radioactive) of all elements. Frequently, the term “isotope” is incorrectly used to mean “nuclide.”

**Photomultiplier Tube (PMT)**

A device capable of converting low levels of light into electrical energy (photoelectrons). Photoelectrons generated in a PMT are multiplied to facilitate their detection.

**Photon**

In the quantum theory of electromagnetic radiation, light is emitted as discrete units of energy called photons.

**Priostat**

A set of capabilities on the Tri-Carb instrument that allow for the interruption of a current protocol in order to count a set of high priority samples, or perform specialized counting functions. For more information, refer to page 192.

**Pulse**

An electrical signal resulting when photons are detected by a PMT.

**Pulse Amplitude Comparison (PAC)**

A technique to reduce background often caused by PMT crosstalk. Pulses generated by true sample events will be very close in amplitude. However, scintillations in PMTs will vary widely due to the distance that light must travel to be detected by an opposing PMT. To eliminate these crosstalk events, the PAC circuit compares the amplitude of coincident event pulses detected by sample PMTs. PAC levels range from 0 - 255, whereas 0 (zero) allows all coincident pulses to be accepted, and 255 rejects pulses with a greater than 20% difference in left and right pulse amplitudes.

**Pulse Shape Analysis (PSA)**

A technique by which nuclide pulses are sorted into separate multichannel analyzers for analysis and quantitation. PSA relies on differences in pulse duration to classify radioactive emission types (alpha, beta, gamma) from a nuclide.

**Quench**

A reduction in scintillation intensity seen by PMTs of a liquid scintillation counter from materials in a scintillation solution that interfere with processes leading to light production or detection. The result is fewer photons per keV of beta particle energy, and often a reduction in counting efficiency.

**Quench Curve**

A mathematical graph which correlates counting efficiency to a Quench Indicating Parameter (QIP). A QIP sample is determined during sample counting. This value is used to interpolate counting efficiency for quench curve samples (where %Efficiency is plotted vs. the QIP). The interpolated efficiency value is used to calculate DPM (where  $DPM = CPM / Efficiency$ ).

**Quench Indicating Parameter (QIP)**

A numerical value used to express a sample quench level (SIS, tSIE).

**Reference Date**

The date on which a radio-labeled material has the specified amount of activity.

**Reference Time**

The time at which a radio-labeled material has the specified amount of activity. Typically, this parameter is described only for radionuclides with brief half-lives.

**Region**

The range of energy over which counts are measured for a nuclide in a liquid scintillation counter. Also referred to as a window or channel.

**Replay**

A feature available on the Tri-Carb instrument that allows reanalysis of previously collected data under various data reduction conditions, without recounting samples. For more information, refer to page 209.

### Rich Text Format (RTF)

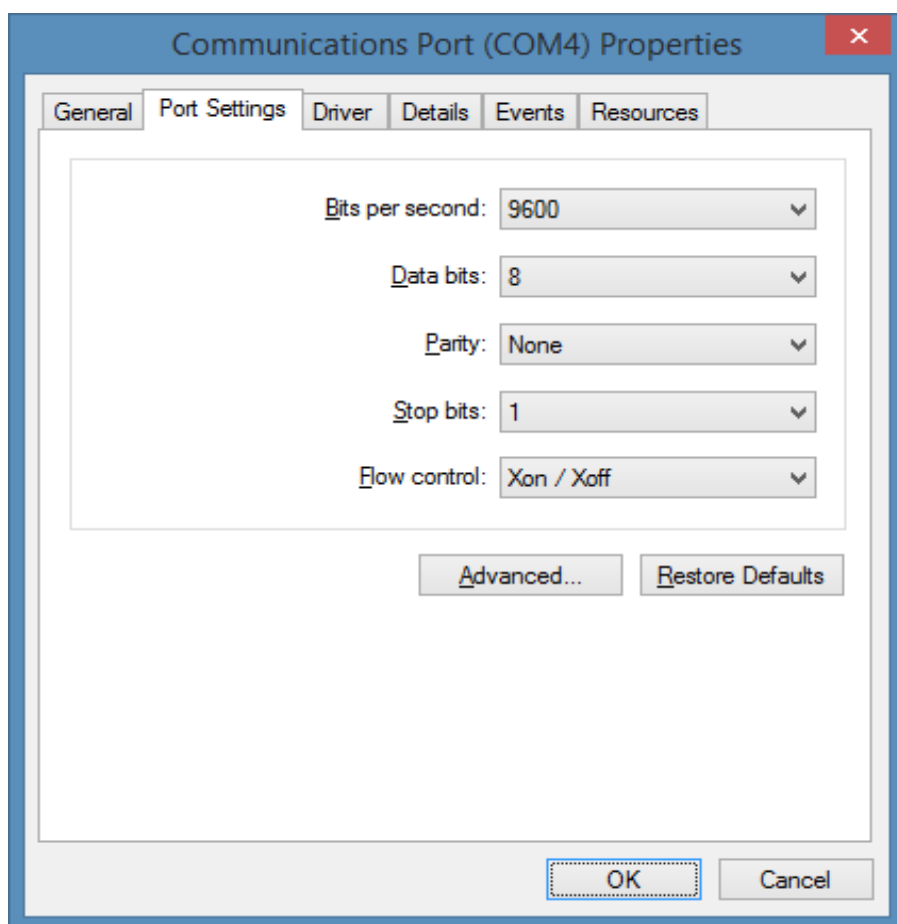
A common ASCII file type with special commands that specify document formatting information, such as fonts and margins. This output type is useful to bring data into a word processing software to perform additional formatting for formal reports.

### RS-232

A standard interface for connecting serial devices to a computer; a USB to RS-232 converter must be used. The default port for RS-232 communications is COM1. A different port may be used by modifying the following registry key:

```
HKEY_LOCAL_MACHINE\SOFTWARE\PACKARD\QuantaSmart (TM)\  
Settings\RS232PortName
```

Serial communications port settings are specified in the Device Manager dialog for the communications port:





**Sample List Library**

A function available in the Worklist portion of the QuantaSmart program, this is used to create a Sample List Library of frequently used sample names. For more information, refer to page 144.

**Scintillation**

A flash of light produced in a scintillator by an ionizing event. A scintillation is the sum of all photons produced by a decay event.

**Shielding**

A process used to reduce the amount of ionizing radiation that reaches a physical area via a shield (lead, tungsten).

**Single Photon Counting (SPC)**

A method used on the Tri-Carb instrument for counting luminescent samples, using only one Photomultiplier Tube (PMT).

**Specific Activity**

The quantity of radioactivity per unit mass (e.g. DPM/g or Ci/g).

**Spectral Index of the Sample (SIS)**

A number obtained from the spectrum analyzer of a liquid scintillation counter calculated from the sample's spectral distribution; this is used as an index for quench levels in a sample.

**Spectral Mapping**

A technique used during single-label DPM sample counting for displaying a sample and quench standards spectra in a three-dimensional view.

**SpectraView**

A window in the QuantaSmart program that displays a two-dimensional, real-time view of a current sample spectrum. For more information, refer to page 55.

**Spectrum Unfolding**

A technique that separates a composite spectrum of a dual-label sample into individual components.

**Spillover**

A term used to describe the situation in dual-label counting where a portion of a spectrum from one radionuclide is included in a region used to count the other radionuclide.

**Static**

Refers to the accumulation of electric charge on an insulated body, such as a scintillation vial. In liquid scintillation counting, a discharge of static may result in spurious pulses from the PMT.

**Tandem Processing**

A process allowing a Tri-Carb instrument to pass data from a protocol to an application program.

**Time Resolved Liquid Scintillation Counting (TR-LSC)**

A process patented by PerkinElmer, Inc., for detection of low level background counts resulting in enhanced sensitivity through the discrimination of true beta from background counts.

**Transformed Spectral Index of the External Standard (tSIE)**

A number obtained from the spectrum analyzer of a liquid scintillation counter calculated from a spectral distribution of external standards, and used as an index for quench levels in a sample.

**Worklist**

A function in the QuantaSmart program used to designate Positive Identification numbers and sample names corresponding to sample numbers on a printout. For more information, refer to page 144.

# Appendix C

## Theory

This appendix contains supplementary information on the theory of the Low Level Counting mode and Alpha/Beta Counting mode (page 270).

## Low Level Counting Theory

In liquid scintillation counting, the limit of detectability is a function of detection efficiency and background noise. By increasing the efficiency of detection, reducing the background (or both) the sensitivity is enhanced. This enhanced sensitivity yields lower limits of detection. In practical terms, this means accurate measurements occur in less time with smaller samples. This is essential when measuring environmental samples for radioactive contamination from nuclear power plants, dump sites, and naturally occurring radiation.

In radiocarbon age dating, to determine the age of archaeological artifacts, only the smallest sample may be spared for measurement without damaging a specimen. In medicine and biomedical research, improved sensitivity facilitates the use of less test substances to determine metabolic pathways.

Most approaches to background reduction employ huge amounts of heavy lead shielding, expensive secondary detection circuits or both. Such systems are very expensive, and due to their design, have very limited utility beyond low level counting. In 1985, however, Packard Instrument Company developed the first electronic burst counting circuitry used in a commercial liquid scintillation counting system. This patented development is the basis of Time Resolved Liquid Scintillation Counting (TR-LSC) in PerkinElmer Tri-Carb liquid scintillation analyzers. In the Tri-Carb Model GCT 6220 analyzer, the burst counting circuitry is further enhanced through the use of a slow scintillating, Bismuth-Germanium Oxide (BGO) detector guard, yielding even higher sensitivity.

Also, PerkinElmer recently released a background reduction method called Guard Compensation Technology (GCT). This patent pending development enhances the action of the BGO crystal to provide, in many cases, lower background levels than TR-LSC while maintaining higher efficiencies.



*Note:      Replay can be used to change GCT values after a run has been acquired.*

---

## Guard Compensation

“Guard Compensation” is a mathematical method which calculates the number of environmental background events that were not blocked or detected by a guard, and then uses this information to reduce sample background counts accordingly.

Guard Compensation Technology (GCT) determines the number of environmental background events which pass through the BGO guard undetected, and then produce scintillation events in the sample. GCT then uses this information to reduce (in real time) sample background counts caused by the environment.

The patent pending GCT process works as follows:

The ability of a BGO guard to detect background events from the environment is measured at our factory. These measurements are stored, and later used to calculate a set of guard efficiencies.

When a customer sample is analyzed, environmental background events are stored in parallel with sample decay events, and using previously measured guard efficiencies, the instrument calculates the number of background events that passed through the BGO guard undetected. The background events which were missed are then subtracted from the sample measurements in real time.

In scintillation counting, if a detector’s efficiency is known, the number of events can be calculated using the equation:

$$\text{ACTUAL EVENTS} = \text{DETECTED EVENTS} / \text{EFFICIENCY}$$

When an unknown sample is counted, the actual number of environmental background events is calculated using the first equation above. The total events the guard missed can then be calculated (ACTUAL – DETECTED) and subtracted from beta sample counts.

Finally, GCT has a tendency of working better than TR-LSC Low Level count mode when plastic or Teflon vials are used.

## Burst Counting

TR-LSC burst counting circuitry uses a background discrimination technique that differentiates aspects of Beta scintillation pulses from non-quenchable background scintillation pulses. A typical Beta scintillation event is composed of at least two components as a function of time. There is a fast (or prompt) component due to the fluorescence of scintillator(s), and a slower (or delayed) component due to the destruction of triplet excited molecules (200–900 nanoseconds). The slow component is present only in the absence of quenching agents (oxygen). When oxygen or other quenching agents exist in a sample (the most common case for routine lab samples), the slow component is reduced. This means that in routine samples prepared in ambient lab air, there is little or no slow component or afterpulses from the sample itself.

TR-LSC increases counting sensitivity by reducing the non-quenchable component of instrument background caused by interaction of high energy cosmic radiation with the sample vial and Photomultiplier (PMT) glass face. Other non-quenchable background interferences including PMT afterpulsing and natural radiation in the PMT and vial construction materials are also reduced by TR-LSC. Approximately 68% of the observed total background is non-quenchable, and can be greatly reduced by this technique.

Non-quenchable background events can be distinguished from true beta events since they are characterized by a series of low amplitude afterpulses that follow the initial prompt pulse. True scintillation pulses have fewer afterpulses associated with them. The figures below show a graphical representation of a background pulse and Tritium Beta pulse. Note that the background pulse has more prominent afterpulse characteristics that extend over time.

TR-LSC is designed to evaluate each event for afterpulses as one criteria to reduce background. When a series of afterpulses is detected, TR-LSC characterizes the event as background and rejects it. The efficacy of this rejection can be increased when a BGO detector guard is used in conjunction with TR-LSC electronics. The BGO guard completely surrounds the sample vial and acts as a cosmic guard to further increase afterpulse rejection, thus reducing the background.

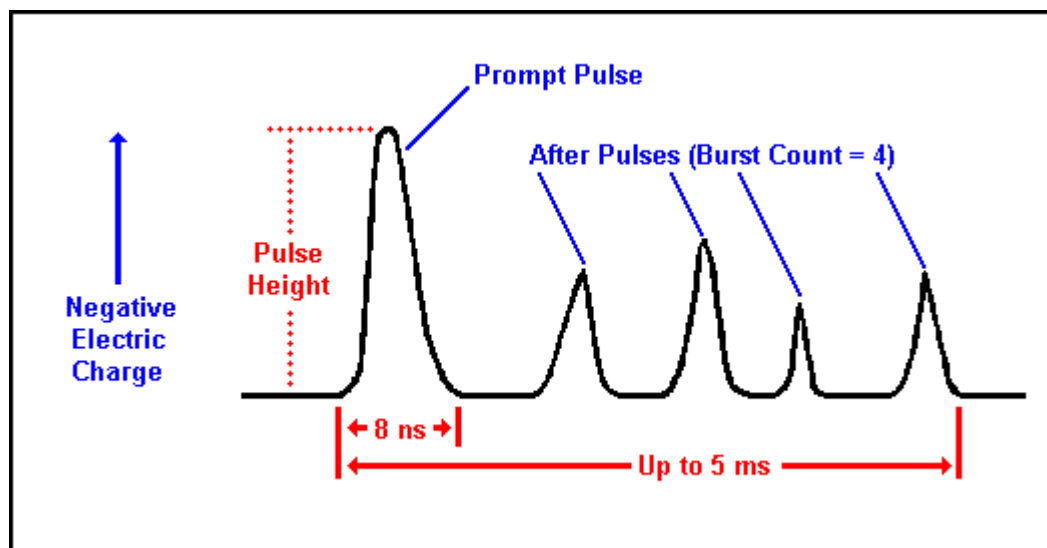


Figure C-1. Liquid Scintillation Background Pulse.

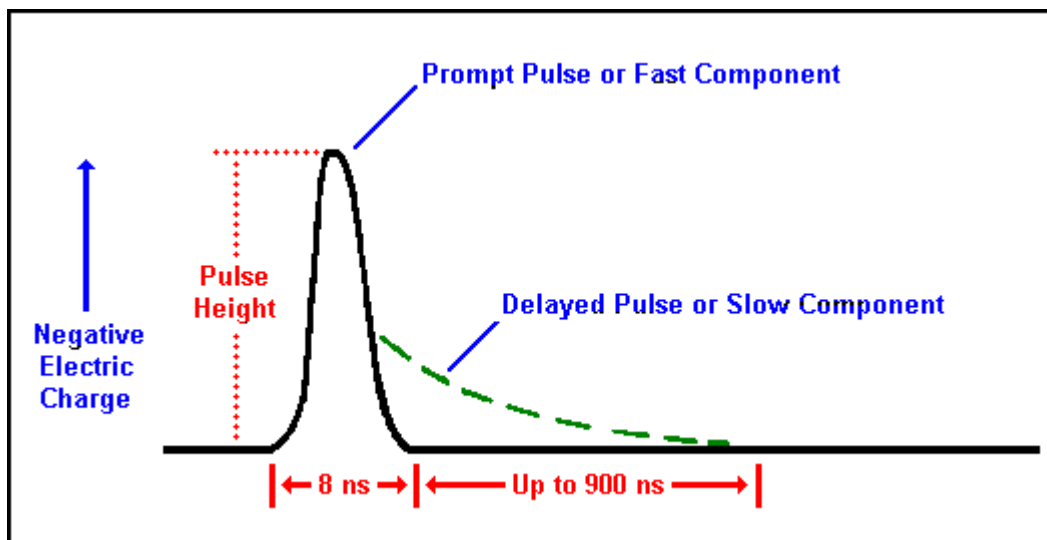


Figure C-2. Liquid Scintillation True Beta Pulse.

TR-LSC can be optimized for the latest generation of safer cocktail formulations, and higher energy beta emitters. This is accomplished through the instrument software by modifying the Delay Before Burst parameter on the Count Corrections tab in Assay Definition. The Delay Before Burst feature functions by implementing a time delay before afterpulse discrimination is enabled. This is necessary because:

- Scintillation cocktails with solvents based on di-isopropyl naphthalene (DIN) and 1-phenylxylylethane (PXE) have long scintillation decay constants (i.e. they produce light pulses of longer duration).
- Higher energy beta emitters produce longer duration pulses.

These phenomena must be considered to minimize the misclassification of beta and background events, as the longer duration pulses arising from these conditions mimic background pulses, and may be eliminated by TR-LSC. By increasing the time delay before afterpulse discrimination begins, counting efficiency losses are minimized and sensitivity is increased.



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## High Sensitivity and Low Level Counting

In the PerkinElmer Tri-Carb series of liquid scintillation analyzers, the patented TR-LSC burst counting circuitry totals the number of afterpulses following a coincident event. This information is used to discriminate background pulses from pulses arising from actual scintillation events in the sample. Thresholds have been established, and are used to reject events producing significant numbers of afterpulses. Thresholds vary with the energy of coincident pulses due to afterpulsing phenomena in PMT tubes. As PMTs can produce energy-dependent afterpulses, this must be factored into background noise discrimination from sample activity.

The PerkinElmer Tri-Carb series liquid scintillation analyzers use this time-resolved discrimination of afterpulses at three levels. These levels are:

- **Normal Count Mode** – This mode employs a minimum amount of discrimination.
- **High Sensitivity Count Mode (HSCM)** – This mode applies an intermediate amount of discrimination.
- **Low Level Count Mode (LLCM)** – This mode provides maximum discrimination.

Progressing from NCM to LLCM yields increasing efficiency to background ratios ( $E^2/B$ ). The improvement is demonstrated in the table of  $^{14}\text{C}$  data (page 266).

PerkinElmer also offers the Tri-Carb Model Quantulus GCT 6220 analyzer, which achieves super low level sensitivity through use of a slow scintillating BGO detector guard. In the Quantulus GCT 6220 analyzer, this special material surrounds the sample as a special detector assembly to further increase the number of photons in the trailing burst from background radiation. The detector assembly replaces the conventional sample changer, and provides a considerable increase in  $E^2/B$  performance compared to the burst counting system alone. This configuration is referred to as the Super Low Level Count Mode (SLLCM).

For environmental water samples, it is often necessary to count as much water as possible as amounts of Tritium found are extremely low, and larger volumes permit shorter counting times. Typical water samples are made using from 9 - 12mL of water in a total volume of 20 - 22mL.

Radiocarbon dating samples are often made of pure benzene from the conversion of raw samples through a benzene synthesis procedure. Such samples are generally only 3 - 5mL total volume. Comparative data is shown in the tables for  $^{14}\text{C}$  samples and Tritium water samples (page 266).

**Example of  $^{14}\text{C}$  in Benzene Sample Performance**

TR-LSC Count Mode	Sample Configuration	Energy (keV)	$^{14}\text{C}$ % Efficiency	BKG CPM	E <sup>2</sup> /B Ratio
None	Sample Only	20.0-113.0	64.99	3.62	1167
NCM	Sample Only	20.5-101.5	64.03	3.28	1250
HSCM	Sample Only	21.5-95.5	61.22	1.36	2756
LLCM	Sample Only	19.5-95.5	54.05	0.76	3844
LLCM (SLLCM)	Sample+BGO Detector	10.0-75.0	70.70	0.54	9256



*Note: The samples were  $^{14}\text{C}$  toluene in benzene cocktail (PPO 6 grams/liter POPOP 0.2 grams/liter). Total sample volume was 3.5mL in standard low 40K 7mL vials, prewashed with 0.1M EDTA, and Teflon cap liners were used.*

**Example of Large Volume Tritium in Water**

TR-LSC Count Mode	Sample Configuration	Energy (keV)	$^3\text{H}$ % Efficiency	BKG CPM	E <sup>2</sup> /B Ratio
None	Sample Only	0.0-18.6	34.2	22.3	52
NCM	Sample Only	0.0-18.6	33.8	17.8	64
HSCM	Sample Only	0.0-18.6	33.9	12.8	90
LLCM	Sample Only	0.0-18.6	29.4	6.2	139
LLCM (SLLCM)	Sample+BGO Detector	0.0-18.6	26.7	2.8	255

### Burst Discrimination Modes

TR-LSC Count Mode	Burst Discrimination Modes
None	Equivalent to conventional LSC systems.
NCM	Minimum or Normal Count Mode.
HSCM	Intermediate or Low Activity, High Sensitivity Count Mode.
LLCM	Maximum or Ultra Low Level Count Mode

Lab performance will depend on various factors. First, in counting environmental water, sources for background samples must be free of contamination by radionuclides (especially Tritium). When counting very low Tritium levels, even the smallest contamination will increase a background sample count rate. This cannot be discriminated out as the contamination is from the sample itself. Therefore, it is necessary to secure a “dead” water source (in terms of radioactivity) for background samples.

For radiocarbon dating samples, ensure that reagents used during sample preparation are free from contaminating  $^{14}\text{C}$ . This includes the actual scintillators and any reagents used to convert the sample into benzene.

Overall, preparation of samples for extremely low level counting must be conducted with extreme care to provide contamination free samples for counting. If background or unknown samples contain extraneous radionuclide sources, performance will be degraded.

In Super Low Level counting, as in other low level count modes, it is important to tailor the scintillation fluor (scintillator) to the counting conditions. Secondary scintillators (BBOT, DPA, POPOP, Me2POPOP, and bis-MSB) produce significantly higher counting efficiencies than are possible with only a primary scintillator.

Although there are many potential combinations of primary and secondary scintillators suitable for use with the TR-LSC, a combination of six grams per liter PPO and 0.2 grams per liter bis-MSB works well for many sample types, and can be used reliably. This is a commonly used combination of scintillators for a variety of counting applications.

## Operational Considerations

The operating procedures for the Tri-Carb Quantulus GCT 6220 liquid scintillation analyzer are described in this documentation. Aside from count rate limitations and differences in the SNC/IPA procedures, operation of the Quantulus GCT 6220 analyzer is exactly the same as other Tri-Carb analyzers.

The selection of counting vials for low level counting is essential to assure low background and high sample counting sensitivity. Low potassium (K) glass vials are recommended when counting low levels of Tritium or  $^{14}\text{C}$ . Certain plastic vials may also be used for large or small samples measuring Tritium in water.

It is recommended that all glass or plastic vials used for low level counting be carefully sealed. Teflon cap liners for vial screw caps improve seals against leakage.

Glass vials should be washed, then rinsed in a dilute ethylene-diamine-tetraacetic acid (EDTA) solution, followed by a “dead” deionized water rinse and allowed to air dry. This will help reduce background and surface contaminants which could contaminate the detector guard.

Maximum vial dimensions are as follows:


- **Small vials** - Must not exceed 17.8mm diameter and 58.0mm height (including cap)
- **Large vials** - Must not exceed 28.1mm diameter and 63.0mm height (including cap).


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## High Sensitivity/Low Level Count Mode Setup

When operating the system in the High Sensitivity or Low Level Count Modes, remember that the maximum sample activity is 100,000 CPM. If a sample exceeds this count rate, the system will automatically switch to Normal Count Mode (GCT, however, will function regardless of the sample count rate). Therefore, when purchasing or making quenched standards or reference standards, this limitation must be observed for proper operation.

When defining a protocol, either the High Sensitivity (HSCM) or Low Level Count Mode (LLCM) must be selected in the Count Conditions window. Selecting LLCM will automatically cause the instrument to operate at that level of afterpulse discrimination. This will enable the TR-LSC background discrimination.

 *Note: The luminescence correction feature is not recommended for use when counting very low CPM samples. For such samples, the Luminescence Correction checkbox in the Count Corrections window should be not be marked.*

 *Note: Do not use High Sensitivity or Low Level Count Modes to count alpha samples in normal CPM or DPM counting assays. These TR-LSC discrimination modes are not appropriate for counting alpha samples. Extremely low alpha count rates will be observed.*

Allow samples to dark adapt before actual count begins. The Tri-Carb analyzer provides sample counting delays up to 99.99 minutes. With a sample counting delay selected, the sample is lowered into the counting chamber, and allowed to dark adapt for the specified delay time before count begins for the indicated counting time. The Pre-Count Delay is selected in the Count Conditions window and is specific for the assay.

## Precautions and Limitations

Note that background radiation varies throughout the world, and will be a factor when determining the instrument background. Higher elevations and areas where geology tends to concentrate uranium, and its decay products will most likely yield higher backgrounds. The exact instrument background and performance for a given location must be determined at the site of the installation.

## Alpha/Beta Counting Theory

Alpha and Beta emitting radionuclides may be counted simultaneously in the same liquid scintillation sample. Some Alpha and Beta nuclide energies may overlap in an LSC environment, and their spectra are not resolvable with simple energy discrimination. To separate Alpha and Beta nuclide energies, take advantage of their differing pulse decay times. The Pulse Shape Analysis (PSA) method of discrimination is used by Tri-Carb instruments equipped with Alpha/Beta capability.

## Alpha/Beta Discriminations Using PSA

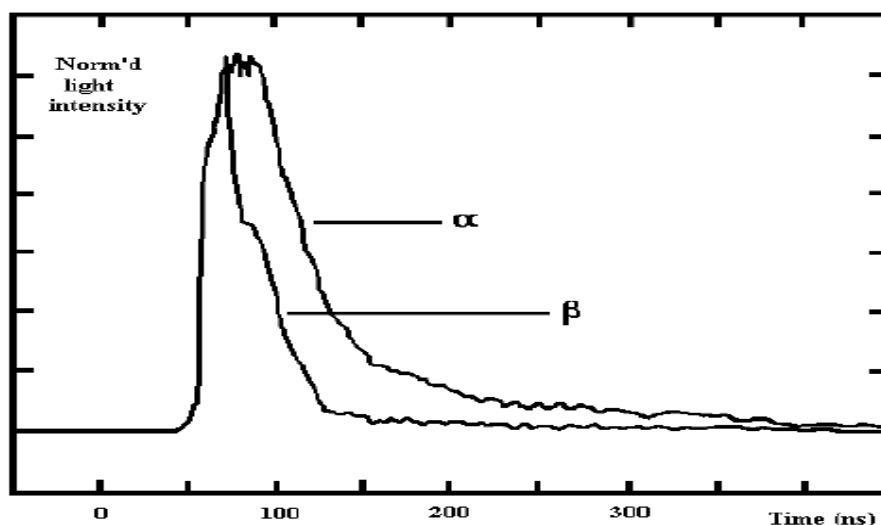
### Physical Background

Alpha particles emit 5 MeV (or more) energy able to create triplet states in a solvent which de-excite to a ground state slower than singlet states produced by Beta particles.

Measurement of pulse decay time (or length) allows identification of the particle which caused it, and enables simultaneous recording of pure Alpha and Beta spectra, respectively. Pulse length also depends on the solvent and fluors used such as fast cocktails containing volatile solvents (e.g. xylene, pseudocumene, toluene, and dioxane). Safe, biodegradable cocktails are slow as those based on diisopropylnaphthalene (DIN).

### PSA Principle

This principle integrates the pulse tail for long enough time to enable differentiation between short and long pulses (see figure below), and normalize pulse length information to pulse height to achieve amplitude independence.



**Figure C-3. Pulse Shape Caused by Alpha/Beta Particles.**

The Alpha/Beta pulse amplitude (energy) spectrum is transformed in this process to 3-D counts vs. pulse amplitude and pulse spectrum (see the following two figures). Electronic division of pulses into Alpha and Beta spectra is done by dividing the pulse amplitude/length plane into two parts by a straight, user adjustable line. Pulses above it are directed into the long pulse spectrum; pulses below it into a short pulse spectrum.

When the dividing line is correctly set, the former spectrum is the pure Alpha spectrum, and the latter is the Beta spectrum. The dividing line position is controlled by PSA level adjustment. This feature allows settings to conform with various solvents, fluors, and quench levels.

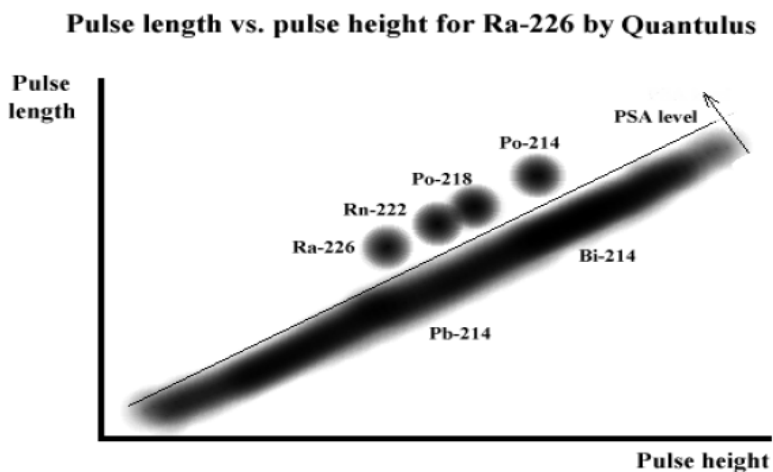


Figure C-4. 3-D Spectrum of Ra-226 vs. Pulse Amplitude (total signal) and Pulse Length (tail signal).

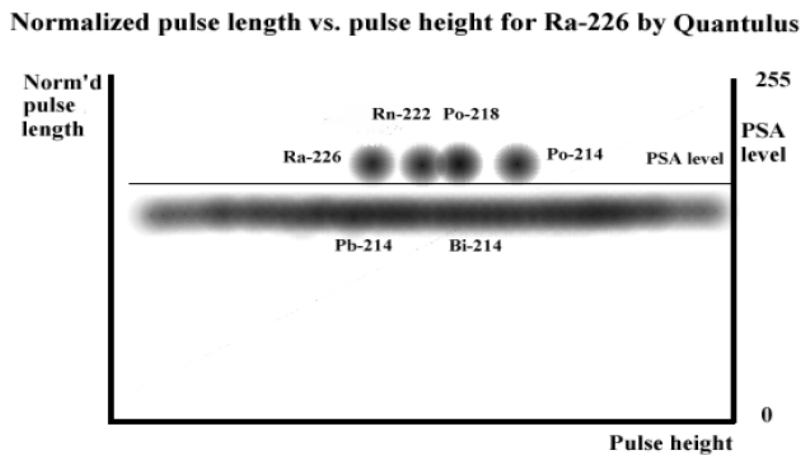


Figure C-5. 3-D Spectrum of Ra-226 vs. Pulse Amplitude and Pulse Length Normalized to Pulse Amplitude.



## Usage of PSA

For Alpha/Beta separation, and extra background reduction in Alpha and Beta counting.

Most LSC background is composed of short pulses, and falls into the Beta spectrum while Alpha background typically remains very small (much less than 1 CPM). Therefore, users may count natural decay series radionuclides with greater sensitivity by measuring Alpha emissions only versus counting total Alpha/Beta activity. Another application is to count very small Alpha activity amidst high Beta activity.

Users may set PSA to cut Beta counting efficiency (e.g. by 5 %), resulting in a great reduction of Beta background particularly in glass vials, further reducing the already low backgrounds achieved by the active anti-coincidence guard detector. Alpha background may be reduced analogously by cutting Alpha counting efficiency.

### Advantages of Alpha Counting by LSC

- 4pi counting geometry (equivalent to geometrical factor = 1)
- No sample self-absorption (e.g. planchet counting)
- 95% counting efficiency (less than 50% in planchet counting and solid state alpha spectrometry)
- Simple sample preparation by mixing with a commercial cocktail
- High throughput - automatic, multiple sample counting
- Large sample capacity
- Simultaneous Alpha/Beta counting (with separation of each spectrum using PSA)
- Low backgrounds and greater sensitivity for Alpha counting

### Pulse Shape Analysis and Quench

- **Pulse Length** - This is a function of sample quench: the higher the quench, the shorter the pulse length. This is a physical phenomenon not introduced by the instrument. When sample quench level is fairly consistent, there is no need to adjust PSA levels between samples (when counting efficiency is constant). If quench variation is large (50 Ch or more), there may be necessary to re-adjust PSA levels for variable quench, or leave PSA levels at the optimum value for the lowest quench sample, and allow Alpha efficiency drop at higher quench. In Quantulus and Tri-Carb, when PSA levels for optimum Alpha/Beta separation are lower, the higher the quench.
- **Counting Efficiency** - Alpha particle counting efficiency remains close to 95% up to very high quench levels, provided that PSA levels are set accordingly. This is due to the number of emitted photons per decay being in the several thousands. Thus, there is room for photon loss, and decay events are still observed. The Alpha spectrum will shift to a lower energy at increasing quench; therefore, the counting window must cover the range of Alpha energies under variable quench.
- **Pulse Shape Analysis and Plastic Vial Effect** - Fast cocktails (e.g. containing toluene, xylene and pseudocumene) will penetrate plastic vial walls resulting in the deterioration of the Alpha spectrum, and instability of Alpha count rates. Plastic vials are not recommended for counting using these cocktails; instead Teflon-coated plastic vials, glass vials, or Teflon vials should be used.

## **Optimum Alpha/Beta Discriminators**

The Alpha/Beta Standards assay is used to determine the optimum discriminators that maximize the Quality Metric for alpha/beta spillover versus efficiency. (See Alpha/Beta Standards Assays (page 109))



## **Appendix D**

### **Sample Type-Specific GCT Optimization Sets**

This appendix contains information on how to improve the performance of GCT through the creation and use of GCT Optimization Sets.

## Overview

PerkinElmer's Guard Compensation Technology (GCT) subtracts background events caused by environmental background radiation while the sample is being counted. The system uses a special detector called a guard to detect the environmental background radiation. When a Quantulus GCT instrument is produced at the factory, a set of GCT guard efficiencies is measured to provide a generic profile of the environmentally caused background events and their contribution to sample backgrounds. These guard efficiencies, in conjunction with the environmental backgrounds detected by the guard while counting a sample, are used to determine the number and energy of environmental background events the guard missed and were counted as sample events. Both the detected and missed background events are then spectrally subtracted from the sample counts in real time.

To accommodate varying environmental conditions and sample formulations, GCT guard efficiencies are subsequently optimized at the installation site. This optimization is accomplished by determining a set of 2 GCT strength factors, Low and High, which can be applied to generate updated GCT guard efficiencies. A background sample matching the customer's typical or most critical low-level sample composition and vial type is counted, and this spectrum is used to generate these 2 optimized GCT strength factors. GCT optimization compensates well for local environmental factors and many normal variations in sample preparation.

A complete "GCT Optimization Set" established at the site is therefore comprised of:

1. The GCT strength factors generated at the installation site which are used with the background spectra to compute the guard efficiencies used for GCT Low and GCT High.
2. Background spectra using the customer-prepared background sample.
3. The guard efficiencies computed for GCT Low and GCT High.

This single GCT Optimization Set will provide excellent results for samples prepared in the same vial material and using products from a similar cocktail family such as the various Ultima Gold products. In many cases, it will also be sufficient for uses with other cocktails and sample preparations.

However, if the GCT strength factor optimization was performed by counting samples prepared with biodegradable scintillation cocktail in a plastic vial, the following variants will likely be significant enough to warrant unique GCT optimizations for these sample types:

- The additional count rate introduced by radioactive impurities in glass vials
- Significant differences in the cocktail type or overall sample matrix

- The reduced background levels in the absence of cocktail when Cherenkov counting


Most low-level counting is performed in plastic vials instead of glass, and low-level Cherenkov counting is not widely used due to the high beta energies required. So these will typically not present the requirement of additional GCT Optimization.

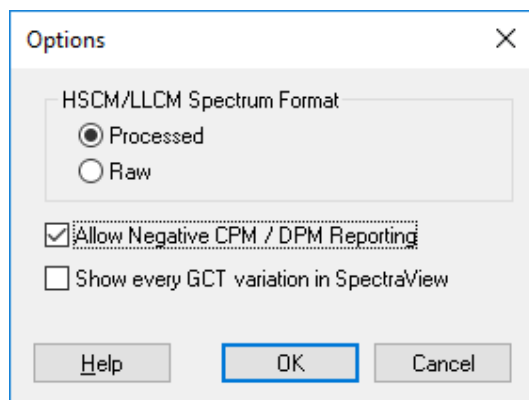
However, the more likely variant is the cocktail formulation. The modern safer, biodegradable cocktails have significantly different chemical composition than the older classical versions. The spectral change observed between different cocktails will vary, so some will be a closer match than others. Therefore, the use of multiple diverse cocktails may require separate GCT Optimization Sets for the best results.

QuantaSmart now allows the user to create multiple sample type-specific GCT Optimization Sets to best accommodate the more significant variants. Once multiple GCT Optimization Sets have been created, the most appropriate GCT Optimization Set may be selected in individual assay definitions.

GCT will provide the best results if the GCT optimizations are generated with a background sample which is not significantly different from the samples being analyzed. When the count rate or spectral shape of the background being subtracted does not adequately match the spectral shape of the unknowns, some channels will potentially subtract more counts as background than were present in the unknown sample. For this reason, the GCT strength factors are generated using an algorithm specifically designed to limit this over-correction possibility. However, if there are significant differences between the sample type used to generate the strength factors and the samples being analyzed, over-correction is more likely to occur.

To help users determine if sample type-specific GCT optimizations are required for their analysis, QuantaSmart has implemented a GCT quality factor check on all samples counted with GCT active. An 'O' reported in the MESSAGES field indicates that over-correction has occurred in the GCT background correction. If this over-correction status is present on unknown samples, it indicates a sample type-specific GCT Optimization may be appropriate.

 *Note: To enable the GCT quality factor in reports, the "Allow Negative CPM / DPM Reporting" must be enabled in the QuantaSmart Tools | Options menu. This setting will apply to all assays.*



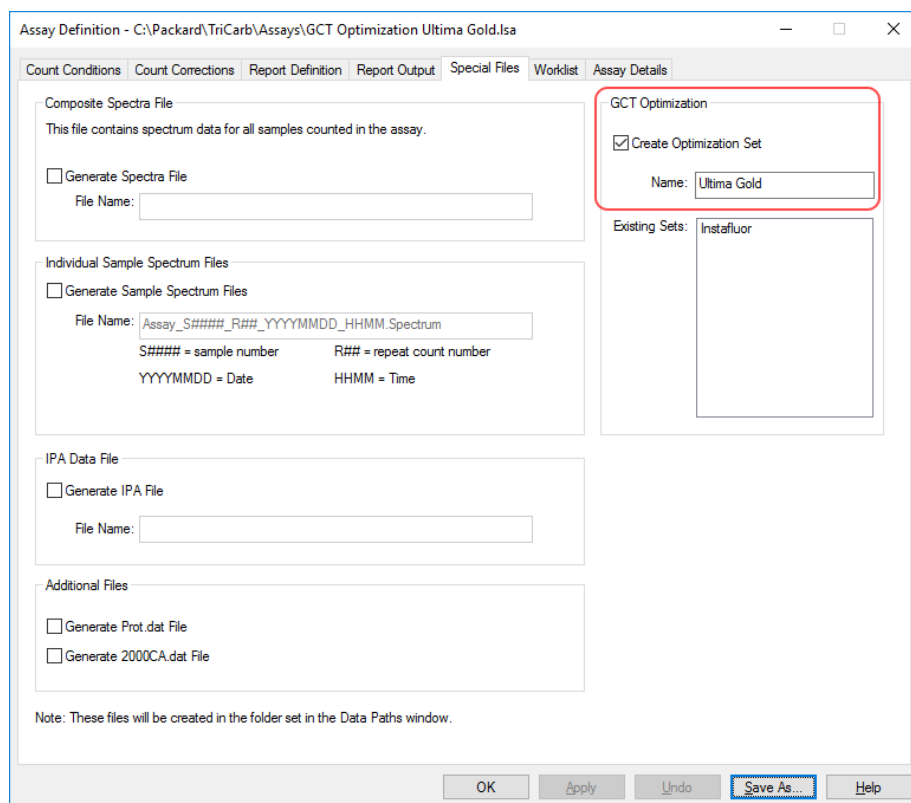
## Comparison of GCT to traditional background sample subtraction

The advantage of using a background sample which matches the unknown samples as closely as possible is not new. Historically, the first vial background subtraction approach has been used effectively for decades to remove the representative background from a series of samples. In this method, a background vial is prepared which matches the composition of the unknown samples. The CPM from this background vial is then subtracted from all unknowns, yielding the net CPM above background. The accuracy of the background subtraction in this method is influenced by the level of similarity between the background vial and the unknown samples. Using a background sample which is significantly different from the unknowns can result in less accurate results, either by subtracting too many counts as background, or not subtracting a representative spectral profile. Similarly, developing GCT Optimization Sets with a matching background sample produces the most accurate results. In both approaches, the match between the background sample and unknown samples is most important when analyzing samples with the lowest levels of activity.



## How to create a GCT Optimization Set

1. Open QuantaSmart
2. Use the menu "File | Open Assay" to open the assay named "Optimize\_GCT\_Strength\_Factors"
3. Use the "Save as" feature to create an assay with a new and descriptive name, such as: Optimize\_GCT\_Strength\_Factors\_UltimaGold".
4. Click on the Special Files tab



- a. Check the box "Create Optimization Set"
  - b. Enter a descriptive name for this optimization set such as the cocktail type.
  - c. A list of existing sets is shown to help pick a unique set name.
  - d. If the name of an existing set is used, the data within that set will be replaced when the assay is counted.
5. NOTES:
- a. A minimum count time of 240 minutes is recommended to acquire sufficient counting statistics.
  - b. This assay must use Normal count mode.

6. Click on "OK" to save the assay
7. Associate the assay created in Step 3 with a protocol flag.
8. Create a background sample that closely matches the sample composition and vial type for this specific GCT Optimization Set.
9. Load the background sample into the first vial position, with no other samples in this cassette. Only one sample should be counted in this assay.
10. Start counting to acquire data using the new GCT optimization assay.

## How to use a GCT Optimization Set

Once the sample type-specific GCT Optimization Set has been created, it may be used in one or more assays to count samples of the same type. To use a specific GCT Optimization Set in an assay:

1. Open the assay
2. Click on the Count Correction tab
3. Select the GCT level, Low or High
4. Select the GCT Optimization set to be used.

Assay Definition - C:\Packard\TriCarb\Assays\14c\_cpm.lsa

Count Conditions | Count Corrections | Report Definition | Report Output | Special Files | Worklist | Assay Details

Special Conditions

Static Controller  
 Luminescence Correction

Coincidence Time (nsec): 18  
 Delay Before Burst (nsec): 75  
 GCT: High  
 GCT Optimization: Ultima Gold  
 Enable PAC   
 Strength: 0  
 Auxiliary Spectrum: TRLSC

Half-life Correction

Apply Half-life Correction  
 Nuclide Group: 14C

	Lower Limit	Upper Limit	Half-life	Units	Reference Date	Reference Time
A	0.0	156.0	5728.49	Years	Start of Assay	Start of Assay
B	4.0	156.0	0.00	Minutes	Start of Assay	Start of Assay
C	0.0	0.0	0.00	Minutes	Start of Assay	Start of Assay

OK Apply Undo Save As... Help

5. Click OK
6. Associate the assay with a protocol clip and place that clip on a the sample cassette
7. Start counting
8. Consult the report generated at the end of the assay for any messages



## **Appendix E**

### **Half-Life Correction**

This appendix features questions and answers on half-life corrections in the QuantaSmart system.

### **When do I use start of assay vs. when do I use manually entered reference date/time?**

The selection of reference date/time depends on which type of assay is using half-life correction. When selecting the date/time, the same method must be used for both date and time. If the assay start is chosen for a reference date, it must also be chosen for the reference time. If a manual reference date is entered, the reference time must also be manual. See the discussion of each assay type for guidance on the correct method for that assay.

### **Why do I use half-life correction in a CPM or DPM assay?**

Half-life correction is typically used for CPM or DPM assays when a nuclide half-life being measured is short versus the time required to measure the sample set. By applying half-life correction, the activity (CPM or DPM) of the samples is easier to compare, as the error associated with half-life decay (which varies for each sample based on its measurement time) has been eliminated.

The reference date/time can be selected as Start of Assay if the user is only interested in a relative comparison of sample activities at the time the assay was started. A manual reference date/time can be selected if the user is interested in comparing the activities at some other time that is more pertinent to their experimental study.

## Why do I use half-life correction in a Quench Standards assay?

For a Quench Standards Assay, half-life correction is used to ensure that the counting efficiencies of quench standards are determined using the correct activity (DPM) of the standards. Quench standards have a known DPM at the time they are prepared. When later measured in a Quench Standards Assay, activity has decreased due to radioactive decay. Half-life correction is used to ensure that the DPM value used in the denominator of the efficiency calculation (CPM / DPM) has taken into account the decay that occurred between the time that the standard was prepared, and the time that it was measured in the Quench Standards Assay.

If half-life correction is not applied, a systematic error is introduced into the efficiencies calculated by the Quench Standards Assay. Those efficiencies are incorrectly low, and when unknown samples are later measured against those efficiencies, the DPM values calculated for the unknown samples are incorrectly high. The magnitude of the error is larger for short half-life nuclides than for long half-life nuclides. To avoid this systematic error, use of half-life correction is recommended for all Quench Standards Assays except those in which the half-life of the standard is long enough that the error caused by ignoring half-life decay is insignificant.

If half-life correction is used for a Quench Standards Assay, when the Quench Standard is defined in the Quench Standards Library, the activity listed on the top of the vial must be entered into the Quench Standards dialog. When the assay is defined, the reference date/time must be entered using the manual entry method (i.e., "Start of Assay" must not be used). The reference date/time are the date/time when the standard was prepared, and is typically printed on top of the vial. However, the time is not always included, unless the half-life standard is extremely short. If the time is not provided, the manually entered reference time can be chosen arbitrarily.

If the half-life correction option is not used for a Quench Standards Assay, then the DPM that is entered when the Quench Standard is defined in the Quench Standards Library must be manually corrected for half-life decay. This can be done by using the Decay Calculator available from the Quench Standards Library dialog. Note that if the half-life correction option is not used for a Quench Standards Assay (and that assay is re-measured), the DPM should be manually corrected, and re-entered into the Quench Standards Library before it is re-measured.

**When would I use half-life correction in both a Quench Standards assay and the DPM assay that uses the results from that Quench Standards assay?**

In general, half-life correction should be used for all Quench Standards assays, as it eliminates the need to manually calculate the half-life corrected DPM of standards before entering them into the Quench Standards Library; it also eliminates the need to re-calculate and re-enter the activity when the assay is re-measured. Half-life correction for a DPM assay is only required if there is interest in comparing sample activity being measured at some specific time.

**When would I use half-life correction in a DPM assay, but not in its corresponding Quench Standards Assay?**

If the nuclide has a sufficiently short half-life that half-life correction is required to compare sample activities in a DPM Assay, then its corresponding Quench Standards Assay should also use half-life correction.



## **Appendix F**

### **Installation of Enhanced Security**

This appendix contains information on installing enhanced security measures for your Tri-Carb instrument.

## Procedure

The Enhanced Security option requires that User Account Control (UAC) is turned off. Prior to installation, please follow these steps:

1. Log in to the instrument as an administrator.
2. Open the command line by pressing the Windows key and “R” - then type “Cmd” and press Enter.
3. Run the group policy editor by typing “gpedit.msc” and press Enter.
4. Navigate through the Local Computer Policy tree via: Computer Configuration > Windows Settings > Security Settings > Local Policies > Security Options.
5. At Security Options, in the right panel, select “User Account Control: Run all administrators in Admin Approval Mode.”
6. Double click on this item, and change the value to Disabled.
7. Close the application, and restart the computer. Enhanced Security measures may now be installed.

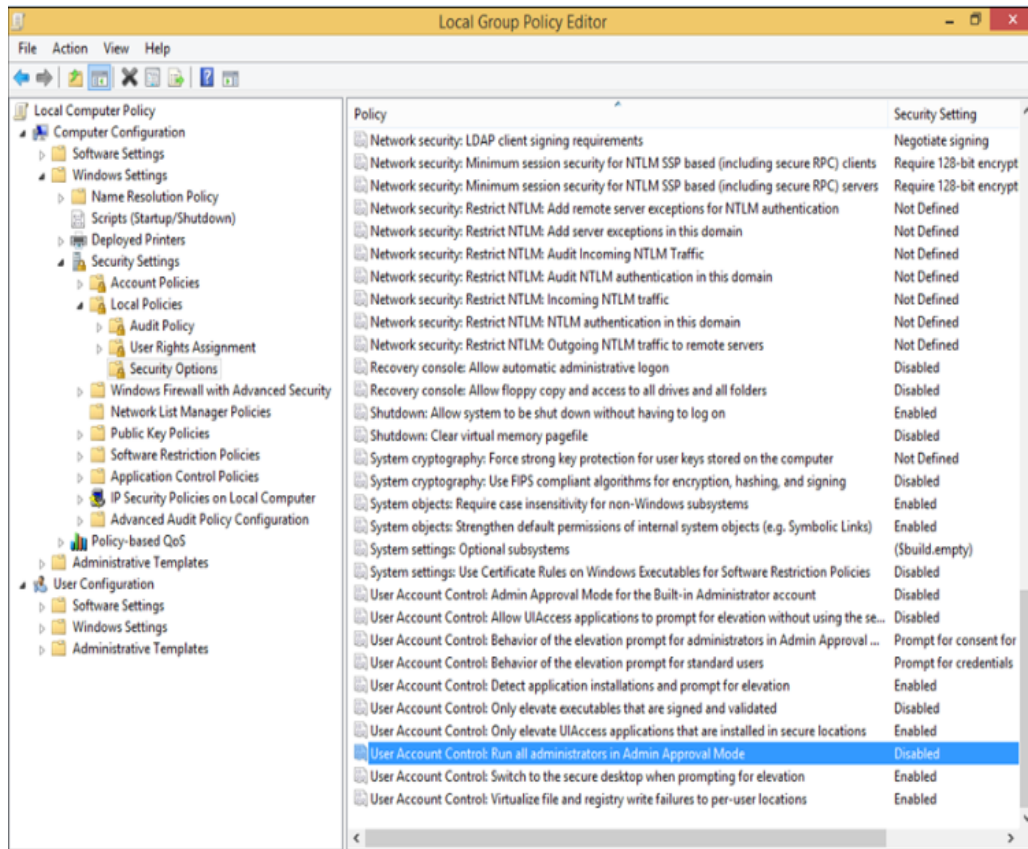


Figure F-1. Local Group Policy Editor.



## **Appendix G**

### **Special Configurations for QuantaSmart**

This appendix describes special configuration files for use with the QuantaSmart system.

## Configurations

The following are special configuration files which enable special configurations for QuantaSmart.

These files can be run by double-clicking on each, and are located in the following directory: c:\packard\tricarb\bin.

- BgoIpaMeasureEveryTimeEnable.reg
  - Run IPA measurement every time a SNC protocol flag is encountered on a BGO instrument. This file has no effect on other instrument models.
- BgoIpaMeasureEveryTimeDisable.reg
  - Run IPA measurement only if 23 hours have elapsed since the last SNC protocol flag on a BGO instrument. This file has no effect on other instrument models.
- IpaPrintToRtfFileEnable.reg
  - At the end of each IPA measurement, create a report in c:\packard\tricarb\ipareults instead of using the printer. The file will have the naming format of IpaResults\_Month\_Day\_Year\_Hour\_Min.rtf
- IpaPrintToRtfFileDisable.reg
  - At the end of each IPA measurement, send a report to the current printer.