

## **Other Test Method 46 (OTM 46) Measurement of Polychlorinated Dibenzo-*p*-Dioxins, Polychlorinated Dibenzofurans, Polychlorinated Biphenyls, and Polycyclic Aromatic Hydrocarbons from Stationary Sources**

### **Background on OTM-46**

The posting of a test method on the Other Test Methods portion of the EMC website is neither an endorsement by EPA regarding the validity of the test method nor a regulatory approval of the test method. The purpose of the Other Test Methods portion of the EMC website is to promote discussion of developing emission measurement methodologies and to provide regulatory agencies, the regulated community, and the public at large with potentially helpful tools. Other Test Methods are test methods which have not yet been subject to the complete Federal rulemaking process. Each of these methods, have been reviewed by the EMC staff and have been found to be potentially useful to the emission measurement community.

The procedures contained in this OTM represent the Agency's current thoughts for consistently sampling, processing, and reporting polychlorinated dibenzo(p)dioxin, dibenzofuran, polycyclic aromatic hydrocarbon and polychlorinated biphenyl emissions from stationary sources of air pollution. OTM methods may be considered for use in federally enforceable State and local programs [e.g., Title V permits, State Implementation Plans (SIP)] provided they are subject to an EPA Regional SIP approval process or permit veto opportunity and public notice with the opportunity for comment. OTMs may also be used to collect data for the purposes of developing or assisting in the development of national standards of performance and national emission standards for hazardous pollutants under sections 111 and/or 112, respectively, of the Clean Air Act as specified in the applicable Information Collection Requests(s) and can be considered for use as alternative methods to meet Federal requirements under 40 CFR Parts 60, 61, and 63. However, an OTM must be approved as an alternative method under Parts 60.8, 61.13, or 63.7(f) before a source may use it for this purpose. Be aware that these methods are subject to change based on the review of additional validation studies or on public comment as a part of adoption as a Federal test method, the Title V permitting process, or inclusion in a SIP.

This OTM is a product of extensive conversations with and feedback from EPA stakeholders including representatives from state regulatory entities, various EPA offices, analytical laboratories, emission testing firms, analytical standards vendors, instrument vendors, and others with experience in sampling and analysis of PCDD and PCDF. We believe this OTM significantly improves on existing methods and find it a significant improvement for collecting emissions data to support development of emissions standards for Polychlorinated Dibenzo-*p*-Dioxins, Polychlorinated Dibenzofurans, Polychlorinated Biphenyls, and Polycyclic Aromatic Hydrocarbons. EPA advises all potential users to review the method and all appendices carefully before application of this method.

Method History - Initial Posting – 1/31/2022

**Other Test Method 46 (OTM 46) Measurement of Polychlorinated Dibenzo-*p*-Dioxins, Polychlorinated Dibenzofurans, Polychlorinated Biphenyls, and Polycyclic Aromatic Hydrocarbons from Stationary Sources**

*1.0 Scope and Application*

1.1 Applicability. This method applies to the measurement of polychlorinated dibenzo-*p*-dioxins and polychlorinated dibenzofurans (PCDD/PCDF), polychlorinated biphenyls (PCB), and/or polycyclic aromatic hydrocarbons (PAH) in emissions from stationary sources. Using this method, you can measure these analyte groups individually or in any combination using a single sample acquisition unless otherwise specified in a rule, regulation, or permit. Tables 23-1 through 23-3 of this method list the applicable target analytes for this method. If all 209 PCB are analyzed, the 17 toxic PCB congeners should be resolved and reported while the other PCB can be reported as totals by homolog, for example, total TrCB.

1.2 Scope. This method describes the sampling and analytical procedures used to measure selected PCDD and PCDF in stationary sources when required in an applicable subpart. This method also describes how the same sampling and analysis technology can be used to measure selected PCB and PAH from stationary source in combination or as each individual compound class when required in an applicable subpart. However, this method incorporates by reference some of the specifications (e.g., equipment and supplies) and procedures (e.g., sampling and analytical) from other methods in this part that are essential to conducting this method. To obtain reliable samples, source sampling teams should be trained and experienced with the following additional EPA test methods: Method 1, Method 2, Method 3, Method 4, and Method 5 of Appendices A-1, A-2, and A-3 to 40 CFR part 60. Laboratory analysis teams should be trained and experienced with Method 1668C (found at: [https://www.epa.gov/sites/production/files/2015-09/documents/method\\_1668c\\_2010.pdf](https://www.epa.gov/sites/production/files/2015-09/documents/method_1668c_2010.pdf)) and Method 1613B of 40 CFR part 136 Appendix A and

have a working knowledge of isotope dilution and the use of high-resolution gas chromatography/high-resolution mass spectrometry (HRGC/HRMS).

1.3 The HRGC/HRMS portions of this method are for use by laboratory analysts experienced with HRGC/HRMS analysis of PCDD, PCDF, PCB, and PAH or under the close supervision of such qualified persons. Each source testing team, including the sampling and laboratory organization(s) that use this method, must demonstrate the ability to generate acceptable results that meet the performance criteria in Section 13 of this method.

1.4 This method is “performance-based” and includes acceptability criteria for assessing sampling and analytical procedures. Users may modify the method to overcome interferences or to substitute superior materials and equipment, provided that they meet all performance criteria in this method. Section 13 of this method presents requirements for method performance.

## *2.0 Summary of Method*

This method identifies and determines the concentration of specific PCDD, PCDF, PCB, and PAH compounds. Gaseous and particulate bound target pollutants are withdrawn from the gas stream isokinetically and collected in the sample probe, on a glass fiber or quartz filter, and on a packed column of adsorbent material. This method is not intended to differentiate between target compounds in particulate or vapor fractions. The target compounds are extracted from the combined sample collection media. Portions of the extract are chromatographically fractionated to remove interferences, separated into individual compounds or simple mixtures by HRGC, and measured with HRMS. This method uses isotopically labeled standards to improve method accuracy and precision through isotope dilution quantitation.

## *3.0 Definitions*

3.1 Alternate Recovery Standards. A group of isotopically labeled compounds that is not otherwise designated in this method for quality control (QC) purposes. Alternate recovery

standards can be used to assess the recovery of a compound class relative to any step in the sampling and analysis procedure that is not already assessed as a mandatory part of this method, such as the cleanup step.

3.2 Benzo[*a*]pyrene Toxic Equivalency Quotient (B[*a*]P-TEQ). One of several schemes that express the toxicity for PAH compounds in terms of the most toxic form of PAH, benzo[*a*]pyrene, as specified in applicable regulations, permits, or other requirements.

3.3 Continuing Calibration Verification (CCV) Standard. A standard prepared at the mid-point concentration of the calibration used to verify the initial calibration. Prepare the CCV standard at the same time as the batch of field samples using the same labeled standards.

3.4 Congener. An individual compound with a common structure (dioxin, furan, or biphenyl), only differing by the number of chlorine or other substituent attached to the structure.

3.5 Estimated Detection Limit (EDL). The minimum qualitatively recognizable signal above background for a target compound. The EDL is a detection limit specific to each sample analysis based on the noise signal measured near the retention time of a target compound or target isomer group. Being sample specific, the EDL is affected by sample size, dilution, recoveries of pre-extraction standard, chemical noise from sample extract, electronic noise from instrument, extract aliquot, relative response of instrument, etc.

3.6 Estimated Maximum Possible Concentration (EMPC). An EMPC is a worst-case estimate of the target compound concentration. Report the results as EMPC when the ion abundance ratio for a target analyte is outside the performance criteria. Calculate the EMPC using both quantitation ions.

3.7 Field Train Proof Blank. A field train proof blank train is a QC sample to evaluate equipment preparation and potential contamination during sample recovery and consists of a fully

assembled train at the sampling site, without actual sampling. The field train proof blank train uses glassware from the same preparation batch as the field samples.

3.8 Homolog. A compound belonging to a series of compounds with the same general molecular formula, differing from each other by the number of repeating units of chlorine.

3.9 Isomer. An individual compound with a common structure (dioxin, furan, or biphenyl), only differing by the position of chlorine atoms attached to the structure.

3.10 Isotope Dilution. A means of determining a naturally occurring (native) compound by reference to the same compound in which one or more atoms has been isotopically enriched.

3.11 Laboratory Method Blank (LMB). A quality control sample to assess background contamination or interference from media, reagents, equipment, etc. An LMB is prepared in the laboratory, composed of clean sampling media (filter and XAD-2), using same labeled standards, media, reagents and materials (sodium sulfate, glass wool, etc.) and processed (extraction, fractionations, cleanup) and analyzed using the same procedures as a field sample.

3.12 Polychlorinated Biphenyl (PCB) congeners. Any or all 209 chlorinated biphenyl congeners. Table 23-3 of this method lists the primary target compounds and Appendix A to this method provides the full list of 209 PCB congeners and isomers.

3.12.1 Monochlorobiphenyl (MoCB). Any or all three monochlorinated biphenyl isomers.

3.12.2 Dichlorobiphenyl (DiCB). Any or all 12 dichlorinated biphenyl isomers.

3.12.3 Trichlorobiphenyl (TrCB). Any or all 24 trichlorinated biphenyl isomers.

3.12.4 Tetrachlorobiphenyl (TeCB). Any or all 42 tetrachlorinated biphenyl isomers.

3.12.5 Pentachlorobiphenyl (PeCB). Any or all 46 pentachlorinated biphenyl isomers.

3.12.6 Hexachlorobiphenyl (HxCB). Any or all 42 hexachlorinated biphenyl isomers.

3.12.7 Heptachlorobiphenyl (HpCB). Any or all 24 heptachlorinated biphenyl isomers.

3.12.8 Octachlorobiphenyl (OcCB). Any or all 12 octachlorinated biphenyl isomers.

3.12.9 Nonachlorobiphenyl (NoCB). Any or all three nonachlorinated biphenyl isomers.

3.12.10 Decachlorobiphenyl (DeCB). Biphenyl fully chlorinated with 10 chlorine atom substituents replacing hydrogen in the parent compound.

3.13 Polychlorinated dibenzo-*p*-dioxin (PCDD) congeners. Any or all 75 chlorinated dibenzo-*p*-dioxin congeners. There are seven 2,3,7,8 substituted PCDD congeners and four PCDD homolog groups listed in Table 23-1 of this method. This method does not measure mono- through tri-PCDD and includes non-2,3,7,8 substituted congeners in the total homolog categories.

3.13.1 Tetrachlorodibenzo-*p*-dioxin (TeCDD). Any or all 22 tetrachlorinated dibenzo-*p*-dioxin isomers.

3.13.2 Pentachlorodibenzo-*p*-dioxin (PeCDD). Any or all 14 pentachlorinated dibenzo-*p*-dioxin isomers.

3.13.3 Hexachlorodibenzo-*p*-dioxin (HxCDD). Any or all 10 hexachlorinated dibenzo-*p*-dioxin isomers.

3.13.4 Heptachlorodibenzo-*p*-dioxin (HpCDD). Any or all two heptachlorinated dibenzo-*p*-dioxin isomers.

3.13.5 Octachlorodibenzo-*p*-dioxin (OCDD). Dibenzodioxin fully chlorinated with eight chlorine atom substituents replacing hydrogen in the parent compound.

3.14 Polychlorinated dibenzofuran (PCDF) congeners. Any or all chlorinated dibenzofuran congeners. There are 10 2,3,7,8 substituted PCDF congeners and four PCDF homolog groups listed in Table 23-1 of this method. This method does not measure mono- through tri-PCDF and includes non-2,3,7,8 substituted congeners in the total homolog categories.

3.14.1 Tetrachlorodibenzofuran (TeCDF). Any or all 38 tetrachlorinated dibenzofuran isomers.

3.14.2 Pentachlorodibenzofuran (PeCDF). Any or all 28 pentachlorinated dibenzofuran isomers.

3.14.3 Hexachlorodibenzofuran (HxCDF). Any or all 16 hexachlorinated dibenzofuran isomers.

3.14.4 Heptachlordibenzofuran (HpCDF). Any or all four heptachlorinated dibenzofuran isomers.

3.14.5 Octachlorodibenzofuran (OCDF). Dibenzofuran fully chlorinated with eight chlorine atom substituents replacing hydrogen in the parent compound.

3.15 Polychlorinated diphenyl ethers (PCDE). Any or all chlorinated substituted diphenyl ethers.

3.15.1 Hexachlorodiphenyl ether (HxCDPE). Any or all 42 hexachlorinated diphenyl ether isomers.

3.15.2. Heptachlorodiphenyl ether (HpCDPE). Any or all 24 heptachlorinated diphenyl ether isomers.

3.15.3 Octachlorodiphenyl ether (OCDPE). Any or all 12 octachlorinated diphenyl ether isomers.

3.15.4 Nonachlorodiphenyl ether (NCDPE). Any or all three nonachlorinated diphenyl ether isomers.

3.15.5. Decachlorodiphenyl ether (DCDPE).

3.16 Polycyclic Aromatic Hydrocarbons (PAH). Any or all aromatic compounds with two or more fused six-member rings. Table 23-2 of this method lists the target PAH compounds for this method. You may add and analyze additional PAH compounds by adding the appropriate <sup>13</sup>C isotopically labeled compound to the pre-extraction standard mixture and by following the other requirements for target PAH compounds in this method.

3.17 Pre-analysis Standard. A group of isotopically labeled compounds added at a known amount immediately prior to analysis and used to monitor instrument response, injection errors, instrument drift and to determine the recovery of the pre-extraction standard compounds. Add pre-analysis standard to every sample (including blank, QC samples, and calibration solutions) at a known amount.

3.18 Pre-extraction Filter Recovery Standard. A group of isotopically labeled compounds added at a known amount to the filter used to indicate the extraction efficiency of the filter media. Add pre-extraction filter recovery standard to the filter samples just prior extraction. The pre-extraction filter recovery standard is not used for quantitating or recovery correction.

3.19 Pre-extraction Standard. A group of isotopically labeled compounds added in a known amount to the XAD-2 adsorbent resin of each sample immediately before extraction and used for quantitation of target and other labeled compounds to correct for extraction, cleanup, and concentration recovery. These isotopically labeled compounds constitute a matrix spike of the resin. Add pre-extraction standard to every sample at the same level (including blank, QC samples, and calibration solutions).

3.20 Pre-sampling Adsorbent Standard. A group of isotopically labeled compounds added in a known amount to the XAD-2 adsorbent prior to sampling used to monitor sampling aspects of the method.

3.21 Pre-transport Standard. Spiking compound from the list of alternative recovery standards that can be added by the laboratory to the sample shipping containers used to transport field equipment rinse and recovery samples prior to sampling. The measured concentration of the pre-transport recovery standard provides a quality check on potential probe rinse sample spillage or mishandling after sample collection and during shipping.

3.22 Quality Control Sample (QCS). A mid-level standard prepared from a second source standard or prepared from a source of standards different from the source of calibration standards. The purpose of the QCS is to verify the integrity of the primary calibration standards. A QCS is analyzed during the initial demonstration of capability and following each initial calibration (at a minimum quarterly) thereafter.



3.23 Relative Response Factor (RRF). The response of the mass spectrometer (MS) to a known amount of an analyte relative to a known amount of an isotopically labeled standard.

3.24 2,3,7,8-Tetrachlorodibenzo-*p*-dioxin Toxic Equivalency Quotient (2,3,7,8-TeCDD TEQ). A procedure that expresses the toxicity of PCDD, PCDF, and PCB in terms of the most toxic dioxin, as specified in applicable regulations, permits, or other requirements.

#### *4.0 Interferences*

Despite interferences, confidence of the data is based on the enhanced selectivity of fractionation, GC separation and detector resolving power, the QC check ions, and monitoring PCDE.

4.1 PCB and PCDE have similar molecular weight and chromatographic properties to PCDD and PCDF. PCB may produce fragment ions at interfering mass-to-charge ratios ( $m/z$ ) when losing chlorine ( $Cl_2$ ) or  $2 Cl_2$  during ionization processes. With HRMS, GC separation, and fractionation, PCB should not pose a problem for PCDD/PCDF identification and quantitation. PCDE also produce interfering  $m/z$  values when losing  $Cl_2$  in the PCDF homolog group with two fewer chlorine atoms (i.e., an octachlorinated PCDE can interfere with a hexachlorinated PCDF). The latter interferences are potentially detected by monitoring an  $m/z$  corresponding to the potentially interfering PCDE; however, the fragmentation patterns of all PCDE may not be known, complicating any attempt to quantify the extent of either interference. Note: Consider monitoring 328  $m/z$  if high levels of PCB are expected.

4.2 Very high amounts of other organic compounds in the matrix may interfere with the analysis. This method provides examples of column-chromatographic cleanup as procedures to reduce, but not necessarily eliminate, matrix effects due to high concentrations of organic compounds (International Agency for Research on Cancer 1991).

4.3 Target compound contaminants or related organics in solvents, reagents, glassware, isotopically labeled spiking standards, and other sample processing hardware are potential method interferences. Routinely evaluate all these materials to demonstrate that they are either free from interferences under the conditions of the analysis, or that the interference does not compromise the quality of the analysis results. Evaluate chemical interference through the preparation and analysis of an LMB. Use high purity reagents, solvents, and standards to minimize interference problems in sample analysis.

4.4 PAH are subject to degradation when exposed to ultraviolet light. Take precautions to shield samples from sunlight or fluorescent light sources during sample collection, recovery, extraction, cleanup, and concentration.

#### *5.0 Safety*

Note: Develop a strict laboratory safety program for the handling of PCDD, PCDF, PCB, and/or PAH.

5.1 Compounds in the PCDD and PCDF classes such as 2,3,7,8-TeCDD are aneugenic, carcinogenic, and teratogenic in laboratory animal studies. Other PCDD and PCDF containing chlorine atoms in positions 2,3,7,8 have toxicities comparable to that of 2,3,7,8-TeCDD.

5.2 PCB and benzo[a]pyrene are classified as known or suspected human or mammalian carcinogens. Be aware of the potential for inhalation and ingestion exposure to laboratory analysts.

5.3 This method recommends that the laboratory purchase dilute standard solutions of the analytes required for this method. However, if preparing primary solutions, use a hood or glove box. Laboratory personnel handling primary solutions should wear personal protective equipment including a toxic gas respirator mask fitted with charcoal filters approved by the National Institute for Occupational Safety and Health (NIOSH)/Mine Safety Health

Administration (MSHA) to prevent the inhalation of airborne particulates if not working in an approved hood or glove box.

5.4 The toxicity or carcinogenicity of other reagents or chemicals used in this method is not precisely defined. However, treat each chemical as a potential health hazard and minimize exposure to these chemicals. The laboratory is responsible for maintaining a current awareness file of Occupational Safety and Health Administration (OSHA) regulations regarding the safe handling of the chemicals specified in this method. Ensure that a reference file or list of internet sites that contain safety data sheets (SDS) is available to all personnel involved in the sampling and chemical analysis of samples known or suspected to contain PCDD, PCDF, PCB, and PAH.

#### *6.0 Equipment and Supplies*

Note: Brand names, suppliers, and part numbers are for illustration purposes only and no endorsement is implied. Apparatus and materials other than those specified in this method may achieve equivalent performance. Meeting the performance requirements of this method is the responsibility of the source testing team and laboratory team.

6.1 Sampling Apparatus. Figure 23-1 of this method shows a schematic for the sampling train. Do not use sealing greases or brominated flame retardant-coated tape in assembling the train. Do not use silicon tubing in direct contact with flue gases. The train is identical to that described in Section 6.1.1 of Method 5 of Appendix A-3 to 40 CFR part 60 with the following additions:

6.1.1 Nozzle. The nozzle must be made of quartz or borosilicate glass or titanium. Stainless steel nozzles should not be used.

6.1.2 Probe Liner. Use either polytetrafluoroethylene (PTFE), borosilicate, or quartz glass probe liners with a heating system capable of maintaining a probe gas temperature of  $120 \pm 14$  °C ( $248 \pm 25$  °F) during sampling, or such other temperature as specified by an applicable subpart of the standards or as approved by the Administrator. Use a PTFE ferrule or single-use PTFE coated O-

ring to achieve the seal at the nozzle end of the probe for stack temperatures up to about 300 °C (572 °F). Use a quartz glass liner and integrated quartz nozzle for stack temperatures between 300 and 1,200 °C (572 and 2,192 °F).

6.1.3 Filter Holder. Use a filter holder of borosilicate glass with a PTFE frit or PTFE-coated wire filter support. The holder design should provide a positive seal against leakage from the outside or around the filter. The holder should be durable, easy to load, leak-free in normal applications, and positioned immediately following the probe and cyclone bypass (or cyclone, if used) with the active side of the filter perpendicular to the source of the flow.

6.1.4 Filter Heating System. Use any heating system capable of monitoring and maintaining the temperature around the filter to ensure that the sample gas temperature exiting the filter is  $120 \pm 14$  °C ( $248 \pm 25$  °F) during sampling or such other temperature as specified by an applicable subpart of the standards or approved by the Administrator for a particular application.

6.1.5 Filter Temperature Sensor. Install a temperature sensor capable of measuring temperature to within  $\pm 3$  °C (5.4 °F) so that the sensing tip protrudes at least 1.3 centimeters (cm) (1/2 in.) into the sample gas exiting the filter. Encase the sensing tip of the sensor in glass or PTFE, if needed.

6.1.6 Sample Transfer Line. The sample transfer line transports gaseous emissions from the heated filter holder to the condenser and must be heat traced and constructed of glass or PTFE with connecting fittings that form leak-free, vacuum-tight connections without using sealing greases or tapes. Keep the sample transfer lines as short as possible and maintain the lines at a temperature of  $120 \text{ °C} \pm 14 \text{ °C}$  ( $248 \text{ °F} \pm 25 \text{ °F}$ ) using active heating when necessary. Orient the sample transfer lines with the downstream end lower than the upstream end so that any condensate will flow away from the filter and into the condenser.

6.1.7 Condenser. Glass, water-jacketed, coil-type with compatible fittings. Orient the condenser to cause moisture to flow down to the adsorbent module to facilitate condensate drainage. Figure 23-2 of this method shows a schematic diagram of the condenser.

6.1.8 Water Circulating Bath. Use a bath pump circulating system capable of providing chilled water flow to the condenser and adsorbent module water jackets. Typically, a submersible pump is placed in the impinger ice water bath to circulate the ice water contained in the bath. Verify the function of this system by measuring the gas temperature at the entrance to the adsorbent module. Maintain this temperature at  $< 20\text{ }^{\circ}\text{C}$  ( $68\text{ }^{\circ}\text{F}$ ).

6.1.9 Adsorbent Module. Use a water-jacketed glass container to hold up to 40 grams (g) of the solid adsorbent. Figure 23–2 of this method shows a schematic diagram of the adsorbent module. Other physical configurations of the adsorbent resin module/condenser assembly are acceptable if the configuration contains the requisite amount of solid adsorbent and maintains the minimum length-to-width adsorbent bed ratio of two-to-one. Orient the adsorbent module vertically to facilitate condensate drainage. The connecting fittings must form leak-free, vacuum-tight seals. Include a coarse glass frit in the adsorbent module to retain the adsorbent.

6.1.10 Impingers. Use five impingers connected in series with leak-free ground glass fittings or any similar leak-free noncontaminating fittings. The first impinger must be a short-stem (water-dropout) design or equivalent. The second, fourth, and fifth impingers must be of the Greenburg-Smith design, modified by replacing the tip with a 1.3 cm (1/2 in.) inside diameter (ID) glass tube extending to approximately 1.3 cm (1/2 in.) from the bottom of the flask. The third impinger must be of the Greenburg-Smith design with the standard tip. The second and third impingers must contain known quantities of water, and the fifth impinger must contain a known weight of silica gel or equivalent desiccant. Alternatively, you may omit the first impinger if you do not expect excess moisture in the sample gas.

## 6.2 Sample Recovery Equipment.

6.2.1 Fitting Caps. Use leak-free ground glass fittings or any similar leak-free non-contaminating fitting to cap the sections of the sampling train exposed to the sample gas. Alternatively, use PTFE tape or contaminant-free aluminum foil for this purpose (see Section 6.2.6 of this method).

6.2.2 Wash Bottles. Use PTFE bottles.

6.2.3 Probe-Liner, Probe-Nozzle, and Filter-Holder Brushes. Use inert bristle brushes with precleaned stainless steel or PTFE handles. Extensions of the probe brush must be made of stainless steel or PTFE and be at least as long as the probe. Use brushes that are properly sized and shaped to remove accumulated material from the nozzle and probe liner if used.

6.2.4 Filter Storage Container. Use a sealed filter holder, wide-mouth amber glass jar with PTFE-lined cap, or glass petri dish sealed with PTFE tape. Purchase precleaned amber glass jars and petri dishes, or clean according to the glassware cleaning procedures listed in Section 8.1.1.1 of this method.

6.2.5 Field Balance. Use a weighing device capable of measurements to an accuracy of 0.5 g.

6.2.6 Aluminum Foil. Use heavy duty aluminum foil cleaned by rinsing three times with hexane or toluene and stored in a pre-cleaned glass petri dish or glass jar. Do not use aluminum foil to wrap or contact filter samples due to the possibility of reaction between the sample and the aluminum.

6.2.7 Silica Adsorbent Storage Container. Use an air-tight container to store silica gel.

6.2.8 Glass Sample Storage Container. Recover samples in amber glass bottles, 500- or 1000-milliliters (mL) with leak-free PTFE-lined caps. Either purchase precleaned bottles or clean containers according to glassware cleaning procedures listed in Section 8.1.1.1 of this method.

## 6.3 Sample Extraction Equipment.

6.3.1 Sample Container. Use 125- and 250-mL amber glass bottles with PTFE-lined caps.

6.3.2 Test Tubes. Use glass test tubes or small (e.g., 5 to 10 mL) amber vials.

6.3.3 Soxhlet/Dean-Stark Extraction Apparatus.

6.3.3.1 Soxhlet Apparatus. Use 200-mL capacity thimble holder capable of holding 43×123-millimeter (mm) extraction thimbles, with receiving flask (typically round-bottom).

6.3.3.2 Moisture Trap. Use Dean-Stark or Barret with fluoropolymer stopcock trap to fit between the Soxhlet extractor body and the condenser as shown in Figure 23-3 of this method. Note: Dean-Stark or Barret traps are used to remove water with extraction solvents that are less dense and insoluble in water.

6.3.3.3 Extraction Thimble. Use quartz, glass, or glass fiber thimble, typically 43 x 123 mm to fit Soxhlet apparatus. The use of cellulose thimbles for sample extraction in this method is prohibited.

6.3.3.4 Heating Mantle. Use a hemispherical shaped heating mantle to fit round-bottom flask.

6.3.4 Kuderna-Danish (KD) Concentrator. Use an apparatus consisting of a three-ball Snyder column, a flask with leak-free joint to accept the three-ball Snyder column at the top, a leak-free joint to receive a graduated concentration tube at the bottom and a heating mantle. Note: Rotary evaporation has only been demonstrated when analyzing PCDD/PCDF. The KD with Snyder column is recommended when analyzing for PAH and PCB to avoid evaporation loss resulting in failed performance criteria for pre-extraction spike recovery.

6.3.5 Nitrogen Evaporative Concentrator. Use a nitrogen evaporative concentrator equipped with a water bath with the temperature controlled in the range of 30 to 60 °C (86 to 140 °F) (N-Evap Organomation Associates, Inc., South Berlin, MA, or equivalent).

6.3.6 Separatory Funnel. Use glass or PTFE 2-liter separatory funnels.

6.4 Glass Liquid Chromatography Columns.

6.4.1 Pasteur Pipettes. Use disposable pipettes, or glass serological pipettes typically 150 mm long x 6 mm ID.

6.4.2 Liquid Chromatography Columns. 200 to 300 mm long x 20 mm ID with 250-mL reservoir.

6.5 Analytical Equipment.

6.5.1 Gas Chromatograph. Use a gas chromatograph consisting of the following components:

6.5.1.1 Oven. Use an oven capable of maintaining the separation column at the proper operating temperature  $\pm 1.0$  °C (1.8 °F) and performing programmed increases in temperature at rates of at least 40 °C/min with isothermal hold.

6.5.1.2 Temperature Monitor. Use a temperature monitor to measure column oven temperature to  $\pm 1.0$  °C (1.8 °F).

6.5.1.3 Flow System. Use an electronic pressure control or equivalent gas metering system to control carrier gas flow or pressure.

6.5.1.4 Injection Port. Use a split/splitless injection port in the splitless mode or on-column injection port for the capillary column.

6.5.2 Capillary Gas Chromatography Column. Use different columns for the analysis of the different target compound classes in this method, if needed. Perform the resolution checks in Sections 10.2.3.5 and 10.2.3.6 of this method to document the required resolution. Compound separation must meet the resolution specifications in Section 10.2.3.5 of this method and the identification specifications found in Section 11.4.3.4 of this method.

6.5.2.1 PCDD/PCDF Column. Recommended column systems for measuring PCDD/PCDF should be capable of achieving separation of the 17 PCDD/PCDF target compounds from the nearest eluting isomer(s) with a valley less than 25 percent (%) of the lower of the two peaks. The system must meet the performance specifications for compound separation and quantitation



in calibration, CCV, and for isotopically labeled standards added to field samples. Use a variety of bonded-phase capillary gas chromatography columns to meet these requirements, if needed.

Note: Fishman, et al. (see Section 16.3 of this method) demonstrated that all TEF isomers can be fully differentiated from closely eluting isomers using either of two sets of non-polar and polar stationary phase combinations. One set consisted of 5% phenyl methylpolysiloxane (DB-5, HP-5MS, Rtx-5MS, Equity-5) and 50% cyanopropylmethyl, 50% phenylmethylsiloxane (DB-225, SP 2331) GC columns and the other set consisted of 5% phenyl, 94% methyl, 1% vinyl silicone bonded-phase (DB-5MS, ZB-5MS, VF-5MS, CP-Sil 8 CB LowBleed/MS) with 50% cyanopropylmethyl, 50%-percent phenylmethylsiloxane (SP-2331).

6.5.2.2 PAH Column. Use column systems for measuring PAH that can achieve separation of anthracene and phenanthrene at  $m/z$  178 such that the valley between the peaks does not exceed 50% of the taller of the two peaks, and benzo[*b*]fluoranthene and benzo[*k*]fluoranthene such that the valley between the peaks is less than 60% of the height of the taller peak. These requirements are achievable using a 30-m narrow bore (0.25 mm ID) 5% phenyl polysilphenylene-siloxane (BPX5 or equivalent) bonded-phase, fused-silica capillary column.

6.5.2.3 PCB Columns. Use column systems for measuring PCB that can achieve unique resolution and identification of the toxics for determination of a  $TEQ_{PCB}$  using toxic equivalency factors (TEF). Isomers may be unresolved if they have the same TEF and RRF and if these unresolved isomers are uniquely resolved from all other congeners. These requirements are achievable using several 30-meter (m) narrow bore (0.25 mm ID) columns including 8% n-phenyl polycarborane-siloxane (HT8), DB-XLB, and poly (50% n-octyl/50%-percent methyl siloxane) (SPB-Octyl). Quantification of unresolved isomers should use the nearest eluting target PCB pre-extraction standard in Appendix A of this method, unless otherwise specified in applicable rule, regulation, or permit.

Note: If all 209 PCB are analyzed the 17 toxic PCB congeners should be resolved and reported while the other PCB can be reported as totals by homolog, for example, total TrCB.

6.5.3 Mass Spectrometer. Instrument employing 28 to 70 electron volt ionization. The instrument and data system must be capable of repetitive monitoring of at least 12 exact  $m/z$  values with a mass resolution defined in Section 10.2.1 within the measurement mass range. The recommended lock-mass ions to be used for mass drift correction are presented in Tables 23-4, 23-5, and 23-6 of this method for PCDD/PCDF, PAH, and PCB, respectively, as applicable to target analytes. Mass drifts of 5 parts per million (ppm) or more can have serious effects on instrument performance.

6.5.4 Mass Spectrometer Data System. Use a data system compatible with the mass spectrometer and capable of sequencing and monitoring multiple groups of selected ions.

6.5.5 Analytical Balance. Use an analytical balance to measure within 0.1 milligram (mg).

### *7.0 Reagents, Media, and Standards*

7.1 Filter. Glass fiber filters, without organic binder, exhibiting at least 99.95% efficiency (<0.05% penetration) on 0.3-micron dioctyl phthalate smoke particles.

7.1.1 Conduct a QC check on the filter lot prior to the field test to demonstrate that filters are free from contamination or interference by extracting and analyzing a minimum of three filters from each lot as follows. Spike with pre-extraction and pre-extraction filter recovery standards for target compounds to be measured and extract each filter separately with toluene as described in Section 11 of this method. After extraction, remove the filters and the solvent from the filters under clean conditions (e.g., a clean nitrogen stream). Analyze the extracts according to the procedures in Section 11 of this method, including adding pre-analysis standard. This filter check analysis must meet the performance requirements in Section 13.1 of this method. Ongoing

analysis of LMB can be used to fulfill this check. If criteria are not met for target compounds, repeat with additional filters from the lot or evaluate another lot.

7.2 Adsorbent Resin. Amberlite® XAD-2 resin. All adsorbent resin must meet the cleanliness criteria described for LMB in Section 13.1 of this method following the same extraction, concentration, cleanup, and analysis steps as field samples. This method recommends using the procedures provided in Appendix B to this method to clean the resin before use, if needed. However, this method allows alternative cleanup procedures that use automated extraction equipment if the adsorbent meets the required performance criteria described for LMB in Section 13.1 of this method.

Note: When using automated systems, the same systems must be used for samples and QC samples, such as blanks and resin checks.

7.2.1 Conduct a QC check on the cleaned adsorbent lot or batch following the extraction and analyses procedures in Section 11 of this method, including adding applicable labeled standards. The cleaned adsorbent must meet the criteria described for LMB in Section 13.1 of this method. An LMB conducted with an adsorbent lot or batch can serve this purpose.

7.2.2 Storage. Store adsorbent in a solvent-rinsed nonporous clean container and secure lid.

7.3 Glass Wool. Clean the glass wool to meet the specifications in Section 13.1 of this method. Glass wool is dried of the solvent and stored in a clean glass container with a PTFE-lined screw cap.

7.4 Water. Use deionized or distilled water meeting requirements in Section 13.1 of this method and store in its original container or in a clean glass container with a PTFE-lined screw cap.

7.5 Silica Gel. Indicating type for sampling, 6–16 mesh. If previously used, dry at 175 °C (347 °F) for two hours. Use new silica gel as received. As an alternative, use other types of desiccants (equivalent or better), subject to the approval of the Administrator.

7.6 Methylene Chloride. Pesticide grade or better.

7.7 Sample Recovery Reagents.

7.7.1 Acetone. Pesticide grade or better.

7.7.2 Toluene. Pesticide grade or better.

7.8 Sample Extraction and Cleanup.

7.8.1 Potassium Hydroxide. American Chemical Society (ACS) grade, 2% (weight/volume) in water.

7.8.2 Sodium Sulfate. Granulated or powdered, reagent grade. Evaluate for cleanliness prior to use with an LMB. The LMB must meet the requirements in Section 13.1 of this method for target compounds. Store in a clean glass container with a PTFE-lined screw cap.

7.8.3 Sulfuric Acid. Reagent grade.

7.8.4 Sodium Hydroxide. 1.0 N. Weigh 40 g of sodium hydroxide into a 1-liter volumetric flask. Dilute to 1 liter with water.

7.8.5 Hexane. Pesticide grade or better.

7.8.6 Methanol. Pesticide grade or better.

7.8.7 Toluene. Pesticide grade or better.

7.8.8 High-Boiling Alkanes Used as Keeper Solvents (e.g., tetradecane, nonane, decane).

Pesticide grade. Note: Lower homologous series alkanes (nonane or decane) are necessary for higher volatility targets such as MoCB and naphthalene to maintain retention during concentration procedures. However, do not take samples to dryness when using these lower alkane homologs.

7.8.9 Liquid Column Chromatography Packing Materials. Use the following column chromatography packing materials, as needed, to prepare sample extracts by fractionation and removal of interferences. Commercially prepacked cleaning columns may be available for this

purpose. The liquid column chromatography packing materials have to be adequate to clean the samples in order to be fit for purpose and meet the performance criteria of this method. All procedures for preparing column chromatography packing materials are recommendations shown to meet the performance specifications required for the recovery of labeled compounds described in Section 13 of this method.

7.8.9.1 Alumina. Use either acidic or basic alumina in the cleanup of sample extracts. Use the same type of alumina for all samples in an analytical sequence, including those used to demonstrate LMB performance.

7.8.9.1.1 Acidic Alumina (Sigma-Aldrich® 199966 or equivalent). Brockmann activity grade 1, 100–200 mesh. Prior to use, activate the alumina by heating for 12 hours at 130 °C (266 °F). Store in a desiccator. You may use pre-activated alumina purchased from a supplier as received.

7.8.9.1.2 Basic Alumina (Sigma-Aldrich® 19943 or equivalent). Brockmann activity grade 1. Activate by heating to 600 °C (1,112 °F) for a minimum of 24 hours. Do not heat to over 700 °C (1,292 °F) because this can lead to reduced capacity for retaining the target compounds. Store at 130 °C (266 °F) in a covered flask. Recommended storage time for acidic alumina is within five days of baking. Use prepacked alumina columns immediately after opening the vacuum-sealed pouch or container.

7.8.9.2 Florisil®. Activated, 60–100 mesh recommended. Heat previously activated Florisil® in a glass container loosely covered with aluminum foil in an oven at 130 to 150 °C (266 to 302 °F) for a minimum of 24 hours. Upon cooling, store activated Florisil® silica prior to use in a desiccator.

7.8.9.3 Silica Gel. Use either activated, acid- or base-coated silica gel in the cleanup of sample extracts. Use the same type of silica gel for all samples in an analytical sequence, including those used to demonstrate LMB performance.

7.8.9.3.1 Activated Silica Gel. Supelco® 1-3651, Bio-Sil® A, 100–200 mesh (or equivalent).

Prior to use, silica gel should be activated by solvent rinsing and heat activation. It is recommended to rinse with methylene chloride and activate the silica gel by heating for at least 1 hour at 180 °C (356 °F). After cooling, rinse the silica gel sequentially with methanol and toluene. Heat the rinsed silica gel at 50 °C (122 °F) for 10 minutes, then increase the temperature gradually to 180 °C (356 °F) over 25 minutes and maintain the gel at this temperature for 90 minutes. Allow to cool in a desiccator to room temperature and store in a glass container with a PTFE-lined screw cap. Alternative conditioning procedure may be used if the performance criteria in Section 13.1 are met for target compounds.

7.8.9.3.2 Acidic Silica Gel (30% weight/weight). Combine 100 g of activated silica gel with 44 g of concentrated sulfuric acid in a clean screw-capped glass container and agitate thoroughly. Disperse the solids with a stirring rod until obtaining a uniform mixture of acid-coated silica gel. Store the mixture in a glass container with a PTFE-lined screw cap.

7.8.9.3.3 Basic Silica Gel. Combine 30 g of 1 N sodium hydroxide with 100 g of activated silica gel in a clean screw-capped glass container and agitate thoroughly. Disperse solids with a stirring rod until obtaining a uniform mixture of base-coated silica gel. Store the mixture in glass container with a PTFE-lined screw cap.

7.8.9.4 Carbon/Celite® 545 (or equivalent solid support). Use of a carbon-based column cleanup material (e.g., one of the many including for example Carbopack® B or C) to further remove non-planar impurities from the samples prior to analysis may be necessary. You must evaluate alternative carbon-based sorbents for this purpose prior to their use. An 18% weight/weight mixture of Carbopack® C and Celite® 545 has been used for this purpose and should be activated at 130 °C (266 °F) for a minimum of 6 hours for this purpose. Allow to cool and store this mixture in a desiccator prior to use.

7.8.10 Nitrogen. 99.999% (ultra-high) purity.

7.9 Sample Analysis.

7.9.1 Helium. 99.999% (ultra-high) purity.

7.9.2 Spiking Standards. Prepare spiking standards quantitatively at a convenient concentration (e.g., 10 nanograms (ng)/mL) or use commercial standards if available, to enable accurate spiking of a labeled standard at various stages of the sample and extract preparation. You may adjust the sample fortification concentrations from those recommended in Tables 23-7, 23-8, and 23-9 of this method to accommodate the concentration of target compounds anticipated in samples if the performance criteria in Section 13 of this method are met. Note: When adjusting the fortification concentrations in the final sample extract, consider variables such as the aliquot of extract used and injection volume of samples and calibration.

7.9.3 Pre-Sampling Adsorbent Standard. Prepare stock standard solutions in nonane to enable spiking of the isotopically labeled compounds for applicable target compound classes in Tables 23-7, 23-8, and 23-9 of this method so that the final sample extract is at the concentration shown under the heading “Pre-sampling Adsorbent Standard.”

7.9.4 Pre-extraction Filter Recovery Standard. Prepare stock standard solutions in nonane to enable spiking of the isotopically labeled compounds for applicable target compound classes in Tables 23-7, 23-8, and 23-9 of this method so that the final sample extract is at the concentration shown under the heading “Pre-extraction Filter Recovery Standard.”

7.9.5 Pre-extraction Standard. Prepare stock standard solutions in nonane to enable spiking of the isotopically labeled compounds for applicable target compound classes in Tables 23-7, 23-8, and 23-9 of this method so that the final sample extract is at the concentration shown under the heading “Pre-extraction Standard.”

7.9.6 Pre-analysis Standard. Prepare stock standard solutions in nonane to enable spiking of the isotopically labeled compounds for applicable target compound classes in Tables 23-7, 23-8, and 23-9 of this method so that the final sample extract is at the concentration shown under the heading “Pre-analysis Standard.”

### *8.0 Sample Collection, Preservation, and Storage*

8.1 Sampling. This method involves collection and recovery of trace concentrations of target semivolatile organic compounds. Therefore, field sampling and recovery staff should be trained and experienced in the best practices for handling and using organic solvents in field environments to recover and protect samples from contamination.

#### 8.1.1 Pretest Preparation.

8.1.1.1 Cleaning Glassware. Clean glassware thoroughly before using. This section provides a recommended procedure, but any protocol that consistently results in contamination-free glassware meeting the LMB criteria in Section 13.1 of this method is acceptable.

8.1.1.1.1 Soak all glassware in hot soapy water (Alconox® or equivalent).

8.1.1.1.2 Rinse with hot tap water.

8.1.1.1.3 Rinse with deionized/distilled water.

8.1.1.1.4 Rinse with methanol.

8.1.1.1.5 Rinse with toluene.

8.1.1.1.6 Baking glassware up to 400 °C (752 °F) for a minimum of 2 hours may be necessary to remove contaminants or interferents from particularly dirty samples. Allow glassware to cool after baking.

Note: Repeated baking of glassware may cause active sites on the glass surface that may irreversibly adsorb target compounds.



8.1.1.1.7 Cover glassware openings with clean glass fitting caps or cleaned aluminum foil (see Section 6.2.6 of this method).

8.1.1.1.8 Rinse glassware immediately before use with acetone and toluene.

Note: To prepare heavily soiled glassware, remove surface residuals from the glassware by soaking in hot soapy water, rinsing with hot water, then soaking with a non-chromic acid oxidizing cleaning reagent in a strong acid (e.g., NOCHROMIX® prepared according to manufacturer's directions). After the acid soak, rinse with hot water and repeat the cleaning procedures in Section 8.1.1.1 of this method.

8.1.1.2 Adsorbent Module. Load the modules in a clean area to avoid contamination. Fill a module with 20 to 40 g of XAD-2. Spike modules before the sampling event, but do not spike the modules in the field. Add the pre-sampling adsorbent standard to the top quarter of the adsorbent bed rather than onto the top or bottom of the adsorbent bed. Add sufficient spike (picograms (pg)/module) to result in the final sample theoretical concentrations specified in Tables 23-7, 23-8, and 23-9 of this method for PCDD/PCDF, PAH, and PCB, respectively, and to be above the lowest calibration concentration to ensure the standard recovery is quantitative. For samples with known or anticipated target compound concentration significantly higher or lower than the specified concentration in these tables, adjust the pre-sampling adsorbent standard concentration to the expected native compound concentration, but no less than 10 times the method detection limit (MDL). Follow the XAD-2 with cleaned glass wool and tightly cap both ends of the module. For analysis that includes PAH, use spiked modules within 14 days of preparation. See Table 23-10 of this method for storage conditions.

8.1.1.3 Sampling Train. Figure 23-1 of this method shows the complete sampling train. Follow the best practices by maintaining all sampling train components according to the procedure

described in APTD-0576 Maintenance, Calibration, and Operation of Isokinetic Source-sampling Equipment (U.S. EPA 1972).

8.1.1.4 Silica Gel. Weigh several 200 to 300 g portions of silica gel in an air-tight container to the nearest 0.5 g. Record the total weight of the silica gel plus container, on the outside of each container. As an alternative, directly weigh the silica gel in its impinger or sampling holder just prior to sampling.

8.1.1.5 Filter. Check each filter against light for irregularities and flaws or pinhole leaks. Pack the filters flat in a clean glass container. Do not mark filters with ink or any other contaminating substance.

8.1.2 Preliminary Determinations. Use the procedures specified in Section 8.2 of Method 5 of Appendix A-3 to 40 CFR Part 60.

8.1.2.1 Sample Volume. Unless otherwise specified in an applicable rule, regulation, or permit, sample for a minimum of 2 minutes at each traverse point. This method recommends sampling a minimum of 2.5 dry standard cubic meters (dscm).

8.1.2.2 For continuously operating processes, use the same sampling time at each traverse point. To avoid timekeeping errors, use an integer, or an integer plus one-half minute, for each traverse point.

8.1.2.3 For batch processes, determine the minimum operating cycle duration, dividing the sampling time evenly between the required numbers of traverse points. After sampling all traverse points once, sample each point again for the same duration of time per sampling point in reverse order until the operating cycle is completed. Sample all traverse points at least once during each test run.

8.1.3 Preparation of Sampling Train.

8.1.3.1 During field preparation and assembly of the sampling train, keep all train openings where contamination can enter sealed until just prior to assembly or until sampling is about to begin. To protect the adsorbent module from radiant heat and sunlight, you must wrap the module with aluminum foil or other suitable material capable of shielding the module from light. The XAD-2 adsorbent resin temperature must never exceed 50 °C (122 °F) because thermal decomposition will occur. Clean and prepare a complete set of sampling train components that will contact the sample for each sampling run, including one complete set to be used as a field train proof blank as a tool to evaluate equipment preparation and potential contamination during sample recovery as described in Section 9.6 of this method.

8.1.3.2 Place approximately 100 mL of water in the second and third impingers but leave the first and fourth impingers empty. Transfer approximately 200 g or more of silica gel from its container to the fifth impinger. Weigh each impinger and the adsorbent module, including the fitting caps, to the nearest 0.5 g using the field balance and record the weight for moisture determination. Remove the aluminum foil from the adsorbent module before weighing. Keep the module out of direct sunlight and rewrap the module with foil immediately after recording the module weight.

8.1.3.3 Using tweezers or clean disposable surgical gloves, place a filter in the filter holder. Be sure that the filter is properly centered, and the gasket properly placed, to prevent the sample gas stream from circumventing the filter. Check the filter for tears after completing the assembly.

8.1.3.4 Prepare the inside of the sampling probe and nozzle by brushing each component while rinsing three times each with acetone and toluene. Install the selected nozzle, using the connecting systems described in Section 6.1.2 of this method. Mark the probe with heat resistant tape or by some other method to denote the proper distance into the stack or duct for each sampling point. Assemble the train as shown in Figure 23-1 of this method. Orient the adsorbent

module vertically so condensed moisture drains into the first impinger. See APTD-0576 Maintenance, Calibration, and Operation of Isokinetic Source-sampling Equipment (U.S. EPA 1972) for details.

8.1.3.5 Turn on the recirculation pump to the adsorbent module and condenser coil and begin monitoring the temperature of the gas entering the adsorbent module. Ensure proper temperature of the gas entering the adsorbent module before proceeding.

8.1.4 Leak-Check Procedure. Same as Section 8.4 of Method 5 of Appendix A-3 to 40 CFR Part 60.

8.1.5 Sampling Train Operation. Same as Sections 8.5.1 through 8.5.9 of Method 5 of Appendix A-3 to 40 CFR Part 60.

8.1.5.1 Monitor the filter temperature with a sensor and record the filter temperature during sampling to ensure a sample gas temperature exiting the filter of  $120\text{ }^{\circ}\text{C} \pm 14\text{ }^{\circ}\text{C}$  ( $248\text{ }^{\circ}\text{F} \pm 25\text{ }^{\circ}\text{F}$ ), or such other temperature as specified by an applicable subpart of the standards or approved by the Administrator for an application of this method.

8.1.5.2 During testing, you must record the temperature of the gas entering the XAD-2 adsorbent module. The temperature of the gas must not exceed  $20\text{ }^{\circ}\text{C}$  ( $68\text{ }^{\circ}\text{F}$ ) for efficient capture of the target compounds.

8.2 Sample Recovery. Begin the cleanup procedure as soon as the probe is removed from the stack at the end of the sampling period. Seal the nozzle end of the sampling probe with PTFE tape or clean (e.g., toluene rinsed) aluminum foil.

8.2.1 When the probe can be safely handled, wipe off all external particulate matter near the tip of the probe. Conduct a post-test leak check. Remove the probe from the train and close off both ends with PTFE tape or clean aluminum foil. Seal off the inlet to the train with PTFE tape, a ground glass cap, or clean aluminum foil.

8.2.2 Transfer the probe and impinger assembly to the cleanup area. This method recommends cleaning and enclosing this area to minimize the chances of losing or contaminating the sample. To avoid sample contamination and unnecessary exposure to toxic chemicals, smoking or eating in the sample recovery area shall not be allowed.

8.2.3 Inspect the train prior to and during disassembly. Note and record any abnormal conditions (e.g., broken filters, colored impinger liquid). Recover and prepare samples for shipping as follows in Sections 8.2.4 through 8.2.12 of this method.

8.2.4 Container No. 1. Either seal the filter holder or carefully remove the filter from the filter holder and place it in its identified container. If it is necessary to remove the filter, use a pair of cleaned tweezers to handle the filter. If necessary, fold the filter such that the particulate cake is inside the fold. Carefully transfer to the container any particulate matter and filter fibers that adhere to the filter holder gasket by using a dry inert bristle brush and a sharp-edged blade. Seal the container and store cool ( $\leq 20$  °C, 68 °F) for transport to the laboratory.

8.2.5 Adsorbent Module Sample. Remove the module from the train, tightly cover both ends with fitting caps and PTFE tape, remove the foil, drain the recirculating water from the module, weigh and record the module weight, and label the adsorbent module. Moisture measurement in the field using the this method requires weighing the adsorbent module before sampling and after sampling as part of the sample recovery.

8.2.6 Container No. 2. Quantitatively recover material deposited in the nozzle, the front half of the filter holder, and the cyclone, if used, by brushing while rinsing three times with acetone followed by three rinses with toluene. Collect all the rinses in Container No. 2.

8.2.7 Rinse the back half of the filter holder three times with acetone followed by three rinses with toluene. Rinse the sample transfer line between the filter and the condenser three times with acetone followed by three rinses with toluene. If using a separate condenser and adsorbent

module, rinse the condenser three times with acetone followed by three rinses with toluene. Collect all the rinses in Container No. 2 and mark the level of the liquid on the container.

8.2.8 Moisture Weight. Weigh the adsorbent module, impingers, and silica gel impinger to within  $\pm 0.5$  g using the field balance and record the weights. This information is required to calculate the moisture content of the effluent gas. For PCDD/PCDF-only measurements, discard the liquid after measuring and recording the weight.

8.2.9 Container No. 3. You must save and analyze impinger water samples if PAH and/or PCB are the target compounds. Quantitatively recover impinger water samples for analysis if PAH and/or PCB are the target compounds by rinsing three times with acetone followed by three rinses with toluene. Collect impinger water and rinses in Container No. 3 and mark the level of the liquid on the container.

8.2.10 Silica Gel. Note the color of the indicating silica gel to determine if it has been completely spent and report its condition on the field data sheet.

8.2.11 Field Sample Handling, Preservation, Storage, and Transport. Store all field samples temporarily in cool ( $\leq 20$  °C, 68 °F) and dark conditions prior to transport to the laboratory. Ship samples cool ( $\leq 20$  °C, 68 °F), shielded from ultraviolet light. In addition, follow the procedures in ASTM D6911-15 (Guide for Packaging and Shipping Environmental Samples for Laboratory Analysis) for all samples, where appropriate. To avoid contamination of the samples, pay special attention to cleanliness during transport, field handling, sampling, recovery, and laboratory analysis, as well as during preparation of the adsorbent cartridges.

8.2.12 Sample Custody. Proper procedures and documentation for sample chain of custody are critical to ensuring data integrity. Follow the chain of custody procedures in ASTM D4840-99(2018)e1 (Standard Guide for Sample Chain-of-Custody Procedures) for all samples (including field samples and blanks).

### 8.3 Sample Storage Conditions and Laboratory Hold Times.

8.3.1 Table 23-10 of this method summarizes the sample storage conditions and laboratory hold times.

8.3.2 Store sampling train rinses and filter samples in the dark at the storage conditions in Table 23-10 from the time the laboratory receives the samples until analysis.

8.3.3 You may store adsorbent samples for PCDD/PCDF or PCB prior to extraction in the dark at 6 °C (43 °F) or less for up to one year from the time the laboratory receives the samples.

Note: The hold times listed in this method for adsorbent samples for PCDD/PCDF and PCB are recommendations as these compounds are very stable under the conditions listed in this section.

8.3.4 Protect adsorbent samples destined for PAH analysis from ultraviolet light. You may store adsorbent samples for PAH analysis in the dark at 6 °C (43 °F) or less for up to 30 days from the time the laboratory receives the samples.

8.3.5 Analyze PAH extracts within 40 days of extraction.

8.3.6 You may store sample aliquots including archived extracts of PCDD/PCDF, PAH and/or PCB samples in the dark at -10 °C (14 °F) or less for up to one year. Sample extracts must not be stored with pierced septa.

Note: The hold times listed in this method for sample aliquots for PCDD/PCDF and PCB are recommendations as these compounds are very stable under the conditions listed in this section.

### *9.0 Quality Control*

Note: In recognition of advances that are occurring in sampling and analytical technology, and to allow the test team to overcome analyte sensitivity and matrix interferences, this method allows certain options to increase sample collection volume and to improve separations and the quality of the analysis results for target analytes. It is the laboratory's responsibility to establish the conditions for optimum sample extraction, cleanup, and concentration to meet the performance

criteria in this method. However, you may not change the fundamental sampling and analysis techniques, isokinetic sampling with an adsorbent collection media followed by sample extraction, and HRMS detection and isotopic dilution quantification procedures. Section 13 of this method specifies the performance criteria to ensure that options employed for a sample set and analytes of interest are equal to or better than the specificity of the techniques in this method. The minimum requirements of this method consist of the initial demonstration of capability (IDC) and ongoing QC requirements. The analysis team shall perform an IDC to demonstrate acceptable accuracy and precision with this method as described in Section 9.3. The ongoing QC includes performing CCVs and LMBs to evaluate an individual laboratory's performance against the criteria in this method. The method includes analysis of samples spiked with labeled compounds to evaluate and document data quality. Laboratory performance is compared to established performance criteria to determine if the results of analyses meet the performance characteristics and requirements of the method.

9.1 Record and report data and information that will allow an independent reviewer to validate the determination of each target compound concentration. Record and report the data as described in Sections 9.1.1 through 9.1.7 of this method and performance criteria results required in Section 13 of this method.

9.1.1 Sample numbers and other sample identifiers. Each sample must have a unique identifier.

9.1.2 Field sample volume.

9.1.3 Field sampling date.

9.1.4 Extraction dates.

9.1.5 Analysis dates and times.

9.1.6 Analysis sequence/run chronology.

9.1.7 Quantitation Reports.



9.1.7.1 This method does not consider EMPC-flagged data to be zero concentrations. Calculate and report the EMPC concentrations.

9.1.7.2 Unless otherwise specified in applicable regulations, permits, or other requirements, when a target compound is measured at or below EDL, use EDL as the concentration for calculating compliance.

9.1.7.3 You must report EDLs for each compound with analytical results as well as the sum of the EDLs, if applicable.

## 9.2 Isotopically Labeled Standard Recovery.

### 9.2.1 Pre-sampling Adsorbent Standard and Pre-extraction Filter Recovery Standard Recoveries.

Pre-sampling adsorbent standard and pre-extraction filter recovery standard recoveries must demonstrate on a per sample basis that recovery of the labeled standard achieved the requirements in Section 13 of this method. Recoveries below the acceptable range for the pre-sampling adsorbent standard may be an indication of breakthrough in the sampling train.

9.2.1.1 If the recovery of all the pre-sampling adsorbent standard compounds is below 70%, the sampling run is not valid, and the stack test must be repeated for invalid analyses. As an alternative, you do not have to repeat the stack test for invalid analyses if the average of all pre-sampling adsorbent standard recoveries is 25% or more and you divide the final results by the average fraction of pre-sampling adsorbent standard recovery.

9.2.1.2 If the recovery of all the pre-extraction filter recovery standard compounds is below 70%, you may reanalyze the sample. If the recovery is still below the limit, the filter sampling extraction is not valid, and you must repeat the stack or vent sampling and subsequent analysis.

9.2.2 Pre-extraction Standard Recoveries. Pre-extraction standard recoveries must demonstrate on a per sample basis that recovery of the labeled standard achieved the requirements in Section 13.15 of this method. If the recovery criteria are not met, you may reanalyze the sample. If the

recovery criteria are still not met, the sampling run is not valid, and the stack test must be repeated. Recoveries outside the acceptable range for pre-extraction standard are an indication that sample preparation procedures did not adequately address sample and or sample matrix processing to recover native target compounds.

9.2.3 Pre-analysis Standard Response. Pre-analysis standard recoveries must demonstrate on a per sample basis that adequate labeled standard signal meets the requirements in Section 13.16 of this method. Add pre-analysis standard to every sample (including blanks, QC samples, and calibration solutions) in a known concentration. If the prepared samples do not meet the pre-analysis standard response criteria you may reanalyze and/or prepare and analyze archive samples to attempt meeting requirements for the compounds that do not meet the pre-analysis standard response criteria. Poor sensitivity compared to initial calibration response may indicate injection errors or instrument drift.

9.3 Initial Demonstration of Capability (IDC). The IDC must be successfully performed prior to analyzing field samples by meeting the QC requirements in Table 23-18. The IDC must be repeated if changes are made to analytical parameters not previously validated during the IDC. This may include, for example, changing the sample volume, selecting alternate quantitation ions, extending the calibration range, adding additional pre-analysis standard, or adding additional pre-extraction standard. The same calibration range used during the IDC must be used for the analysis of field samples.

9.3.1 Perform initial calibration following the procedures in Section 10. The lowest calibration standard used to establish the initial calibration must not be less than three times the MDL. The initial calibration must meet performance criteria in Section 13.9.

9.3.2 Lowest Calibration Concentration Confirmation. Establish a target concentration for the lowest calibration standard based on the intended use of the method. The lowest calibration

concentration may be established by a laboratory or programmatic lowest quantitative reporting requirement. The laboratory calibration curve must be set at or below this level. Perform seven replicate analyses of a calibration sample prepared at proposed lowest calibration concentration. The replicate analyses of the lowest calibration concentrations standards must meet the criteria in Sections 13.9 and 13.17.1.

Note: Consider that establishing the lowest calibration concentration too low may cause repeated failure of ongoing QC requirements.

9.3.3 Calculate Lowest Calibration Statistics. Calculate the mean and standard deviation for each analyte in these replicates (those used in Section 9.3.2). Determine the Half Range for the Prediction Interval of Results (HRPIR) using Equation 23-13. Calculate the Upper and Lower Limits for the Prediction Interval of Results (PIR) with Equations 23-14 and 23-15.

9.3.4 Lowest Calibration Point Acceptance Criteria. The laboratory's ability to measure analyte concentrations down to the lowest calibration point is confirmed if the criteria presented in Section 13.17.1 are met. If these criteria are not met, the lowest calibration point as been set too low and must be confirmed at a higher concentration.

9.3.5 LMB. Analyze an LMB after the highest standard in the calibration range. If an automated extraction system is used, an LMB must be extracted on each port. Performance criteria are presented in Section 13.1.

9.3.6 Initial Calibration Verification. A QCS must be analyzed during the IDC, and then following each initial calibration thereafter (at a minimum quarterly). A QCS is a mid-level standard prepared from a second source standard or prepared from a source of standards different from the source of calibration standards. The purpose of the QCS is to verify the integrity of the primary calibration standards. The acceptance criterion is presented in Section 13.11.

9.3.7 MDL. Perform an MDL determination using a minimum of seven spiked combined filter/sorbent media samples, spiked within 2 to 10 times of the expected MDL, and seven LMBs (combined filter/sorbent media) through all the steps of the method following the requirements in 40 CFR Part 136 Appendix B. Confirm target compounds meet the qualitative identification criteria in Sections 13.12 and 13.13. The criteria for the MDL determination are presented in Section 13.6.1 of this method.

9.3.8 MDL Confirmation. Confirm newly determined MDLs by preparing a low-level spiked combined filter/sorbent media sample by spiking the sorbent with native target compounds at 1 to 5 times the MDL and pre-extraction standard at the concentration used to analyze field samples and analyze. The criterion for the MDL confirmation is presented in Section 13.6.1 of this method.

9.3.9 Demonstration of Precision. Prepare, extract, and analyze seven replicate spiked samples in a valid Extraction Batch. Fortify the spiked samples near the midpoint of the initial calibration curve. The criterion is presented in Section 13.17.2 and Table 23-18. Demonstration is be repeated for failed compounds only.

9.3.10 Demonstration of Accuracy. Using the same set of replicate data generated for Section 9.3.9 of this method, calculate the average % recovery. The criterion is presented in Section 13.17.3 and Table 23-18. Demonstration is be repeated for failed compounds only.

9.4 LMBs. Evaluate background contamination from glassware, equipment, solvents, standards and media used for sample batches using an LMB prepared and analyzed identically to the field samples, including the same labeled standards, media, sodium sulfate, glass wool, glassware, solvents, etc. An LMB must be extracted with every batch of samples. Analyze an LMB at least once during each analytical sequence or every 12 hours, whichever period is shorter. Section 13.1 of this method describes the performance criteria for the LMB.

9.5 EDL. Calculate the EDL using Equation 23-11 of this method. If the field train proof blank or the LMB results are above the EDL, report the EDLs as equal to the sample-specific EDL, the LMB or the field train proof blank, whichever is larger.

Note: If the applicable compliance limit is total dioxin or total furan, report the sum of the EDLs for all the target compounds. If the applicable rule limit is a TEQ value, report the sum of the EDLs for all target compounds multiplied by their corresponding compound specific TEF.

9.6 Field Train Proof Blank Assessment. Conduct at least one field train proof blank for each test series at a single facility. A field train proof blank is used to evaluate equipment preparation and potential contamination during sample recovery and consists of a fully assembled train at the sampling site. Prepare and assemble the field train proof blank train in a manner identical to that described in Sections 8.1.3 and 8.1.4 of this method using glassware from the same preparation batch as the field samples. The field train proof blank train must remain assembled for the same average amount of time samples are collected. Recover the field train proof blank train as described in Section 8.2 of this method. Follow all subsequent steps for field train proof blank train sample preparation and analysis used for field samples including data reporting. Section 13.1 of this method describes the criteria for the field train proof blank.

#### *10.0 Calibration and Standardization*

10.1 Sampling System. Same as Sections 6.1 and 10.1 through 10.7 of Method 5 of Appendix A-3 to 40 CFR Part 60.

10.2 HRGC/HRMS System.

10.2.1 Mass Resolution. Tune the HRMS instrument to a resolving power of at least 10,000 at 10% percent of the peak height or 25,000 at 50% percent of the peak height. The resolving power for PAH and PCB analysis may be 8,000 at 10% of the peak height or 15,000 at 50% of the peak height. Assess the resolution at three exact  $m/z$ 's representing the low, mid and high

m/z range of the masses used to measure the target compound class. You may use peak matching and the chosen perfluoro-kerosene (PFK) or perfluorotributylamine (FC43) reference peak to verify that the exact mass is within 5 ppm of the required value.

10.2.2 Initial Calibration. Calibrate the HRGC/HRMS system using a minimum of five concentrations over a range that brackets expected field sample concentrations and the concentration of isotopically labeled standards in spiked samples. Tables 23-11, 23-12, and/or 23-13 of this method show the calibration concentrations recommended by this method, as applicable to the target compound classes. Perform calibration and subsequent analyses on an absolute mass (pg/microliter ( $\mu\text{L}$ )) basis. Determine the initial relative response factors for the target compounds and isotopically labeled standards using the initial calibration. Criteria for the initial calibration is in Section 13.9 of this method.

10.2.2.1 Lock-Mass Ions. Tables 23-4, 23-5, and 23-6 of this method present the recommended mass spectrometer lock-mass ions for PCDD/PCDF, PAH, and PCB, respectively. The reference compounds PFK or FC43 have ions that may be selected as your lock-mass and QC check ions. Monitor the QC check ions specified in these tables to verify instrument stability during the analysis (see Section 13.8 for performance criteria). Additional cleanup of the sample extract (or archive extract) and reanalysis is necessary for failure to maintain the lock-mass during analysis.

10.2.2.2 The relative standard deviation (RSD) for the mean relative response factor from each of the unlabeled analytes and isotopically labeled compounds used in an analysis must be less than or equal to the values in Table 23-14 of this method.

10.2.2.3 The signal-to-noise (S/N) ratio for the GC/MS signal present in every selected ion current profile must be greater than or equal to 10 in all concentrations of calibration standards for unlabeled targets and isotopically labeled standards. The ion abundance ratios must be within the control limits in Table 23-15 of this method.

Note: An interference with PFK  $m/z$  223.9872 may preclude meeting 10:1 S/N for the DiCB congeners at the optional Cal 1 level (Table 23-11). If this interference occurs, 10:1 S/N must be met at the Cal 2 level.

### 10.2.3 Continuing Calibration Verification.

10.2.3.1 Prepare the CCV standard at the same time as the batch of field samples using the same labeled standards. Prepare CCV standards at mid-level of the calibration (C3 level from Tables 23-11, 23-12, or 23-13 of this method). Inject a CCV standard, for the target compound class at least once every 12 hours during an analysis sequence. Calculate the RRF for each compound and compare each RRF to the corresponding mean RRF obtained during the initial calibration. The RRF for each native compound measured in a CCV must not deviate from the initial calibration by more than the limits shown in Table 23-14.

10.2.3.2 The ion abundance ratios must be within the allowable control limits shown in Table 23-15 of this method.

10.2.3.3 The S/N ratio for the GC/MS signal present in every selected ion current profile must be greater than or equal to 10.

10.2.3.4 Repeat the initial calibration when there is a failure to meet the requirements for acceptable CCV standard analysis.

10.2.3.5 Column Separation Check. Use the results from a CCV to verify and document the resolution required in Section 13.2, 13.3, or 13.4 of this method for the target compound classes analyzed with this method. If target compounds are not sufficiently resolved to meet the requirement, an analysis on a confirmation column is recommended (Section 13.5 of this method).

10.2.3.6 If you use a confirmation column, perform the resolution check in Section 10.2.3.5 of this method to document the required resolution on the confirmation column. See Section 13.5 of this method on confirmation columns, if needed.

### *11.0 Analysis Procedure*

11.1 Sample Extraction and Concentration. The sample extraction procedures in this method are the same for PCDD, PCDF, PCB and PAH targets. Figure 23-4 provides a flow chart showing sample container combination and extraction steps. Do not allow samples and extracts destined for PAH or PCB analysis to concentrate to dryness because the lower molecular weight PAH and the mono- through tri-chlorobiphenyls may be totally or partially lost. Note: Rotary evaporation is applicable when analyzing for PCDD/PCDF only. Snyder column apparatus is recommended when analyzing for PAH and PCB.

11.1.1 Optional Soxhlet Precleaning. Place an extraction thimble (see Section 6.3.3.3 of this method) and a plug of glass wool into the Soxhlet apparatus equipped with a Dean-Stark trap, charge the apparatus with toluene, and reflux for a minimum of 3 hours. Remove the toluene and discard it. Remove the extraction thimble from the extraction system and place it in a glass beaker to catch the solvent rinses from sample transfer to the extraction thimble. Retain the clean glass wool plug. Alternatively, confirm that the LMB for associated reagents, materials, and media meets the performance requirements in Section 13.1 of this method.

11.1.2 Container No. 1 (Filter) Preparation. Spike the filter with the appropriate pre-extraction filter recovery standard to result in the final sample extract concentrations shown in Tables 23-7, 23-8, and 23-9 of this method taking care that all spike liquid is distributed on the filter. Allow the filter to dry enough to prevent overspill, then transfer the filter and the contents of Container No. 1 directly to the glass extraction thimble in the glass solvent rinse catch beaker so that the filter will be completely immersed in the solvent during extraction.



11.1.3 Adsorbent Module. Spike the adsorbent with the appropriate pre-extraction standard to result in the final sample extract concentrations shown in Tables 23-7, 23-8, and 23-9 of this method, as applicable, spiked into the adsorbent, not on top of the adsorbent. Transfer the adsorbent material to the glass extraction thimble in the glass solvent rinse catch beaker. Rinse the module into the thimble in the beaker with the contents of Container No. 1. Alternatively, suspend the adsorbent module directly over the extraction thimble in a beaker, then, using a wash bottle containing methanol, flush the XAD-2 into the thimble onto the filter. Thoroughly rinse the interior of the glass module that contained the XAD-2 with toluene.

11.1.4 Container No. 2 (Acetone and Toluene Rinses). Concentrate the sample to a volume of no less than 5 mL. Concentrate samples containing toluene using a heating mantle and three-ball Snyder column or a rotary evaporator. Rinse sample Container No. 2 three times with small portions of toluene and add these to the concentrated solution and concentrate further to no less than 5 mL. This residue contains particulate matter removed in the rinse of the train probe and nozzle. Rinse the concentrated material from Container No. 2 into the glass extraction thimble containing the filter and the XAD-2 resin.

11.1.5 Transfer the solvent contained in the glass solvent rinse catch beaker to the extraction apparatus solvent reservoir. Rinse the beaker into the Soxhlet extraction apparatus solvent reservoir three times with small portions of toluene.

11.1.6 Container No. 3 (Impinger Water and Rinses). For PAH and PCB analysis, transfer the contents of Container No. 3 to a separatory funnel. Adjust to pH 2 with 6 N sulfuric acid, if necessary. Rinse the sample container with three successive 10-mL aliquots of the toluene and add these rinses to the separatory funnel. Extract the sample by vigorously shaking the separatory funnel for 5 minutes. After complete separation of the phases, remove the solvent and filter it through a bed of precleaned, dry sodium sulfate into the Soxhlet extraction apparatus

solvent reservoir. Repeat the extraction step two additional times. Adjust the pH to 11 with 6 N sodium hydroxide, re-extract the impinger water and rinses, and filter it through a bed of pre-cleaned, dry sodium sulfate into the Soxhlet extraction apparatus solvent reservoir. Rinse the sodium sulfate into the extraction apparatus solvent reservoir with fresh solvent and discard the sodium sulfate.

11.1.7 Add the appropriate pre-extraction standard for the target compound classes (at the final sample extract concentrations shown in Tables 23-7, 23-8, and 23-9 of this method) to the extraction thimble containing the combined filter and adsorbent sample fractions. Cover the contents of the extraction thimble with the cleaned glass wool plug to prevent the XAD-2 resin from splashing into the solvent reservoir of the extractor. Place the extraction thimble into the Soxhlet extraction apparatus.

11.1.8 Pour additional toluene to fill the solvent reservoir to approximately two-thirds capacity. Add PTFE boiling chips and assemble the apparatus.

11.1.9 Adjust the heat source to cause the extractor to cycle approximately three times per hour. Extract the sample for sufficient time to meet the pre-extraction standard recovery performance criteria in Section 13.15 of this method. The solvent should cycle completely through the system a minimum of 48 times.

11.2 Sample Aliquots for Cleanup and Analysis.

11.2.1 After extraction, allow the Soxhlet apparatus to cool.

11.2.2 Initial Extract Concentration. You may perform an initial concentration of the sample extract using the techniques (e.g., Kuderna Danish, rotary evaporation, nitrogen blowdown) found to recover the pre-extraction standard sufficient to meet the performance criteria in Section 13.15 of this method. Concentrate initial extracts in toluene using a heating mantle and three-ball

Snyder column or a rotary evaporator. Concentrate the field train proof blank and LMB samples in the same manner as samples.

Note: For samples requiring PCB or PAH analysis, it is recommended to perform the initial concentration using a three-ball Snyder column on the original extraction receiver flask. To meet isotopically labeled standard recoveries for low molecular weight PCB and PAH, do not evaporate samples to dryness and do not use a rotary evaporator to concentrate extracts.

11.2.3 Allow the sample extract to cool. You should use a minimum of one half of the sample extract for PCDD/PCDF analysis. You may archive the remaining sample extract or further split the sample extract for PCB and/or PAH analysis and archive.

Note: If using amount other than half the sample extract, adjust the spiking amount of the labeled standards accordingly.

11.2.4 If necessary, further concentrate the sample extract for cleanup and analysis using concentration techniques (e.g., Kuderna Danish, rotary evaporation, nitrogen blowdown) found to recover the pre-extraction standard sufficient to meet the performance criteria in Section 13 of this method.

11.3 Sample Cleanup and Fractionation. You may process a separate aliquot/split of the sample extract for each of the compound classes analyzed by this method. Sample cleanup for each compound class may include techniques in addition to column chromatography such as acid/base back-extraction, Gel Permeation Chromatography or high-performance liquid chromatography (HPLC) to isolate target compounds from interferences. This section includes a description of column chromatography shown to meet the performance criteria in Sections 9.2 and 13 of this method. The following sample cleanup and fractionation procedures are recommended but not required. You may modify cleanup column dimensions to meet manual or automated cleanup procedures as technology changes and improves. You must evaluate the cleanup and

fractionation procedures used to confirm acceptable recovery of isotopically labeled standards.

The alternative procedures must provide sufficient cleanup to meet method identification criteria (Section 11.4.3.4 of this method) and recovery criteria (Section 9.2 of this method). Section 13 of this method summarizes the method performance requirements.

Note: Recommendations in this section provide a cleanup approach that may allow multiple compound class measurement from a single aliquot of the original sample extract. Typically, Florisil® and alumina are used to separate PAH and PCDE from PCDD and PCDF target compounds. Use acid, neutral, and basic silica gel and cleanup procedures to remove nonpolar and polar interferences from samples destined for PCB and PCDD/PCDF analysis. Use Carbowack®/Celite® (or other equivalent carbon-based column material) to remove other nonpolar interferences.

11.3.1 PAH and PCDE Fractionation and Cleanup. You may use a Florisil® column to remove PAH and PCDE from the sample extract. You may also fractionate sample extracts using Florisil® as the first cleanup step to separate PAH for analysis.

Note: High concentrations of PAH may interfere, leading to failure of performance criteria for PCDD/PCDF or PCB analysis.

11.3.1.1 Pack a 6-mm ID chromatographic column or equivalent diameter glass pipet with a glass wool plug followed by approximately 1.5 g (approximately 2 mL) of activated Florisil®. Add approximately 1 cm (approximately 1 mL) of anhydrous sodium sulfate followed by a glass wool plug to the head of the column. Pre-elute the column with 10 mL of methylene chloride followed by 10 mL of hexane and discard the eluate.

11.3.1.2 When the solvent is within 1 mm of the packing, transfer the concentrated extract (up to 5 mL) to the top of the Florisil® column, rinse the sample container twice with 1 to 2 mL of hexane, adding each rinse to the column, and elute the column with 35 mL of 5%

dichloromethane in hexane. This fraction (Fraction 1) should contain target PCB, and selected hydrocarbons and chlorinated monoaromatic compounds.

11.3.1.3 Elute the column with 35 mL of 15% of dichloromethane in hexane and collect the eluate. This fraction (Fraction 2) should contain target PCDD/PCDF compounds.

11.3.1.4 Elute the column with 50 mL of 50% dichloromethane in hexane. The fraction (Fraction 3) should contain target PAH.

11.3.1.5 If necessary to remove any remaining polar organic compounds, elute the column with 70 mL of 15% acetone in hexane.

11.3.2 PCDD/PCDF and PCB Fractionation and Cleanup. You may remove PAH from the original aliquot of sample extract used for PCDD/PCDF analysis as described in Section 11.3.1 of this method. Design the column cleanup chromatography for PCDD/PCDF and PCB such that two consecutive fractions are collected (one with PCDD/PCDF and one with PCB) without impacting the detection limits. Depending on the source and sample matrix of the original sample, one or more of the following column cleanup approaches may be necessary to further remove polyhalogenated diphenyl ethers. You may use any number of permutations found in the referenced literature for this cleanup if the pre-extraction standard recoveries from field and LMB samples meet the associated performance criteria in Section 13 of this method.

Alternatively, you may use an automated cleanup approach that meets the labeled spike recovery requirements in Section 13 of this method.

11.3.2.1 Silica Gel Column Chromatography. Pack one end of a glass column, approximately 20 mm ID x 230 mm long, with glass wool. Add in sequence to the glass column, 1 g of silica gel, 2 g of sodium hydroxide impregnated silica gel, 1 g of silica gel, 4 g of acid-modified silica gel, 1 g of silica gel, and 1 cm layer of anhydrous sodium sulfate. Pre-elute the column with 30 to 50 mL of hexane leaving a small quantity of hexane above the sodium sulfate layer. Discard the pre-

elution hexane. Add the sample extract, dissolved in 5 mL of hexane to the head of the column. Allow the sample to flow into the column leaving a small quantity of hexane above the sodium sulfate layer. Rinse the extract container with two additional 5-mL rinses of hexane and apply each rinse to the column separately as the previous addition elutes. Elute the column with an additional 90 mL of hexane and retain the entire eluate. Concentrate this solution to a volume of about 1 mL using the nitrogen evaporative concentrator (see Section 6.3.5 of this method).

11.3.2.2 Silver Nitrate Silica Gel Column Chromatography. Pack a column (6 mm ID, 150 mm in length) sequentially with 1 g of silica gel and 1 g of 10% silver nitrate silica gel followed by a layer of about 10 mm of sodium sulfate (anhydrous). Wash the column sufficiently with hexane, elute until the liquid level reaches to the upper end of the column, and then transfer the concentrated sample (about 5 mL). Rinse the container several times with a small amount of hexane, elute with 200 mL of hexane at a flow rate about 2.5 mL/min (approximately one drop per second) to elute PCDD/PCDF.

11.3.2.3 Multi-layer Silica Gel Column Chromatography. You may use a multi-layer silica gel column in place of separate silica columns. Pack a column of 20 mm ID and 300 mm in length sequentially by the dry pack method with 0.9 g of silica gel, 3.0 g of 2% potassium hydroxide silica gel, 0.9 g of silica gel, 4.5 g of 44% sulfuric acid silica gel, 6.0 g of 22% sulfuric acid silica gel, 0.9 g of silica gel, 3.0 g of 10% silver nitrate silica gel, 2.0 g of silica gel and 6.0 g of sodium sulfate (anhydrous). Wash the column sufficiently with hexane, elute until the liquid level reaches to the upper end of the column, and then load the sample solution. Rinse the container several times with a small amount of hexane, elute with 150-200 mL of hexane at a flow rate about 2.5 mL/min (approximately one drop per second) to elute PCDD/PCDF.

11.3.2.4 Basic Alumina Column Chromatography. Pack a column (20 mm ID, 300 mm in length) with approximately 6 to 12 g of basic alumina. Pre-elute the column with 50 to 100 mL of

hexane. Transfer the concentrated extract from the previous column cleanup to the top of the basic alumina column. Allow the sample to flow into the column leaving a small quantity of solvent above the top of the bed. Rinse the extract container with two additional 1-mL rinses of hexane and apply each rinse to the column separately as the previous addition elutes. Elute the column with 100 mL hexane to remove the interferences. Elute the PCDD/PCDF from the column with 20 to 40 mL of 50% methylene chloride in hexane. The ratio of methylene chloride to hexane may vary depending on the activity of the alumina used in the column preparation. Do not let the head of the column go without solvent. The first 100 mL hexane eluate is not used for subsequent PCDD/PCDF analysis. The eluate is concentrated to approximately 0.5 mL using the nitrogen evaporative concentrator.

11.3.2.5 Carbopack® C/Celite® 545 Column or Equivalent. Cut both ends from a 10 mL disposable Pasteur pipette (see Section 6.4.1 of this method) to produce a 10 cm column. Fire-polish both ends and flare both ends if desired. Insert a glass wool plug at one end and pack the column with 0.55 g of Carbopack®/Celite® (see Section 7.8.9.4 of this method) to form an adsorbent bed approximately 2 cm long. Insert a glass wool plug on top of the bed to hold the adsorbent in place. Pre-elute the column with 5 mL of toluene followed by 2 mL of methylene chloride:methanol:toluene (15:4:1 v/v), 1 mL of methylene chloride:cyclohexane (1:1 v/v), and 5 mL of hexane. If the flow rate of eluate exceeds 0.5 mL/minute, discard the column. Do not let the head of the column go without solvent. Add the sample extract to the column. Rinse the sample container twice with 1 mL portions of hexane and apply separately to the column. Apply 2 mL of hexane to the head of the column to complete the transfer. Elute the interfering compounds with two 3 mL portions of hexane, 2 mL of methylene chloride:cyclohexane (1:1 v/v), and 2 mL of methylene chloride:methanol:toluene (15:4:1 v/v). Discard the eluate. Invert the column and elute the PCDD/PCDF with 20 mL of toluene. If carbon particles are present in

the eluate, filter through glass-fiber filter paper. Concentrate the eluate to approximately 0.5 mL using the nitrogen evaporative concentrator for further cleanup or analysis by HRGC/HRMS.

#### 11.4 PCDD, PCDF, PCB and PAH Analysis.

11.4.1 Analyze the sample extract with an HRGC/HRMS using the instrumental parameters in Sections 11.4.2 and 11.4.3 of this method.

11.4.1.1 Immediately prior to analysis, add an aliquot (typically 20 microliters ( $\mu\text{l}$ )) of the pre-analysis standard to result in the final sample extract concentrations in Tables 23-7, 23-8, and 23-9 of this method to each sample as appropriate for the compounds you are measuring by this method.

11.4.1.2 Inject an aliquot of the sample extract into the GC, typically 1  $\mu\text{l}$ . You may perform separate analyses using different GC columns for each of the target compound classes. Perform calibration and sample analysis for each target compound class using the same instrument operating conditions including injection volume.

11.4.1.2.1 If target compounds are not resolved sufficiently from other target compounds or interferences in the sample to meet the requirements in Section 10.2.3.5 or 10.2.3.6 of this method, as applicable to the compound class being analyzed, or as otherwise specified in an applicable regulation, permit, or other requirement, analyze another aliquot of the sample using an alternative column that provides elution order to uniquely quantify the target compounds subject to interference on the first GC column.

11.4.1.2.2 You may use column systems other than those recommended in this method provided the analyst is able to demonstrate, using calibration and CCVs, that the alternative column system is able to meet the applicable specifications of Section 10.2.3.5 or 10.2.3.6 of this method.

#### 11.4.2 Example Gas Chromatograph Operating Conditions.



11.4.2.1 Injector. Configured for capillary column, splitless, 250 °C (482 °F).

11.4.2.2 Carrier Gas. Helium, 1 to 2 mL/min.

11.4.2.3 Oven. Optimize the GC temperature program to achieve the required separation and target compound recovery for the GC column in use. Table 23-16 of this method presents the typical conditions for a DB5-MS column.

11.4.3 High-Resolution Mass Spectrometer.

11.4.3.1 Ionization Mode. Electron ionization.

11.4.3.2 Source Temperature. Maintain the source temperature in the range of 250 to 300 °C (482 to 572 °F).

11.4.3.3 Ion Monitoring Mode. Tables 23-4, 23-5, and 23-6 of this method summarize the various ions to be monitored for PCDD/PCDF, PAH, and PCB, respectively.

11.4.3.4 Identification Criteria for Target Compounds. Use the following identification criteria for the characterization of target compounds in this method. The available native and isotopically labeled standards allow the unique identification of all PCDD/PCDF, PAH, and selected PCB congeners required in this method. Also see Sections 13.12 and 13.13 of this method for identification criteria for PCDD/PCDF/PCB and PAH target compounds, respectively.

11.4.3.4.1 For PCDD/PCDF and PCB, Table 23-15 of this method provides acceptance limits for the integrated ion abundance ratio of primary and secondary target compound ions. When the ion abundance ratio for a target analyte is outside the performance criteria, you may reanalyze samples on an alternative GC column to resolve chemical interferences, tune the mass spectrometer to operate at a higher mass resolution to discriminate against the interference(s), and/or further cleanup an archived sample to remove the interference(s). Report analysis results as an EMPC when a response meets identification criteria except the ion abundance ratio criteria

or when a peak representing a PCDE has been detected at the retention time. This method does not consider EMPC-flagged data to be zero concentrations.

Note: Some EMPCs may be caused by poor ion statistics when the concentration of the target compound is at or near the DL.

11.4.3.4.2 The retention time for the analytes must be within 3 seconds of the corresponding labeled pre-extraction standard.

11.4.3.4.3 The signals for the two exact masses in Tables 23-4 and 23-6 of this method for PCDD/PCDF and PCB, respectively, must be present and must reach their maximum response within two seconds of each other.

11.4.3.4.4 Identify and quantify specific target compounds or isomers that do not have corresponding pre-extraction standard compounds by comparing to the pre-extraction standard of the same compound class with the nearest retention time to target compound.

11.4.3.4.5 For the identification of specific PCB congeners, the retention time of the native congener must be within 0.006 relative retention time (RRT) units of the pre-extraction standard.

11.4.3.4.6 For qualitative identification, the S/N ratio for the GC signal present in every selected ion current profile for native compound response must be greater than or equal to 2.5.

11.4.3.4.7 The separation of target compounds, including 2,3,7,8–TeCDD and 2,3,7,8–TeCDF, must satisfy the separation criteria in Section 10.2.3.5 of this method and all the identification criteria specified in Sections 11.4.3.4.1 through 11.4.3.4.6 of this method. See Section 13.5 of this method on confirmation columns, if needed.

11.4.3.4.8 Chlorodiphenyl Ether Interference. If chromatographic peaks are detected at the retention time of any PCDF in any of the m/z channels used to monitor PCDE, there is evidence of a positive interference and you may opt to flag data noting the interference and keep the value to calculate PCDF concentration as EMPC or reanalyze to remove or shift the interference. This

method recommends alumina (see Section 11.3.2.4 of this method) and Florisil® (see Section 11.3.1 of this method) liquid column chromatography packing materials for removal of PCDE during sample cleanup.

11.4.3.4.9 Set the MS lock-mass ions as specified in Tables 23-4, 23-5, and 23-6 of this method for PCDD/PCDF, PAH, and PCB, respectively. Monitor the QC check ions to verify instrument stability during the analysis. If the QC check ion signal varies by more than 25% from the average response across the run, flag results for all isomers at corresponding retention time as the lock-mass ions or QC check ions. You have the option to reanalyze after additional cleanup on the sample (or an archived portion of the sample if the archive is available), or after dilution of the sample. Alternately, determine through additional quality review whether the target analyte and its corresponding isotopically labeled standard are equally affected by the change in lock-mass ions and/or QC check ions. When you reanalyze a sample, ensure all concentration calculations are reported from the reanalyzed sample.

11.4.3.4.10 For the identification of PAH, the RRT of each native to its labeled compound must be within 0.006 RRT units compared to the corresponding RRTs in the continuing calibration. The signals for the characteristic ion listed in Table 23-5 of this method must be present.

11.4.3.5 Quantitation. Measure the response of each native target compound and the corresponding pre-extraction standard. Using the CCV RRF, calculate the mass of each target compound, using equations in Section 12.7 of this method. Use the pre-extraction standard to correct the native target compounds result for variations in performance of the extraction, cleanup, and concentration steps of the analysis. Recovery of pre-extraction standard must meet minimum specifications (in Section 9.2. of this method) to ensure that the method performance and reliability have not been compromised by unacceptable losses during sample processing. Table 23-17 of this method shows the assignments for pre-extraction standard compounds for

use in calculating the response factor and the concentrations of PCB. Recoveries of all labeled standard compounds must meet the minimum recovery specifications in Section 13 of this method. Note: Unacceptably low recoveries can be an indication of a sample processing step that caused the low recoveries, such as spiking errors.

11.4.3.5.1 Use Equation 23-7 to calculate the amount of each target compound or group in the sample.

11.4.3.5.2 Use Equation 23-8 to calculate the concentration per dscm of each target compound or group in the gas.

11.4.3.5.3 Quantify native PCDD and PCDF in its homologous series using the corresponding native and pre-extraction standard response in its homologous series. For example, use  $^{13}\text{C}_{12}$ -2,3,7,8-TeCDD to calculate the concentrations of all other tetra chlorinated isomers.

11.4.3.5.4 As an option or as required or specified in applicable regulations, permits, or other requirements, you may quantify any or all other PCB congeners as resolved or coeluting combinations using the RRF of the nearest eluting native target PCB in the same homolog group and the pre-extraction standard assigned in Appendix A to this method.

11.4.3.5.5 As an option or as required or specified in applicable regulations, permits, or other requirements, report the total concentration of congeners at a given level of chlorination (homolog; i.e., total TrCB, total PeCB, total HxCB) by summing the concentrations of all congeners identified in the retention time window for the homologs as assigned in Appendix A to this method.

11.4.3.5.6 As an option or if required in an applicable regulation, permit or other requirement, total PCB may be reported by summing all congeners identified at all window-defining congeners (WDCs) as assigned in Appendix A to this method.

## *12.0 Data Analysis and Calculations*

Note: Same as Section 12 of Method 5 of Appendix A-3 to 40 CFR part 60, with the following additions.

12.1 Nomenclature.

$A_{1n}$  = Integrated ion current of the primary m/z values for the target native compound.

$A_{1pe}$  = Integrated ion current of the primary m/z values for the pre-extraction standard compound (assigned in Tables 23-4, 23-5, and 23-6 of this method).

$A_{1pa}$  = Integrated ion current of the primary m/z values for the pre-analysis standard compound.

$A_{2n}$  = Integrated ion current of the secondary m/z values for the target native compound. For PAH  $A_{2n} = 0$ .

$A_{2pe}$  = Integrated ion current of the secondary m/z's for the pre-extraction standard compound. For PAH  $A_{2l} = 0$ .

$A_{2pa}$  = Integrated ion current of the secondary m/z values for the pre-analysis standard compound.

$Q_n$  = Quantity of the target native compound, pg.

$Q_{pe}$  = Quantity of the pre-extraction standard, pg.

$Q_{pa}$  = Quantity of the pre-analysis standard, pg.

$C_i$  = Mass of compound i in the sample, pg.

$C_{idscm}$  = Concentration of target native compound i in the emission gas, pg/dscm.

$C_T$  = Total mass of target compounds in the sample, pg/sample.

dscm = Dry standard cubic meters of gas volume sample measured by the dry gas meter, corrected to standard conditions.

$H_{ai}$  = Summed heights of the noise for each quantitation ion for native target compounds.

$H_{ci}$  = Summed heights of the noise at the primary and secondary m/z's of the pre-extraction standard i.

$L_{PIR}$  = Lower limit for the prediction interval of results.

$n$  = Number of values.

PD = Percent Difference in the RRF of the continuing calibration verification compared to the average RRF of the initial calibration, %.

R = Recovery of pre-sampling adsorbent standard and pre-extraction filter recovery standard, %.

$R_{pe}$  = Recovery of pre-extraction standard, %.

$RRF_i$  = Relative response factor of a native target compound or pre-sampling adsorbent standard and pre-extraction filter recovery standard at calibration level  $i$ .

$RRF_{pe}$  = Relative response factor of a pre-extraction standard compound.

$RRF_{ccv}$  = Relative response factor of a native target compound or pre-sampling adsorbent standard and pre-extraction filter recovery standard in the continuing calibration verification.

RSD = Relative standard deviation, in this case, of RRFs over the calibration levels, %.

SD = Standard deviation.

$SD_{RRF}$  = Standard deviation of initial calibration RRFs.

$U_{PIR}$  = Upper limit for the prediction interval of results.

WDC = Window-defining congener representing an isotopically labeled compound that defines the beginning or end of a retention time window bracketing a target homolog.

12.2 Individual Compound RRF for Each Calibration Level  $i$ . Equation 23-1 for the response factor of each target native compound relative to its labeled pre-extraction standard analog includes the integrated ion current of both the primary and secondary  $m/z$  values for each compound in the calibration standard, excluding PAH, which use only primary  $m/z$  values. Use Equation 23-2 to calculate the RRF for pre-extraction standard.

$$RRF_i = \frac{(A1_n + A2_n)Q_{pe}}{(A1_{pe} + A2_{pe})Q_n} \quad \text{Eq. 23-1}$$

$$RRF_{pe} = \frac{(A1_{pe} + A2_{pe})Q_{pa}}{(A1_{pa} + A2_{pa})Q_{pe}} \quad \text{Eq. 23-2}$$

Note: the units for  $Q_{pe}$  and  $Q_n$  in Eq. 23-1 and the units for  $Q_{pa}$  and  $Q_{pe}$  in Eq. 23-2 must be the same.

12.3 Average RRF for Each Compound Over the Minimum of Five Calibration Levels.

$$\overline{RRF} = \frac{1}{n} \sum_{i=1}^n RRF_i \quad \text{Eq. 23-3}$$

12.4 Percent RSD of the RRFs for a Compound Over the Calibration Levels. The requirement for the initial calibration RSD is in Section 13.9 and Table 23-14 of this method.

$$\%RSD = \frac{SD_{RRF}}{RRF} \times 100\% \quad \text{Eq. 23-4}$$

12.5 Standard Deviation of the RRFs for a Compound Over the Calibration Levels.

$$SD_{RRF} = \sqrt{\sum_{i=1}^n \frac{(x_i - \bar{x})^2}{n-1}} \quad \text{Eq. 23-5}$$

12.6 Percent Difference of the RRF of the Continuing Calibration Verification Compared to the Average RRF from the Initial Calibration for Each Target Compound. Use Equation 23-1 to calculate the RRF for the continuing calibration verification for comparison to the average RRF from the initial calibration. The requirement for the continuing calibration verification % difference is in Section 13.10 and Table 23-14 of this method.

$$PD = \frac{RRF_{ccv} - \overline{RRF}}{\overline{RRF}} \times 100\% \quad \text{Eq. 23-6}$$

12.7 Amount of Individual Target Compound  $i$  in the Sample by Isotope Dilution (pg). This equation corrects for the target native compound recovery based on its labeled pre-extraction standard analog. This equation is also used to calculate the amount of pre-sampling adsorbent standard and pre-extraction filter recovery standard recovered.

$$C_i = \left[ \frac{Q_{pe} (A1_n + A2_n)}{(A1_{pe} + A2_{pe}) RRF_{CCV}} \right] \quad \text{Eq. 23-7}$$

### 12.8 Concentration of the Individual Target Compound or Group i in the Emission Gas

(pg/dscm). The total concentration of a target compound group in the sample can be calculated by substituting  $C_T$  from Eq. 23-12 for  $C_i$  in Eq 23-8.

$$C_{idscm} = \frac{C_i}{dscm} \quad \text{Eq. 23-8}$$

12.9 Recovery of Labeled Compound Standards. Use Equation 23-9 to determine the recovery of pre-sampling adsorbent standard and the pre-extraction filter recovery standard. Use Equation 23-10 to determine the recovery of the pre-extraction standard. The recovery performance criteria for these standards are in Sections 13.14, 13.15, and 13.16 of this method.

$$R = \frac{\text{conc. found}}{\text{conc. spiked}} \times 100\% \quad \text{Eq. 23-9}$$

$$R_{pe} = \left[ \frac{Q_{pa} (A1_{pe} + A2_{pe})}{(A1_{pa} + A2_{pa}) (Q_{pe}) (RRF_{pe})} \right] \times 100\% \quad \text{Eq. 23-10}$$

Note:  $R_{pe}$  must be corrected for the fraction of the original sample extract used for analysis. (e.g., if half of the extract is used for analysis of the target class,  $R_{pe}$  must be multiplied by a factor of 2).

### 12.10 Estimated Detection Limit (EDL).

$$EDL = \frac{2.5 (H_{ai}) Q_{pe}}{H_{ci} \times RRF_{CCV}} \quad \text{Eq. 23-11}$$

### 12.11 Total Target Compound Mass.

$$C_T = \sum_{i=1}^n C_i \quad \text{Eq. 23-12}$$



Note: Unless otherwise specified in applicable regulations, permits or other requirements, count any target compounds reported as non-detected as EDL when calculating the concentration of target compounds in the sample.

### 12.12 Upper and Lower Limits for the Prediction Interval of Results (PIR)

Half Range (HR) for the Prediction Interval of Results

$$HR_{PIR} = (3.963)(S) \quad \text{Eq. 23-13}$$

Note: 3.963 is a constant value for seven replicates.

Upper and Lower Limits for the Prediction Interval of Results

$$U_{PIR} = \left[ \frac{(Mean + HR_{PIR})}{[Spike Concentration]} \right] 100\% \quad \text{Eq. 23-14}$$

$$L_{PIR} = \left[ \frac{(Mean - HR_{PIR})}{[Spike Concentration]} \right] 100\% \quad \text{Eq. 23-15}$$

### 13.0 Method Performance

Data generated with this method must be fit for purpose. Applicable results of method performance criteria in this section must be reported. Consequences of failed quality criteria are provided with the criteria in this section.

13.1 Background Assessment - Field Train Proof Blank, LMB and Materials. Determine the contribution to target compound concentration from reagents, media and glassware used to make target compound measurements. Conduct at least one field train proof blank for each test series at a single facility. Analyze at least one LMB sample during an analytical sequence or every 12 hours, whichever is shorter. The field train proof blank, LMB and materials assessment must meet the performance specifications in Tables 23-7, 23-8, and 23-9, as applicable to the compound target list. Native target compound concentrations must be less than or equal to three times the EDL of the method or 10 times lower than the quantitation limit required by the end use of the data (e.g., compliance limit or other limits set by consent decree or permit), whichever

is higher. If field train proof blank or LMB fails this criterion, flag associated sample data with an explanation. Failure to meet field train proof blank requirements may invalidate the test results at the discretion of the regulatory authority or end data user. If the field train proof blank or the LMB results are above the EDL, report the EDLs as equal to the sample-specific EDL, the LMB, or the field train proof blank, whichever is larger.

13.2 GC column or column systems used to measure PCDD/PCDF must meet the column separation requirements in Section 6.5.2.1 of this method and the applicable requirements in Sections 10.2.3.5 and 11.4.3.4 of this method using the continuing calibration verification.

Failure to meet this chromatographic resolution criterion requires data from this analysis to be flagged explaining the potential bias of the results.

13.3 GC column or column systems used to measure PAH must meet the column separation requirements in Section 6.5.2.2 of this method and the applicable requirements in Sections 10.2.3.5 and 11.4.3.4 of this method using the continuing calibration check. Failure to meet this chromatographic resolution criterion requires data from this analysis to be flagged explaining the potential bias of the results.

13.4 GC column or column systems used to measure PCB must meet the column separation requirements in Section 6.5.2.3 of this method and the applicable requirements in Sections 10.2.3.5 and 11.4.3.4 of this method using the continuing calibration check and be able to achieve unique resolution and identification of the toxics for determination of a  $TEQ_{PCB}$ . The rule requiring the use of this method will establish which WHO TEF to use. Failure to meet this chromatographic resolution criterion requires data from this analysis to be flagged explaining the potential bias of the results.

13.5 Confirmation Column. If target compounds are not sufficiently resolved from other target compounds or interferences in the sample to meet the requirements for target compounds in

Sections 13.2, 13.3, and/or 13.4 of this method, analyze another aliquot of the sample in a separate run using an alternative column that provides elution order to uniquely quantify the target compounds subject to interference on the first GC column. When using a confirmation column, document the required resolution.

### 13.6 Detection Limits.

13.6.1 MDL. The MDLs are determined following the procedures in Section 9.3.7 of this method. MDLs are confirmed by preparing and analyzing a spiked sample (spiked at 1 to 5 times the determined MDL, see Section 9.3.8), then confirm that the target compounds meet the qualitative identification criteria in Section 11.4.3.4 of this method. If the MDL confirmation criteria are not met, the MDL determination is repeated with a higher spike concentration until criteria are met.

13.6.2 EDL. If the sample specific EDLs are less than 50% of the emission standard, the EDLs are acceptable. If the field train proof blank or the LMB results are above the EDL, calculate and report the test-specific and compound-specific EDLs as equal to the sample-specific EDL, or the measured concentration in the LMB or field train proof blank, whichever is larger.

13.7 Tune. The groups of monitored ions are listed in Tables 23-4, 23-5, and 23-6 of this method, as applicable for the target compound class. Tune the instrument to meet the required resolving power in Section 10.2.1 for the desired target compound class. Assess the resolution at three exact  $m/z$ 's representing the low, mid and high  $m/z$  range of the masses used to measure the target compound class. You may use peak matching and the chosen PFK (or FC43) reference peak to verify that the exact mass is within 5 ppm of the required value.

13.8 Lock-Mass Ions. The MS lock-mass and QC check ions in Tables 23-4, 23-5, and 23-6 of this method are recommended for PCDD/PCDF, PCB, or PAH, respectively. The reference compounds PFK or FC43 have ions that may be selected as your lock-mass and QC check ions.

Monitor the QC check ions specified in these tables to verify instrument stability during the analysis; these must not vary > 25% from the average response. Additional cleanup on sample extract (or archive extract) and reanalysis is necessary for failure to maintain lock-mass during analysis.

### 13.9 Initial Calibration.

13.9.1 The RSD for mean RRF from each of the target analytes and labeled standards in the calibration samples must not exceed the values in Table 23-14 of this method.

13.9.2 The S/N in every selected ion current profile must be  $\geq 10$  for all unlabeled targets and labeled standards in the calibration samples.

13.9.3 The ion abundance ratios must be within the control limits in Table 23-15 of this method.

### 13.10 Continuing Calibration Verification.

13.10.1 The RRF for each unlabeled and labeled compound measured in a CCV must not deviate from the initial calibration by more than the limits shown in Table 23-14 of this method.

13.10.2 The ion abundance ratios must be within the control limits in Table 23-15 of this method.

13.10.3 The S/N ratio for the GC/MS signal present in every selected ion current profile must be greater than or equal to 10.

13.10.4 Repeat the initial calibration when there is a failure to meet the requirements for an acceptable CCV analysis.

13.10.5 Column Separation Check. Use the results from a CCV to verify and document the resolution required in Sections 13.2, 13.3, or 13.4 of this method for the target compound classes analyzed with this method. The separation criteria are applicable to all the compounds in a target class whether analyzed by a single or multiple GC columns. If a confirmation column is used, document required resolution (Section 13.5).

13.11 QCS. A QCS must be analyzed during the IDC and after initial calibrations (at a minimum quarterly). The acceptance criterion for the QCS is 70–130% of the true value. If the accuracy for any analyte fails the recovery criterion, prepare fresh standard dilutions and repeat. If the freshly prepared QCS fails, determine the cause, recalibrate the instrument if necessary and reanalyze the QCS.

13.12 Compound Identification for PCDD/PCDF and PCB.

13.12.1 Target compounds must have ion abundance ratios within the control limits in Table 23-15 of this method. PAH target compounds have single ion identifiers with no ion abundance ratio requirement. Report analysis results as an EMPC when a response meets identification criteria but fails the ion abundance ratio criteria or when a peak representing a PCDE has been detected at the target compound retention time.

13.12.2 The retention time for the analytes must be within 3 seconds of the corresponding pre-extraction standard.

13.12.3 The monitored ions, shown in Table 23-4 of this method for a given PCDD/PCDF, must reach their maximum response within 2 seconds of each other.

13.12.4 The monitored ions, shown in Table 23-6 of this method for a given PCB, must reach their maximum response within 2 seconds of each other.

13.12.5 For the identification of specific PCB, the RRT of the native congener must be within 0.006 RRT units of the pre-extraction standard RRT.

13.12.6 The S/N ratio for the monitored ions for native compounds must be greater than or equal to 2.5.

13.12.7 Identify and quantify isomers that do not have corresponding pre-extraction standard compounds by comparing to the pre-extraction standard of the same compound class with the nearest retention time to the target compound.

13.12.8 If chromatographic peaks are detected at the retention time of any PCDD/PCDF in any of the m/z channels used to monitor chlorophenyl ethers, there is evidence of interference and positive bias. Data must be flagged to indicate an interference. You may report the total with bias for the affected target. To reduce the bias, you may use a confirmatory column or perform additional clean up on an archived sample followed by reanalysis.

### 13.13 Compound Identification for PAH.

13.13.1 The signals for the characteristic ion listed in Table 23-5 of this method must be present.

13.13.2 The RRT between each native and labeled compound must be within 0.006 RRT units.

### 13.14 Pre-sampling Adsorbent Standard and Pre-extraction Filter Recovery Standard Recovery.

Recoveries of pre-sampling standard added to the sample and pre-extraction filter recovery standard added to the filter must be between 70 and 130% (Tables 23-7, 23-8, and 23-9 of this method).

13.14.1 If the recovery of all the pre-sampling adsorbent standard compounds is below 70%, the sampling runs are not valid, and you must repeat the stack or vent sampling and subsequent analysis. As an alternative, you do not have to repeat the test if the average pre-sampling adsorbent standard recovery is 25% or more and you divide the final results by the average fraction of pre-sampling adsorbent standard recovery.

13.14.2 If the recovery of all the pre-extraction filter recovery standard compounds is below 70%, you may reanalyze the sample. If the recovery criteria are still not met, the sampling recovery is not valid, and you must repeat the stack or vent sampling and subsequent analysis.

13.15 Pre-extraction Standard Recovery. Recoveries of all pre-extraction standard compounds added to the sample must be between 20 to 130% for PCDD/PCDF and PAH (Tables 23-7 and 23-8 of this method) and between 20 to 145% for PCB (Table 23-9 of this method). If the recovery criteria are not met, you may reanalyze the sample and/or prepare and analyze the

archive sample. If the recovery criteria are still not met, the sampling run is not valid, and the stack test must be repeated.

13.16 Pre-analysis Standard Response. Response of all pre-analysis standard compounds must show a S/N for every selected ion current profile of  $\geq 10$ . If the minimum response is not met, you must reanalyze the sample. Poor sensitivity compared to initial calibration response may indicate injection errors or instrument drift.

13.17 IDC - Lowest calibration concentration, Demonstration of precision, Demonstration of accuracy.

13.17.1 Lowest calibration concentration. The Upper PIR Limit must be less than, or equal to, 150%; and the Lower PIR Limit must be greater than, or equal to, 50%. If these criteria are not met, the lowest calibration point has been set too low and must be confirmed at a higher concentration.

13.17.2 Demonstration of precision. The percent relative standard deviation (%RSD) of the concentrations from the replicate analyses must be less than 20% for all target analytes.

Demonstration would be repeated for failed compounds only.

13.17.3 Demonstration of accuracy. The average % recovery for each target analyte must be within 70 to 130%. Demonstration would be repeated for failed compounds only.

13.18 Requirements for Equivalency. The Administrator considers any modification of this method, beyond those expressly permitted in this method as options, to be a major modification subject to application and approval of alternative test procedures following EPA Guidance Document 22 currently found at: <https://www.epa.gov/emc/emc-guideline-documents>.

13.19 Records. As part of the laboratory's quality system, the laboratory must maintain records of modifications to this method.

#### *14.0 Pollution Prevention*

The target compounds used as standards in this method are prepared in extremely small amounts and pose little threat to the environment when managed properly. Prepare standards in volumes consistent with laboratory use to minimize the disposal of excess volumes of expired standards.

### *15.0 Waste Management*

15.1 The laboratory is responsible for complying with all federal, state, and local regulations governing waste management, particularly the hazardous waste identification rules and land disposal restrictions, and for protecting the air, water, and land by minimizing and controlling all releases from fume hoods and bench operations. The laboratory must also comply with any sewage discharge permits and regulations. The EPA's *Environmental Management Guide for Small Laboratories* (EPA 233-B-98-001) provides an overview of requirements.

15.2 Samples containing hydrogen chloride or sulfuric acid to pH <2 are hazardous and must be handled and disposed in accordance with federal, state, and local regulations.

15.3 For further information on waste management, consult *The Waste Management Manual for Laboratory Personnel* and *Less is Better-Laboratory Chemical Management for Waste Reduction*, available from the American Chemical Society's Department of Government Relations and Science Policy, 1155 16th Street N.W., Washington, D.C. 20036.

### *16.0 Bibliography*

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17.0 Tables, Diagrams, Flowcharts, and Validation Data

**Table OTM46-1. Polychlorinated Dibenzo-*p*-dioxin and Polychlorinated Dibenzofuran Target Analytes**

Polychlorinated Dibenzo- <i>p</i> -dioxins	CAS <sup>a</sup> Registry Number	Polychlorinated Dibenzofurans	CAS Registry Number
2,3,7,8-TeCDD	1746-01-6	2,3,7,8-TeCDF	51207-31-9
1,2,3,7,8-PeCDD	40321-76-4	1,2,3,7,8-PeCDF	57117-41-6
1,2,3,4,7,8-HxCDD	39227-28-6	2,3,4,7,8-PeCDF	57117-31-4
1,2,3,6,7,8-HxCDD	57653-85-7	1,2,3,4,7,8-HxCDF	70648-26-9
1,2,3,7,8,9-HxCDD	19408-74-3	1,2,3,6,7,8-HxCDF	57117-44-9
1,2,3,4,6,7,8-HpCDD	35822-46-9	1,2,3,7,8,9-HxCDF	72918-21-9
Total TeCDD	41903-57-5	2,3,4,6,7,8-HxCDF	60851-34-5
Total PeCDD	36088-22-9	1,2,3,4,6,7,8-HpCDF	67562-39-4
Total HxCDD	34465-46-8	1,2,3,4,7,8,9-HpCDF	55673-89-7
Total HpCDD	37871-00-4	Total TeCDF	55722-27-5
OCDD	3268-87-9	Total PeCDF	30402-15-4
		Total HxCDF	55684-94-1
		Total HpCDF	38998-75-3
		OCDF	39001-02-0

**Table OTM46-2. Polycyclic Aromatic Hydrocarbon Target Analytes**

Polycyclic Aromatic Hydrocarbons	CAS <sup>a</sup> Registry Number	Polycyclic Aromatic Hydrocarbons	CAS <sup>a</sup> Registry Number
Naphthalene	91-20-3	Chrysene	218-01-9
2-Methylnaphthalene	91-57-6	Benzo[ <i>b</i> ]fluoranthene	205-99-2
Acenaphthylene	208-96-8	Benzo[ <i>k</i> ]fluoranthene	207-08-9
Acenaphthene	83-32-9	Perylene	198-55-8
Fluorene	86-73-7	Benzo[ <i>a</i> ]pyrene	50-32-8
Anthracene	120-12-7	Benzo[ <i>e</i> ]pyrene	192-92-2
Phenanthrene	85-01-8	Benzo[ <i>g,h,i</i> ]perylene	191-24-2
Fluoranthene	206-44-0	Indeno[ <i>1,2,3-cd</i> ]pyrene	193-39-5
Pyrene	129-00-0	Dibenz[ <i>a,h</i> ]anthracene	53-70-3
Benz[ <i>a</i> ]anthracene	56-55-3		

**Table OTM46-3. Polychlorinated Biphenyl Target Analytes**

PCB Congener	BZ No. <sup>a</sup>	CAS <sup>b</sup> Registry Number	PCB Congener	BZ No. <sup>a</sup>	CAS <sup>b</sup> Registry Number
2,4'-DiCB	8	34883-43-7	2,2',3,3',4,4'-HxCB	128	38380-07-3

PCB Congener	BZ No. <sup>a</sup>	CAS <sup>b</sup> Registry Number	PCB Congener	BZ No. <sup>a</sup>	CAS <sup>b</sup> Registry Number
2,2',5-TrCB	18	37680-65-2	2,2',3,4,4',5'-HxCB	138	35065-28-2
2,4,4'-TrCB	28	7012-37-5	2,2',4,4',5,5'-HxCB	153	35065-27-1
2,2',3,5'-TeCB	44	41464-39-5	2,3,3',4,4',5-HxCB	156	38380-08-4
2,2',5,5'-TeCB	52	35693-99-3	2,3,3',4,4',5'-HxCB	157	69782-90-7
2,3',4,4'-TeCB	66	32598-10-0	2,3',4,4',5,5'-HxCB	167	52663-72-6
3,3',4,4'-TeCB	77	32598-13-3	3,3',4,4',5,5'-HxCB	169	32774-16-6
3,4,4',5-TeCB	81	70362-50-4	2,2',3,3',4,4',5-HpCB	170	35065-30-6
2,2',4,5,5'-PeCB	101	37680-73-2	2,2',3,4,4',5,5'-HpCB	180	35065-29-3
2,3,3',4,4'-PeCB	105	32598-14-4	2,2',3,4',5,5',6-HpCB	187	52663-68-0
2,3,4,4',5-PeCB	114	74472-37-0	2,3,3',4,4',5,5'-HpCB	189	39635-31-9
2,3',4,4',5-PeCB	118	31508-00-6	2,2',3,3',4,4',5,6-OcCB	195	52663-78-2
2',3,4,4',5-PeCB	123	65510-44-3	2,2',3,3',4,4',5,5',6-NoCB	206	40186-72-9
3,3',4,4',5-PeCB	126	57465-28-8	2,2',3,3',4,4',5,5',6,6'-DeCB	209	2051-24-3

a BZ No.: Ballschmiter and Zell 1980, or International Union of Pure and Applied Chemistry (IUPAC) number.

b Chemical Abstract Service.

**Table OTM46-4. Elemental Compositions and Exact Masses of the Ions Monitored by High-Resolution Mass Spectrometry for PCDD and PCDF**

Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte <sup>b</sup>	Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte <sup>b</sup>
263.9871	LOCK	C <sub>5</sub> F <sub>10</sub> N	FC43	383.8639	M	<sup>13</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>6</sub> O	HxCDF (S)
292.9825	LOCK	C <sub>7</sub> F <sub>11</sub>	PFK	385.8610	M+2	<sup>13</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> ClO	HxCDF (S)
303.9016	M	C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>4</sub> O	TeCDF	389.8157	M+2	C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> ClO <sub>2</sub>	HxCDD
305.8987	M+2	C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sup>37</sup> ClO	TeCDF	391.8127	M+4	C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl <sub>2</sub> O <sub>2</sub>	HxCDD
313.9839	QC	C <sub>6</sub> F <sub>12</sub> N	FC43	392.9760	LOCK	C <sub>9</sub> F <sub>15</sub>	PFK
315.9419	M	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>4</sub> O	TeCDF (S)	401.8559	M+2	<sup>13</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> ClO <sub>2</sub>	HxCDD (S)
316.9745	M+2	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> ClO	TeCDF (S)	403.8529	M+4	<sup>13</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl <sub>2</sub> O	HxCDD (S)
317.9389	M+2	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>2</sub> <sup>37</sup> ClO	TeCDF (S)	425.9775	QC	C <sub>9</sub> F <sub>16</sub> N	FC43
319.8965	M	C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>4</sub> O <sub>2</sub>	TeCDD	445.7555	M+4	C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl <sub>2</sub> O	OCDPE
321.8936	M+2	C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> ClO <sub>2</sub>	TeCDD	407.7818	M+2	C <sub>12</sub> H <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> ClO	HpCDF
325.9839	QC	C <sub>7</sub> F <sub>12</sub> N	FC43	409.7789	M+4	C <sub>12</sub> H <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl <sub>2</sub> O	HpCDF
330.9792	QC	C <sub>7</sub> F <sub>13</sub>	PFK	417.8253	M	<sup>13</sup> C <sub>12</sub> H <sup>35</sup> Cl <sub>7</sub> O	HpCDF (S)
331.9368	M	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>4</sub> O <sub>2</sub>	TeCDD (S)	419.8220	M+2	<sup>13</sup> C <sub>12</sub> H <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> ClO	HpCDF (S)
333.9339	M+2	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> ClO <sub>2</sub>	TeCDD (S)	423.7766	M+2	C <sub>12</sub> H <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> ClO <sub>2</sub>	HpCDD
339.8597	M+2	C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> ClO	PeCDF	425.7737	M+4	C <sub>12</sub> H <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl <sub>2</sub> O <sub>2</sub>	HpCDD
341.8567	M+4	C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>2</sub> O	PeCDF	430.9729	QC	C <sub>9</sub> F <sub>17</sub>	PFK
354.9792	LOCK	C <sub>9</sub> F <sub>13</sub>	PFK	435.8169	M+2	<sup>13</sup> C <sub>12</sub> H <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> ClO <sub>2</sub>	HpCDD (S)
351.9000	M+2	<sup>13</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> ClO	PeCDF (S)	437.8140	M+4	<sup>13</sup> C <sub>12</sub> H <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl <sub>2</sub> O <sub>2</sub>	HpCDD (S)

Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte <sup>b</sup>	Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte <sup>b</sup>
353.8970	M+4	<sup>13</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>2</sub> O	PeCDF (S)	442.9728	LOCK	C <sub>10</sub> F <sub>17</sub>	PFK
355.8546	M+2	C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> ClO <sub>2</sub>	PeCDD	479.7165	M+4	C <sub>12</sub> H <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> Cl <sub>2</sub> O	NCPDE
357.8516	M+4	C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>2</sub> O <sub>2</sub>	PeCDD	430.9729	LOCK	C <sub>9</sub> F <sub>17</sub>	PFK
367.8949	M+2	<sup>13</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> ClO <sub>2</sub>	PeCDD (S)	441.7428	M+2	C <sub>12</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> ClO	OCDF
369.8919	M+4	<sup>13</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>2</sub> O <sub>2</sub>	PeCDD (S)	443.7399	M+4	C <sub>12</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl <sub>2</sub> O	OCDF
375.9807	QC	C <sub>8</sub> F <sub>14</sub> N	FC43	457.7377	M+2	C <sub>12</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> ClO <sub>2</sub>	OCDD
375.8364	M+2	C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> ClO	HxCDFPE	459.7348	M+4	C <sub>12</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl <sub>2</sub> O <sub>2</sub>	OCDD
409.7974	M+2	C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> ClO	HpCPDE	463.9743	QC	C <sub>9</sub> F <sub>18</sub> N	FC43
373.8208	M+2	C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> ClO	HxCDF	469.7779	M+2	<sup>13</sup> C <sub>12</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> ClO <sub>2</sub>	OCDD (S)
375.8178	M+4	C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl <sub>2</sub> O	HxCDF	471.7750	M+4	<sup>13</sup> C <sub>12</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl <sub>2</sub> O <sub>2</sub>	OCDD (S)
375.9807	QC	C <sub>8</sub> F <sub>14</sub> N	FC43	513.6775	M+4	C <sub>12</sub> <sup>35</sup> Cl <sub>8</sub> <sup>37</sup> Cl <sub>2</sub> O <sub>2</sub>	DCDPE
				442.9728	QC	C <sub>10</sub> F <sub>17</sub>	PFK

<sup>a</sup> The following nuclidic masses were used to calculate exact masses: H = 1.007825, C = 12.000000, <sup>13</sup>C = 13.003355, F = 18.9984, O = 15.994915, <sup>35</sup>C l = 34.968853, <sup>37</sup>Cl = 36.965903.

<sup>b</sup> (S) = Labeled Standard. LOCK = Lock-Mass Ion PFK or FC43. QC = Quality Control Check Ion. Note: Consider monitoring 328 m/z if high level of PCB is expected.

**Table OTM46-5. Elemental Compositions and Exact Masses of the Ions Monitored by High-Resolution Mass Spectrometry for PAH**

Aromatic Ring Number	Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte
2	128.0624	M	C <sub>10</sub> H <sub>8</sub>	Naphthalene
	130.9920	LOCK		PFK/FC43
2	134.0828	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>4</sub> H <sub>8</sub>	<sup>13</sup> C <sub>6</sub> -Naphthalene
2	142.078	M	C <sub>11</sub> H <sub>10</sub>	2-Methylnaphthalene
2	148.0984	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>5</sub> H <sub>10</sub>	<sup>13</sup> C <sub>6</sub> -2-Methylnaphthalene
2	152.0624	M	C <sub>12</sub> H <sub>8</sub>	Acenaphthylene
2	158.0828	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>6</sub> H <sub>8</sub>	<sup>13</sup> C <sub>6</sub> -Acenaphthylene
2	154.078	M	C <sub>12</sub> H <sub>10</sub>	Acenaphthene
2	160.078	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>6</sub> H <sub>10</sub>	<sup>13</sup> C <sub>6</sub> -Acenaphthene
2	166.078	M	C <sub>13</sub> H <sub>10</sub>	Fluorene
	169.988	QC		PFK/FC43
2	172.0984	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>7</sub> H <sub>10</sub>	<sup>13</sup> C <sub>6</sub> -Fluorene
3	178.078	M	C <sub>14</sub> H <sub>10</sub>	Phenanthrene
3	184.0984	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>8</sub> H <sub>10</sub>	<sup>13</sup> C <sub>6</sub> -Phenanthrene
3	178.078	M	C <sub>14</sub> H <sub>10</sub>	Anthracene
3	184.078	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>8</sub> H <sub>10</sub>	<sup>13</sup> C <sub>6</sub> -Anthracene
3	202.078	M	C <sub>16</sub> H <sub>10</sub>	Fluoranthene
	204.9888	QC		PFK
3	208.0984	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>10</sub> H <sub>10</sub>	<sup>13</sup> C <sub>6</sub> -Fluoranthene

Aromatic Ring Number	Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte
4	202.078	M	C <sub>16</sub> H <sub>10</sub>	Pyrene
4	205.078	M	<sup>13</sup> C <sub>3</sub> <sup>12</sup> C <sub>13</sub> H <sub>10</sub>	<sup>13</sup> C <sub>3</sub> -Pyrene
	213.9898	QC		FC43
	218.9856	LOCK		FC43
4	228.0936	M	C <sub>18</sub> H <sub>12</sub>	Benz[ <i>a</i> ]anthracene
	230.9856	LOCK		PFK
4	234.114	M	<sup>13</sup> C <sub>6</sub> C <sub>12</sub> H <sub>12</sub>	<sup>13</sup> C <sub>6</sub> -Benz[ <i>a</i> ]anthracene
4	228.0936	M	C <sub>18</sub> H <sub>12</sub>	Chrysene
4	234.114	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>12</sub> H <sub>12</sub>	<sup>13</sup> C <sub>6</sub> -Chrysene
4	252.0936	M	C <sub>20</sub> H <sub>12</sub>	Benzo[ <i>b</i> ]fluoranthene
4	258.114	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>14</sub> H <sub>12</sub>	<sup>13</sup> C <sub>6</sub> -Benzo[ <i>b</i> ]fluoranthene
4	252.32	M	C <sub>20</sub> H <sub>12</sub>	Benzo[ <i>k</i> ]fluoranthene
4	258.114	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>14</sub> H <sub>12</sub>	<sup>13</sup> C <sub>6</sub> -Benzo[ <i>k</i> ]fluoranthene
5	252.0936	M	C <sub>20</sub> H <sub>12</sub>	Benzo[ <i>e</i> ]pyrene
5	256.1072	M	<sup>13</sup> C <sub>4</sub> <sup>12</sup> C <sub>16</sub> H <sub>12</sub>	<sup>13</sup> C <sub>4</sub> -Benzo[ <i>e</i> ]pyrene
5	256.1072	M	<sup>13</sup> C <sub>4</sub> <sup>12</sup> C <sub>16</sub> H <sub>12</sub>	<sup>13</sup> C <sub>4</sub> -Benzo[ <i>a</i> ]pyrene
5	252.0936	M	C <sub>20</sub> H <sub>12</sub>	Benzo[ <i>a</i> ]pyrene
5	252.0936	M	C <sub>20</sub> H <sub>12</sub>	Perylene
5	264.1692	M	C <sub>20</sub> D <sub>12</sub>	d <sub>12</sub> -Perylene
	268.9824	QC		PFK
	263.9871	LOCK		FC43
6	276.0936	M	C <sub>22</sub> H <sub>12</sub>	Indeno[ <i>1,2,3-cd</i> ]pyrene
6	282.114	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>16</sub> H <sub>12</sub>	<sup>13</sup> C <sub>6</sub> -Indeno[ <i>1,2,3-cd</i> ]pyrene
5	278.1092	M	C <sub>22</sub> H <sub>14</sub>	Dibenz[ <i>a,h</i> ]anthracene
	280.9824	LOCK		PFK
5	284.1296	M	<sup>13</sup> C <sub>6</sub> <sup>12</sup> C <sub>16</sub> H <sub>14</sub>	<sup>13</sup> C <sub>6</sub> -Dibenz[ <i>a,h</i> ]anthracene
6	276.0936	M	C <sub>22</sub> H <sub>12</sub>	Benzo[ <i>g,h,i</i> ]perylene
6	288.1344	M	<sup>13</sup> C <sub>12</sub> <sup>12</sup> C <sub>10</sub> H <sub>12</sub>	<sup>13</sup> C <sub>12</sub> -Benzo[ <i>g,h,i</i> ]perylene
	313.9839	QC		FC43

<sup>a</sup> Isotopic masses used for accurate mass calculation: <sup>1</sup>H = 1.0078, <sup>12</sup>C = 12.0000, <sup>13</sup>C = 13.0034, <sup>2</sup>H = 2.0141.

<sup>b</sup> LOCK = Lock-Mass Ion PFK or FC43. QC = Quality Control Check Ion.

**Table OTM46-6. Elemental Compositions and Exact Masses of the Ions Monitored by High-Resolution Mass Spectrometry for PCB**

Chlorine Substitution	Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte	Chlorine Substitution	Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte
Fn-1; Cl-1	188.0393	M	<sup>12</sup> C <sub>12</sub> H <sub>9</sub> <sup>35</sup> Cl	Cl-1 PCB	Fn-5; Cl-5,6,7	323.8834	M	<sup>12</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>5</sub>	Cl-5 PCB
	190.0363	M+2	<sup>12</sup> C <sub>12</sub> H <sub>9</sub> <sup>37</sup> Cl	Cl-1 PCB		325.8804	M+2	<sup>12</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl	Cl-5 PCB
	200.0795	M	<sup>13</sup> C <sub>12</sub> H <sub>9</sub> <sup>35</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-1 PCB		327.8775	M+4	<sup>12</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-5 PCB
	202.0766	M+2	<sup>12</sup> C <sub>12</sub> H <sub>9</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-1 PCB		337.9207	M+2	<sup>13</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-5 PCB

Chlorine Substitution	Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte	Chlorine Substitution	Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte
	218.9856	LOCK	C <sub>4</sub> F <sub>9</sub>	PFK		339.9178	M+4	<sup>13</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-5 PCB
Fn-2; Cl-2,3	222.0003	M	<sup>12</sup> C <sub>12</sub> H <sub>8</sub> <sup>35</sup> Cl <sub>2</sub>	Cl-2 PCB		354.9792	LOCK	C <sub>9</sub> F <sub>13</sub>	PFK
	223.9974	M+2	<sup>12</sup> C <sub>12</sub> H <sub>8</sub> <sup>35</sup> Cl <sup>37</sup> Cl	Cl-2 PCB		359.8415	M+2	<sup>12</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl	Cl-6 PCB
	225.9944	M+4	<sup>12</sup> C <sub>12</sub> H <sub>8</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-2 PCB		361.8385	M+4	<sup>12</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-6 PCB
	234.0406	M	<sup>13</sup> C <sub>12</sub> H <sub>8</sub> <sup>35</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-2 PCB		363.8356	M+6	<sup>12</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>3</sub>	Cl-6 PCB
	236.0376	M+2	<sup>13</sup> C <sub>12</sub> H <sub>8</sub> <sup>35</sup> Cl <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-2 PCB		371.8817	M+2	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-6 PCB
	242.9856	LOCK	C <sub>4</sub> F <sub>9</sub>	PFK		373.8788	M+4	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-6 PCB
	255.9613	M	<sup>12</sup> C <sub>12</sub> H <sub>7</sub> <sup>35</sup> Cl <sub>3</sub>	Cl-3 PCB		393.8025	M+2	<sup>12</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl	Cl-7 PCB
	257.9584	M+2	<sup>12</sup> C <sub>12</sub> H <sub>7</sub> <sup>35</sup> Cl <sub>2</sub> <sup>37</sup> Cl	Cl-3 PCB		395.7995	M+4	<sup>12</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-7 PCB
	268.0016	M	<sup>13</sup> C <sub>12</sub> H <sub>7</sub> <sup>35</sup> Cl <sub>3</sub>	<sup>13</sup> C <sub>12</sub> Cl-3 PCB		397.7966	M+6	<sup>12</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl <sub>3</sub>	<sup>37</sup> Cl <sub>3</sub> Cl-7 PCB
	269.9986	M+2	<sup>13</sup> C <sub>12</sub> H <sub>7</sub> <sup>35</sup> Cl <sub>2</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-3 PCB		405.8428	M+2	<sup>13</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-7 PCB
Fn-3; Cl-3,4,5	255.9613	M	<sup>12</sup> C <sub>12</sub> H <sub>7</sub> <sup>35</sup> Cl <sub>3</sub>	Cl-3 PCB		407.8398	M+4	<sup>13</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-7 PCB
	257.9584	M+2	<sup>12</sup> C <sub>12</sub> H <sub>7</sub> <sup>35</sup> Cl <sub>2</sub> <sup>37</sup> Cl	Cl-3 PCB		454.9728	QC	C <sub>11</sub> F <sub>17</sub>	PFK
	259.9554	M+4	<sup>12</sup> C <sub>12</sub> H <sub>7</sub> <sup>35</sup> Cl <sup>37</sup> Cl <sub>2</sub>	Cl-3 PCB	Fn-6; Cl-7,8,9,10	393.8025	M+2	<sup>12</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl	Cl-7 PCB
	268.0016	M	<sup>13</sup> C <sub>12</sub> H <sub>7</sub> <sup>35</sup> Cl <sub>3</sub>	<sup>13</sup> C <sub>12</sub> Cl-3 PCB		395.7995	M+4	<sup>12</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-7 PCB
	269.9986	M+2	<sup>13</sup> C <sub>12</sub> H <sub>7</sub> <sup>35</sup> Cl <sub>2</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-3 PCB		397.7966	M+6	<sup>12</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl <sub>3</sub>	Cl-7 PCB
	280.9825	LOCK	C <sub>6</sub> F <sub>11</sub>	PFK		405.8428	M+2	<sup>13</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-7 PCB
	289.9224	M	<sup>12</sup> C <sub>12</sub> H <sub>6</sub> <sup>35</sup> Cl <sub>4</sub>	Cl-4 PCB		407.8398	M+4	<sup>13</sup> C <sub>12</sub> H <sub>3</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-7 PCB
	291.9194	M+2	<sup>12</sup> C <sub>12</sub> H <sub>6</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl	Cl-4 PCB		427.7635	M+2	<sup>12</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> Cl	Cl-8 PCB
	293.9165	M+4	<sup>12</sup> C <sub>12</sub> H <sub>6</sub> <sup>35</sup> Cl <sub>2</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-4 PCB		429.7606	M+4	<sup>12</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-8 PCB
	301.9626	M	<sup>13</sup> C <sub>12</sub> H <sub>6</sub> <sup>35</sup> Cl <sub>4</sub>	<sup>13</sup> C <sub>12</sub> Cl-4 PCB		431.7576	M+6	<sup>12</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl <sub>3</sub>	Cl-8 PCB
	303.9597	M+2	<sup>13</sup> C <sub>12</sub> H <sub>6</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-4 PCB		439.8038	M+2	<sup>13</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-8 PCB
	323.8834	M	<sup>12</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>5</sub>	Cl-5 PCB		441.8008	M+4	<sup>13</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-8 PCB
	325.8804	M+2	<sup>12</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl	Cl-5 PCB		454.9728	QC	C <sub>11</sub> F <sub>17</sub>	PFK
	327.8775	M+4	<sup>12</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-5 PCB		427.7635	M+2	<sup>12</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> Cl	Cl-8 PCB
	337.9207	M+2	<sup>13</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-5 PCB		429.7606	M+4	<sup>12</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-8 PCB
	339.9178	M+4	<sup>13</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-5 PCB		431.7576	M+6	<sup>12</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl <sub>3</sub>	Cl-8 PCB
	Fn-4; Cl-4,5,6	289.9224	M	<sup>12</sup> C <sub>12</sub> H <sub>6</sub> <sup>35</sup> Cl <sub>4</sub>		Cl-4 PCB	439.8038	M+2	<sup>13</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> Cl
291.9194		M+2	<sup>12</sup> C <sub>12</sub> H <sub>6</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl	Cl-4 PCB		441.8008	M+4	<sup>13</sup> C <sub>12</sub> H <sub>2</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-8 PCB

Chlorine Substitution	Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte	Chlorine Substitution	Mass <sup>a</sup>	Ion Type <sup>b</sup>	Elemental Composition	Target Analyte
	293.9165	M+4	<sup>12</sup> C <sub>12</sub> H <sub>6</sub> <sup>35</sup> Cl <sub>2</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-4 PCB		442.9728	QC	C <sub>10</sub> F <sub>17</sub>	PFK
	301.9626	M+2	<sup>13</sup> C <sub>12</sub> H <sub>6</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-4 PCB		454.9728	LOCK	C <sub>11</sub> F <sub>17</sub>	PFK
	303.9597	M+4	<sup>13</sup> C <sub>12</sub> H <sub>6</sub> <sup>35</sup> Cl <sub>2</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-4 PCB		461.7246	M+2	<sup>12</sup> C <sub>12</sub> H <sub>1</sub> <sup>35</sup> Cl <sub>8</sub> <sup>37</sup> Cl	Cl-9 PCB
	323.8834	M	<sup>12</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>5</sub>	Cl-5 PCB		463.7216	M+4	<sup>12</sup> C <sub>12</sub> H <sub>1</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-9 PCB
	325.8804	M+2	<sup>12</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl	Cl-5 PCB		465.7187	M+6	<sup>12</sup> C <sub>12</sub> H <sub>1</sub> <sup>35</sup> Cl <sub>6</sub> <sup>37</sup> Cl <sub>3</sub>	Cl-9 PCB
	327.8775	M+4	<sup>12</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-5 PCB		473.7648	M+2	<sup>13</sup> C <sub>12</sub> H <sub>1</sub> <sup>35</sup> Cl <sub>8</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-9 PCB
	330.9792	LOCK	C <sub>7</sub> F <sub>15</sub>	PFK		475.7619	M+4	<sup>13</sup> C <sub>12</sub> H <sub>1</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-9 PCB
	337.9207	M+2	<sup>13</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-5 PCB		495.6856	M+2	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>5</sup> Cl <sub>9</sub> <sup>37</sup> Cl	Cl-10 PCB
	339.9178	M+4	<sup>13</sup> C <sub>12</sub> H <sub>5</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-5 PCB		499.6797	M+6	<sup>12</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>8</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-10 PCB
	359.8415	M+2	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl	Cl-6 PCB		501.6767	M+8	<sup>12</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> Cl <sub>3</sub>	Cl-10 PCB
	361.8385	M+4	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl <sub>2</sub>	Cl-6 PCB		507.7258	M+2	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>9</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-10 PCB
	363.8356	M+6	<sup>12</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>3</sub> <sup>37</sup> Cl <sub>3</sub>	Cl-6 PCB		509.7229	M+4	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>8</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-10 PCB
	371.8817	M+2	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>5</sub> <sup>37</sup> Cl	<sup>13</sup> C <sub>12</sub> Cl-6 PCB		511.7199	M+6	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>7</sub> <sup>37</sup> Cl <sub>3</sub>	<sup>13</sup> C <sub>12</sub> Cl-10 PCB
	373.8788	M+4	<sup>13</sup> C <sub>12</sub> H <sub>4</sub> <sup>35</sup> Cl <sub>4</sub> <sup>37</sup> Cl <sub>2</sub>	<sup>13</sup> C <sub>12</sub> Cl-6 PCB					

<sup>a</sup> Isotopic masses used for accurate mass calculation: <sup>1</sup>H = 1.0078, <sup>12</sup>C = 12.0000, <sup>13</sup>C = 13.0034, <sup>35</sup>Cl = 34.9689, <sup>37</sup>Cl = 36.9659, <sup>19</sup>F = 18.9984. An interference with PFK m/z 223.9872 may preclude meeting 10:1 S/N for the DiCB congeners at optional Cal 1 level (Table 23-11). If this interference occurs, 10:1 S/N must be met at the Cal 2 level

<sup>b</sup> LOCK = Lock-Mass Ion PFK or FC43. QC = Quality Control Check Ion.

**Table OTM46-7. Concentration of the Sample Fortification for PCDD and PCDFa**

Compound	pg/μL in final extract <sup>b</sup>	Spike Recovery
<b>Pre-sampling Adsorbent Standard</b>		
<sup>13</sup> C <sub>12</sub> -1,2,3,4-TeCDD	50	70-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,4,7-PeCDD	50	70-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,4,6-PeCDF	50	70-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,4,6,9-HxCDF	50	70-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,4,6,8,9-HpCDF	50	70-130%
<b>Pre-extraction Filter Recovery Standard</b>		
<sup>13</sup> C <sub>12</sub> -1,2,7,8-TeCDF	50	70-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,4,6,8-HxCDD	50	70-130%
<b>Pre-extraction Standard</b>		
<sup>13</sup> C <sub>12</sub> -2,3,7,8-TeCDD	50	20-130%
<sup>13</sup> C <sub>12</sub> -2,3,7,8-TeCDF	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,7,8-PeCDD	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,7,8-PeCDF	50	20-130%



Compound	pg/ $\mu$ L in final extract <sup>b</sup>	Spike Recovery
<sup>13</sup> C <sub>12</sub> -2,3,4,7,8-PeCDF	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,4,7,8-HxCDD	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,6,7,8-HxCDD	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,7,8,9-HxCDD	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,4,7,8-HxCDF	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,6,7,8-HxCDF	50	20-130%
<sup>13</sup> C <sub>12</sub> -2,3,4,6,7,8-HxCDF	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,7,8,9-HxCDF	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,4,6,7,8-HpCDD	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,4,6,7,8-HpCDF	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,3,4,7,8,9-HpCDF	50	20-130%
<sup>13</sup> C <sub>12</sub> -OCDD	100	20-130%
<sup>13</sup> C <sub>12</sub> -OCDF	100	20-130%
<b>Pre-analysis Standard</b>		
<sup>13</sup> C <sub>12</sub> -1,3,6,8-TeCDD	50	S/N $\geq$ 10
<sup>13</sup> C <sub>12</sub> -1,2,3,4-TeCDF	50	S/N $\geq$ 10
<sup>13</sup> C <sub>12</sub> -1,2,3,4,6,7-HxCDD	50	S/N $\geq$ 10
<sup>13</sup> C <sub>12</sub> -1,2,3,4,6,7,9-HpCDD	50	S/N $\geq$ 10
<b>Alternate Recovery Standard</b>		
<sup>13</sup> C <sub>12</sub> -1,3,7,8-TeCDD	50	20-130%
<sup>13</sup> C <sub>12</sub> -1,2,4,7,8-PeCDD	50	20-130%

<sup>a</sup> Changes in the amounts of labeled standards added to the sample or its representative extract will necessitate an adjustment of the calibration solutions to prevent the introduction of inconsistencies. Spike concentration assumes 1 $\mu$ L sample injection volume for analysis or the injection volume for standards and samples is the same.

<sup>b</sup> Spike levels assume half of the extract will be archived before cleanup. Spike levels may be adjusted for different split levels.

Note: all standards used should be reported.

**Table OTM46-8. Concentration of the Sample Fortification for PAH<sup>a</sup>**

Compound	pg/ $\mu$ L in final extract <sup>b</sup>	Spike Recovery
<b>Pre-sampling Adsorbent Standard</b>		
<sup>13</sup> C <sub>6</sub> -Benzo[ <i>c</i> ]fluorene	100	70-130%
<sup>13</sup> C <sub>12</sub> -Benzo[ <i>j</i> ]fluoranthene	100	70-130%
<b>Pre-extraction Filter Recovery Standard</b>		
d <sub>10</sub> -Anthracene	100	70-130%
<b>Pre-extraction Standard</b>		
<sup>13</sup> C <sub>6</sub> -Naphthalene	100	20-130%
<sup>13</sup> C <sub>6</sub> -2-Methylnaphthalene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Acenaphthylene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Acenaphthene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Fluorene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Phenanthrene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Anthracene	100	20-130%

Compound	pg/ $\mu$ L in final extract <sup>b</sup>	Spike Recovery
<sup>13</sup> C <sub>6</sub> -Fluoranthene	100	20-130%
<sup>13</sup> C <sub>3</sub> -Pyrene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Benz[ <i>a</i> ]anthracene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Chrysene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Benzo[ <i>b</i> ]fluoranthene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Benzo[ <i>k</i> ]fluoranthene	100	20-130%
<sup>13</sup> C <sub>4</sub> -Benzo[ <i>e</i> ]pyrene	100	20-130%
<sup>13</sup> C <sub>4</sub> -Benzo[ <i>a</i> ]pyrene	100	20-130%
d <sub>12</sub> -Perylene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Indeno[ <i>1,2,3-cd</i> ]pyrene	100	20-130%
<sup>13</sup> C <sub>6</sub> -Dibenz[ <i>a,h</i> ]anthracene	100	20-130%
<sup>13</sup> C <sub>12</sub> -Benzo[ <i>g,h,i</i> ]perylene	100	20-130%
<b>Pre-analysis Standard</b>		
Acenaphthene-d <sub>10</sub>	100	S/N $\geq$ 10
d <sub>10</sub> -Pyrene	100	S/N $\geq$ 10
d <sub>12</sub> -Benzo[ <i>e</i> ]pyrene	100	S/N $\geq$ 10

<sup>a</sup> Changes in the amounts of labeled standards added to the sample or its representative extract will necessitate an adjustment of the calibration solutions to prevent the introduction of inconsistencies

<sup>b</sup> Spike levels assume half of the extract will be archived before cleanup. You may adjust spike levels for different split levels.

Note: all standards used should be reported.

**Table OTM46-9. Concentration of the Sample Fortification for PCB<sup>a</sup>**

Compound	BZ No. <sup>b</sup>	pg/ $\mu$ L in final extract <sup>c</sup>	Spike Recovery
<b>Pre-sampling Adsorbent Standard</b>			
<sup>13</sup> C <sub>12</sub> -3,3'-DiCB	11L	100	70-130%
<sup>13</sup> C <sub>12</sub> -2,4',5-TrCB	31L	100	70-130%
<sup>13</sup> C <sub>12</sub> -2,2',3,5',6-PeCB	95L	100	70-130%
<sup>13</sup> C <sub>12</sub> -2,2',4,4',5,5'-HxCB	153L	100	70-130%
<b>Pre-extraction Filter Recovery Standard</b>			
<sup>13</sup> C <sub>12</sub> -2,3,3',4,5,5'-HxCB	159L	100	70-130%
<b>Pre-extraction Standard</b>			
<sup>13</sup> C <sub>12</sub> -2-MoCB (WDC)	1L	100	20-145%
<sup>13</sup> C <sub>12</sub> -4-MoCB (WDC)	3L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2'-DiCB (WDC)	4L	100	20-145%
<sup>13</sup> C <sub>12</sub> -4,4'-DiCB (WDC)	15L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB (WDC)	19L	100	20-145%
<sup>13</sup> C <sub>12</sub> -3,4',4'-TrCB (WDC)	37L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB (WDC)	54L	100	20-145%
<sup>13</sup> C <sub>12</sub> -3,3',4,4'-TeCB (WDC) (WHOT) (NOAAT)	77L	100	20-145%
<sup>13</sup> C <sub>12</sub> -3,4,4',5-TeCB (WHOT)	81L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB (WDC)	104L	100	20-145%

Compound	BZ No. <sup>b</sup>	pg/ $\mu$ L in final extract <sup>c</sup>	Spike Recovery
<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB (WHOT)	105L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,3,4,4',5-PeCB (WHO)	114L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,3',4,4',5-PeCB (WHOT)	118L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2',3,4,4',5-PeCB (WHOT)	123L	100	20-145%
<sup>13</sup> C <sub>12</sub> -3,3',4,4',5-PeCB (WDC) (WHOT)	126L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB (WDC)	155L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5-HxCB (WHOT)	156L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB (WHOT)	157L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,3',4,4',5,5'-HxCB (WHOT)	167L	100	20-145%
<sup>13</sup> C <sub>12</sub> -3,3',4,4',5,5'-HxCB (WDC) (WHOT) (NOAAT)	169L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2',3,3',4,4',5'-HpCB (NOAAT)	170L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2',3,4,4',5,5'-HpCB (NOAAT)	180L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB (WDC)	188L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5,5'-HpCB (WDC) (WHOT)	189L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2',3,3',5,5',6,6'-OcCB (WDC)	202L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,3',3',4,4',5,5',6-OcCB (WDC)	205L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2',3,3',4,4',5,5',6-NoCB (WDC)	206L	100	20-145%
<sup>13</sup> C <sub>12</sub> -2,2',3,3',4,5,5',6,6'-NoCB (WDC)	208L	100	20-145%
<sup>13</sup> C <sub>12</sub> -DeCB (WDC)	209L	100	20-145%
<b>Pre-analysis Standard</b>			
<sup>13</sup> C <sub>12</sub> -2,5-DiCB	9L	100	S/N $\geq$ 10
<sup>13</sup> C <sub>12</sub> -2,2',5,5'-TeCB (NOAAT)	52L	100	S/N $\geq$ 10
<sup>13</sup> C <sub>12</sub> -2,2',4,5,5'-PeCB (NOAAT)	101L	100	S/N $\geq$ 10
<sup>13</sup> C <sub>12</sub> -2,2',3,4,4',5'-HxCB (NOAAT)	138L	100	S/N $\geq$ 10
<sup>13</sup> C <sub>12</sub> -2,2',3,3',4,4',5,5'-OcCB	194L	100	S/N $\geq$ 10
<b>Optional Cleanup Standard</b>			
<sup>13</sup> C <sub>12</sub> -2-MoCB (NOAAT)	28L	100	20-130%
<sup>13</sup> C <sub>12</sub> -2,2',4,5,5'-PeCB	111L	100	20-130%
<sup>13</sup> C <sub>12</sub> -2,2',3,3',5,5',6,6'-OcCB	178L	100	20-130%
<b>Alternate Recovery Standard</b>			
<sup>13</sup> C <sub>12</sub> -2,3',4',5'-TeCB	70L	100	20-130%
<sup>13</sup> C <sub>12</sub> -2,3,4,4'-TeCB	60L	100	20-130%
<sup>13</sup> C <sub>12</sub> -3,3',4,5,5'-PeCB	127L	100	20-130%

<sup>a</sup> Changes in the amounts of spike standards added to the sample or its representative extract will necessitate an adjustment of the calibration solutions to prevent the introduction of inconsistencies

<sup>b</sup> BZ No.: Ballschmitter and Zell 1980, or IUPAC number.

<sup>c</sup> Spike levels assume half of the extract will be archived before cleanup. Spike levels may be adjusted for different split levels.

NOAAT = PCB considered toxic by the National Oceanic and Atmospheric Administration.

WHOT = PCB considered toxic by the World Health Organization.

Note: all standards used should be reported.

**Table OTM46-10. Sample Storage Conditions<sup>a</sup> and Laboratory Hold Times<sup>b</sup>**

Sample Type	PCDD/PCDF	PAH	PCB
<b>Field Storage and Shipping Conditions</b>			
All Field Samples	≤ 20 °C, (68 °F)	≤ 20 °C, (68 °F)	≤ 20 °C, (68 °F)
<b>Laboratory Storage Conditions</b>			
Sampling Train Rinses and Filters	≤ 6 °C (43 °F)	≤ 6 °C (43 °F)	≤ 6 °C (43 °F)
Adsorbent	≤ 6 °C (43 °F)	≤ 6 °C (43 °F)	≤ 6 °C (43 °F)
Extract and Archive	< -10 °C (14 °F)	< -10 °C (14 °F)	< -10 °C (14 °F)
<b>Laboratory Hold Times</b>			
Extract and Archive	One year	45 Days	One year

<sup>a</sup> Samples and extracts must be stored in the dark.

<sup>b</sup> Hold times begin from the time the laboratory receives the sample.

Note: Hold times for PCDD/PCDF and PCB are recommendations.

**Table OTM46-11. Concentration of the Initial Calibration Standard Solutions for PCDD and PCDF<sup>a</sup> (pg/μL)**

Standard Compound	Cal 1 (optional)	Cal 2	Cal 3	Cal 4	Cal 5	Cal 6	Cal 7 (optional)
Target (Unlabeled) Analytes	0.50	1.0	5.0	10.0	25	50	100
Pre-sampling Adsorbent Standard	50	50	50	50	50	50	50
Pre-extraction Filter Recovery Standard	50	50	50	50	50	50	50
Pre-extraction Standard ( <sup>13</sup> C <sub>12</sub> -OCDD, <sup>13</sup> C <sub>12</sub> -OCDF – 100 pg/μL)	50	50	50	50	50	50	50
Pre-analysis Standard	50	50	50	50	50	50	50
Alternate Recovery Standard	50	50	50	50	50	50	50

<sup>a</sup> Assumes 1 μL injection volume or the injection volume for standards and samples is the same.

**Table OTM46-12. Concentration of the Initial Calibration Standard Solutions for PAH<sup>a</sup> (pg/μL)**

Standard Compound	Cal 1 (optional)	Cal 2	Cal 3	Cal 4	Cal 5	Cal 6	Cal 7 (optional)
Target (Unlabeled) Analytes	1	2	4	20	80	400	1,000
Pre-sampling Adsorbent Standard	100	100	100	100	100	100	100
Pre-extraction Filter Recovery Standard	100	100	100	100	100	100	100
Pre-extraction Standard	100	100	100	100	100	100	100
Pre-analysis Standard	100	100	100	100	100	100	100

<sup>a</sup> Assumes 1 μL injection volume.

**Table OTM46-13. Concentration of the Initial Calibration Standard Solutions for PCB<sup>a</sup> (pg/ $\mu$ L)**

<b>Standard Compound</b>	<b>Cal 1 (optional)</b>	<b>Cal 2</b>	<b>Cal 3</b>	<b>Cal 4</b>	<b>Cal 5</b>	<b>Cal 6</b>	<b>Cal 7 (optional)</b>
Target (Unlabeled) Analytes	0.50	1	5	10	50	400	2,000
Pre-sampling Adsorbent Standard	100	100	100	100	100	100	100
Pre-extraction Filter Recovery Standard	100	100	100	100	100	100	100
Pre-extraction Standard	100	100	100	100	100	100	100
Pre-analysis Standard	100	100	100	100	100	100	100
Alternate Standard	100	100	100	100	100	100	100

<sup>a</sup> Assumes 1  $\mu$ L injection volume.**Table OTM46-14. Minimum Requirements for Initial and Continuing Calibration Response Factors for Isotopically Labeled and Native Compounds**

<b>Analyte Group</b>	<b>Relative Response Factors</b>	
	<b>Initial Calibration RSD</b>	<b>Continuing Calibration compared to ICAL (PD)</b>
Native (Unlabeled) Analytes	10	25
Pre-sampling Adsorbent Standard	20	25
Pre-extraction Filter Recovery Standard	20	25
Pre-extraction Standard	20	30
Alternative Recovery Standard	20	30

**Table OTM46-15. Recommended Ion Type and Acceptable Ion Abundance Ratios**

<b>No. of Chlorine Atoms</b>	<b>Ion Type</b>	<b>Theoretical Ratio</b>	<b>Control Limits</b>	
			<b>Lower</b>	<b>Upper</b>
1	M/M+2	3.13	2.66	3.60
2	M/M+2	1.56	1.33	1.79
3	M/M+2	1.04	0.88	1.20
4	M/M+2	0.77	0.65	0.89

**Table OTM46-15. Recommended Ion Type and Acceptable Ion Abundance Ratios**

No. of Chlorine Atoms	Ion Type	Theoretical Ratio	Control Limits	
			Lower	Upper
5	M+2/M+4	1.55	1.32	1.78
6	M+2/M+4	1.24	1.05	1.43
6 <sup>a</sup>	M/M+2	0.51	0.43	0.59
7	M+2/M+4	1.05	0.89	1.21
7 <sup>b</sup>	M/M+2	0.44	0.37	0.51
8	M+2/M+4	0.89	0.76	1.02
9	M+2/M+4	0.77	0.65	0.89
10	M+4/M+6	1.16	0.99	1.33

<sup>a</sup> Used only for <sup>13</sup>C-HxCDF.

<sup>b</sup> Used only for <sup>13</sup>C-HpCDF.

**Table OTM46-16. Typical DB5-MS Column Conditions**

Column Parameter	Analyte		
	PCDD/PCDF	PAH	PCB
Injector temperature	250 °C	320 °C	270 °C
Initial oven temperature	100 °C	100 °C	100 °C
Initial hold time (minutes)	2	2	2
Temperature program	100 to 190 °C at 40 °C/min, then 190 to 300 °C at 3°C/min	100 to 300 °C at 8°C/min	100 to 150 °C at 15 °C/min, then 150 to 290 °C at 2.5 °C/min

**Table OTM46-17. Assignment of Pre-extraction Standards for Quantitation of Target PCB<sup>b</sup>**

PCB Congener	BZ No. <sup>a</sup>	Labeled Analog	BZ No.
2,4'-DiCB (NOAAT)	8	<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L
2,2',5-TrCB (NOAAT)	18	<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L
2,4,4'-TrCB (NOAAT)	28	<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L
2,2',3,5'-TeCB (NOAAT)	52	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L

PCB Congener	BZ No. <sup>a</sup>	Labeled Analog	BZ No.
2,2',5,5'-TeCB (NOAAT)	52	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L
2,3',4,4'-TeCB (NOAAT)	66	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L
3,3',4,4'-TeCB (NOAAT) (WHOT)	77	<sup>13</sup> C <sub>12</sub> -3,3',4,4'-TeCB	77L
3,4,4',5'-TeCB (WHOT)	81	<sup>13</sup> C <sub>12</sub> -3,4,4',5'-TeCB	81L
2,2',4,5,5'-PeCB (NOAAT)	101	<sup>13</sup> C <sub>12</sub> -2,2',4,5,5'-PeCB	104L
2,3,3',4,4'-PeCB (NOAAT) (WHOT)	105	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB	105L
2,3,4,4',5'-PeCB (WHOT)	114	<sup>13</sup> C <sub>12</sub> -2,3,4,4',5'-PeCB	114L
2,3',4,4',5'-PeCB (WHOT)	118	<sup>13</sup> C <sub>12</sub> -2,3',4,4',5'-PeCB	118L
2',3,4,4',5'-PeCB (WHOT)	123	<sup>13</sup> C <sub>12</sub> -2',3,4,4',5'-PeCB	123L
3,3',4,4',5'-PeCB (NOAAT) (WHOT)	126	<sup>13</sup> C <sub>12</sub> -3,3',4,4',5'-PeCB	126L
2,2',3,3',4,4'-HxCB (NOAAT)	128	<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155L
2,2',3,4,4',5'-HxCB (NOAAT)	138	<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155L
2,2',4,4',5,5'-HxCB (NOAAT)	153	<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155L
2,3,3',4,4',5'-HxCB (WHOT)	156	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	156L
2,3,3',4,4',5'-HxCB (WHOT)	157	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157L
2,3',4,4',5,5'-HxCB (WHOT)	167	<sup>13</sup> C <sub>12</sub> -2,3',4,4',5,5'-HxCB	167L
3,3',4,4',5,5'-HxCB (NOAAT) (WHOT)	169	<sup>13</sup> C <sub>12</sub> -3,3',4,4',5,5'-HxCB	169L
2,2',3,3',4,4',5'-HpCB (NOAAT)	170	<sup>13</sup> C <sub>12</sub> -2,2',3,3',4,4',5'-HpCB	170L
2,2',3,4,4',5,5'-HpCB (NOAAT)	180	<sup>13</sup> C <sub>12</sub> -2,2',3,4,4',5,5'-HpCB	180L
2,2',3,4,5,5',6'-HpCB (NOAAT)	187	<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188L
2,3,3',4,4',5,5'-HpCB (WHOT)	189	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5,5'-HpCB	189L
2,2',3,3',4,4',5,6'-OxCB (NOAAT)	195	<sup>13</sup> C <sub>12</sub> -2,2',3,3',5,5',6,6'-OxCB	202L
2,2',3,3',4,4',5,5',6'-NoCB (NOAAT)	206	<sup>13</sup> C <sub>12</sub> -2,2',3,3',4,4',5,5',6'-NoCB	206L
2,2',3,3',4,4',5,5',6,6'-DeCB (NOAAT)	209	<sup>13</sup> C <sub>12</sub> -DeCB	209L

<sup>a</sup> BZ No.: Ballschmiter and Zell 1980, or IUPAC number.

<sup>b</sup> Assignments assume the use of the SPB-Octyl column. In the event you choose another column, you may select the labeled standard having the same number of chlorine substituents and the closest retention time to the target analyte in question as the labeled standard to use for quantitation.

NOAAT = PCB considered toxic by the National Oceanic and Atmospheric Administration.

WHOT = PCB considered toxic by the World Health Organization.

**Table OTM46-18. Initial Demonstration of Capability QC Requirements**

<b>Section</b>	<b>Requirement</b>	<b>Specification and Frequency</b>	<b>Acceptance Criteria</b>
9.3.5	Demonstration of low system background	Analyze an LMB after the highest calibration standard. Note: If an automated extraction system is used, an LMB must be extracted on each port.	Confirm that the LMB is free from contamination as defined in Section 13.1.
9.3.7	Determination of MDL	Prepare, extract, and analyze 7 replicate spiked samples (spiked within 2 to 10 times of the expected MDL) and 7 LMBs.  See 40 CFR Part 136 Appendix B	See MDL confirmation
9.3.8	MDL confirmation	Prepare, extract, and analyze a spiked sample (spiked at the MDL).	Confirm that the target compounds meet the qualitative identification criteria in Section 11.4.3.4 of this method.
9.3.9	Demonstration of precision	Prepare, extract, and analyze 7 replicate spiked samples (spiked near mid-range).	Percent relative standard deviation must be $\leq 20\%$ .
9.3.10	Demonstration of accuracy	Calculate mean recovery for replicate spiked samples in Section 9.3.9.	Mean recovery within 70-130% of true value.
9.3.2	Lowest Calibration Concentration Confirmation	Establish a target concentration for the lowest calibration based on the intended use of the method.	Upper PIR $\leq 150\%$ Lower PIR $\geq 50\%$
9.3.6	Calibration Verification	Analyze a mid-level QCS.	Within limits in Section 13.11.



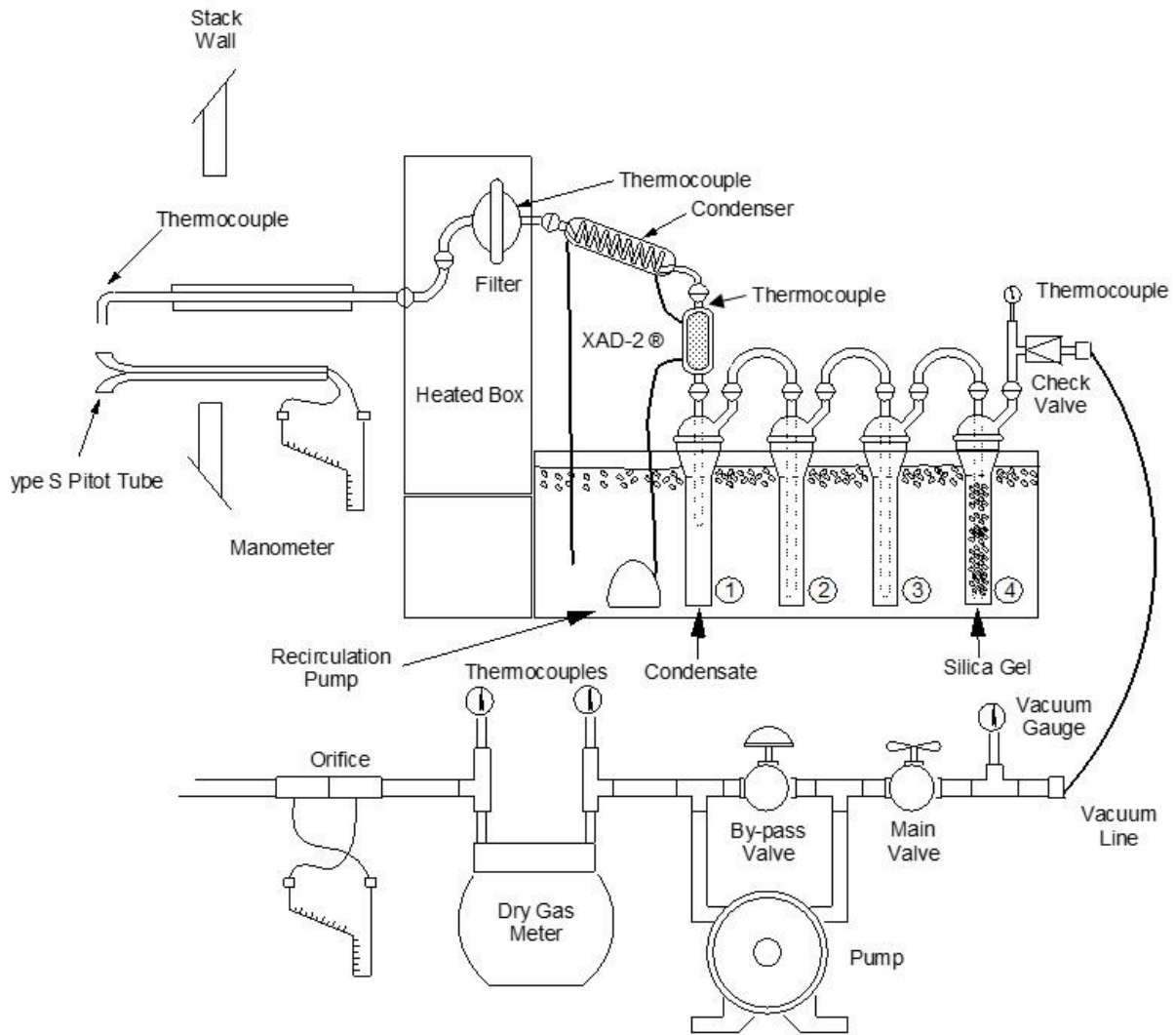


Figure 23-1. Sampling Train

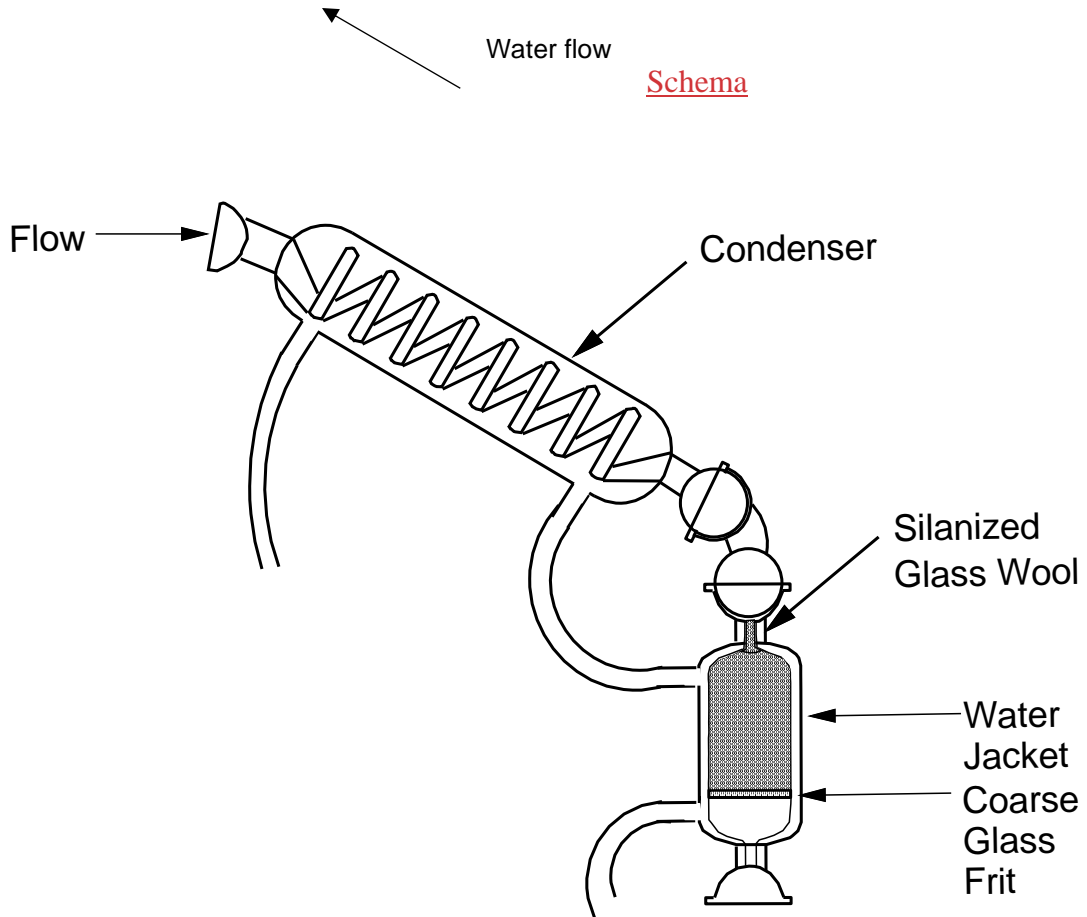


Figure 23-2. Condenser and Adsorbent Module

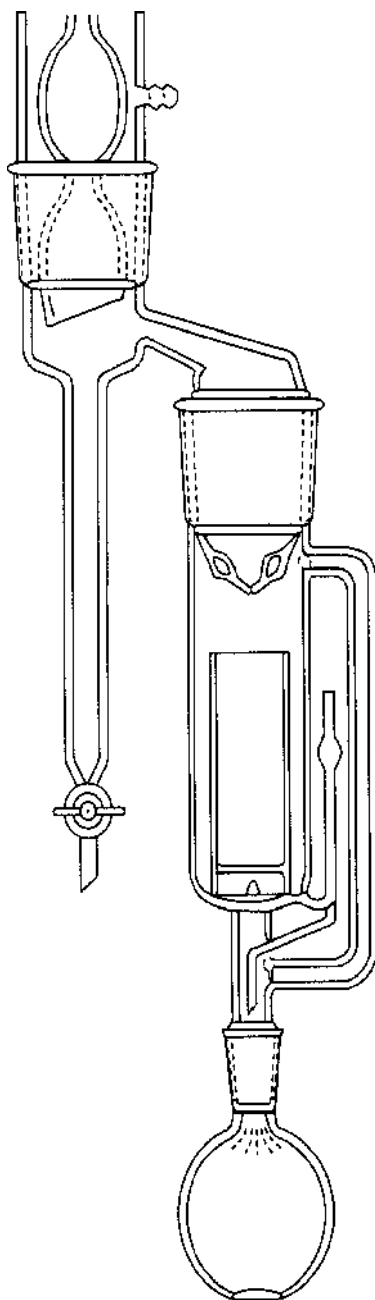


Figure 23-3. Soxhlet/Dean-Stark Extractor

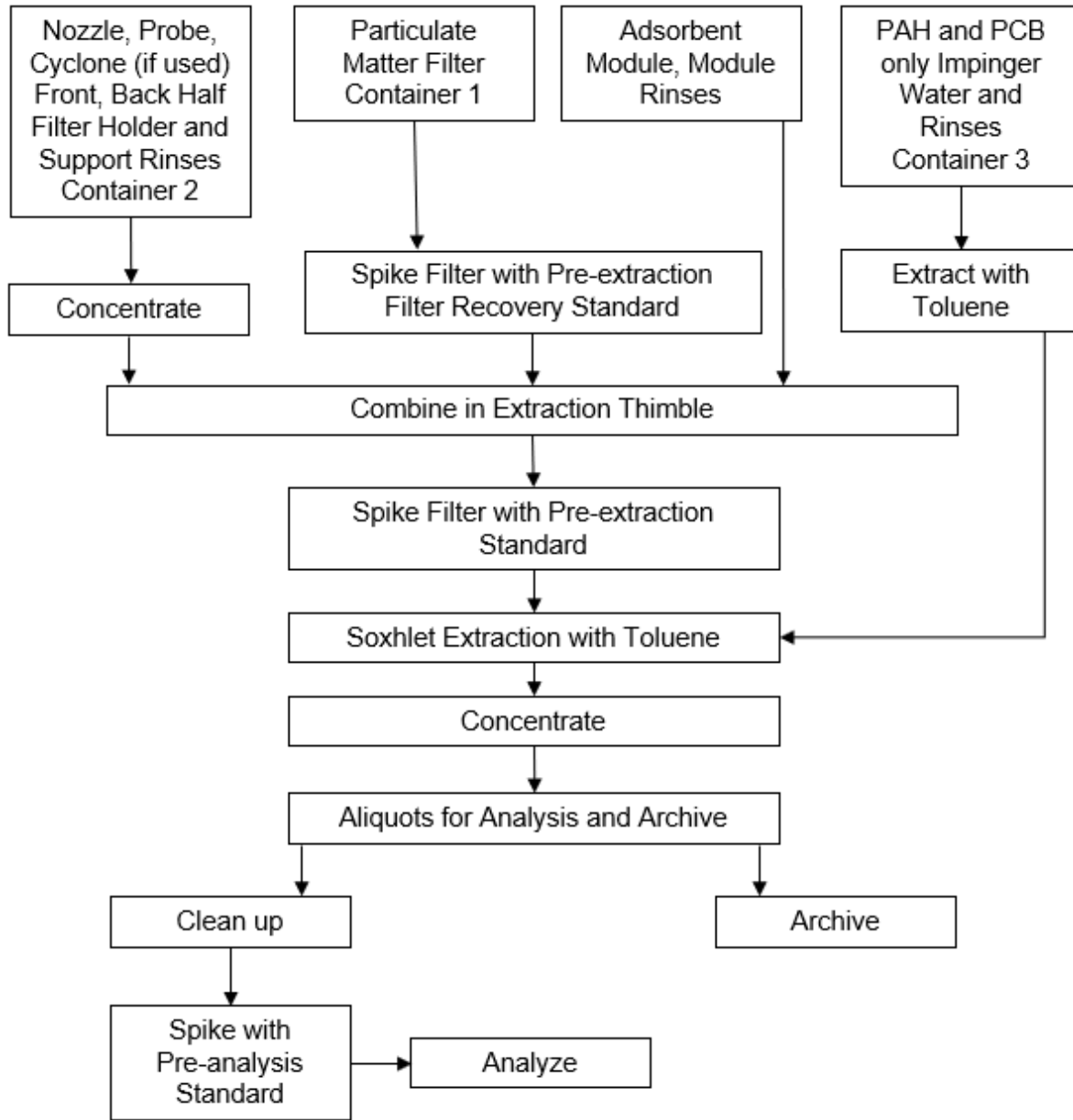


Figure 23-4. Sample Preparation Flow Chart

## APPENDIX A

**Complete List of 209 PCB Congeners and Their Isomers with Corresponding Isotope  
Dilution Quantitation Standards<sup>a</sup>**

Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.	Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.
<b>MoCB</b>				<b>DiCB</b>			
<sup>13</sup> C <sub>12</sub> -2-MoCB	1L	2-MoCB	1	<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	2,2'-DiCB	4
<sup>13</sup> C <sub>12</sub> -2-MoCB	1L	3-MoCB	2	<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	2,3-DiCB	5
<sup>13</sup> C <sub>12</sub> -4-MoCB	3L	4-MoCB	3	<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	2,3'-DiCB	6
				<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	2,4-DiCB	7
				<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	2,4'-DiCB	8
				<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	2,5-DiCB	9
				<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	2,6-DiCB	10
				<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	3,3'-DiCB	11
				<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	3,4-DiCB	12
				<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	3,4'-DiCB	13
				<sup>13</sup> C <sub>12</sub> -2,2'-DiCB	4L	3,5-DiCB	14
				<sup>13</sup> C <sub>12</sub> -4,4'-DiCB	15L	4,4'-DiCB	15
<b>TrCB</b>							
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,2',3-TrCB	16	<sup>13</sup> C <sub>12</sub> -3,4,4'-TrCB	19L	2,4,4'-TrCB	28
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,2',4-TrCB	17	<sup>13</sup> C <sub>12</sub> -3,4,4'-TrCB	19L	2,4,5-TrCB	29
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,2',5-TrCB	18	<sup>13</sup> C <sub>12</sub> -3,4,4'-TrCB	19L	2,4,6-TrCB	30
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,2',6-TrCB	19	<sup>13</sup> C <sub>12</sub> -3,4,4'-TrCB	19L	2,4',5-TrCB	31
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,3,3'-TrCB	20	<sup>13</sup> C <sub>12</sub> -3,4,4'-TrCB	19L	2,4',6-TrCB	32
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,3,4-TrCB	21	<sup>13</sup> C <sub>12</sub> -3,4,4'-TrCB	19L	2',3,4-TrCB	33
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,3,4'-TrCB	22	<sup>13</sup> C <sub>12</sub> -3,4,4'-TrCB	19L	2',3,5-TrCB	34
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,3,5-TrCB	23	<sup>13</sup> C <sub>12</sub> -3,4,4'-TrCB	19L	3,3',4-TrCB	35
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,3,6-TrCB	23	<sup>13</sup> C <sub>12</sub> -3,4,4'-TrCB	19L	3,3',5-TrCB	36
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,3',4-TrCB	25	<sup>13</sup> C <sub>12</sub> -3,4',4'-TrCB	37L	3,4,4'-TrCB	37
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,3',5-TrCB	26	<sup>13</sup> C <sub>12</sub> -3,4',4'-TrCB	37L	3,4,5-TrCB	38
<sup>13</sup> C <sub>12</sub> -2,2',6-TrCB	19L	2,3',6-TrCB	27	<sup>13</sup> C <sub>12</sub> -3,4',4'-TrCB	37L	3,4',5-TrCB	39
<b>TeCB</b>							
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',3,3'-TeCB	40	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,4,5-TeCB	61
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',3,4-TeCB	41	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,4,6-TeCB	62
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',3,4'-TeCB	42	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,4',5-TeCB	63
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',3,5-TeCB	43	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,4',6-TeCB	64
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',3,5'-TeCB	44	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,5,6-TeCB	65

Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.	Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',3,6-TeCB	45	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3',4,4'-TeCB	66
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',3,6'-TeCB	46	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3',4,5-TeCB	67
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',4,4'-TeCB	47	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3',4,5'-TeCB	68
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',4,5-TeCB	48	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3',4,6-TeCB	69
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',4,5'-TeCB	49	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3',4',5-TeCB	70
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',4,6-TeCB	50	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3',4',6-TeCB	71
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',4,6'-TeCB	51	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3',5,5'-TeCB	72
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',5,5'-TeCB	52	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3',5',6-TeCB	73
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',5,6'-TeCB	53	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,4,4',5-TeCB	74
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,2',6,6'-TeCB	54	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,4,4',6-TeCB	75
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,3',4'-TeCB	55	<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2',3,4,5-TeCB	76
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,3',4'-TeCB	56	<sup>13</sup> C <sub>12</sub> -3,3',4,4'-TeCB	77L	3,3',4,4'-TeCB	77
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,3',5-TeCB	57	<sup>13</sup> C <sub>12</sub> -3,3',4,4'-TeCB	77L	3,3',4,5-TeCB	78
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,3',5'-TeCB	58	<sup>13</sup> C <sub>12</sub> -3,3',4,4'-TeCB	77L	3,3',4,5'-TeCB	79
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,3',6-TeCB	59	<sup>13</sup> C <sub>12</sub> -3,3',4,4'-TeCB	77L	3,3',5,5'-TeCB	80
<sup>13</sup> C <sub>12</sub> -2,2',6,6'-TeCB	54L	2,3,4,4'-TeCB	60	<sup>13</sup> C <sub>12</sub> -3,4,4',5-TeCB	81L	3,4,4',5-TeCB	81
<b>PeCB</b>							
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,3',4-PeCB	82	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB	105 L	2,3,3',4,4'-PeCB	105
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,3',5-PeCB	83	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB	105 L	2,3,3',4,5-PeCB	106
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,3',6-PeCB	84	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB	105 L	2,3,3',4',5-PeCB	107
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,4,4'-PeCB	85	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB	105 L	2,3,3',4,5'-PeCB	108
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,4,5-PeCB	86	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB	105 L	2,3,3',4,6-PeCB	109

Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.	Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,4,5'-PeCB	87	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB	105 L	2,3,3',4',6-PeCB	110
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,4,6-PeCB	88	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB	105 L	2,3,3',5,5'-PeCB	111
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,4,6'-PeCB	89	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB	105 L	2,3,3',5,6-PeCB	112
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,4',5-PeCB	90	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4'-PeCB	105 L	2,3,3',5',6-PeCB	113
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,4',6-PeCB	91	<sup>13</sup> C <sub>12</sub> -2,3,4,4',5-PeCB	114 L	2,3,4,4',5-PeCB	114
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,5,5'-PeCB	92	<sup>13</sup> C <sub>12</sub> -2,3,4,4',5-PeCB	114 L	2,3,4,4',6-PeCB	115
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,5,6-PeCB	93	<sup>13</sup> C <sub>12</sub> -2,3,4,4',5-PeCB	114 L	2,3,4,5,6-PeCB	116
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,5,6'-PeCB	94	<sup>13</sup> C <sub>12</sub> -2,3,4,4',5-PeCB	114 L	2,3,4',5,6-PeCB	117
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,5',6-PeCB	95	<sup>13</sup> C <sub>12</sub> -2,3',4,4',5-PeCB	118 L	2,3',4,4',5-PeCB	118
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3,6,6'-PeCB	96	<sup>13</sup> C <sub>12</sub> -2,3',4,4',5-PeCB	118 L	2,3',4,4',6-PeCB	119
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3',4,5-PeCB	97	<sup>13</sup> C <sub>12</sub> -2,3',4,4',5-PeCB	118 L	2,3',4,5,5'-PeCB	120
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',3',4,6-PeCB	98	<sup>13</sup> C <sub>12</sub> -2,3',4,4',5-PeCB	118 L	2,3',4,5,'6-PeCB	121
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',4,4',5-PeCB	99	<sup>13</sup> C <sub>12</sub> -2,3',4,4',5-PeCB	118 L	2',3,3',4,5-PeCB	122
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',4,4',6-PeCB	100	<sup>13</sup> C <sub>12</sub> -2',3,4,4',5-PeCB	123 L	2',3,4,4',5-PeCB	123
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',4,5,5'-PeCB	101	<sup>13</sup> C <sub>12</sub> -2',3,4,4',5-PeCB	123 L	2',3,4,5,5'-PeCB	124
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',4,5,6'-PeCB	102	<sup>13</sup> C <sub>12</sub> -2',3,4,4',5-PeCB	123 L	2',3,4,5,6'-PeCB	125
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',4,5,'6-PeCB	103	<sup>13</sup> C <sub>12</sub> -3,3',4,4',5-PeCB	126 L	3,3',4,4',5-PeCB	126
<sup>13</sup> C <sub>12</sub> -2,2',4,6,6'-PeCB	104 L	2,2',4,6,6'-PeCB	104	<sup>13</sup> C <sub>12</sub> -3,3',4,4',5-PeCB	126 L	3,3',4,5,5'-PeCB	127
<b>HxCB</b>							
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,3',4,4'-HxCB	128	<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4',5',6-HxCB	149
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,3',4,5'-HxCB	129	<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4',6,6'-HxCB	150

Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.	Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,3',4,5'-HxCB	130	<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,5,5',6'-HxCB	151
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,3',4,6'-HxCB	131	<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,5,6,6'-HxCB	152
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,3',4,6'-HxCB	132	<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',4,4',5,5'-HxCB	153
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,3',5,5'-HxCB	133	<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',4,4',5',6'-HxCB	154
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,3',5,6'-HxCB	134	<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',4,4',6,6'-HxCB	155
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,3',5,6'-HxCB	135	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	156 L	2,3,3',4,4',5'-HxCB	156
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,3',6,6'-HxCB	136	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157 L	2,3,3',4,4',5'-HxCB	157
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4,4',5'-HxCB	137	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157 L	2,3,3',4,4',6'-HxCB	158
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4,4',5'-HxCB	138	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157 L	2,3,3',4,5,5'-HxCB	158
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4,4',6'-HxCB	139	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157 L	2,3,3',4,5,6'-HxCB	160
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4,4',6'-HxCB	140	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157 L	2,3,3',4,5',6'-HxCB	161
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4,5,5'-HxCB	141	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157 L	2,3,3',4',5,5'-HxCB	162
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4,5,6'-HxCB	142	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157 L	2,3,3',4',5,6'-HxCB	163
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4,5,6'-HxCB	143	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157 L	2,3,3',4',5',6'-HxCB	164
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4,5',6'-HxCB	144	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157 L	2,3,3',5,5',6'-HxCB	165



Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.	Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4,6,6'-HxCB	145	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5'-HxCB	157 L	2,3,4,4',5,6'-HxCB	166
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4',5,5'-HxCB	146	<sup>13</sup> C <sub>12</sub> -2,3',4,4',5,5'-HxCB	167 L	2,3',4,4',5,5'-HxCB	167
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4',5,6'-HxCB	147	<sup>13</sup> C <sub>12</sub> -2,3',4,4',5,5'-HxCB	167 L	2,3',4,4',5',6'-HxCB	168
<sup>13</sup> C <sub>12</sub> -2,2',4,4',6,6'-HxCB	155 L	2,2',3,4',5,6'-HxCB	148	<sup>13</sup> C <sub>12</sub> -3,3',4,4',5,5'-HxCB	169 L	3,3',4,4',5,5'-HxCB	169
<b>HpCB</b>							
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,3',4,4',5'-HpCB	170	<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,4,4',5,6'-HpCB	182
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,3',4,4',6'-HpCB	171	<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,4,4',5',6'-HpCB	183
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,3',4,5,5'-HpCB	172	<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,4,4',5',6'-HpCB	184
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,3',4,5,6'-HpCB	173	<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,4,4',6,6'-HpCB	185
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,3',4,5,6'-HpCB	174	<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,4,5,5',6'-HpCB	186
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,3',4,5',6'-HpCB	175	<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,4',5,5',6'-HpCB	187
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,3',4,6,6'-HpCB	176	<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,4',5,6,6'-HpCB	188
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,3',4',5,6'-HpCB	177	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5,5'-HpCB	189 L	2,3,3',4,4',5,5'-HpCB	189
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,3',5,5',6'-HpCB	178	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5,5'-HpCB	189 L	2,3,3',4,4',5,6'-HpCB	190
<sup>13</sup> C <sub>12</sub> -2,2',3,4',5,6,6'-HpCB	188 L	2,2',3,3',5,6,6'-HpCB	179	<sup>13</sup> C <sub>12</sub> -2,3,3',4,4',5,5'-HpCB	189 L	2,3,3',4,4',5',6'-HpCB	191

Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.	Pre-extraction Standard	BZ <sup>b</sup> No.	Unlabeled Target Analyte	BZ <sup>b</sup> No.
<sup>13</sup> C <sub>12</sub> - 2,2',3,4',5,6,6'- HpCB	188 L	2,2',3,4,4',5,5'- HpCB	180	<sup>13</sup> C <sub>12</sub> - 2,3,3',4,4',5,5'- HpCB	189 L	2,3,3',4,5,5',6- HpCB	192
<sup>13</sup> C <sub>12</sub> - 2,2',3,4',5,6,6'- HpCB	188 L	2,2',3,4,4',5,6- HpCB	181	<sup>13</sup> C <sub>12</sub> - 2,3,3',4,4',5,5'- HpCB	189 L	2,3,3',4',5,5',6- HpCB	193
<b>OcCB</b>				<b>NoCB</b>			
<sup>13</sup> C <sub>12</sub> - 2,2',3,3',5,5',6,6'- OcCB	202 L	2,2',3,3',4,4',5, 5'-OcCB	194	<sup>13</sup> C <sub>12</sub> - 2,2',3,3',4,4',5,5',6 -NoCB	206 L	2,2',3,3',4,4',5,5', ,6-NoCB	206
<sup>13</sup> C <sub>12</sub> - 2,2',3,3',5,5',6,6'- OcCB	202 L	2,2',3,3',4,4',5, 6-OcCB	195	<sup>13</sup> C <sub>12</sub> - 2,2',3,3',4,4',5,5',6 -NoCB	206 L	2,2',3,3',4,4',5,6, 6'-NoCB	207
<sup>13</sup> C <sub>12</sub> - 2,2',3,3',5,5',6,6'- OcCB	202 L	2,2',3,3',4,4',5, 6'-OcCB	196	<sup>13</sup> C <sub>12</sub> - 2,2',3,3',4,5,5',6,6' -NoCB	208 L	2,2',3,3',4,5,5',6, 6'- NoCB	208
<sup>13</sup> C <sub>12</sub> - 2,2',3,3',5,5',6,6'- OcCB	202 L	2,2',3,3',4,4',6, 6'-OcCB	197	<b>DeCB</b>			
<sup>13</sup> C <sub>12</sub> - 2,2',3,3',5,5',6,6'- OcCB	202 L	2,2',3,3',4,5,5', 6-OcCB		<sup>13</sup> C <sub>12</sub> -DeCB	209 L	2,2',3,3',4,4',5,5', ,6,6'-DeCB	209
<sup>13</sup> C <sub>12</sub> - 2,2',3,3',5,5',6,6'- OcCB	202 L	2,2',3,3',4,5,5', 6'-OcCB	199				
<sup>13</sup> C <sub>12</sub> - 2,2',3,3',5,5',6,6'- OcCB	202 L	2,2',3,3',4,5,6,6 '-OcCB	200				
<sup>13</sup> C <sub>12</sub> - 2,2',3,3',5,5',6,6'- OcCB	202 L	2,2',3,3',4,5',6, 6'-OcCB	201				
<sup>13</sup> C <sub>12</sub> - 2,2',3,3',5,5',6,6'- OcCB	202 L	2,2',3,3',5,5',6, 6'-OcCB	202				
<sup>13</sup> C <sub>12</sub> - 2,3',3',4,4',5,5',6- OcCB	205 L	2,2',3,4,4',5,5', 6-OcCB	203				
<sup>13</sup> C <sub>12</sub> - 2,3',3',4,4',5,5',6- OcCB	205 L	2,2',3,4,4',5,6,6 '-OcCB	204				
<sup>13</sup> C <sub>12</sub> - 2,3',3',4,4',5,5',6- OcCB	205 L	2,3,3',4,4',5,5', 6-OcCB	205				

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<sup>a</sup> Assignments assume the use of the SPB-Octyl column. In the event you choose another column, you may select the labeled standard having the same number of chlorine substituents and the closest retention time to the target analyte in question as the labeled standard to use for quantitation.

<sup>b</sup>BZ No.: Ballschmiter and Zell 1980, also referred to as IUPAC number.

## Appendix B

### Preparation of XAD-2 Adsorbent Resin

#### *1.0 Scope and Application*

XAD-2® resin, as supplied by the original manufacturer, is impregnated with a bicarbonate solution to inhibit microbial growth during storage. Remove both the salt solution and any residual extractable chemicals used in the polymerization process before use. Prepare the resin by a series of water and organic extractions, followed by careful drying.

#### *2.0 Extraction*

2.1 You may perform the extraction using a Soxhlet extractor or other apparatus that generates resin meeting the requirements in Section 13.1 of this method. Use an all-glass thimble containing an extra-coarse frit for extraction of the resin. The frit is recessed 10-15 mm above a crenellated ring at the bottom of the thimble to facilitate drainage. Because the resin floats on methylene chloride, carefully retain the resin in the extractor cup with a glass wool plug and stainless-steel screen. This process involves sequential extraction with the following recommended solvents in the listed order.

- Water initial rinse: Place resin in a suitable container, soak for approximately 5 min with Type II water, remove fine floating resin particles and discard the water. Fill with Type II water a second time, let stand overnight, remove fine floating resin particles and discard the water.
- Hot water: Extract with water for 8 hr.
- Methyl alcohol: Extract for 22 hr.
- Methylene chloride: Extract for 22 hr.
- Toluene: Extract for 22 hr.
- Methylene chloride: Extract for 22 hr.

Note: You may store the resin in a sealed glass container filled with toluene prior to the final toluene extraction. It may be necessary to repeat the final methylene chloride extractions to meet the cleanliness requirements in Section 13.1 of this method.

2.2 You may use alternative extraction procedures to clean large batches of resin. Any size extractor may be constructed; the choice depends on the needs of the sampling programs. The resin is held in a glass or stainless-steel cylinder between a pair of coarse and fine screens. Spacers placed under the bottom screen allow for even distribution of clean solvent. Clean solvent is circulated through the resin for extraction. A flow rate is maintained upward through the resin to allow maximum solvent contact and prevent channeling.

2.2.1 Experience has shown that 1 mL/g of resin extracted is the minimum necessary to extract and clean the resin. The aqueous rinse is critical to the subsequent organic rinses and may be accomplished by simply flushing the canister with about 1 liter of distilled water for every 25 g of resin. A small pump may be useful for pumping the water through the canister. You should perform the water extraction at the rate of about 20 to 40 mL/min.

2.2.2 All materials of construction are glass, PTFE, or stainless steel. Pumps, if used, should not contain extractable materials.

### *3.0 Drying*

3.1 Dry the adsorbent of extraction solvent before use. This section provides a recommended procedure to dry adsorbent that is wet with solvent. However, you may use other procedures if the cleanliness requirements in Section 13.1 of this method are met.

3.2 Drying Column. A simple column with suitable retainers will hold all the XAD-2 from the extractor or the Soxhlet extractor, as shown in Figure B-1, with sufficient space for drying the bed while generating a minimum backpressure in the column.

3.3 Drying Procedure: Dry the adsorbent using clean inert gas. Liquid nitrogen from a standard commercial liquid nitrogen cylinder has proven to be a reliable source of large volumes of gas free from organic contaminants. You may use high-purity tank nitrogen to dry the resin.

However, you should pass the high-purity nitrogen through a bed of activated charcoal approximately 150 mL in volume prior to entering the drying apparatus.

3.3.1 Connect the gas vent of a liquid nitrogen cylinder or the exit of the activated carbon scrubber to the column by a length of precleaned copper tubing (e.g., 0.95 cm ID) coiled to pass through a heat source. A convenient heat source is a water bath heated from a steam line. The final nitrogen temperature should only be warm to the touch and not over 40 °C.

3.3.2 Allow the methylene chloride to drain from the resin prior to placing the resin in the drying apparatus.

3.3.3 Flow nitrogen through the drying apparatus at a rate that does not fluidize or agitate the resin. Continue the nitrogen flow until the residual solvent is removed.

Note: Experience has shown that about 500 g of resin may be dried overnight by consuming a full 160-L cylinder of liquid nitrogen.

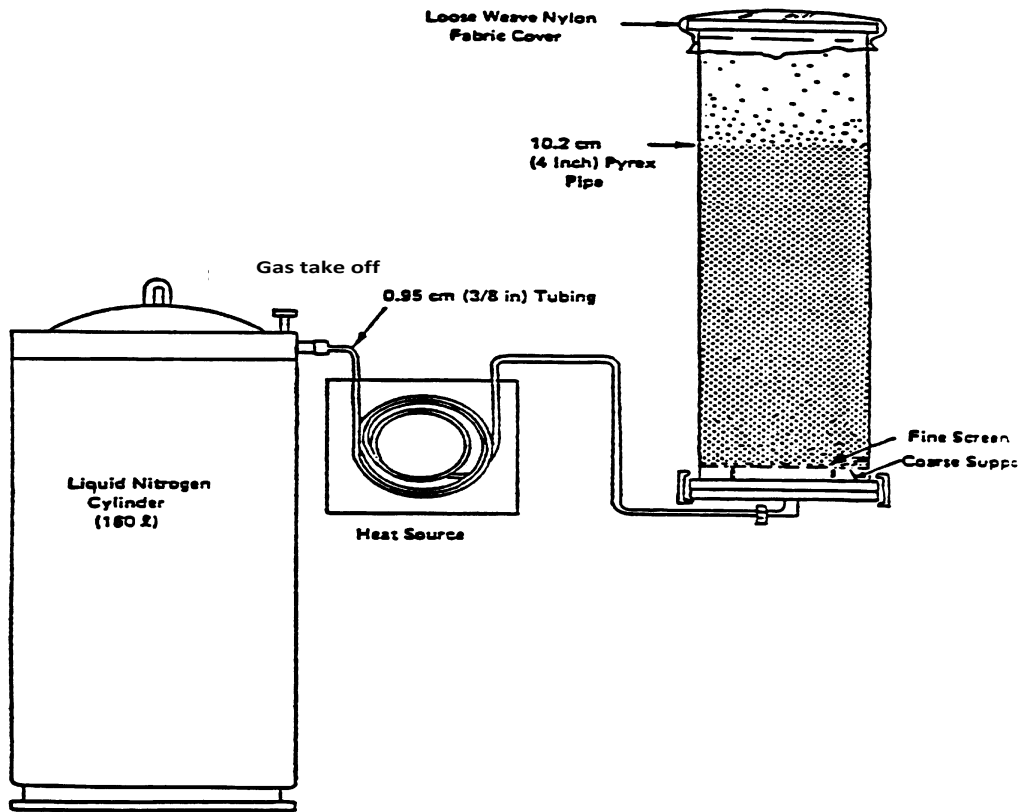


Figure B-1. XAD-2 fluidized-bed drying apparatus