REPORT

# Correction of Analytical Biases in the 1991-1997 GE Hudson River PCB Database

General Electric Company
Corporate Environmental Programs
Albany, New York

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O'BRIEN & GERE
ENGINEERS, INC.

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# 1. Introduction

## 1.1. Background

On behalf of the General Electric Company (GE), O'Brien & Gere Engineers, Inc. (O'Brien & Gere) prepared this report to document corrections implemented to address PCB analytical bias in the GE Hudson River database. HydroQual (1997) identified analytical bias in the database, and developed correction factors to correct for the bias. This report presents detailed documentation of the corrections as applied to the database.

### 1.1.1. Analytical method summary

Sampling and analysis for PCBs in the Hudson River by GE and its contractors has been performed in accordance with the Quality Assurance Project Plan (QAPP) developed for the site (O'Brien & Gere 1992). The PCB analytical method used for the Hudson River sampling programs, Method NEA608CAP, has been performed by Northeast Analytical Laboratories, Inc. (Northeast Analytical) for the Hudson River project since 1991.

Method NEA608CAP involves the analysis of PCBs, extracted from the sample matrix, by gas chromatographic (GC) separation of PCB congeners on a DB-1 capillary column, with electron capture detection (O'Brien & Gere 1997a). Calibration of the DB-1 column is based on the method developed by the U.S. Environmental Protection Agency (USEPA) for the Green Bay Mass Balance Study (USEPA 1987). The Green Bay Method involves GC standardization using a 25:18:18 mixture of Aroclors 1232, 1248, and 1262. Individual DB-1 peak response factors[1] are calculated based on standard peak weight percent values originally developed by the USEPA (USEPA 1987). These response factors are then used to calculate PCB content of environmental samples. The DB-1 column separates PCBs into 118 unique chromatogram peaks. Several of these peaks contain multiple (coeluting) congeners (Table 1-1).

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[1] The response factor is defined as the PCB congener mass per unit area of chromatogram peak.

### 1.1.2. Summary of GE Hudson River PCB database

The GE Hudson River PCB database was developed to store data collected from the Hudson River by GE and its contractors in association with the USEPA Reassessment Remedial Investigation and Feasibility Study (RRI/FS). The database contains congener PCB data for approximately 3,000 environmental samples collected from the Hudson River between 1990 and 1997. Sampling programs include the Post-Construction Remnant Deposit Monitoring Program (PCRDMP; O'Brien & Gere 1993a, 1994, 1995, 1996a, 1997a) Temporal Water Column Monitoring Program (O'Brien & Gere 1993c), 1991 Sediment Sampling Program (O'Brien & Gere 1993b), and others (O'Brien & Gere 1993d,e,f; 1996b; 1997b,c,d)

Hudson River PCB data are contained in two related databases.

*GE (environmental) database*. Information in the GE database consists of:

- Total PCB, PCB homolog distributions and chlorines per biphenyl obtained from Method NEA608CAP PCB congener analyses
- analytical results from conventional parameters such as total suspended solids, organic carbon, and total PCBs obtained from analytical methods other than NEA608CAP
- sample field logs and chain of custody information
- Hudson River USGS gaging station discharge data
- sampling program and investigating contractor responsible for sample collection.

*CP (congener peak) database*. Information in the CP database consists of data from Method NEA608CAP analyses:

- sample identification information
- PCB congener peak concentrations for 118 peaks resolved on a DB-1 capillary column
- total PCB concentrations
- average molecular weight
- total micromoles of PCB within sample

Additional fields have been added to both databases to reflect the revisions made to compensate for analytical biases. These revisions are described in Chapter 2. Revised file structure tables for the databases are contained in Appendix A.

**1.1.3. Identification and quantification of analytical biases**
HydroQual identified and quantified analytical biases in the GE Hudson River database (HydroQual 1997). A brief synopsis of those findings is provided below.

HydroQual (1997) compared water column PCB concentrations in samples collected by GE in 1993 from the Fort Edward (HRM 194.2) and Thompson Island dam (HRM 188.5) monitoring stations (O'Brien & Gere 1994) with those measured as part of the USEPA RRI/FS Phase II study (USEPA 1995). Although total PCB levels exhibited consistency in magnitude and temporal trends, individual PCB congeners differed significantly (HydroQual 1997).

HydroQual (1997) identified analytical biases as the predominant cause of observed differences between GE and USEPA data. These analytical biases were associated with the Green Bay mixed Aroclor standard used to calibrate the DB-1 capillary column system (HydroQual 1997). These analytical biases, briefly summarized below, are of two types: calibration errors and coelution biases (HydroQual 1997).

*Calibration errors.* Differences between the GE and USEPA congener PCB data can be partly attributed to an error in the original calibration of the PCB standard used by GE for DB-1 analyses (USEPA 1987). The congener distribution of the Green Bay standard was apparently miscalculated, predominantly for components of DB-1 Peak 5, and a revision to the calibration was later published (USEPA 1994). The congener distribution miscalculation introduced systematic analytical biases in the GE data because underestimation of DB-1 Peak 5 in the calibration standard resulted in underestimation of DB-1 Peak 5 in the Hudson River environmental samples. Since the error was in the interpretation of the calibration standard composition, not the PCB mass, it affected data for all 118 DB-1 peaks. Specifically, underestimation of DB-1 Peak 5 resulted in overestimation of the other peaks (HydroQual 1997).

Original and revised DB-1 peak weight percent data for the Green Bay standard were used to develop correction factors to account for the calibration error in the original standard (HydroQual 1997). These correction factors were used to implement this portion of the database correction.

*Coelution bias.* Another cause of bias in the GE database is related to the methods used to separate and quantify PCB congeners (HydroQual 1997). Mass estimates of coeluting congeners with differing response factors are sensitive to the assumption made regarding the relative amounts of the congeners that coelute in a single DB-1 peak (HydroQual 1997). Currently, the assumptions for deconvolution of peaks containing congeners with different chlorination levels (mixed peaks) are based on mass spectrometry analysis of Aroclor mixtures (Frame et al, 1996). As mixed-peak congener mass ratios in Hudson River environmental samples deviate from those of commercial Aroclors, measurement errors are introduced into results for these peaks. Furthermore, differences in coeluting peak congener compositions between Hudson River environmental samples and those of the DB-1 calibration standard will result in similar errors (HydroQual 1997).

HydroQual (1997) ranked the DB-1 capillary column peaks with coeluting congeners for potential bias based on differences in congener response factors and the relative abundance of these peaks in Hudson River environmental samples. Mixed DB-1 peak deconvolution assumptions used for PCB analysis were derived from literature (Mullin et al, 1984; Frame and others 1996; Frame 1997). Peaks possessing the largest potential bias (Peaks 5, 8, and 14) were further evaluated through the analysis of selected water column and sediment archived sample extracts on a different analytical column (Chromopack, Inc. CP-SIL5/C18 (C18) capillary column). The C18 column separates target congeners that coelute in the DB-1 capillary column Peaks 5, 8 and 14. HydroQual (1997) quantitatively compared individual congener results from the C18 column with the original DB-1 column results and developed coelution correction factors for both sediment and water column samples.

Based on these findings, HydroQual developed correction factors to be used to correct PCB calibration (Table 1-2) and coelution biases (Table 1-3) in the historical GE database, and changes to the GE Hudson River PCB analytical program (HydroQual 1997).

## 1.2. Objective

The principal objective of database correction was to correct the 1991-1997 GE Hudson River PCB database for both calibration errors and coelution biases identified and quantified by HydroQual (1997). This document accompanies the revised GE Hudson River database (Appendix B).

## 1.3. Approach

O'Brien & Gere developed the following approach to implement the corrections to the GE Hudson River PCB database:

1. Prepare the CP, GE and reference databases:
   - archiving a copy of the existing databases
   - editing of the databases to separate the records of samples analyzed using the Green Bay standard from those not using the Green Bay standard
   - developing reference databases used to implement the corrections.

2. Implement analytical bias corrections to the CP database:
   - applying correction factors for both the calibration and coelution biases to the congener concentrations
   - recalculating total PCBs, average molecular weight, and total micromoles of PCB.

3. Manual and electronic Quality Control (QC) review of the corrected CP database.

4. Implement analytical bias corrections to the GE database including recalculating homolog distributions, and ortho-, meta+para- and total chlorines per biphenyl.

5. Manual and electronic QC review of the corrected GE database.

6. Finally, the corrected CP and GE databases were reconstructed with the non-corrected records.

This approach was implemented electronically, using routines written in Microsoft FoxPro software. A detailed algorithm is presented in Appendix C.

## 2. Implementation of database corrections

The PCB analytical bias correction factors developed by HydroQual (1997) were applied to the 1991-1997 GE Hudson River database (Tables 1-2 and 1-3). Corrections for analytical biases affected numerous field entries in the Hudson River databases including:

- DB-1 PCB peak concentrations
- Total PCB concentrations
- PCB composition information

The specific fields within the databases that were corrected for analytical biases are identified in the following table:

| Data | CP Database | GE Database |
|---|---|---|
| DB-1 peak concentrations | PK2_AMT[1] through PK118AMT | -- |
| Total PCB concentration | PCB_CONC | NEA_TOT, PCB_CAP, DL_CAP |
| PCB composition information | Total micromoles PCB (MIC_MOLS) | Homolog distributions, weight percent and mole percent MONO_WT through DECA_WT MONO_ML through DECA_ML |
| | Average molecular weight (AVG_MWT) | Chlorine substitution patterns (ORTHO_CL, MP_CL, TOT_CL) |

Notes:
[1]PK1_AMT (biphenyl) does not have a defined correction factor. This peak is not considered for PCB analysis of Hudson River environmental samples (HydroQual 1997).

*Source:* O'Brien & Gere Engineers, Inc.

Database corrections also required addition of new fields to the GE Hudson River PCB database. These new fields are summarized in Table 2-1.

Other reference information used to implement database corrections (Appendix D) were obtained from HydroQual (1997) and Northeast Analytical.

## 2.1. Database preparation

Prior to implementing the corrections programs, two copies of the existing databases were made: one copy was archived; a second, working copy was prepared for revision in a three-step procedure (Figure 2-1):

1. Editing the GE and CP databases - The GE database was edited to remove those records containing data not obtained using the Green Bay standard and for which the corrections did not apply. The CP database was also edited, using the field ID that links the GE and CP databases, to remove those records not requiring correction. The data not requiring correction were Harza (INVEST = HAR) sediment and fish data collected prior to 1990 and GE Corporate Research and Development (INVEST = CRD) archived fish data. New fields were added to the CP database to provide additional space to document the corrections implemented (Table 2.2).

2. Separating the databases by media - Since some of the corrections have media-specific correction factors, the CP and GE databases were separated by the media categories for water column, sediment/porewater, and fish/biota.

3. Developing additional reference databases - The information in these databases included data from C18 analyses, correction factors for the calibration bias, sample-specific indicators of analytical method, and DB-1 congener peak molecular weights (Table 1-2, Appendix D).

Once the databases were prepared, the corrections were implemented (Sections 2.2 and 2.3).

## 2.2. Analytical bias corrections: CP database

### 2.2.1. Procedure

Two analytical bias corrections to the CP databases were implemented for the three media data sets. Separate algorithms were written for the three media. For each record (or sample), four steps were completed (Figure 2-2):

1. The calibration bias was corrected by applying the appropriate correction factor from the reference database to the existing DB-1 congener peak

data in the selected database for water, sediment, porewater, fish and biota samples.

2. The coelution peak bias was corrected by applying the appropriate, media-specific, correction factor to DB-1 Peaks 5, 8 and 14. The additional fields (CF_PK5, CF_PK8, CF_PK14) contain the correction factors used for the given sample.

3. The data obtained from C18 analyses of archived extracts from water column, sediment, and porewater samples were compiled in the reference database C18_DATA (Appendix D). Values from the reference database were copied into the fields BZ4_AMT, BZ10_AMT, BZ5_AMT, BZ8_AMT, BZ15_AMT, and BZ18_AMT in the congener database. The database field C18_CHK indicates by "Y" or "N" if the sample was analyzed using the C18 column.

4. Three fields were recalculated once the calibration and coelution biases were corrected. First, the revised concentrations of the DB-1 peaks were summed for a PCB total that was placed in the field PCB_CONC. Then, the average molecular weight and the total micromoles were calculated and the resulting values placed in the fields AVG_MWT and MIC_MOLS, respectively.

### 2.2.2. Media-specific concerns

Two media-specific concerns with respect to the correction of coelution bias are summarized below:

*Fish and biota coelution correction factors.* Coelution correction factors were developed for water, sediment and porewater data sets, but were not developed for fish and biota samples. HydroQual evaluated the potential for coelution bias in the fish and biota samples, and concluded that higher-chlorinated coeluting congeners had the most potential for bias in the fish and biota samples. HydroQual indicated that separation of these higher chlorinated congeners could be difficult on a single-column system, and therefore coelution correction factors were not developed (HydroQual 1997).

*Change in calibration protocols for sediment and porewater.* During the original analysis of samples obtained during the 1991 Sediment Sampling Program (O'Brien & Gere 1993b), the DB-1 calibration protocol was altered to account for elevated DB-1 peak 5 concentrations within the samples (Northeast Analytical 1997a). Early in the sampling program, the calibration standard was changed from the Green Bay mixed Aroclor standard to the Green Bay standard plus an independent Peak 5 standard consisting of a 4:1 ratio of BZ4 and BZ10. This alleviated a DB-1 Peak 5 calibration range problem. Samples analyzed using the Green Bay standard only are identified in the database field GBS_BZ with "N". Samples analyzed by Green Bay standard with the BZ standard are identified with "Y" in the database field GBS_BZ. Sediment samples collected in 1996 (Particle Transport Study) and 1997 (High Flow Bed Load Sampling) were also analyzed using the Green Bay standard only. The different correction factors used for these two calibration protocols are included in Table 1-2.

### 2.2.3. Rounding

PCB congener concentrations in the database are in *ppm* units, and the database fields for congener concentrations (PK1_AMT to PK118AMT) extend to eleven decimal places. To minimize rounding errors in the calculations, the structure of the field PCB_CONC was adjusted to match that of the individual congener fields. The correction program performs calculations to fifteen decimal places, then rounds the resulting value to fit the structure of the field.

### 2.2.4. Correction of database errors

During the QC phase of the database correction task, several errors in the original database became apparent. These errors, listed below, have been corrected in the course of this task:

- MIC_MOLS field - The data in this field should be in micromole units throughout the database. The water column values in this field, however, were in picomole units. To maintain consistency in the MIC_MOLS field, the structure of the field was adjusted to allow picomole data to be presented in micromole units.

- Fish samples analyzed in 1995 from frozen tissues collected by Law Environmental in 1990 - The congener peak data in the original CP database were under reported by $10^6$, resulting in values reported by the laboratory in *ppm* units to be shown in the database in *ppt* units. Total PCBs in the original CP and GE databases were properly reported in *ppm* units. The congener peak data was corrected to the *ppm* units prior to adjustment for calibration bias. In addition, data for DB-1 Peak 89 were missing from the original database for this set of fish samples. Prior to database correction, these missing data were entered and checked.

- Change of the field name OBG-ID in the GE databases to CONV_ID - OBG_ID was originally used to identify the sample number assigned by O'Brien & Gere Laboratories (OBG) which performed conventional parameters analyses (*e.g.*, TOC, TSS). However, the laboratory was changed to NEA and this field name is no longer relevant. Therefore, the field name CONV_ID for conventional parameters laboratory sample ID is a more appropriate descriptor.

## 2.3. Analytical bias corrections: GE database

Upon completion and QC review of the corrections to the CP databases for the three media data sets, the revisions to the GE databases using the corrected CP data were implemented. For each record (or sample), three steps were completed (Figure 2-3):

1. The total PCB values calculated in the CP databases (field PCB_CONC) were copied into the fields NEA_TOT and PCB_CAP in the GE database. The field structures for NEA_TOT and PCB_CAP were adjusted to match that of PCB_CONC to minimize potential rounding errors. Data from PCB_CONC which were less than the media detection limit are identified by labels in the DL_CAP field, and by negative values in the NEA_TOT and PCB_CAP fields.

2. Homolog distributions were recalculated on both a weight percent and mole percent basis. The reference database MOL_WT, used to provide the information to the database on the distribution of DB-1 peaks in the ten homolog groups, is presented in Appendix D.

3. The average chlorination levels were recalculated for ortho, meta-para, and total chlorines per biphenyl. The reference database MOL_WT, which provided the information on the chlorination levels of the DB-1 congener peaks, is presented in Appendix D.

# 3. QC protocols development, implementation, and results

QC protocols were developed by O'Brien & Gere to check the accuracy of the corrections executed by the computer programs. In addition, HydroQual developed QC protocols and reviewed database changes as an independent quality check of the database. O'Brien & Gere worked closely with HydroQual during the QC process to validate the accuracy of changes to the database.

QC protocols were implemented in three phases: electronic QC review, manual QC review, and HydroQual review.

## 3.1. Electronic QC review

Electronic QC review consisted of electronically applying calibration and coelution correction factors to original congener peak data and comparing the result to the computer program revised congener peak data. In addition, total PCB, homolog distributions and chlorination levels were checked for accuracy. QC criteria included:

- Revised congener data matched original data times correction factors, with a rounding error of $\pm 1 \times 10^{-11}$ ppm.
- The sum of homolog weight percents and the sum of the homolog mole percents were within ±0.02% of 100%.
- The sum of the congeners equaled the values in fields PCB_CONC, NEA_TOT and PCB_CAP.

## 3.2. Manual QC review

Manual QC review was conducted on 5% of the database records, which were randomly selected from the three media-specific CP- and GE-adjusted databases. The corresponding original records were copied from the archived original CP and GE databases. The calibration and coelution correction factors were applied, in QuattroPro spreadsheet format, to the original records. The calculations to obtain total PCB, average molecular weight, total micromoles, homolog distributions and chlorination levels were also performed within the spreadsheet. The results were compared with the program-generated data in the adjusted databases. QC criteria included:

- Congener values corrected in the spreadsheet matched congener values corrected by the computer program within $\pm 1 \times 10^{-11}$ ppm.
- Total PCBs, total micromoles, and average molecular weight values calculated in the spreadsheet matched, within one significant decimal place, the values calculated by the computer program.
- Ortho, meta-para and total chlorines per biphenyl values calculated in the spreadsheet matched, within ±0.01 chlorines per biphenyl, the values calculated by the computer program.
- Homolog distributions, both weight percent and mole percent, calculated in the spreadsheet matched the values calculated by the computer program, and totaled 100% ±0.02%.
- Total chlorines per biphenyl, which represents the average chlorination level in the sample, was compared to the homolog distributions to qualitatively assess agreement between the two values.

## 3.3. HydroQual QC Review

HydroQual independently developed QC protocols and reviewed database changes as a secondary QC check after O'Brien & Gere completed its QC protocols.

# 4. Impact of analytical bias corrections on databases

Application of the analytical bias correction factors has impacted the quantification of PCB data and related parameters. The following sections provide a brief summary of changes in Hudson River PCB capillary column data, potential impact on the method detection limit, and potential impact to data validation qualifiers.

## 4.1. Magnitude of change in PCB data

Changes in PCB congener concentrations resulting from the analytical bias correction has impacted Method NEA608CAP PCB data. Total PCB concentration, total micromoles of PCB, average molecular weight, homolog distributions, and chlorines per biphenyl changed. The degree of alteration depended on the congener composition of the individual sample.

### 4.1.1. Magnitude of congener concentration changes

Congener concentrations were adjusted for two forms of bias, calibration and coelution (Section 1.1.3). Calibration bias correction factors were applied to the 118 DB-1 capillary column peaks, whereas coelution bias correction factors were applied only to DB-1 Peaks 5, 8 and 14.

On average, corrected congener peak concentrations were approximately 13% greater than the original data. The greatest increase occurred for DB-1 Peaks 5, 6, 8, 14, 60, and 66 (Tables 1-2 and 1-3). Samples with high concentrations of these congener peaks exhibited the greatest change in total PCB concentrations and homolog distributions. A cursory evaluation of the magnitude of change in total PCB concentrations, homolog distributions, and chlorines per biphenyl are briefly summarized for the three media databases in the following subsections.

### 4.1.2. Water column data

Preliminary review of water column data indicate that the corrections increased water column total PCB concentrations by an average of 7.7 ppt (median = 1.6 ppt), and ranged from a decrease of 135 ppt to an increase of 127 ppt.

The change in water column homolog groups mono through deca averaged from -3% weight to 2% weight. Overall, change in homologs on a weight percent basis ranged from -15% to 26%.

On average, changes in total chlorines per biphenyl ranged from -0.56 to 0.33 chlorines per biphenyl.

#### 4.1.3. Sediment and porewater data

Preliminary review of the sediment and porewater data indicate that the corrections increased total PCB concentrations by an average of 4 ppm (median = 0.42 ppm), and ranged from -0.05 ppm to approximately 440 ppm.

The change in sediment and porewater homolog groups mono through deca averaged from -3% weight to 3% weight. Overall, change in homologs on a weight percent basis ranged from -34% to 36%.

On average, total chlorines per biphenyl increased by 0.02, and ranged from -0.32 to 0.31 chlorines per biphenyl.

#### 4.1.4. Fish and biota data

Preliminary review of the fish and biota data indicate that the corrections increased total PCB concentrations by an average of 0.37 ppm (median = 0.13 ppm), and ranged from -1.25 ppm to 7.8 ppm.

The change in fish and biota homolog groups mono through deca averaged from -3% weight to 4% weight. Overall, change in homologs on a weight percent basis ranged from -6% to 7%.

On average, total chlorines per biphenyl decreased by 0.05, and ranged from -0.25 to 0.03 chlorines per biphenyl.

### 4.2. Method detection limit

The analytical biases may have impacted quantification of the method detection limit. This issue is currently under investigation.

## 4.3. Data validation qualifiers

Data validation qualifiers in the field QL_CAP indicate to the user whether the quality of the PCB capillary column data are affected by analytical or handling problems. Data validation technical memorandums that accompanied data summary reports provide specific details about the qualifiers used (O'Brien & Gere 1993a, 1994, 1995, 1996a, 1997a).

In general, most of the data validation criteria are not affected by the analytical bias. However, certain criteria are evaluated based on comparisons of DB-1 peak concentrations in a sample to a known concentration in a spike solution. Qualification of the data using these criteria may be affected by the analytical bias. Table 4-1 presents the data validation criteria, the qualifiers associated with those criteria, and description of how correction of the analytical bias may impact the relevance of the qualifiers originally assigned to uncorrected data. This issue is currently under investigation.

# 5. Modifications to future analytical and database deliverables

Modifications to future analytical and database deliverables will be implemented to reflect the database corrections.

## 5.1. Analytical changes for future analyses

Hudson River samples collected after September 1, 1997 will be quantified using the revised calibration standard (Northeast Analytical 1997b, Appendix E). The laboratory will quantify PCBs using the revised Green Bay standard and calculate total PCBs, average molecular weight, total micromoles, homolog distributions (for both weight percent and mole percent), and chlorines per biphenyl. These data will be delivered to O'Brien & Gere in both hard copy and electronic format.

Media-specific coelution correction factors will be applied to the data after receipt from the laboratory. The coelution correction factors were developed using Hudson River data; therefore, these factors are specific to the Hudson River project and represent an additional level of data interpretation beyond the purview of the laboratory. Specifically, congener DB-1 peaks 5, 8 and 14 will be adjusted using the media-specific coelution correction factors calculated by HydroQual (HydroQual 1997; Appendix D).

Following coelution bias adjustment of the three peaks, the remaining PCB data will be recalculated as part of the monthly database update procedure performed by O'Brien & Gere. These include the database fields: MIC_MOLS, AVG_MWT, PCB_CONC, NEA_TOT, PCB_CAP, homologs MONO_WT through DECA_WT and MONO_ML through DECA_ML, and chlorination levels ORTHO_CL, MP_CL and TOT_CL.

The data will be periodically reviewed to evaluate whether changes in PCB composition in river samples will require adjustment of the media-specific coelution correction factors. Additional analysis on the C18 column will be conducted on a proportion of samples. These data will provide resolution of coeluting congeners in DB-1 Peaks 5, 8, and 14 to verify the coelution correction factors. These data will be added to the database fields BZ4_AMT, BZ10_AMT, BZ5_AMT, BZ8_AMT, BZ15_AMT and BZ18_AMT. The database field C18_CHK will indicate by "Y" or "N" whether confirmation analysis on the C18 column was conducted for a given sample.

## 5.2. Database deliverable changes

The database deliverable in the future will include revised file structure tables and a data table containing the calibration correction factors for each DB-1 peak.

Revisions of future submittals of the database will incorporate structure changes as discussed in Sections 2.1 and 2.2 of this report. These are summarized below:

- Update and revision of field name OBG_ID to CONV_ID
- Identification of samples with total PCB concentrations reported less than the method detection limit by using negative detection limit values in the GE database (NEA_TOT and PCB_CAP fields)
- Additional field in the database containing identification of samples analyzed with the original Green Bay standard which have been corrected
- Additional fields in the CP database to include sample-specific coelution bias correction factors for DB-1 Peaks 5, 8, and 14
- Additional fields in the CP database to include congener concentrations for BZ4 and BZ10 (Peak 5), BZ5 and BZ8 (Peak 8), and BZ15 and BZ18 (Peak 14) obtained from C18 analyses.

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TABLES

Table 1.1. DB-1 chromatogram peaks and corresponding congeners.

| DB-1 Peak No. | Congener BZ No. | Chlorination Structure |
|---|---|---|
| 1 | 0 | biphenyl |
| 2 | 1 | 2 |
| 3 | 2 | 3 |
| 4 | 3 | 4 |
| 5 | 4 | 2,2' |
| 5 | 10 | 2,6 |
| 6 | 7 | 2,4 |
| 6 | 9 | 2,5 |
| 7 | 6 | 2,3' |
| 8 | 5 | 2,3 |
| 8 | 8 | 2,4' |
| 9 | 14 | 3,5 |
| 10 | 19 | 2,2',6 |
| 11 | 30 | 2,4,6 |
| 12 | 11 | 3,3' |
| 13 | 12 | 3,4 |
| 13 | 13 | 3,4' |
| 14 | 15 | 4,4' |
| 14 | 18 | 2,2',5 |
| 15 | 17 | 2,2',4 |
| 16 | 24 | 2,3,6 |
| 16 | 27 | 2,3',6 |
| 17 | 16 | 2,2',3 |
| 17 | 32 | 2,4',6 |
| 18 | 23 | 2,3,5 |
| 19 | 34 | 2',3,5 |
| 19 | 54 | 2,2',6,6' |
| 20 | 29 | 2,4,5 |
| 21 | 26 | 2,3',5 |
| 22 | 25 | 2,3',4 |
| 23 | 31 | 2,4',5 |
| 24 | 28 | 2,4,4' |
| 24 | 50 | 2,2',4,6 |
| 25 | 21 | 2,3,4 |
| 25 | 33 | 2',3,4 |
| 25 | 53 | 2,2',5,6' |
| 26 | 22 | 2,3,4' |
| 26 | 51 | 2,2',4,6' |
| 27 | 45 | 2,2',3,6 |
| 28 | 36 | 3,3',5 |
| 29 | 46 | 2,2',3,6' |
| 30 | 39 | 3,4',5 |
| 31 | 52 | 2,2',5,5' |
| 31 | 73 | 2,3',5',6 |
| 32 | 49 | 2,2',4,5' |
| 33 | 47 | 2,2',4,4' |
| 34 | 48 | 2,2',4,5 |
| 34 | 75 | 2,4,4',6 |
| 35 | 62 | 2,3,4,6 |
| 35 | 65 | 2,3,5,6 |
| 36 | 35 | 3,3',4 |
| 37 | 44 | 2,2',3,5' |
| 37 | 104 | 2,2',4,6,6' |
| 38 | 37 | 3,4,4' |
| 38 | 42 | 2,2',3,4' |
| 38 | 59 | 2,3,3',6 |
| 39 | 64 | 2,3,4',6 |
| 39 | 71 | 2,3',4',6 |
| 40 | 68 | 2,3',4,5' |
| 41 | 96 | 2,2',3,6,6' |
| 42 | 40 | 2,2',3,3' |
| 43 | 57 | 2,3,3',5 |
| 43 | 103 | 2,2',4,5',6 |
| 44 | 67 | 2,3',4,5 |
| 44 | 100 | 2,2',4,4',6 |
| 45 | 58 | 2,3,3',5' |
| 45 | 63 | 2,3,4',5 |
| 46 | 74 | 2,4,4',5 |
| 46 | 94 | 2,2',3,5,6' |
| 47 | 61 | 2,3,4,5 |
| 47 | 70 | 2,3',4',5 |
| 47 | 76 | 2',3,4,5 |
| 48 | 66 | 2,3',4,4' |
| 48 | 93 | 2,2',3,5,6 |
| 48 | 95 | 2,2',3,5',6 |
| 49 | 55 | 2,3,3',4 |
| 49 | 91 | 2,2',3,4',6 |
| 49 | 98 | 2,2',3',4,6 |
| 50 | 56 | 2,3,3',4' |
| 50 | 60 | 2,3,4,4' |
| 51 | 84 | 2,2',3,3',6 |
| 51 | 92 | 2,2',3,5,5' |
| 51 | 155 | 2,2',4,4',6,6' |
| 52 | 89 | 2,2',3,4,6' |
| 53 | 90 | 2,2',3,4',5 |
| 53 | 101 | 2,2',4,5,5' |
| 54 | 99 | 2,2',4,4',5 |
| 55 | 112 | 2,3,3',5,6 |
| 55 | 119 | 2,3',4,4',6 |
| 55 | 150 | 2,2',3,4',6,6' |
| 56 | 83 | 2,2',3,3',5 |
| 56 | 109 | 2,3,3',4,6 |
| 57 | 86 | 2,2',3,4,5 |
| 57 | 97 | 2,2',3',4,5 |
| 57 | 152 | 2,2',3,5,6,6' |
| 58 | 87 | 2,2',3,4,5' |
| 58 | 111 | 2,3,3',5,5' |
| 58 | 115 | 2,3,4,4',6 |
| 59 | 85 | 2,2',3,4,4' |
| 59 | 116 | 2,3,4,5,6 |
| 60 | 136 | 2,2',3,3',6,6' |
| 61 | 77 | 3,3',4,4' |
| 61 | 110 | 2,3,3',4',6 |
| 62 | 154 | 2,2',4,4',5,6' |
| 63 | 82 | 2,2',3,3',4 |
| 64 | 151 | 2,2',3,5,5',6 |
| 65 | 124 | 2',3,4,5,5' |
| 65 | 135 | 2,2',3,3',5,6' |
| 66 | 144 | 2,2',3,4,5',6 |
| 67 | 107 | 2,3,3',4',5 |
| 67 | 108 | 2,3,3',4,5' |
| 67 | 147 | 2,2',3,4',5,6 |
| 68 | 123 | 2',3,4,4',5 |
| 69 | 106 | 2,3,3',4,5 |
| 69 | 118 | 2,3',4,4',5 |
| 69 | 149 | 2,2',3,4',5',6 |
| 70 | 139 | 2,2',3,4,4',6 |
| 70 | 140 | 2,2',3,4,4',6' |
| 71 | 114 | 2,3,4,4',5 |
| 71 | 134 | 2,2',3,3',5,6 |
| 71 | 143 | 2,2',3,4,5,6' |
| 72 | 122 | 2',3,3',4,5 |
| 72 | 131 | 2,2',3,3',4,6 |
| 72 | 133 | 2,2',3,3',5,5' |
| 73 | 146 | 2,2',3,4',5,5' |
| 73 | 161 | 2,3,3',4,5',6 |
| 74 | 105 | 2,3,3',4,4' |
| 74 | 132 | 2,2',3,3',4,6' |
| 75 | 153 | 2,2',4,4',5,5' |
| 76 | 168 | 2,3',4,4',5',6 |
| 77 | 141 | 2,2',3,4,5,5' |
| 78 | 179 | 2,2',3,3',5,6,6' |
| 79 | 130 | 2,2',3,3',4,5' |
| 80 | 137 | 2,2',3,4,4',5 |
| 81 | 176 | 2,2',3,3',4,6,6' |
| 82 | 138 | 2,2',3,4,4',5' |
| 82 | 163 | 2,3,3',4',5,6 |
| 83 | 158 | 2,3,3',4,4',6 |
| 84 | 129 | 2,2',3,3',4,5 |
| 85 | 178 | 2,2',3,3',5,5',6 |
| 86 | 166 | 2,3,4,4',5,6 |
| 87 | 175 | 2,2',3,3',4,5',6 |
| 88 | 182 | 2,2',3,4,4',5,6' |
| 88 | 187 | 2,2',3,4',5,5',6 |
| 89 | 128 | 2,2',3,3',4,4' |
| 90 | 183 | 2,2',3,4,4',5',6 |
| 91 | 167 | 2,3',4,4',5,5' |
| 92 | 185 | 2,2',3,4,5,5',6 |
| 93 | 174 | 2,2',3,3',4,5,6' |
| 93 | 181 | 2,2',3,4,4',5,6 |
| 94 | 177 | 2,2',3,3',4',5,6 |
| 95 | 156 | 2,3,3',4,4',5 |
| 95 | 171 | 2,2',3,3',4,4',6 |
| 96 | 202 | 2,2',3,3',5,5',6,6' |
| 97 | 157 | 2,3,3',4,4',5' |
| 98 | 173 | 2,2',3,3',4,5,6 |
| 99 | 200 | 2,2',3,3',4,5,6,6' |
| 99 | 204 | 2,2',3,4,4',5,6,6' |
| 100 | 172 | 2,2',3,3',4,5,5' |
| 100 | 192 | 2,3,3',4,5,5',6 |
| 101 | 197 | 2,2',3,3',4,4',6,6' |
| 102 | 180 | 2,2',3,4,4',5,5' |
| 103 | 193 | 2,3,3',4',5,5',6 |
| 104 | 191 | 2,3,3',4,4',5',6 |
| 105 | 199 | 2,2',3,3',4,5,5',6' |
| 106 | 170 | 2,2',3,3',4,4',5 |
| 107 | 190 | 2,3,3',4,4',5,6 |
| 108 | 198 | 2,2',3,3',4,5,5',6 |
| 109 | 201 | 2,2',3,3',4,5',6,6' |
| 110 | 196 | 2,2',3,3',4,4',5,6' |
| 110 | 203 | 2,2',3,4,4',5,5',6 |
| 111 | 189 | 2,3,3',4,4',5,5' |
| 112 | 195 | 2,2',3,3',4,4',5,6 |
| 113 | 208 | 2,2',3,3',4,5,5',6,6' |
| 114 | 207 | 2,2',3,3',4,4',5,6,6' |
| 115 | 194 | 2,2',3,3',4,4',5,5' |
| 116 | 205 | 2,3,3',4,4',5,5',6 |
| 117 | 206 | 2,2',3,3',4,4',5,5',6 |
| 118 | 209 | 2,2',3,3',4,4',5,5',6,6' |
| NQ | 20 | 2,3,3' |
| NQ | 38 | 3,4,5 |
| NQ | 41 | 2,2',3,4 |
| NQ | 43 | 2,2',3,5 |
| NQ | 69 | 2,3',4,6 |
| NQ | 72 | 2,3',5,5' |
| NQ | 78 | 3,3',4,5 |
| NQ | 79 | 3,3',4,5' |
| NQ | 80 | 3,3',5,5' |
| NQ | 81 | 3,4,4',5 |
| NQ | 88 | 2,2',3,4,6 |
| NQ | 102 | 2,2',4,5,6' |
| NQ | 113 | 2,3,3',5'6 |
| NQ | 117 | 2,3,4',5,6 |
| NQ | 120 | 2,3',4,5,5' |
| NQ | 121 | 2,3',4,5',6 |
| NQ | 125 | 2',3,4,5,6' |
| NQ | 126 | 3,3',4,4',5 |
| NQ | 127 | 3,3',4,5,5' |
| NQ | 142 | 2,2',3,4,5,6 |
| NQ | 145 | 2,2',3,4,6,6' |
| NQ | 148 | 2,2',3,4',5,6' |
| NQ | 159 | 2,3,3',4,5,5' |
| NQ | 160 | 2,3,3',4,5,6 |
| NQ | 162 | 2,3,3',4',5,5' |
| NQ | 164 | 2,3,3',4',5',6 |
| NQ | 165 | 2,3,3',5,5',6 |
| NQ | 169 | 3,3',4,4',5,5' |
| NQ | 184 | 2,2',3,4,4',6,6' |
| NQ | 186 | 2,2',3,4,5,6,6' |
| NQ | 188 | 2,2',3,4',5,6,6' |

Note: NQ = not quantified in DB-1 method. The congener assignments presented in this table are those used for the historic GE/Hudson River PCB database. Updates to PCB congener assignments have been made for the DB-1 system (Frame, 1996), but are not reported here for consistency with the historic laboratory records.

*SOURCES:*

*HydroQual 1997* *Northeast Analytical Laboratories* *"Analytical Chemistry of PCBs" - Erickson, 1992 (Appendix A)*

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**Table 1-2. HydroQual calibration correction factors (reference database CORFACTOR.DBF).**

| DB-1 Peak | Correction Factor | DB-1 Peak | Correction Factor | DB-1 Peak | Correction Factor |
|---|---|---|---|---|---|
| 1 | 1.0000 | 41 | 1.0000 | 81 | 1.0000 |
| 2 | 1.0441 | 42 | 1.0657 | 82 | 1.0308 |
| 3 | 1.0000 | 43 | 1.0000 | 83 | 0.7794 |
| 4 | 1.0073 | 44 | 0.8231 | 84 | 0.1621 |
| 5 | 4.5431 | 45 | 1.0617 | 85 | 1.2104 |
| 6 | 2.0407 | 46 | 0.8776 | 86 | 1.0000 |
| 7 | 1.6925 | 47 | 0.6057 | 87 | 1.2471 |
| 8 | 1.0476 | 48 | 0.9904 | 88 | 0.8979 |
| 9 | 1.0000 | 49 | 1.3629 | 89 | 0.7960 |
| 10 | 1.0476 | 50 | 0.7275 | 90 | 0.8260 |
| 11 | 1.0000 | 51 | 1.5661 | 91 | 1.6666 |
| 12 | 1.0000 | 52 | 1.2471 | 92 | 0.7993 |
| 13 | 1.0858 | 53 | 1.4030 | 93 | 1.0884 |
| 14 | 1.0648 | 54 | 1.2037 | 94 | 1.1158 |
| 15 | 1.8707 | 55 | 0.5820 | 95 | 0.8010 |
| 16 | 1.1054 | 56 | 1.5589 | 96 | 0.7460 |
| 17 | 1.1138 | 57 | 1.1027 | 97 | 1.0000 |
| 18 | 1.0000 | 58 | 1.3072 | 98 | 1.1168 |
| 19 | 1.0000 | 59 | 1.2471 | 99 | 0.7050 |
| 20 | 1.1016 | 60 | 2.0043 | 100 | 1.0912 |
| 21 | 1.1712 | 61 | 1.1224 | 101 | 1.8878 |
| 22 | 1.1972 | 62 | 1.0000 | 102 | 0.9509 |
| 23 | 0.9293 | 63 | 1.2663 | 103 | 1.1224 |
| 24 | 0.9226 | 64 | 1.1158 | 104 | 0.9977 |
| 25 | 0.8819 | 65 | 0.4628 | 105 | 1.6088 |
| 26 | 0.9297 | 66 | 9.9882 | 106 | 0.5257 |
| 27 | 1.2333 | 67 | 1.4739 | 107 | 0.5255 |
| 28 | 1.0000 | 68 | 1.0000 | 108 | 0.6701 |
| 29 | 1.0690 | 69 | 1.0321 | 109 | 1.0476 |
| 30 | 1.0000 | 70 | 1.0000 | 110 | 0.9463 |
| 31 | 1.3824 | 71 | 0.8891 | 111 | 0.8314 |
| 32 | 0.9561 | 72 | 1.1923 | 112 | 0.3701 |
| 33 | 0.7483 | 73 | 0.9120 | 113 | 0.3711 |
| 34 | 0.9353 | 74 | 0.7451 | 114 | 0.7249 |
| 35 | 1.0000 | 75 | 0.7447 | 115 | 0.9760 |
| 36 | 1.0000 | 76 | 1.0000 | 116 | 1.0289 |
| 37 | 1.0725 | 77 | 1.2231 | 117 | 0.6057 |
| 38 | 1.1054 | 78 | 1.0000 | 118 | 0.4726 |
| 39 | 0.9411 | 79 | 1.1224 | | |
| 40 | 1.0000 | 80 | 0.7008 | | |

*Source: HydroQual (1997)*

**Table 1-3. HydroQual coelution correction factors.**

| DB-1 Peak | Water Column[1] | Sediment/Porewater (GBS only[2]) | Sediment/Porewater (GBS with BZ[3]) | Fish/Biota[4] |
|---|---|---|---|---|
| Peak 5 | 0.65 | 1.25 | 1.37 | – |
| Peak 8 | 0.45 | 0.58 | 0.58 | – |
| Peak 14 | 1.44 | 2.23 | 2.23 | – |

Notes:
[1]Includes 1996 Particle Transport and 1997 High Flow Bedload sediment samples (Section 2.2.2).
[2]Green Bay mixed Aroclor standard only; Peak 5 adjusted by both the calibration and coelution correction factors (Section 2.2.2).
[3]Green Bay standard with BZ4/BZ10 congener standard; Peak 5 adjusted by only the coelution correction factor (Section 2.2.2).
[4]Fish data were not adjusted for coelution bias (Section 2.2.2).

*Source: HydroQual 1997*

**Table 2-1. Summary of new database fields and definitions.**

| Required Additional Information | Field Name | Entry Type | Definition |
|---|---|---|---|
| Media-specific coelution bias correction factors to allow for reversal of corrections if required. | CF_PK5<br>CF_PK8<br>CF_PK14 | 0.65, 1.25, 1.37<br>0.45, 0.58<br>1.44, 2.23 | Coelution correction factors used to adjust for peak coelution bias in DB-1 Peaks 5, 8 and 14 |
| C18 column confirmation analysis data. | C18_CHK | Y, N | Yes or no, whether analysis on a C18 column was conducted. |
| | BZ4_AMT<br>BZ10_AMT<br>BZ5_AMT<br>BZ8_AMT<br>BZ15_AMT<br>BZ18_AMT | 0.00012345<br>0.00012345<br>0.00012345<br>0.00012345<br>0.00012345<br>0.00012345 | C-18 column confirmation analytical results for congeners BZ4 and BZ10 (DB-1 Peak 5), BZ5 and BZ8 (DB-1 Peak 8), and BZ15 and BZ18 (DB-1 Peak 14). |
| Identify different standards used for sediment and porewater analyses[1]. | GBS_BZ | Y, N | Yes or no, whether sediment and porewater samples were analyzed with both GB[2] and BZ[3] standards. |
| In GE and CP, indicate whether samples adjusted for analytical bias | ADJUST | Y, N | Yes or no, whether database record was adjusted for analytical biases. |

Notes: [1]During original analysis of 1991 Sediment Survey samples, the DB-1 calibration protocol was altered to account for elevated DB-1 Peak 5 concentrations within sediment and porewater samples (Northeast Analytical, 1997a). See Section 2.2 of this report for additional details.

[2]GB = Green Bay mixed Aroclor standard consisting of 25:18 = 18 mixture of Aroclors 1232, 1248 and 1262

[3]BZ = independent Peak 5 standard consisting of 4:1 ratio of BZ4 and 10

*Source: O'Brien & Gere Engineers, Inc.*

**Table 4-1. Data validation criteria review and potential impacts due to analytical bias corrections.**

| Validation Criteria | Definition | Validation Qualifiers | Impact from analytical bias | Rationale |
|---|---|---|---|---|
| Documentation completeness | full package includes required documentation | d.o.e. | No impact | Bias does not affect documentation |
| Holding times | 7 days from collection to extraction; 40 days from extraction to analysis | J, UJ, R | No impact | Bias does not affect holding times |
| Instrument performance | 23456-2346 NCBP retention time shift | J, UJ, R | No impact | Bias does not affect retention times |
| | baseline stability | d.o.e. | No impact | Bias does not affect stability |
| | chromatographic resolution | J, R | No impact | Measured in peak height (mm) |
| | internal standard area performance | J, R | No impact | Area under peak not affected |
| Calibration | initial linearity check | J, R | Potentially | Bias affects calculation of response factors |
| | analytical sequence verification | d.o.e. | No impact | Bias does not affect sequence |
| | calibration verification | J, R | Potentially | Bias affects congener concentrations |
| Blank analysis | field blank; method blank | U | Potentially | Bias adjustment could increase blank concentrations above detection limit |
| Surrogate recovery | percent recovery between 70 and 130 | J, R | Potentially | Bias adjustment affects quantification of congener concentration; dependent on whether quantification of congener in surrogate solution was based on Green Bay standard. |
| Matrix spike analysis | percent recovery between 70 and 130 | J, R | Potentially | Bias adjustment affects quantification of congener concentration; adjustment affects sample concentration, which affects calculation of MS %recovery; dependent on whether quantification of congener in matrix spike solution was based onGreen Bay standard. |
| Duplicate analysis | relative percent difference less than 35 | J | No impact | Bias affects both sample and duplicate equally |

**Table 4-1. Data validation criteria review and potential impacts due to analytical bias corrections.**

| Validation Criteria | Definition | Validation Qualifiers | Impact from analytical bias | Rationale |
|---|---|---|---|---|
| Spike blank | percent recovery between 70 and 130 | J, R | Potentially | Bias adjustment affects quantification of congener concentration; dependent on whether quantification of congener in spike solution was based on Green Bay Standard. |
| Compound identification | peak retention times within continuing calibration retention time window. | J, R | No impact | Bias does not affect retention times |
| Compound quantitation | manually validated; recalculate sample concentration from instrument response | J | No impact | Bias affects original result and recalculation equally |
| Overall data assessment | manual assessment of cumulative effects of excursions | d.o.e. | Potentially | Depends on whether the excursions are impacted by bias adjustment |

Notes:
d.o.e. = depends on excursion
J = result approximated due to deviation from data validation criteria
U = not detected due to blank contamination
UJ = approximated detection limit
R = unusable data due to significant excursion from data validation criteria

FIGURES

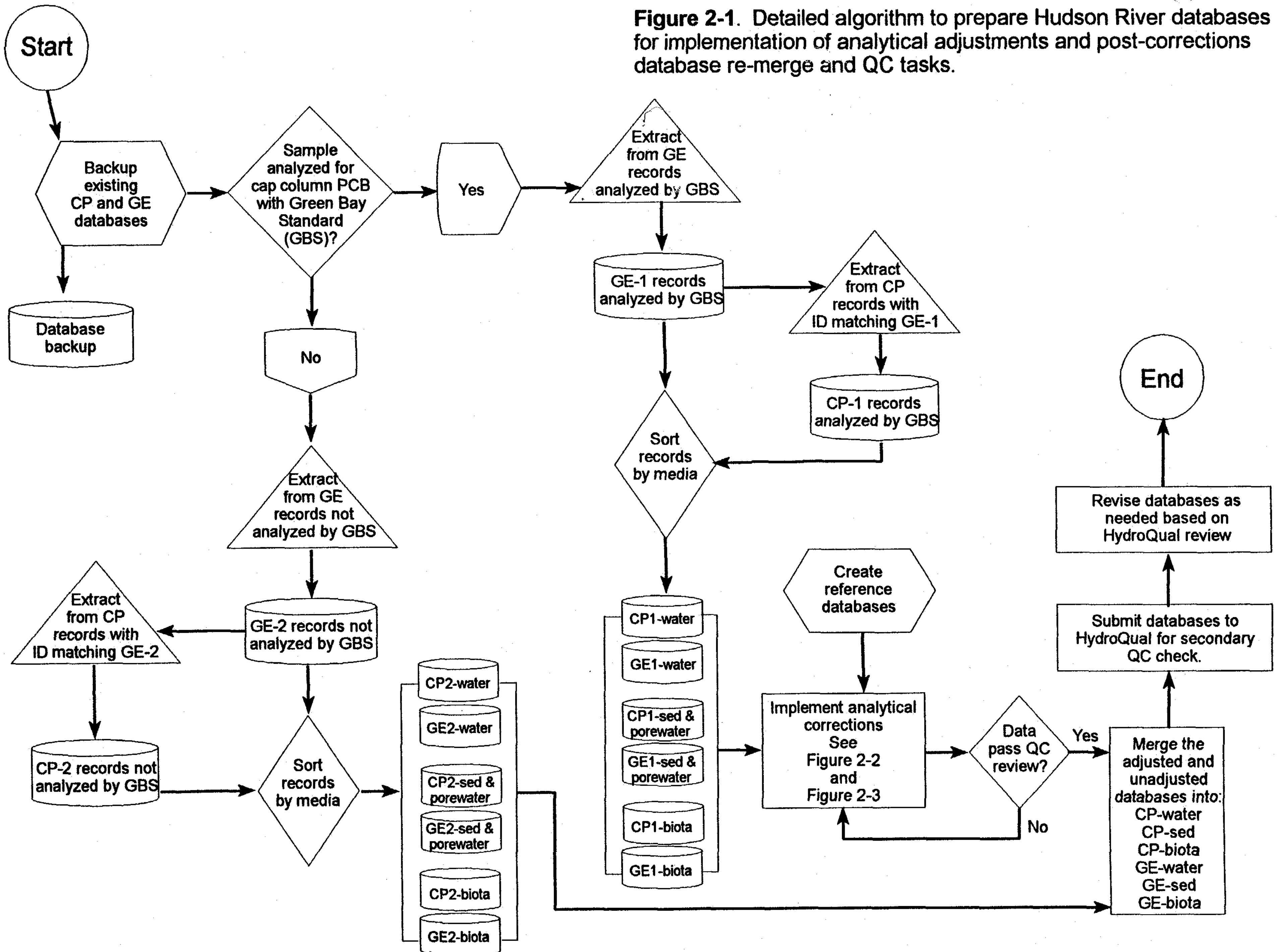


**Figure 2-1**. Detailed algorithm to prepare Hudson River databases for implementation of analytical adjustments and post-corrections database re-merge and QC tasks.

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**Figure 2-2.** Detailed algorithm to implement corrections to the CP databases.

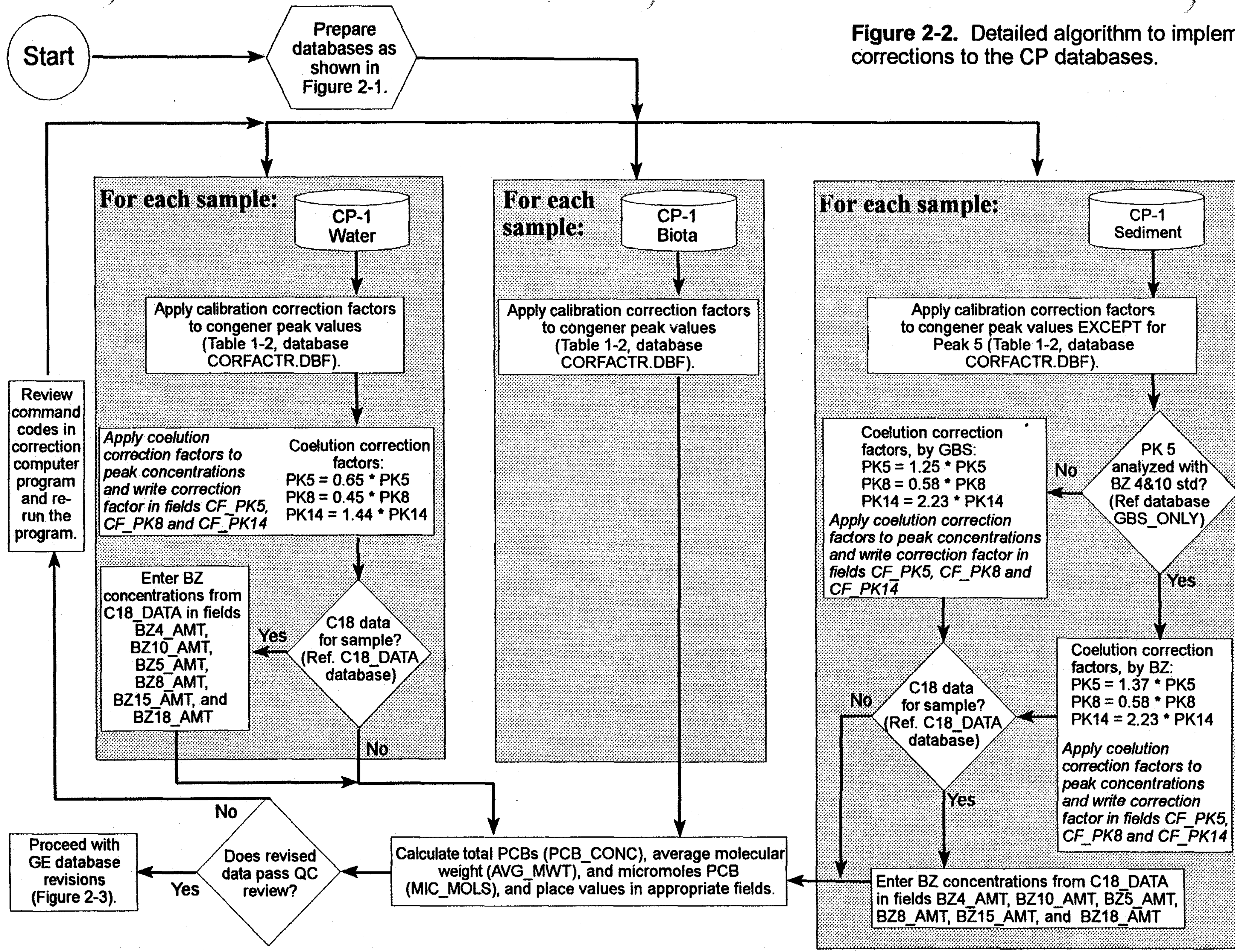


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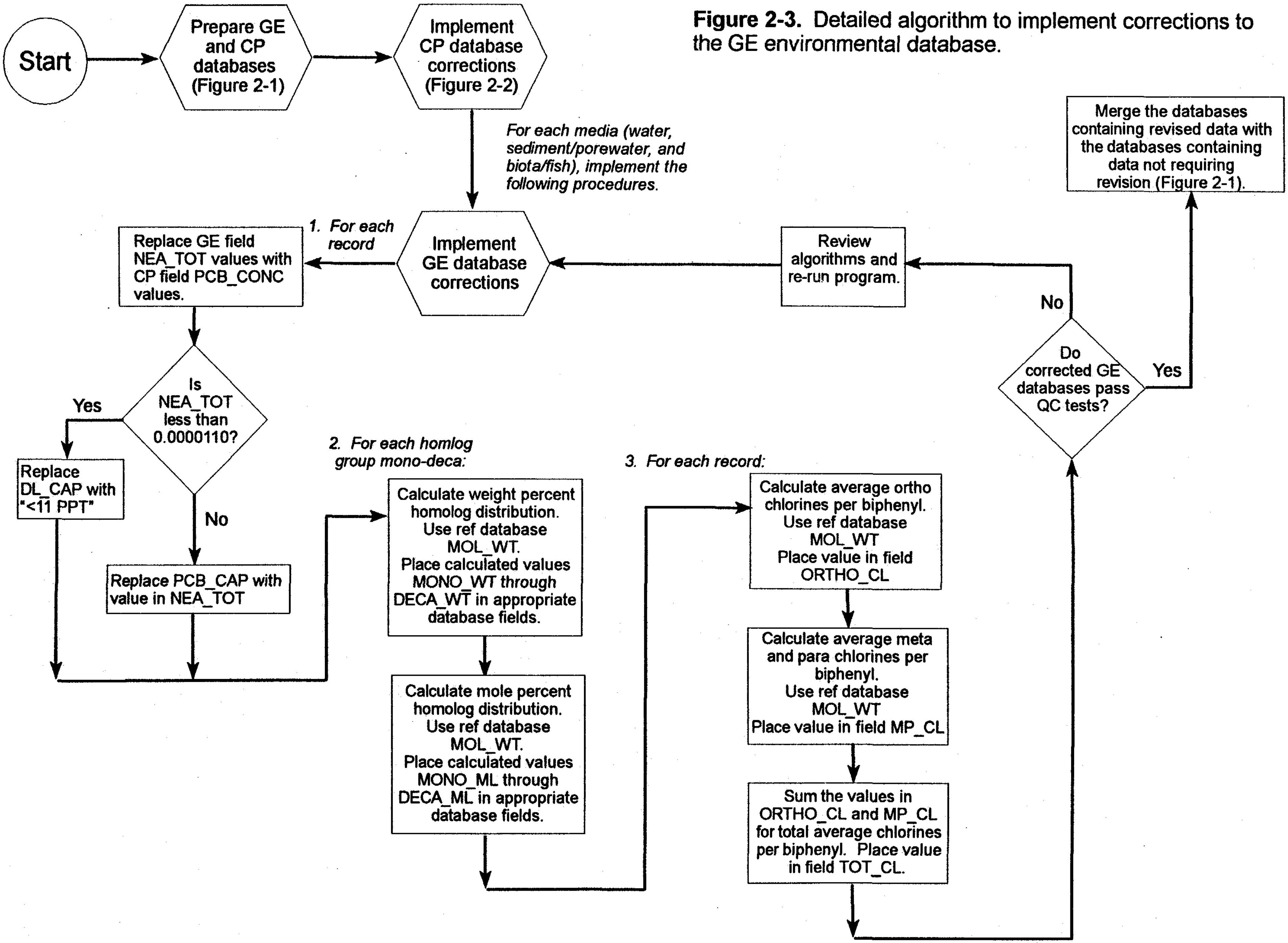
Figure 2-3. Detailed algorithm to implement corrections to the GE environmental database.

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APPENDICES

# Revised database file structure tables

| Field | Field Name | Length | Dec | Type | Entry Types<br>Water Column, Sediment, Pore Water, Fish and Biota | Comments |
|---|---|---|---|---|---|---|
| 1 | NEA_FILE | 7 | 0 | CHARACTER | 911606F or 911345X | NEA file identification as reported on the PCB Congener Amount Report. An "X" is only indicated in the NEA_FILE field if the sample is a Temporal Water Column sample analyzed for dissolved PCBs. "R" indicates sample was reanalyzed. |
| 2 | NEA_DESC | 50 | 0 | CHARACTER | 8A-F1(0-5) or BAKER FALLS BRIDGE or 806 0920 | NEA file description as reported on PCB summary report sheet |
| 3 | REACH | 20 | 0 | CHARACTER | 8A | River reach where sediment samples were collected. Reach 9 is above Thompson Island Pool, Reach 1 is above Troy Dam. |
| 4 | SAMPSED | 20 | 0 | CHARACTER | F1 | Sediment sample texture (F = fine, C = coarse) and ordinal descriptor. |
| 5 | ST_DPTH | 8 | 0 | NUMERIC | 0 | Starting depth of sediment core (cm) or composite water sample |
| 6 | END_DPTH | 8 | 0 | NUMERIC | 5 | Ending depth of sediment core (cm) or composite water sample (ft) |
| 7 | DATE_COL | 8 | 0 | DATE | 08/17/91 | Date of sample collection |
| 8 | ID | 12 | 0 | CHARACTER | 25 | The unique sample identifier assigned in the field to each environmental sample collected. |
| 9 | LOCATION | 25 | 0 | CHARACTER | 8A-22 or<br>B.F.Br<br>Rt.197 Br.<br>TID-West<br>Rt.29 Br.<br>S.W.Br.<br>Rt.4 Br.<br>Hoosic R.<br>Bat. Kill<br><br>COMPOSITE | Sampling location. The actual location where the sample was collected. Water column sample locations: B.F.Br = Baker Falls Bridge (HRM 197.0); HRM 196.8 = Canoe Carry; Rt.197 Br. = Rt. 197 Bridge Fort Edward (HRM 194.2); TID = Thompson Island Dam (HRM 188.5); Rt.29 Br. = Rt. 29 Bridge Schuylerville; S.W.Br. = Stillwater Bridge; Rt.4 Br. = Rt. 4 Bridge Waterford; Hoosic R. = Hoosic River; Bat Kill = Batten Kill. "COMPOSITE" refers to sediment samples composited from more than one location. "EQBL" refers to equipment blanks (included only where total PCB concentration exceeds MDL). HRM = approximate Hudson River mile. HRM 0.0 is located at the Battery in New York City. Sample locations within the river may be further differentiated by W = west (shore or channel), C = center (of channel), E = east (shore or channel). "R" indicates the archive sample for a given location. |

| Field | Field Name | Length | Dec | Type | Entry Types<br>Water Column, Sediment, Pore Water, Fish and Biota | Comments |
|---|---|---|---|---|---|---|
| 10 | MEDIA | 1 | 0 | CHARACTER | f,w,a,b,p,s | Type of matrix: f=fish, w=water, a=air, b=biota, p=pore water, s=sediment |
| 11 | MIX_TYPE | 1 | 0 | CHARACTER | S | The type of mixed peak deconvolution as reported on the PCB Congener Amount Report. |
| 12 | PK1_AMT | 17 | 11 | NUMERIC | 0.00000 | Amount of PCB (ppm) detected in Peak #1 as reported on the PCB Congener Amount Report. |
| 13 | PK2_AMT | 17 | 11 | NUMERIC | 1.35323 | Amount of PCB (ppm) detected in Peak #2 as reported on the PCB Congener Amount Report. |
| 14 | PK3_AMT | 17 | 11 | NUMERIC | 0.21430 | Amount of PCB (ppm) detected in Peak #3 as reported on the PCB Congener Amount Report. |
| 15 | PK4_AMT | 17 | 11 | NUMERIC | 2.03247 | Amount of PCB (ppm) detected in Peak #4 as reported on the PCB Congener Amount Report. |
| 16 | PK5_AMT | 17 | 11 | NUMERIC | 0.01879 | Amount of PCB (ppm) detected in Peak #5 as reported on the PCB Congener Amount Report. |
| 17 | PK6_AMT | 17 | 11 | NUMERIC | 0.14898 | Amount of PCB (ppm) detected in Peak #6 as reported on the PCB Congener Amount Report. |
| 18 | PK7_AMT | 17 | 11 | NUMERIC | 1.59697 | Amount of PCB (ppm) detected in Peak #7 as reported on the PCB Congener Amount Report. |
| 19 | PK8_AMT | 18 | 11 | NUMERIC | 0.23654 | Amount of PCB (ppm) detected in Peak #8 as reported on the PCB Congener Amount Report. |
| 20 | PK9_AMT | 17 | 11 | NUMERIC | 0.00000 | Amount of PCB (ppm) detected in Peak #9 as reported on the PCB Congener Amount Report. |
| 21 | PK10_AMT | 17 | 11 | NUMERIC | 0.56981 | Amount of PCB (ppm) detected in Peak #10 as reported on the PCB Congener Amount Report. |
| 22 | PK11_AMT | 17 | 11 | NUMERIC | 0.25781 | Amount of PCB (ppm) detected in Peak #11 as reported on the PCB Congener Amount Report. |

310486

| Field | Field Name | Length | Dec | Type | Entry Types | Comments |
|---|---|---|---|---|---|---|
| | | | | | Water Column, Sediment, Pore Water, Fish and Biota | |
| 23 | PK12_AMT | 17 | 11 | NUMERIC | 0.56984 | Amount of PCB (ppm) detected in Peak #12 as reported on the PCB Congener Amount Report. |
| 24 | PK13_AMT | 17 | 11 | NUMERIC | 0.00254 | Amount of PCB (ppm) detected in Peak #13 as reported on the PCB Congener Amount Report. |
| 25 | PK14_AMT | 17 | 11 | NUMERIC | 0.05671 | Amount of PCB (ppm) detected in Peak #14 as reported on the PCB Congener Amount Report. |
| 26 | PK15_AMT | 17 | 11 | NUMERIC | 0.23681 | Amount of PCB (ppm) detected in Peak #15 as reported on the PCB Congener Amount Report. |
| 27 | PK16_AMT | 17 | 11 | NUMERIC | 0.00004 | Amount of PCB (ppm) detected in Peak #16 as reported on the PCB Congener Amount Report. |
| 28 | PK17_AMT | 17 | 11 | NUMERIC | 0.00045 | Amount of PCB (ppm) detected in Peak #17 as reported on the PCB Congener Amount Report. |
| 29 | PK18_AMT | 17 | 11 | NUMERIC | 0.25981 | Amount of PCB (ppm) detected in Peak #18 as reported on the PCB Congener Amount Report. |
| 30 | PK19_AMT | 17 | 11 | NUMERIC | 0.25874 | Amount of PCB (ppm) detected in Peak #19 as reported on the PCB Congener Amount Report. |
| 31 | PK20_AMT | 17 | 11 | NUMERIC | 0.12584 | Amount of PCB (ppm) detected in Peak #20 as reported on the PCB Congener Amount Report. |
| 32 | PK21_AMT | 17 | 11 | NUMERIC | 0.40014 | Amount of PCB (ppm) detected in Peak #21 as reported on the PCB Congener Amount Report. |
| 33 | PK22_AMT | 17 | 11 | NUMERIC | 0.25804 | Amount of PCB (ppm) detected in Peak #22 as reported on the PCB Congener Amount Report. |
| 34 | PK23_AMT | 17 | 11 | NUMERIC | 0.84621 | Amount of PCB (ppm) detected in Peak #23 as reported on the PCB Congener Amount Report. |
| 35 | PK24_AMT | 17 | 11 | NUMERIC | 0.25041 | Amount of PCB (ppm) detected in Peak #24 as reported on the PCB Congener Amount Report. |

310487

| Field | Field Name | Length | Dec | Type | Entry Types<br>Water Column, Sediment, Pore Water, Fish and Biota | Comments |
|---|---|---|---|---|---|---|
| 36 | PK25_AMT | 17 | 11 | NUMERIC | 0.21430 | Amount of PCB (ppm) detected in Peak #25 as reported on the PCB Congener Amount Report. |
| 37 | PK26_AMT | 17 | 11 | NUMERIC | 2.03247 | Amount of PCB (ppm) detected in Peak #26 as reported on the PCB Congener Amount Report. |
| 38 | PK27_AMT | 17 | 11 | NUMERIC | 0.01879 | Amount of PCB (ppm) detected in Peak #27 as reported on the PCB Congener Amount Report. |
| 39 | PK28_AMT | 17 | 11 | NUMERIC | 0.14898 | Amount of PCB (ppm) detected in Peak #28 as reported on the PCB Congener Amount Report. |
| 40 | PK29_AMT | 17 | 11 | NUMERIC | 1.59697 | Amount of PCB (ppm) detected in Peak #29 as reported on the PCB Congener Amount Report. |
| 41 | PK30_AMT | 17 | 11 | NUMERIC | 0.23654 | Amount of PCB (ppm) detected in Peak #30 as reported on the PCB Congener Amount Report. |
| 42 | PK31_AMT | 17 | 11 | NUMERIC | 0.00000 | Amount of PCB (ppm) detected in Peak #31 as reported on the PCB Congener Amount Report. |
| 43 | PK32_AMT | 17 | 11 | NUMERIC | 0.56981 | Amount of PCB (ppm) detected in Peak #32 as reported on the PCB Congener Amount Report. |
| 44 | PK33_AMT | 17 | 11 | NUMERIC | 0.25781 | Amount of PCB (ppm) detected in Peak #33 as reported on the PCB Congener Amount Report. |
| 45 | PK34_AMT | 17 | 11 | NUMERIC | 0.56984 | Amount of PCB (ppm) detected in Peak #34 as reported on the PCB Congener Amount Report. |
| 46 | PK35_AMT | 17 | 11 | NUMERIC | 0.00254 | Amount of PCB (ppm) detected in Peak #35 as reported on the PCB Congener Amount Report. |
| 47 | PK36_AMT | 17 | 11 | NUMERIC | 0.05671 | Amount of PCB (ppm) detected in Peak #36 as reported on the PCB Congener Amount Report. |
| 48 | PK37_AMT | 17 | 11 | NUMERIC | 0.23681 | Amount of PCB (ppm) detected in Peak #37 as reported on the PCB Congener Amount Report. |

310488

| Field | Field Name | Length | Dec | Type | Entry Types<br>Water Column, Sediment, Pore Water, Fish and Biota | Comments |
|---|---|---|---|---|---|---|
| 49 | PK38_AMT | 17 | 11 | NUMERIC | 0.00004 | Amount of PCB (ppm) detected in Peak #38 as reported on the PCB Congener Amount Report. |
| 50 | PK39_AMT | 17 | 11 | NUMERIC | 0.00045 | Amount of PCB (ppm) detected in Peak #39 as reported on the PCB Congener Amount Report. |
| 51 | PK40_AMT | 17 | 11 | NUMERIC | 0.25981 | Amount of PCB (ppm) detected in Peak #40 as reported on the PCB Congener Amount Report. |
| 52 | PK41_AMT | 17 | 11 | NUMERIC | 0.25874 | Amount of PCB (ppm) detected in Peak #41 as reported on the PCB Congener Amount Report. |
| 53 | PK42_AMT | 17 | 11 | NUMERIC | 0.12584 | Amount of PCB (ppm) detected in Peak #42 as reported on the PCB Congener Amount Report. |
| 54 | PK43_AMT | 17 | 11 | NUMERIC | 0.40014 | Amount of PCB (ppm) detected in Peak #43 as reported on the PCB Congener Amount Report. |
| 55 | PK44_AMT | 17 | 11 | NUMERIC | 0.25804 | Amount of PCB (ppm) detected in Peak #44 as reported on the PCB Congener Amount Report. |
| 56 | PK45_AMT | 17 | 11 | NUMERIC | 0.84621 | Amount of PCB (ppm) detected in Peak #45 as reported on the PCB Congener Amount Report. |
| 57 | PK46_AMT | 17 | 11 | NUMERIC | 0.25041 | Amount of PCB (ppm) detected in Peak #46 as reported on the PCB Congener Amount Report. |
| 58 | PK47_AMT | 17 | 11 | NUMERIC | 0.21430 | Amount of PCB (ppm) detected in Peak #47 as reported on the PCB Congener Amount Report. |
| 59 | PK48_AMT | 17 | 11 | NUMERIC | 2.03247 | Amount of PCB (ppm) detected in Peak #48 as reported on the PCB Congener Amount Report. |
| 60 | PK49_AMT | 17 | 11 | NUMERIC | 0.01879 | Amount of PCB (ppm) detected in Peak #49 as reported on the PCB Congener Amount Report. |
| 61 | PK50_AMT | 17 | 11 | NUMERIC | 0.14898 | Amount of PCB (ppm) detected in Peak #50 as reported on the PCB Congener Amount Report. |

| Field | Field Name | Length | Dec | Type | Entry Types | Comments |
|---|---|---|---|---|---|---|
| | | | | | Water Column, Sediment, Pore Water, Fish and Biota | |
| 62 | PK51_AMT | 17 | 11 | NUMERIC | 1.59697 | Amount of PCB (ppm) detected in Peak #51 as reported on the PCB Congener Amount Report. |
| 63 | PK52_AMT | 17 | 11 | NUMERIC | 0.23654 | Amount of PCB (ppm) detected in Peak #52 as reported on the PCB Congener Amount Report. |
| 64 | PK53_AMT | 17 | 11 | NUMERIC | 0.00000 | Amount of PCB (ppm) detected in Peak #53 as reported on the PCB Congener Amount Report. |
| 65 | PK54_AMT | 17 | 11 | NUMERIC | 0.56981 | Amount of PCB (ppm) detected in Peak #54 as reported on the PCB Congener Amount Report. |
| 66 | PK55_AMT | 17 | 11 | NUMERIC | 0.25781 | Amount of PCB (ppm) detected in Peak #55 as reported on the PCB Congener Amount Report. |
| 67 | PK56_AMT | 17 | 11 | NUMERIC | 0.56984 | Amount of PCB (ppm) detected in Peak #56 as reported on the PCB Congener Amount Report. |
| 68 | PK57_AMT | 17 | 11 | NUMERIC | 0.00254 | Amount of PCB (ppm) detected in Peak #57 as reported on the PCB Congener Amount Report. |
| 69 | PK58_AMT | 17 | 11 | NUMERIC | 0.05671 | Amount of PCB (ppm) detected in Peak #58 as reported on the PCB Congener Amount Report. |
| 70 | PK59_AMT | 17 | 11 | NUMERIC | 0.23681 | Amount of PCB (ppm) detected in Peak #59 as reported on the PCB Congener Amount Report. |
| 71 | PK60_AMT | 17 | 11 | NUMERIC | 0.00004 | Amount of PCB (ppm) detected in Peak #60 as reported on the PCB Congener Amount Report. |
| 72 | PK61_AMT | 17 | 11 | NUMERIC | 0.00045 | Amount of PCB (ppm) detected in Peak #61 as reported on the PCB Congener Amount Report. |
| 73 | PK62_AMT | 17 | 11 | NUMERIC | 0.25981 | Amount of PCB (ppm) detected in Peak #62 as reported on the PCB Congener Amount Report. |
| 74 | PK63_AMT | 17 | 11 | NUMERIC | 0.25874 | Amount of PCB (ppm) detected in Peak #63 as reported on the PCB Congener Amount Report. |

310490

| Field | Field Name | Length | Dec | Type | Entry Types<br>Water Column, Sediment, Pore Water, Fish and Biota | Comments |
|---|---|---|---|---|---|---|
| 75 | PK64_AMT | 17 | 11 | NUMERIC | 0.12584 | Amount of PCB (ppm) detected in Peak #64 as reported on the PCB Congener Amount Report. |
| 76 | PK65_AMT | 17 | 11 | NUMERIC | 0.40014 | Amount of PCB (ppm) detected in Peak #65 as reported on the PCB Congener Amount Report. |
| 77 | PK66_AMT | 17 | 11 | NUMERIC | 0.25804 | Amount of PCB (ppm) detected in Peak #66 as reported on the PCB Congener Amount Report. |
| 78 | PK67_AMT | 17 | 11 | NUMERIC | 0.84621 | Amount of PCB (ppm) detected in Peak #67 as reported on the PCB Congener Amount Report. |
| 79 | PK68_AMT | 17 | 11 | NUMERIC | 0.25041 | Amount of PCB (ppm) detected in Peak #68 as reported on the PCB Congener Amount Report. |
| 80 | PK69_AMT | 17 | 11 | NUMERIC | 0.21430 | Amount of PCB (ppm) detected in Peak #69 as reported on the PCB Congener Amount Report. |
| 81 | PK70_AMT | 17 | 11 | NUMERIC | 2.03247 | Amount of PCB (ppm) detected in Peak #70 as reported on the PCB Congener Amount Report. |
| 82 | PK71_AMT | 17 | 11 | NUMERIC | 0.01879 | Amount of PCB (ppm) detected in Peak #71 as reported on the PCB Congener Amount Report. |
| 83 | PK72_AMT | 17 | 11 | NUMERIC | 0.14898 | Amount of PCB (ppm) detected in Peak #72 as reported on the PCB Congener Amount Report. |
| 84 | PK73_AMT | 17 | 11 | NUMERIC | 1.59697 | Amount of PCB (ppm) detected in Peak #73 as reported on the PCB Congener Amount Report. |
| 85 | PK74_AMT | 17 | 11 | NUMERIC | 0.23654 | Amount of PCB (ppm) detected in Peak #74 as reported on the PCB Congener Amount Report. |
| 86 | PK75_AMT | 17 | 11 | NUMERIC | 0.00000 | Amount of PCB (ppm) detected in Peak #75 as reported on the PCB Congener Amount Report. |
| 87 | PK76_AMT | 17 | 11 | NUMERIC | 0.56981 | Amount of PCB (ppm) detected in Peak #76 as reported on the PCB Congener Amount Report. |

310491

| Field | Field Name | Length | Dec | Type | Entry Types | Comments |
|---|---|---|---|---|---|---|
| | | | | | Water Column, Sediment, Pore Water, Fish and Biota | |
| 88 | PK77_AMT | 17 | 11 | NUMERIC | 0.25781 | Amount of PCB (ppm) detected in Peak #77 as reported on the PCB Congener Amount Report. |
| 89 | PK78_AMT | 17 | 11 | NUMERIC | 0.56984 | Amount of PCB (ppm) detected in Peak #78 as reported on the PCB Congener Amount Report. |
| 90 | PK79_AMT | 17 | 11 | NUMERIC | 0.00254 | Amount of PCB (ppm) detected in Peak #79 as reported on the PCB Congener Amount Report. |
| 91 | PK80_AMT | 17 | 11 | NUMERIC | 0.05671 | Amount of PCB (ppm) detected in Peak #80 as reported on the PCB Congener Amount Report. |
| 92 | PK81_AMT | 17 | 11 | NUMERIC | 0.23681 | Amount of PCB (ppm) detected in Peak #81 as reported on the PCB Congener Amount Report. |
| 93 | PK82_AMT | 17 | 11 | NUMERIC | 0.00004 | Amount of PCB (ppm) detected in Peak #82 as reported on the PCB Congener Amount Report. |
| 94 | PK83_AMT | 17 | 11 | NUMERIC | 0.00045 | Amount of PCB (ppm) detected in Peak #83 as reported on the PCB Congener Amount Report. |
| 95 | PK84_AMT | 17 | 11 | NUMERIC | 0.25981 | Amount of PCB (ppm) detected in Peak #84 as reported on the PCB Congener Amount Report. |
| 96 | PK85_AMT | 17 | 11 | NUMERIC | 0.25874 | Amount of PCB (ppm) detected in Peak #85 as reported on the PCB Congener Amount Report. |
| 97 | PK86_AMT | 17 | 11 | NUMERIC | 0.12584 | Amount of PCB (ppm) detected in Peak #86 as reported on the PCB Congener Amount Report. |
| 98 | PK87_AMT | 17 | 11 | NUMERIC | 0.40014 | Amount of PCB (ppm) detected in Peak #87 as reported on the PCB Congener Amount Report. |
| 99 | PK88_AMT | 17 | 11 | NUMERIC | 0.25804 | Amount of PCB (ppm) detected in Peak #88 as reported on the PCB Congener Amount Report. |
| 100 | PK89_AMT | 17 | 11 | NUMERIC | 0.84621 | Amount of PCB (ppm) detected in Peak #89 as reported on the PCB Congener Amount Report. |

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| Field | Field Name | Length | Dec | Type | Entry Types<br>Water Column, Sediment, Pore Water, Fish and Biota | Comments |
|---|---|---|---|---|---|---|
| 101 | PK90_AMT | 17 | 11 | NUMERIC | 0.25041 | Amount of PCB (ppm) detected in Peak #90 as reported on the PCB Congener Amount Report. |
| 102 | PK91_AMT | 17 | 11 | NUMERIC | 0.56981 | Amount of PCB (ppm) detected in Peak #91 as reported on the PCB Congener Amount Report. |
| 103 | PK92_AMT | 17 | 11 | NUMERIC | 0.25781 | Amount of PCB (ppm) detected in Peak #92 as reported on the PCB Congener Amount Report. |
| 104 | PK93_AMT | 17 | 11 | NUMERIC | 0.56984 | Amount of PCB (ppm) detected in Peak #93 as reported on the PCB Congener Amount Report. |
| 105 | PK94_AMT | 17 | 11 | NUMERIC | 0.00254 | Amount of PCB (ppm) detected in Peak #94 as reported on the PCB Congener Amount Report. |
| 106 | PK95_AMT | 17 | 11 | NUMERIC | 0.05671 | Amount of PCB (ppm) detected in Peak #95 as reported on the PCB Congener Amount Report. |
| 107 | PK96_AMT | 17 | 11 | NUMERIC | 0.23681 | Amount of PCB (ppm) detected in Peak #96 as reported on the PCB Congener Amount Report. |
| 108 | PK97_AMT | 17 | 11 | NUMERIC | 0.00004 | Amount of PCB (ppm) detected in Peak #97 as reported on the PCB Congener Amount Report. |
| 109 | PK98_AMT | 17 | 11 | NUMERIC | 0.00045 | Amount of PCB (ppm) detected in Peak #98 as reported on the PCB Congener Amount Report. |
| 110 | PK99_AMT | 17 | 11 | NUMERIC | 0.25981 | Amount of PCB (ppm) detected in Peak #99 as reported on the PCB Congener Amount Report. |
| 111 | PK100AMT | 17 | 11 | NUMERIC | 0.25874 | Amount of PCB (ppm) detected in Peak #100 as reported on the PCB Congener Amount Report. |
| 112 | PK101AMT | 17 | 11 | NUMERIC | 0.12584 | Amount of PCB (ppm) detected in Peak #101 as reported on the PCB Congener Amount Report. |
| 113 | PK102AMT | 17 | 11 | NUMERIC | 0.40014 | Amount of PCB (ppm) detected in Peak #102 as reported on the PCB Congener Amount Report. |

310493

| Field | Field Name | Length | Dec | Type | Entry Types<br>Water Column, Sediment, Pore Water, Fish and Biota | Comments |
|---|---|---|---|---|---|---|
| 114 | PK103AMT | 17 | 11 | NUMERIC | 0.25804 | Amount of PCB (ppm) detected in Peak #103 as reported on the PCB Congener Amount Report. |
| 115 | PK104AMT | 17 | 11 | NUMERIC | 0.84621 | Amount of PCB (ppm) detected in Peak #104 as reported on the PCB Congener Amount Report. |
| 116 | PK105AMT | 17 | 11 | NUMERIC | 0.25041 | Amount of PCB (ppm) detected in Peak #105 as reported on the PCB Congener Amount Report. |
| 117 | PK106AMT | 17 | 11 | NUMERIC | 0.56981 | Amount of PCB (ppm) detected in Peak #106 as reported on the PCB Congener Amount Report. |
| 118 | PK107AMT | 17 | 11 | NUMERIC | 0.25781 | Amount of PCB (ppm) detected in Peak #107 as reported on the PCB Congener Amount Report. |
| 119 | PK108AMT | 17 | 11 | NUMERIC | 0.56984 | Amount of PCB (ppm) detected in Peak #108 as reported on the PCB Congener Amount Report. |
| 120 | PK109AMT | 17 | 11 | NUMERIC | 0.00254 | Amount of PCB (ppm) detected in Peak #109 as reported on the PCB Congener Amount Report. |
| 121 | PK110AMT | 17 | 11 | NUMERIC | 0.05671 | Amount of PCB (ppm) detected in Peak #110 as reported on the PCB Congener Amount Report. |
| 122 | PK111AMT | 17 | 11 | NUMERIC | 0.23681 | Amount of PCB (ppm) detected in Peak #111 as reported on the PCB Congener Amount Report. |
| 123 | PK112AMT | 17 | 11 | NUMERIC | 0.00004 | Amount of PCB (ppm) detected in Peak #112 as reported on the PCB Congener Amount Report. |
| 124 | PK113AMT | 17 | 11 | NUMERIC | 0.00045 | Amount of PCB (ppm) detected in Peak #113 as reported on the PCB Congener Amount Report. |
| 125 | PK114AMT | 17 | 11 | NUMERIC | 0.25981 | Amount of PCB (ppm) detected in Peak #114 as reported on the PCB Congener Amount Report. |
| 126 | PK115AMT | 17 | 11 | NUMERIC | 0.25874 | Amount of PCB (ppm) detected in Peak #115 as reported on the PCB Congener Amount Report. |

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| Field | Field Name | Length | Dec | Type | Entry Types | Comments |
|---|---|---|---|---|---|---|
| | | | | | Water Column, Sediment, Pore Water, Fish and Biota | |
| 127 | PK116AMT | 17 | 11 | NUMERIC | 0.12584 | Amount of PCB (ppm) detected in Peak #116 as reported on the PCB Congener Amount Report. |
| 128 | PK117AMT | 17 | 11 | NUMERIC | 0.40014 | Amount of PCB (ppm) detected in Peak #117 as reported on the PCB Congener Amount Report. |
| 129 | PK118AMT | 17 | 11 | NUMERIC | 0.25804 | Amount of PCB (ppm) detected in Peak #118 as reported on the PCB Congener Amount Report. |
| 130 | PCB_CONC | 17 | 11 | NUMERIC | 11.542 | Total PCB concentration (ppm) as reported on the PCB Congener Amount Report. |
| 131 | MIC_MOLS | 13 | 10 | NUMERIC | 0.04761 | Total micromoles as reported on the PCB Congener Amount Report. |
| 132 | AVG_MWT | 7 | 2 | NUMERIC | 242.3 | Average molecular weight as reported on the PCB Congener Amount Report. |
| 133 | PEAKS | 3 | 0 | NUMERIC | 107 | The number of calibrated peaks detected as reported on the PCB Congener Amount Report. |
| 134 | C18_CHK | 1 | 0 | CHARACTER | Y, N | Yes or no, whether confirmation analysis on a C18 column was conducted for this sample. |
| 135 | CF_PK5 | 17 | 11 | NUMERIC | 0.65, 1.25, 1.37 | Coelution correction factor used to adjust for peak coelution bias in DB-1 Peak 5 |
| 136 | CF_PK8 | 17 | 11 | NUMERIC | 0.45, 0.58 | Coelution correction factor used to adjust for peak coelution bias in DB-1 Peak 8 |
| 137 | CF_PK14 | 17 | 11 | NUMERIC | 1.44, 2.23 | Coelution correction factor used to adjust for peak coelution bias in DB-1 Peak 14 |
| 138 | BZ4_AMT | 17 | 11 | NUMERIC | 0.00012345678 | C-18 confirmation analysis results for congener BZ4 (ppm), first of two coeluting congeners in DB-1 Peak 5 |

310495

| Field | Field Name | Length | Dec | Type | Entry Types: Water Column, Sediment, Pore Water, Fish and Biota | Comments |
|---|---|---|---|---|---|---|
| 139 | BZ10_AMT | 17 | 11 | NUMERIC | 0.00012345678 | C-18 confirmation analysis results for congener BZ10 (ppm), second of two coeluting congeners in DB-1 Peak 5 |
| 140 | BZ5_AMT | 17 | 11 | NUMERIC | 0.00012345678 | C-18 confirmation analysis results for congener BZ5 (ppm), first of two coeluting congeners in DB-1 Peak 8 |
| 141 | BZ8_AMT | 17 | 11 | NUMERIC | 0.00012345678 | C-18 confirmation anaysis results for congener BZ8 (ppm), second of two coeluting congeners in DB-1 Peak 8 |
| 142 | BZ15_AMT | 17 | 11 | NUMERIC | 0.00012345678 | C-18 confirmation analysis results for congener BZ15 (ppm), first of two coleuting congeners in DB-1 Peak 14 |
| 143 | BZ18_AMT | 17 | 11 | NUMERIC | 0.00012345678 | C-18 confirmation analysis results for congener BZ18 (ppm), first of two coeluting congeners in DB-1 Peak 14 |
| 144 | GBS_BZ | 1 | 0 | CHARACTER | Y, N | Yes or no, whether sediment or porewater samples were analyzed with both Green Bay (GBS) and BZ standards |
| 145 | ADJUST | 1 | 0 | CHARACTER | Y, N | Indicates which records have been adjusted for analytical biases. |

310496

| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 1 | ID | | 12 | 0 | CHARACTER | 25 | 10037 | | The unique sample identifier assigned in the field to each environmental sample collected or tested. If a sample is collected and archived, a unique identifier will be given to it and the sample will be entered into an Archive Database. This is the DATABASE KEY field. Each record in the database has a unique ID. This ID is used to relate into the QA/QC database. |
| 2 | LOCATION | | 10 | 0 | CHARACTER | 8A-22<br>For a composite enter: COMPOSIT E | B.F.Br<br>Rt.197 Br.<br>TID-West<br>Rt.29 Br.<br>S.W.Br.<br>Rt.4 Br.<br>Hoosic R.<br>Bat. Kill<br>BFI AREA | | Sampling location. The actual location where the sample was collected. Water column sample locations: B.F.Br = Baker Falls Bridge (HRM 197.0); HRM 196.8 = Canoe Carry; Rt.197 Br. = Rt. 197 Bridge Fort Edward (HRM 194.2); TID = Thompson Island Dam (HRM 188.5), Rt.29 Br. = Rt. 29 Bridge Schuylerville; S.W.Br. = Stillwater Bridge; Rt.4 Br. = Rt. 4 Bridge Waterford; Hoosic R. = Hoosic River; Bat Kill = Batten Kill. "COMPOSITE" refers to sediment samples composited from more than one location. "EQBL" refers to equipment blanks (included only where PCB concentration exceeds MDL). HRM = approximate Hudson River mile. HRM 0.0 is located at the Battery in New York City. Sample locations within the river may be further differentiated by W = west (shore or channel), C = center (of channel), E = east (shore or channel). "R" indicates the archive sample for a given location. |

310497

Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".

| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 3 | MEDIA | | 1 | 0 | CHARACTER | f,w,a,b,p,s | f,w,a,b,p,s | | Type of matrix: f=fish, w=water, a=air, b=biota, p=pore water, s=sediment |
| 4 | INVEST | | 3 | 0 | CHARACTER | OBG, HAR, D&M | OBG, HAR, D&M | DEC, LAW, EPA, CRD | The organization that collected the sample: OBG = O'Brien & Gere; HAR = Harza; D&M = Dames & Moore; DEC = NYS Dept. Environ. Conserv.; LAW = Law Environmental; EPA = US Environ. Protect. Agency; CRD = GE Corporate Research and Development. |
| 5 | DESC | | 150 | 0 | CHARACTER | ST/CL-8A-1, 8A-12, 8A-2, 8A-3, 8A-5, 8A-7, 8A-15, 8A-6, 8A-13, 8A-4 | | Brown bullhead Atlantic tomcod American eel | Sample description. Possible sediment descriptions: CS=coarse sand, MS=medium sand, FS=fine sand, G=gravel, ST=silt, CL=clay, FS/ST=fine sand/silt, ST/CL=silt/clay, WC=wood chips, PD=plant debris, SH=shells. Fish species are abbreviated in Field SPP (number 23) and are spelled out in this Description field. For composites: Enter the description of the composite sample along with the locations of each sample involved in the composite. |
| 6 | MILE | mi | 5 | 1 | NUMERIC | | | | Approximate Hudson River Mile (HRM). HRM 0.0 is located at the Battery in New York City. The river mile for the Batten Kill and Hoosic River (Temporal Water Column Sampling locations) were estimated at the confluent. The river miles entered for the Float Survey sampling locations are also estimated. In addition, the river mile was estimated at the midpoint of each of the sampling reaches for the Sediment Survey. |

310498

Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".

| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 7 | NORTHING | ft | 9 | 1 | NUMERIC | 1189500.0 | 1185467.0 | | Northing coordinate according to the 1927 State Plane Coordinate System, this coordinate is estimated. |
| 8 | EASTING | ft | 9 | 1 | NUMERIC | 699400.0 | 699450.0 | | Easting coordinate according to the 1927 State Plane Coordinate System, this coordinate is estimated. |
| 9 | ELEV | ft | 5 | 1 | NUMERIC | 950.0 | 950.0 | | River Elevation, this value is estimated. |
| 10 | DATE_COL | | 8 | 0 | DATE | 03/09/91 | 04/12/91 | | Date of sample collection (MM/DD/YY) |
| 11 | HRCOL | hours | 2 | 0 | NUMERIC | NA | 14 | | This value represents the hour of the day that the sample was collected. |
| 12 | MINCOL | minutes | 2 | 0 | NUMERIC | NA | 45 | | This value represents the minute of the day that the sample was collected. |
| 13 | WTR_DPTH | ft | 5 | 1 | NUMERIC | 8.4 | 18.0 | | Depth of water at sample location |
| 14 | ST_DPTH | cm or ft | 5 | 1 | NUMERIC | 0.0 | 0.0 | | Starting depth of sediment core (cm) or composite water sample (ft) |
| 15 | END_DPTH | cm or ft | 5 | 1 | NUMERIC | 5.0 | 18.0 | | Ending depth of sediment core (cm) or composite water sample (ft) |
| 16 | LAB | | 8 | 0 | CHARACTER | NEA | NEA | | The laboratory that performed the sample analysis |
| 17 | TOT_SOL | % | 4 | 1 | NUMERIC | 78.3 | NA | | Total percent solids for sediment core composite samples only |
| 18 | VOL_SOL | % | 4 | 1 | NUMERIC | 45.6 | NA | | Volume solids for sediment core composite samples only |
| 19 | DENSITY | g(dry)/ml(wet) | 4 | 2 | NUMERIC | 1.3 | NA | | Bulk density for sediment core composite samples only |

Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".



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| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 20 | MOIST | % | 4 | 1 | NUMERIC | 92.4 | NA | | Percent moisture for sediment core composite samples only |
| 21 | TOC | mg/kg or mg/l | 6 | 0 | NUMERIC | 23000 | 50 | | Total organic carbon in sediment core composite samples (mg/kg) or water composite samples (mg/l) |
| 22 | AGE | yr | 1 | 0 | CHARACTER | NA | NA | 1 | Age of fish in years |
| 23 | SPP | | 4 | 0 | CHARACTER | NA | NA | BB | Fish Species abbreviated: Largemouth Bass, Brown Bullhead, Smallmouth Bass, Pumpkinseed. |
| 24 | PCLPD | % | 5 | 2 | NUMERIC | NA | NA | 34.56 | Percent lipids |
| 25 | LEN | mm | 6 | 1 | NUMERIC | NA | NA | 14.1 | Fish length |
| 26 | WGT | grams | 9 | 2 | NUMERIC | NA | NA | 3.34 | Fish weight |
| 27 | SEX | | 1 | 0 | CHARACTER | NA | NA | M,F | Sex of fish: m=male, f=female, U=undetermined |
| 28 | PREP | | 3 | 0 | CHARACTER | NA | NA | F,W, CF, CW | Preparation method: F=fillet, W=whole fish, CF=composite fillets, CW=composite whole fish |
| 29 | OBG_ID | | 8 | 0 | CHARACTER | M2241 | M2241 | | O'Brien and Gere sample identification for fields 30 to 34. If this field is blank then there will be no data available for entry into fields 30 to 34, and zeros can be regarded as "null values". |
| 30 | TSS | mg/l | 5 | 0 | NUMERIC | NA | 6 | | Total suspended solids in water samples only. Results presented to tenths place for 1995 data, otherwise rounded to whole numbers. Results less than detection limit shown as "11111". |

Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".

| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 31 | TDS | mg/l | 5 | 0 | NUMERIC | NA | 59 | | Total dissolved solids in water samples only |
| 32 | SP_COND | umho/cm | 6 | 0 | NUMERIC | NA | 89 | | Specific conductivity in water samples only |
| 33 | TOT_ALK | mg/l as CaCO3 | 5 | 0 | NUMERIC | NA | 11 | | Total alkalinity in water samples only |
| 34 | TOC_F | mg/l | 5 | 0 | NUMERIC | NA | 15 | | Total organic carbon in filtered water samples only |
| 35 | FTEDFLOW | cubic ft/sec | 8 | 0 | NUMERIC | NA | 7150 | | United States Department of the Interior USGS daily average flow data for the Hudson River at Fort Edward, NY (station number 01327750). Instantaneous flows are entered for recent dates (typically going back about 3 months) for which preliminary daily average data is not yet available. Preliminary flows are updated quarterly. |
| 36 | WTFDFLOW | cubic ft/sec | 8 | 0 | NUMERIC | NA | 8400 | | United States Department of the Interior USGS daily average flow data for the Hudson River at Waterford, NY (station number 01335754). Preliminary and finalized values are included. |
| 37 | SWTRFLOW | cubic ft/sec | 8 | 0 | NUMERIC | NA | 3520 | | United States Department of the Interior USGS daily average flow data for the Hudson River at Stillwater, NY (station number 01331095). Preliminary and finalized values are included. |
| 38 | WTR_TMP | Degrees Celsius | 4 | 0 | NUMERIC | NA | 9 | | Water temperature for water samples only |

Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".

| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 39 | PCB_WM | ppm | 12 | 7 | NUMERIC | | 0.0000126 | | Total PCB concentration by Webb & McCall Method or USEPA Method 8080, this entry will be reported as a "zero value" if the sample concentration is less than the detection limit. See field 45 to distinguish a below detection limit entry from a "null value". |
| 40 | PCB_USGS | ppm | 12 | 7 | NUMERIC | | 0.0000025 | | Total PCB concentration by USGS Method, this entry will be reported as a "zero value" if the sample concentration is less than the detection limit. See field 44 to distinguish a below detection limit entry from a "null value". |
| 41 | PCB_CAP | ppm | 17 | 11 | NUMERIC | 65.7800000 | 0.0000198 | | Total PCB concentration by Capillary Column Method NEA608CAP, this entry will be reported as a "zero value" if the sample concentration is less than the detection limit. See field 46 to distinguish a below detection limit entry from a "null value". |
| 42 | AROC_ID | | 20 | 0 | CHARACTER | A1242<br>Altered<br>A1242<br>A1248<br>None | A1242<br>Altered<br>A1242<br>A1248<br>None | | Visually identified nominal Aroclor pattern reported by NEA for Webb & McCall or Method 8080 analyses. |
| 43 | TOT_DISS | | 1 | 0 | CHARACTER | T,D | T,D | | Total or Dissolved (derived from a filtered water sample) |
| 44 | DL_USGS | | 7 | 0 | CHARACTER | | <11PPT | | USGS method detection limit. This field will be blank if the sample was not analyzed by this method and will indicate that a zero in field 40 is a "null value". |

Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".

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| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 45 | DL_WM | | 7 | 0 | CHARACTER | | <11PPT | | Webb & McCall or Method 8080 method detection limit. This field will be blank if the sample was not analyzed by this method and will indicate that a zero in field 39 is a "null value". |
| 46 | DL_CAP | | 7 | 0 | CHARACTER | <1PPM | <11PPT | | Capillary Column method detection limit. This field will be blank if the sample was not analyzed by this method and will indicate that a zero in field 41 is a "null value". It should be noted that the method detection limit for pore water analyses will be <100PPB. |
| 47 | COL_TYP1 | | 1 | 0 | CHARACTER | P,C | P,C | | Type of column used to generate Webb & McCall data: P=packed column, C=capillary column |
| 48 | COL_TYP2 | | 1 | 0 | CHARACTER | P,C | P,C | | Type of column used to generate homolog values: P=packed column, C=capillary column. If a packed column was used to generate homolog values, the homolog values are estimates. |
| 49 | NEA_FILE | | 12 | 0 | CHARACTER | 910606F or N/A | 910566F or 910878X | | NEA file identification as reported on PCB summary report sheet. An "X" is only included in the NEA_FILE field if the sample is a Temporal Water Column sample analyzed for dissolved PCBs. N/A applies to samples not analyzed by NEA (e.g. Channel Characterization samples.) "R" indicates reanalyzed sample. |
| 50 | CUSTOMER | | 20 | 0 | CHARACTER | O'BRIEN & GERE | O'BRIEN & GERE | GE:CR and D | NEA Customer identification as reported on the PCB summary report sheet |



Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".

| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 51 | NEA_DESC | | 40 | 0 | CHARACTER | 8A-F1(0-5) | BAKER FALLS BRIDGE (DISSOLVE D) | 806 0855 | NEA file description as reported on PCB summary report sheet. RalTech #s reported for Archived Fish analyses. |
| 52 | NEA_COM | | 40 | 0 | CHARACTER | 1991 HUDSON RIVER SEDIMENT SURVEY COC:7/16/9 1 | 1991 HUDSON RIVER H2O SURVEY COC:5/3/91 | | NEA comment as reported on PCB summary report sheet |
| 53 | NEA_TOT | ppm | 17 | 11 | NUMERIC | 67.8900000 | 0.0000182 | | NEA total PCB concentration as reported on PCB summary report sheet. Value is equal to the value reported for "PCB_CAP" in field 41. |
| 54 | MONO_WT | % | 5 | 2 | NUMERIC | 17.40 | 50.00 | | Weight % of monochlorinated PCB by Capillary Column Chromatography |
| 55 | DI_WT | % | 5 | 2 | NUMERIC | 17.90 | 0.0 | | Weight % of dichlorinated PCB by Capillary Column Chromatography |
| 56 | TRI_WT | % | 5 | 2 | NUMERIC | 27.00 | 18.47 | | Weight % of trichlorinated PCB by Capillary Column Chromatography |
| 57 | TERA_WT | % | 5 | 2 | NUMERIC | 25.20 | 30.62 | | Weight % of terachlorinated (tetrachlorinated) PCB by Capillary Column Chromatography |
| 58 | PENTA_WT | % | 5 | 2 | NUMERIC | 9.30 | 17.63 | | Weight % of pentachlorinated PCB by Capillary Column Chromatography |
| 59 | HEXA_WT | % | 5 | 2 | NUMERIC | 2.10 | 14.62 | | Weight % of hexachlorinated PCB by Capillary Column Chromatography |

Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".

| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 60 | HEPTA_WT | % | 5 | 2 | NUMERIC | 0.90 | 15.32 | | Weight % of heptachlorinated PCB by Capillary Column Chromatography |
| 61 | OCTA_WT | % | 5 | 2 | NUMERIC | 0.10 | 3.34 | | Weight % of octachlorinated PCB by Capillary Column Chromatography |
| 62 | NONA_WT | % | 5 | 2 | NUMERIC | 0.10 | 0.00 | | Weight % of nonachlorinated PCB by Capillary Column Chromatography |
| 63 | DECA_WT | % | 5 | 2 | NUMERIC | 0.10 | 0.00 | | Weight % of decachlorinated PCB by Capillary Column Chromatography |
| 64 | MONO_ML | % | 5 | 2 | NUMERIC | 23.00 | 0.00 | | Mole % of monochlorinated PCB by Capillary Column Chromatography |
| 65 | DI_ML | % | 5 | 2 | NUMERIC | 19.90 | 0.00 | | Mole % of dichlorinated PCB by Capillary Column Chromatography |
| 66 | TRI_ML | % | 5 | 2 | NUMERIC | 26.10 | 22.98 | | Mole % of trichlorinated PCB by Capillary Column Chromatography |
| 67 | TERA_ML | % | 5 | 2 | NUMERIC | 21.60 | 33.29 | | Mole % of terachlorinated (tetrachlorinated) PCB by Capillary Column Chromatography |
| 68 | PENTA_ML | % | 5 | 2 | NUMERIC | 7.20 | 16.92 | | Mole % of pentachlorinated PCB by Capillary Column Chromatography |
| 69 | HEXA_ML | % | 5 | 2 | NUMERIC | 1.50 | 12.43 | | Mole % of hexachlorinated PCB by Capillary Column Chromatography |
| 70 | HEPTA_ML | % | 5 | 2 | NUMERIC | 0.60 | 12.01 | | Mole % of heptachlorinated PCB by Capillary Column Chromatography |
| 71 | OCTA_ML | % | 5 | 2 | NUMERIC | 0.10 | 2.36 | | Mole % of octachlorinated PCB by Capillary Column Chromatography |

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Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".

| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 72 | NONA_ML | % | 5 | 2 | NUMERIC | 0.10 | 0.00 | | Mole % of nonachlorinated PCB by Capillary Column Chromatography |
| 73 | DECA_ML | % | 5 | 2 | NUMERIC | 0.10 | 0.00 | | Mole % of decachlorinated PCB by Capillary Column Chromatography |
| 74 | ORTHO_CL | | 4 | 2 | NUMERIC | 1.39 | 1.55 | | Mole ratio of ortho chlorines per biphenyl |
| 75 | MP_CL | | 4 | 2 | NUMERIC | 1.38 | 2.09 | | Mole ratio of meta and para chlorines per biphenyl |
| 76 | TOT_CL | | 4 | 2 | NUMERIC | 2.77 | 3.64 | | Mole ratio of total chlorines per biphenyl |
| 77 | VERIFIED | | 3 | 0 | CHARACTER | YES | YES | | Verified data has been checked for accuracy and validated |
| 78 | QL_WM | | 2 | 0 | CHARACTER | U,J,UJ | U,J,UJ | | Data Validation Qualifier for the Webb & McCall PCB results:<br>J=approximate sample result<br>U=approximate the detection limit<br>UJ=approximate the sample result and the detection limit<br>R=reject the sample result or the detection limit |
| 79 | QL_USGS | | 2 | 0 | CHARACTER | U,J,UJ | U,J,UJ | | Data Validation Qualifier for the USGS PCB results:<br>J=approximate sample result<br>U=approximate the detection limit<br>UJ=approximate the sample result and the detection limit<br>R=reject the sample result or the detection limit |

310506

Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".

| Field | Field Name | Units | Length | Dec | Type | Entry Types | | | Comments |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Sediment | Water column | Other | |
| 80 | QL_CAP | | 2 | 0 | CHARACTER | U,J,UJ | U,J,UJ | | Data Validation Qualifier for the Capillary Column PCB results:<br>J=approximate sample result<br>U=approximate the detection limit<br>UJ=approximate the sample result and the detection limit<br>R=reject the sample result or the detection limit |
| 81 | PROGRAM | | 20 | 0 | CHARACTER | SEDIMENT, FOOD CHAIN, BFI, | TWCMP, HIGHFLOW, BFI, PCRDMP | FOOD CHAIN LOWER HUDSON | This field indicates the sampling program under which the sample was collected. Examples:<br>TWCMP = Temporal Water Column Monitoring Program 91-92<br>PCRDMP = Post Construction Remnant Deposit Monitoring Program 92-96+<br>SEDIMENT = Sediment Sampling and Analysis Program 91<br>BFI = Bakers Falls Investigation 92-93 |
| 82 | ADJUST | | 1 | 0 | CHARACTER | Y,N | Y,N | Y,N | Indicates which records have been adjusted for analytical biases. |

310507

Note: NA = Not Applicable
Numeric fields containing zeros (0) may indicate either a "zero value" or a "null value". See comments to identify individual numeric fields where zero entries reflect "null values".

# Data disk:
# GE Hudson River PCB database

## EPA REGION II
## SCANNING TRACKING SHEET

DOC ID # 67288

DOC TITLE/SUBJECT:

**HUDSON RIVER PCBS UPDATE #7**
**GE HUDSON RIVER PCB DATABASE**
**(FILE FORMAT:dBASEIV)**
**(Page: 310509)**

THIS DOCUMENT IS ON A DISKETTE AND CAN BE LOCATED IN THE ADMINISTRATIVE RECORD FILE AT THE

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# Computer program algorithm to implement database corrections

# Appendix C. Algorithm for the correction of the analytical biases in the GE Hudson River PCB database[1]

## I. Prepare the databases

A. Backup the existing databases GE (environmental) and CP (congener peak)

B. Edit the GE database for samples analyzed using Green Bay Standard (GBS).

1. Select samples (records) which will be modified
   a. criteria: **INVEST** ≠ "HAR" (*excludes the Harza sediment and biota data*)
   b. criteria: **DATE_COL** > {01/01/90} (*excludes the GE CR&D archived fish results from 1977-1982*)

2. Copy records to be modified to a temporary database GE-1

3. Reverse selection process to select samples which will not be modified
   a. criteria: **INVEST** = "HAR" (*includes the Harza sediment and biota data*)
   b. criteria: **DATE_COL** < {01/01/90} (*includes the GE CR&D archived fish results from 1977-1982*)

4. Copy records which will not be modified to a temporary database GE-2.

C. Edit the CP (congener peak) database

1. Add the following fields to the CP database
   a. **C18_CHK**
   b. **CF_PK5**
   c. **CF_PK8**
   d. **CF_PK14**
   e. **BZ4_AMT**
   f. **BZ10_AMT**
   g. **BZ5_AMT**
   h. **BZ8_AMT**

---

1 Note that bold and capitalized text indicates actual field names in the databases. The format **GE.INVEST** indicates the field **INVEST** is in the GE database.

i. **BZ15_AMT**
j. **BZ18_AMT**
k. **GBS_BZ**

2. Select the records that will be modified
   a. criteria: **CP.ID** LIKE **GE-1.ID**
      *Note that the ID fields in both databases contain unique sample identification numbers which link the GE and CP database records. In this step, the* **ID** *field in the edited GE-1 database is used to select the records for modification in the CP database. This step will remove from CP those records from the Archived Fish and Harza Lower Hudson programs.*
   b. Copy the records to be modified to a temporary database CP-1.

3. Reverse selection process to select samples which will not be modified
   a. criteria: **GE-2.ID** LIKE **CP.ID**
      *In this step, the* **ID** *field in the edited GE-2 database is used to select the records which will not be modified in the CP database.*
   b. Copy the records not to be modified to a temporary database CP-2.

D. Sort the temporary databases by media

1. Using GE-1, sort the database into three databases by media
   a. water column ("W") data - GE-1W
   b. sediment ("S") and porewater ("P") data - GE-1S
   c. fish ("F") and biota ("B") data - GE-1B

2. Using GE-2, sort the database into three databases by media
   a. water column ("W") data - GE-2W
   b. sediment ("S") and porewater ("P") data - GE-2S
   c. fish ("F") and biota ("B") data - GE-2B

3. Using CP-1, sort the database into three databases by media
   a. water column ("W") data - CP-1W
   b. sediment ("S") and porewater ("P") data - CP-1S
   c. fish ("F") and biota ("B") data - CP-1B

4. Using CP-2, sort the database into three databases by media
    a. water column ("W") data - CP-2W
    b. sediment ("S") and porewater ("P") data - CP-2S
    c. fish ("F") and biota ("B") data - CP-2B

E. Store the temporary databases which will not be modified (e.g. GE-2W, GE-2S, GE-2B, CP-2W, CP-2S, CP-2B).

F. Create the additional reference databases

1. C18_DATA (HydroQual 1997, Tables A-9, A-11, and A-15) - create using the C18 data obtained from additional C18 capillary analyses to quantify the coeluting congeners in DB-1 Peaks 5, 8, and 14.

2. COR_FACTOR (HydroQual 1997, Table A-6) - contains the corrections factors for calibration bias correction.

3. GBS_ONLY (HydroQual 1997, Tables A-14 and A-17) contains identification information for sediment and porewater samples analyzed using only the GBS, not supplemented with the BZ Standard (BZS). *This database will contain 101 sediment samples and 54 porewater samples.*

4. MOL_WT - contains the molecular weights of each DB-1 peak, chlorination levels, and homolog distribution ratios to be used in the calculation of average molecular weight, total micromoles, ortho-, meta-para-, and total chlorines per biphenyl, and homolog distributions. *Derived from work by Frame and others, 1996.*

## II. Implement the analytical bias corrections - congener peak (CP) databases

*The analytical bias corrections will be implemented in order by media. Each sample (record) will be adjusted for the calibration bias and the coelution bias before the next record is selected.*

*Table B-1 defines which fields will be affected by the database revisions, and those which will not be affected.*

**Table B-1. Field status in CP databases**

| Fields that will be affected | Fields that will not be affected |
|---|---|
| Congener peak concentrations (PK2_AMT through PK118AMT) | Sample description fields (NEA_FILE, NEA_DESC, ID, MEDIA) |
| Total PCBs (PCB_CONC) | Field log information (DATE_COL, LOCATION, ST_DPTH, END_DPTH, SAMPSED, REACH) |
| Total micromoles PCB (MIC_MOLS) | Type of mixed peak deconvolution (MIX_TYPE) |
| Average molecular weight (AVG_MWT) | Biphenyl concentration (PK1_AMT) |
| | Number of peaks quantified (PEAKS) |

A. Correct the CP-W1 temporary water column database.

1. Correct calibration bias - For each sample, starting with the first one and ending with the last one, complete the following steps:
   a. apply the appropriate correction factor from COR_FACTOR reference database to each peak concentration value in the fields **PK2_AMT** through **PK118AMT**. *Note that the correction factor for DB-1 Peak 1 (***PK1_AMT***) is undefined. This peak is not considered for PCB analysis of Hudson River environmental samples.*
      (1) **PK2_AMT** × 1.0441
      (2) **PK3_AMT** × 1.0000
      (3) **PK4_AMT** × 1.0073
      (4) **PK5_AMT** × 4.5431
      •
      •
      •
      (117) **PK118_AMT** × 0.4726

2. Correct coelution bias - For each sample, starting with the first one and ending with the last one, complete the following steps:
   a. Replace the following peak values using the correction factor shown.
      (1) replace **CP-1W.PK5_AMT** with (0.65 × **CP-1W.PK5_AMT**)
      (2) replace **CP-1W.PK8_AMT** with (0.45 × **CP-1W.PK8_AMT**)
      (3) replace **CP-1W.PK14_AMT** with (1.44 × **CP-1W.PK14_AMT**)
      (4) write value 0.65 into field **CP-1W.CF_PK5**
      (5) write value 0.45 into field **CP-1W.CF_PK8**
      (6) write value 1.44 into field **CP-1W.CF_PK14**
   b. If the record is present in C18_DATA reference database, then fill in the following fields with data from C18_DATA.
      (1) write "Y" into field **CP-1W.C18_CHK**
      (2) write value in **C18_DATA.BZ4_AMT** to **CP-1W.BZ4_AMT**
      (3) write value in **C18_DATA.BZ10_AMT** to **CP-1W.BZ10_AMT**
      (4) write value in **C18_DATA.BZ5_AMT** to **CP-1W.BZ5_AMT**
      (5) write value in **C18_DATA.BZ8_AMT** to **CP-1W.BZ8_AMT**
      (6) write value in **C18_DATA.BZ15_AMT** to **CP-1W.BZ15_AMT**
      (7) write value in **C18_DATA.BZ18_AMT** to **CP-1W.BZ18_AMT**
   c. if the record is not present in C18_DATA and was therefore not measured for C18 data, then write "N" into field **CP-1W.C18_CHK**

3. Update additional field in CP-1W
   a. Calculate total PCB concentration (∑**PK1_AMT** through **PK118AMT**) and put the sum value in field **PCB_CONC**
   b. Calculate the total micromoles using values in the reference database MOL_WT and the following formula:

**(1)** Equation II.A.3.b.
*Calculation for total micromoles of PCB (MIC_MOLS).*

$$\sum \frac{C_i}{MWT_i} = \sum MICMOL_i = MICMOLS$$

   where $C_i$ is the concentration in ppm of the individual congener peak, and $MWT_i$ is the molecular weight of the same congener peak from the reference database MOL_WT, resulting in the micromole concentration for the individual DB-1 capillary column peak ($MICMOL_i$). Put the calculated value in the field **MIC_MOLS**.
   c. Calculate the average molecular weight using the reference values in database MOL_WT and put the calculated value in the field **AVG_MWT**, using the following formula:

**(2)** Equation II.A.3.c.
*Calculation for average molecular weight (AVG_MWT)*

$$\frac{PCBCONC}{MICMOLS} = AVGMWT$$

where PCBCONC is the total PCB concentration (**CP-1W.PCB_CONC**) and MICMOLS is total micromoles (**CP-1W.MIC_MOLS**).

4. Close the CP-1W database after the last sample has been adjusted.

B. Correct the temporary fish/biota database CP-1B

1. Correct calibration bias - For each sample, starting with the first one and ending with the last one, complete the following steps:
   a. apply the appropriate correction factor from COR_FACTOR to each peak concentration value in the fields **PK2_AMT** through **PK118AMT**.
   *Note that the correction factor for DB-1 Peak 1 (***PK1_AMT***) is undefined. This peak is not considered for PCB analysis of Hudson River environmental samples.*
   (1) **PK2_AMT** × 1.0441
   (2) **PK3_AMT** × 1.0000
   (3) **PK4_AMT** × 1.0073
   (4) **PK5_AMT** × 4.5431
   •
   •
   •
   (117) **PK118_AMT** × 0.4726

2. Coelution bias: note that coelution bias corrections have not been developed for the biota data (HydroQual 1997).

3. Correct additional fields in CP-B1
   a. Calculate total PCB concentration (∑**PK1_AMT** through **PK118AMT**) and put the sum value in field **PCB_CONC**
   b. Calculate the total micromoles using reference values in database MOL_WT and put the calculated value in the field **MIC_MOLS** (see Equation II.A.3.b).
   c. Calculate the average molecular weight using the reference values in database MOL_WT and put the calculated value in the field **AVG_MWT** (see Equation II.A.3.c.).
4. Close the CP-1B database after the last sample has been adjusted

C. Correct the temporary sediment/porewater database CP-1S

1. Coelution bias correction - For each sample, starting with the first one and ending with the last one, complete the following steps:
   a. apply the appropriate correction factor from COR_FACTOR to each peak concentration value in the fields **PK2_AMT** through **PK118AMT**, except for **PK5_AMT**.

*Note that the correction factor for DB-1 Peak 1 (***PK1_AMT***) is undefined. This peak is not considered for PCB analysis of Hudson River environmental samples.*

*Also note that some sediment and porewater samples were analyzed using only the Green Bay mixed Aroclor calibration standard, whereas other samples were analyzed with both the Green Bay and BZ#4-BZ#10 standard to refine calibration of Peak 5. Correction of calibration bias for Peak 5 is not required for samples analyzed using both standards, but is required for samples analyzed using only the GBS standard. These calibration bias for Peak 5 will be applied as appropriate at the time the coelution biases are applied (Section II.C.2.)*

(1) **PK2_AMT** × 1.0441
(2) **PK3_AMT** × 1.0000
(3) **PK4_AMT** × 1.0073
(4) **PK6_AMT** × 2.0407
•
•
•
(116) **PK118_AMT** × 0.4726

2. Correct coelution bias - For each sample, starting with the first one and ending with the last one, complete the following steps:
   a. use database GBS_ONLY to evaluate if the record was analyzed by GBS only, or GBS supplemented with BZS
   *Note: A group of sediment samples collected in association with the 1996 Particle Study (HydroQual) and the 1997 High Flow Bedload Study (HydroQual) were not significantly altered from a commercial Aroclor congener pattern. Therefore, the water column coelution bias corrections factors were deemed more appropriate for these data than the sediment coelution corrections factors.*
   (1) if the record is present in GBS_ONLY (having been analyzed using the Green Bay standard only) and the **DATE_COL** is earlier than January 1, 1996, then:
      (a) replace **CP-1S.PK5_AMT** with (1.25 × 4.5431 × **CP-1S.PK5_AMT**)
      (b) replace **CP-1S.PK8_AMT** with (0.58 × **CP-1S.PK8_AMT**)
      (c) replace **CP-1S.PK14_AMT** with (2.23 × **CP-1S.PK14_AMT**)
      (d) write value 1.25 into field **CP-1S.CF_PK5**
      (e) write value 0.58 into field **CP-1S.CF_PK8**
      (f) write value 2.23 into field **CP-1S.CF_PK14**
      (g) write "N" in the field **GBS_BZ**
   (2) if the record is present in GBS_ONLY (having been analyzed using the Green Bay standard only) and the **DATE_COL** is the same or later than January 1, 1996, then:
      (a) replace **CP-1S.PK5_AMT** with (0.65 × 4.5431 × **CP-1S.PK5_AMT**)
      (b) replace **CP-1S.PK8_AMT** with (0.45 × **CP-1S.PK8_AMT**)

        (c) replace **CP-1S.PK14_AMT** with (1.44 × **CP-1S.PK14_AMT**)
        (d) write value 0.65 into field **CP-1S.CF_PK5**
        (e) write value 0.45 into field **CP-1S.CF_PK8**
        (f) write value 1.44 into field **CP-1S.CF_PK14**
        (g) write "N" in the field **GBS_BZ**
    (3) if the record is not present in GBS_ONLY database (the record has been analyzed with Green Bay standard and the BZ#4-BZ#10 standard):
        (a) replace **CP-1S.PK5_AMT** with (1.37 × **CP-1S.PK5_AMT**)
        (b) replace **CP-1S.PK8_AMT** with (0.58 × **CP-1S.PK8_AMT**)
        (c) replace **CP-1S.PK14_AMT** with (2.23 × **CP-1S.PK14_AMT**)
        (d) write value 1.37 into field **CP-1S.CF_PK5**
        (e) write value 0.58 into field **CP-1S.CF_PK8**
        (f) write value 2.23 into field **CP-1S.CF_PK14**
        (g) write "Y" in the field **GBS_&_BZ**

b. Use the database C18_DATA to evaluate if the sample was analyzed using the C-18 capillary column.
    (1) If the record is present in C18_DATA then write the following values into the fields specified:
        (a) write "Y" into field **CP-1S.C18_CHK**
        (b) write value in **C18_DATA.BZ4_AMT** to **CP-1S.BZ4_AMT**
        (c) write value in **C18_DATA.BZ10_AMT** to **CP-1S.BZ10_AMT**
        (d) write value in **C18_DATA.BZ5_AMT** to **CP-1S.BZ5_AMT**
        (e) write value in **C18_DATA.BZ8_AMT** to **CP-1S.BZ8_AMT**
        (f) write value in **C18_DATA.BZ15_AMT** to **CP-1S.BZ15_AMT**
        (g) write value in **C18_DATA.BZ18_AMT** to **CP-1S.BZ18_AMT**
    (2) if the record is not present in C18_DATA, write "N" in the field **CP-1S.C18_CHK**.

3. Correct additional fields in CP-S1
    a. Calculate total PCB concentration (∑**PK1_AMT** through **PK118AMT**) and put the sum value in field **PCB_CONC**
    b. Calculate the total micromoles using reference values in database MOL_WT and put the calculated value in the field **MIC_MOLS** (see Equation II.A.3.b.).
    c. Calculate the average molecular weight using the reference values in database MOL_WT and put the calculated value in the field **AVG_MWT** (see Equation II.A.3.c.).

4. Close the CP-1S database after the last sample has been adjusted.

## III. Quality Control (QC) check of the CP databases

*QC evaluation of the databases will be the same procedure for each media (water column, sediment/porewater, and biota/fish). A copy of the original database will be used as a reference*

A. Electronic QC of 100% of the data - using the original and revised databases.

1. For each congener concentration in DB-1 Peaks 2 through 118 (**PK2_AMT** through **PK118AMT**)
   a. multiply the uncorrected value in the original CP database by the appropriate correction factor from database COR_FACTOR and, as applicable, by the coelution correction factor (Peaks 5, 8 and 14)
   b. compare the result to the corresponding record in the revised database
      (1) if the values match within $\pm 1 \times 10^{-11}$ (e.g., 0.00001 parts per trillion), then the field passes this QC test; proceed with next field
      (2) if the values do not match within $\pm 1 \times 10^{-11}$, then the field fails
         (a) write sample information and the peak that failed to a temporary database for later evaluation
         (b) proceed with next field

2. For each record, recalculate the total PCB as the sum of the 118 congener peaks and compare the result to the value in the field **PCB_CONC**
   a. if the values match within $\pm 1 \times 10^{-11}$ (e.g., 0.00001 parts per trillion), then the record passes this QC test; proceed with next step
   b. if the values do not match within $\pm 1 \times 10^{-11}$, then the record fails
      1. write sample information and reason for failure to a temporary database for later evaluation
      2. proceed with next step

3. Upon completion of evaluation, close the CP database in use and proceed with next media database.

B. Review the electronic "fail" databases, identify the sources of error and implement corrections

C. Manual QC of 5% of the records. Records will be randomly selected from the original database, and extracted to a spreadsheet. Within the spreadsheet, the analytical bias corrections will be applied to the data. In addition to the same review described in Section III.A., the following will be reviewed:
1. Recalculate the average molecular weight using the reference database MOL_WT and compare the result to the value in the field **AVG_MWT**
   a. if the values match within 0.1, then the record passes this QC test; proceed with next step
   b. if the values do not match within 0.1, then the record fails

(1) write sample information and reason for failure to a temporary database for later evaluation

(2) proceed with next step

2. Recalculate the total micromoles using the reference database MOL_WT and compare the result to the value in the field **MIC_MOLS**
   a. if the values match within 0.00001, then the record passes this QC test; proceed with next record
   b. if the values do not match within 0.00001, then the record fails
      (1) write sample information and reason for failure to a temporary database for later evaluation
      (2) proceed with next record

D. Compile the information on the records which failed the QC tests, evaluate the data, and identify the source of error. Correct the computer program as necessary and proceed with Section II of this algorithm. After all the records have passed the QC tests, proceed with Section IV of this algorithm.

## IV. Implement the analytical bias corrections - environmental (GE) databases

*The analytical bias corrections will be implemented in order by media. Each sample (record) will be adjusted in the CP databases for calibration and coelution bias and pass QC criteria before this series of corrections is undertaken.*

*Table B-2 defines which fields will be affected by the database revisions and those which will not be affected.*

**Table B-2. Field status for GE database.**

| Fields that will be affected | Fields that will not be affected |
|---|---|
| Total PCBs (NEA_TOT, PCB_CAP, DL_CAP) | Sample description fields (NEA_FILE, NEA_DESC, ID, MEDIA, INVEST, LAB, DESC, OBG_ID, CUSTOMER, NEA_COM) |
| Homologs weight percent (MONO_WT through DECA_WT) | Field log information (DATE_COL, HRCOL, MINCOL, LOCATION, WTR_DPTH, ST_DPTH, END_DPTH, MILE, NORTHING, EASTING, ELEV, WTR_TMP) |
| Homologs mole percent (MONO_ML through DECA_ML) | Other parameters (TOT_SOL, VOL_SOL, DENSITY, MOIST, TOC, AGE, SPP, PCLPD, LEN, WGT, SEX, PREP, TSS, TDS, SP_COND, TOT_ALK, TOC_F, TOT_DISS, VERIFIED, PROGRAM) |
| Chlorination level (ORTHO_CL, MP_CL, TOT_CL) | River flow data (FTEDFLOW, WTFDFLOW, SWTRFLOW) |
| Validation qualifiers (QL_CAP) | PCB data by methods other than NEA608CAP (PCB_WM, PCB_USGS, AROC_ID, DL_USGS, DL_WM, COL_TYP1, COL_TYP2, QL_WM, QL_USGS) |

A. Correct each media GE database by implementing the following steps.

1. Correct the total PCB fields - For each sample, starting with the first one and ending with the last one, complete the following steps:
    a. Use the ID field to identify matching records between the corrected CP-1 database and GE-1 database
    b. Replace **GE.NEA_TOT** with **CP.PCB_CONC**
    c. Check if the total PCB concentration is greater than the method detection limit
        (1) If **GE.NEA_TOT** is greater than or equal to the detection limit, then replace all values in the field **GE.PCB_CAP** with the value in **GE.NEA_TOT**

(2) If **GE.NEA_TOT** is less than the detection limit, then replace all labels in the field **GE.DL_CAP** with the detection limit label

2. Calculate the homolog distribution
   a. weight percent basis: for each homolog group
      (1) Calculate the sum concentration of the DB-1 peaks from the CP database for the homolog group, referencing database MOL_WT for the peak distribution and coelution ratios.

**(3)** Equation IV.A.2.a.
*Calculation for homolog weight percent*

$$\frac{\sum (PK_i AMT \times HOMVALUE)}{PCBCONC} \times 100 = Homolog WT\%$$

where $PK_i$AMT is the congener peak concentration for DB-1 peaks 1 through 118, HOMVALUE is taken from the MOL_WT database for $PK_i$ and the homolog group being calculated, and PCBCONC is the total PCB concentration in field **GE.NEA_TOT**. Table B-3 summarizes the congener distribution among the homolog groups.

**Table B-3. Congener-homolog deconvolution rules.**

| Homolog Group | DB-1 Peaks, or percentage thereof |
|---|---|
| mono | 2, 3, 4, |
| di | 5, 6, 7, 8, 9, 12, 13, (*24.8%*14) |
| tri | 10, 11, (*75.2%*14), 15, 16, 17, 18, (*70.0%*19), 20, 21, 22, 23, 24, (*94.4%*25), (*96.6%*26), 28, 30, 36, (*57.0%*38) |
| tetra | (*30.0%*19), (5.6%25), (*3.4%*26), 27, 29, 31, 32, 33, 34, 35, 37, (*43.0%*38), 39, 40, 42, (*80.0%*43), (*80.0%*44), 45, 46, 47, (*95.5%*48), (*5.0%*49), 50 |
| penta | 41, (*20.0%*43), (*20.0%*44), (*4.5%*48), (*95.0%*49), 51, 52, 53, 54, 55, 56, 57, 58, 59, 61, 63, (*30.0%*65), (*70.0%*67), 68, (*68.0%*69), (*38%*71), (*70.0%*72), (*38.0%*74) |
| hexa | 60, 62, 64, (*70.0%*65), 66, (*30.0%*67), (*32.0%*69), 70, (*62%*71), (*30.0%*72), 73, (*62.0%*74), 75, 76, 77, 79, 80, 82, 83, 84, 86, 89, 91, (*38.0%*95), 97 |
| hepta | 78, 81, 85, 87, 88, 90, 92, 93, 94, (*62.0%*95), 98, 100, 102, 103, 104, 106, 107, 111 |

**Table B-3. Congener-homolog deconvolution rules.**

| Homolog Group | DB-1 Peaks, or percentage thereof |
|---|---|
| octa | 96, 99, 101, 105, 108, 109, 110, 112, 115, 116 |
| nona | 113, 114, 117 |
| deca | 118 |

(2) Place the calculated weight percent value in the appropriate homolog field **(GE.MONO_WT** through **GE.DECA_WT**).
(3) Repeat for each homolog group

b. mole percent basis: for each homolog group
(1) Calculate the sum micromoles of the DB-1 peaks from the CP database for the homolog group, referencing database MOL_WT for the peak distribution and coelution ratios.

(4) Equation IV.A.2.b.
*Calculation for homolog mole percent.*

$$\frac{\sum\left(\frac{PK_iAMT}{MWT_i} \times HOMVALUE\right)}{\sum\left(\frac{PK_iAMT}{MWT_i}\right)} \times 100 = HomologMole\%$$

where $PK_iAMT$ is the congener peak concentration for DB-1 peaks 1 through 118, $MWT_i$ is the molecular weight of the congener peak from MOL_WT database, and HOMVALUE is taken from the MOL_WT database for $PK_i$ and the homolog group being calculated.
Table B-3 summarizes the congener distribution among the homolog groups.

(2) Place the calculated mole percent value in the appropriate homolog field **(GE.MONO_ML** through **GE.DECA_ML**).
(3) Repeat for each homolog group

c. Calculate the chlorination level - chlorination level is based on the ratio of total chlorines to one of two options: ortho chlorines, meta-para chlorines. DB-1 peak chlorination levels are listed in the MOL_WT reference database. Repeat the following steps for each chlorination level:
(1) Select a record
(2) calculate the ortho-chlorination level using the following equation:

$$\sum\left(\frac{\left(\frac{PK_iAMT}{MWT_i}\right)}{\sum\left(\frac{PK_iAMT}{MWT_i}\right)}\times CLORTHO\right)=Avg.ORTHO.CLperBP$$

**(5)** Equation IV.A.2.c.(2)
*Calculation for ortho chlorines per biphenyl*

where $PK_iAMT$ is the congener peak concentration for DB-1 peaks 1 through 118, $MWT_i$ is the molecular weight of the congener peak from MOL_WT database, and CLORTHO is taken from the MOL_WT database for $PK_i$.

(3) place the calculated value for ortho-chlorines per biphenyl in the field **GE.ORTHO_CL**.

(4) calculate the meta-para-chlorination level using the following equation:

$$\sum\left(\frac{\left(\frac{PK_iAMT}{MWT_i}\right)}{\sum\left(\frac{PK_iAMT}{MWT_i}\right)}\times CL.MP\right)=Avg.MP.CLperBP$$

**(6)** Equation IV.A.2.c.(4)
*Calculation for meta-para chlorines per biphenyl*

where $PK_iAMT$ is the congener peak concentration for DB-1 peaks 1 through 118, $MWT_i$ is the molecular weight of the congener peak from MOL_WT database, and CL.MP is taken from the MOL_WT database for $PK_i$.

(5) place the calculated value for meta-para-chlorines per biphenyl in the field **GE.MP_CL**.

(6) Add together the values in the fields **GE.ORTHO_CL** and **GE.MP_CL**, and place the resulting value in the field **GE.TOT_CL**.

(7) Select the next record and repeat steps (2) through (7) until all the records have been recalculated.

B. close the GE database upon completion. Repeat for each media database until completed.

## V. QC check of the adjusted GE database

*QC evaluation of the databases will be the same procedure for each media (water column, sediment/porewater, and biota/fish). A copy of the original database will be used as a reference*

A. Electronic QC of 100% of the data - using the corrected databases.

1. Check the total PCB fields - For each record from first to last, select one record and proceed with the following steps:
   a. Confirm that the value in **GE.NEA_TOT** equals the value in **CP.PCB_CONC**.
      (1) if the values do not match, tabulate the record and continue to next step
      (2) if the values match, continue with next step
   b. Confirm that values in the field **GE.PCB_CAP** are greater than or equal to the detection limit value for the media
      (1) if the values do not match, tabulate the record and continue to next step
      (2) if the values match, continue with next step
   c. Confirm that the detection limit label in **GE.DL_CAP** correspond to values less than the media detection limit in **GE.NEA_TOT**.
      (1) if the labels and values do not correspond, tabulate the record and continue to next step
      (2) if the labels and values correspond, continue with next step

2. Check the calculation of the homolog distributions
   a. Weight percent values - sum the weight percents of the ten homolog groups (**GE.MONO_WT** through **GE.DECA_WT**)
      (1) if the result is greater than or less than 100% by 0.02%, tabulate the record and continue to next step
      (2) if the result equals 100% ± 0.02%, continue with next step
   b. Mole percent values - sum the mole percents of the ten homolog groups (**GE.MONO_ML** through **GE.DECA_ML**)
      (1) if the result is greater than or less than 100% by 0.02%, tabulate the record and continue to next step
      (2) if the result equals 100% ± 0.02%, continue with next step
3. Check the calculation of the average of ortho, meta, para, and total chlorines per biphenyl, for each record:
   a. sum the values for the ortho, and meta-para chlorines per biphenyl (**GE.ORTHO_CL** + **GE.MP_CL**)
   b. compare the resulting sum to the value in the field **GE.TOT_CL**
      (1) if the values match within 0.01, then the record passes this QC test; proceed with next record

(2) if the values do not match within 0.01, then the record fails
(a) write sample information and reason for failure to a temporary database for later evaluation
(b) proceed with next record

4. Upon completion of evaluation, close the GE database in use and proceed with next media database.

B. Review the electronic "fail" databases, identify the sources of error and implement corrections

C. Manual QC of 5% of the records. Records from the original database will be randomly selected, and extracted to a spreadsheet. Within the spreadsheet, the analytical bias corrections will be applied to the data. In addition to the review described in Section V.A., the following will be reviewed:

1. Recalculate the homolog distributions using the reference database MOL_WT and compare the results to the values in the homolog distribution fields of the revised database
   a. if the values match within 0.02%, then the record passes this QC test; proceed with the next step.
   b. if the values do not match within 0.02%, then the record fails
      (1) note the sample information and reason for failure for later evaluation
      (2) proceed with the next step.
2. Recalculate the chlorination levels using the reference database MOL_WT and compare the results to the values in the fields **ORTHO_CL**, **MP_CL** and **TOT_CL** in the revised database
   a. if the values match within 0.02 chlorines per biphenyl, then the record passes this QC test; proceed with the next step.
   b. if the values do not match within 0.02 chlorines per biphenyl, then the record fails
      (1) note the sample information and reason for failure for later evaluation
      (2) proceed with the next step.
3. Qualitatively assess the reasonableness of the homolog and chlorines per biphenyl calculations: The average total chlorines per biphenyl (**TOT_CL**) for a given sample should reasonably approximate the homolog group with the highest percentage of representation in the sample. For example, if **TOT_CL** equals 3.5, then the highest percentages in the homolog distribution should be between the tri-chlorinated and tetra-chlorinated groups (**TRI_WT**, **TETRA_WT**, **TRI_ML**, and **TETRA_ML**).
   a. if the value for TOT_CL reasonably approximates the homolog distribution, then the record passes this QC test; proceed with the next step.
   b. if the value for TOT_CL does not reasonably approximate the homolog distribution, then the record fails this QC test. Tabulate the record information for later evaluation.

D. Compile the information on the records which failed the QC tests, evaluate the data, and identify the source of error. Correct the computer program as necessary and proceed with Section IV of this algorithm. After all the records have passed the QC tests, proceed with Subsection V.E of this algorithm.

E. QC corrections - HydroQual

*Once OBG has completed the corrections and run through QC procedures, the database will be sent to HydroQual, where another round of independent QC procedures will be run. OBG will work with HydroQual to address any QC issues which arise resulting from their QC evaluation.*

## VI. Re-Merging of the databases

A. Water column data

1. Re-merge the database CP-W1 (adjusted and QC corrected) to CP-W2 (unadjusted data). The merged database will be called CPW

2. Re-merge the database GE-W1 (adjusted and QC corrected) to GE-W2 (unadjusted data). The merged database will be called GEW

B. Biota data

1. Re-merge the database CP-B1 (adjusted and QC corrected) to CP-B2 (unadjusted data). The merged database will be called CPB

2. Re-merge the database GE-B1 (adjusted and QC corrected) to GE-B2 (unadjusted data). The merged database will be called GEB

C. Sediment data

1. Re-merge the database CP-S1 (adjusted and QC corrected) to CP-S2 (unadjusted data). The merged database will be called CPS

2. Re-merge the database GE-S1 (adjusted and QC corrected) to GE-S2 (unadjusted data). The merged database will be called GES

D. Prior to database delivery, merge the separate media GE and CP databases together into one GE database and one CP database.

# Reference databases to implement database corrections

**Table D-1(a). Congener-specific information for calculating total micromoles, average molecular weight, and chlorines per biphenyl (reference database MOL_WT.DBF)**

| | Database Peak Label | DB-1 Peak Number | Congener BZ Number | Molecular Structure of PCB Congener | DB-1 Peak Molecular Weight | DB-1 Peak Chlorines per Biphenyl Total | Ortho | Meta-Para |
|---|---|---|---|---|---|---|---|---|
| *Fields:* | *PEAKLABL* | *PEAK_NO* | *BZ_NO* | *MOL_STRU* | *MWT* | *CL_TOT* | *CL_ORTHO* | *CL_MP* |
| | PK1_AMT | 1 | 0 | biphenyl | 154.20 | 0.000 | 0.000 | 0.000 |
| | PK2_AMT | 2 | 1 | 2 | 188.70 | 1.000 | 1.000 | 0.000 |
| | PK3_AMT | 3 | 2 | 3 | 188.70 | 1.000 | 0.000 | 1.000 |
| | PK4_AMT | 4 | 3 | 4 | 188.70 | 1.000 | 0.000 | 1.000 |
| | PK5_AMT | 5 | 4, 10 | 2 2'; 2 6 | 223.10 | 2.000 | 2.000 | 0.000 |
| | PK6_AMT | 6 | 7, 9 | 2 4; 2 5 | 223.10 | 2.000 | 1.000 | 1.000 |
| | PK7_AMT | 7 | 6 | 2 3' | 223.10 | 2.000 | 1.000 | 1.000 |
| | PK8_AMT | 8 | 5, 8 | 2 3; 2 4' | 223.10 | 2.000 | 1.000 | 1.000 |
| | PK9_AMT | 9 | 14 | 3 5 | 223.10 | 2.000 | 0.000 | 2.000 |
| | PK10_AMT | 10 | 19 | 2 2'6 | 257.50 | 3.000 | 3.000 | 0.000 |
| | PK11_AMT | 11 | 30 | 2 4 6 | 257.50 | 3.000 | 2.000 | 1.000 |
| | PK12_AMT | 12 | 11 | 3 3' | 223.10 | 2.000 | 0.000 | 2.000 |
| | PK13_AMT | 13 | 12, 13 | 3 4; 3 4' | 223.10 | 2.000 | 0.000 | 2.000 |
| | PK14_AMT | 14 | 15, 18 | 4 4'; 2 2'5 | 249.00 | 2.752 | 1.504 | 1.248 |
| | PK15_AMT | 15 | 17 | 2 2'4 | 257.50 | 3.000 | 2.000 | 1.000 |
| | PK16_AMT | 16 | 24, 27 | 2 3 6; 2 3'6 | 257.50 | 3.000 | 2.000 | 1.000 |
| | PK17_AMT | 17 | 16, 32 | 2 2'3; 2 4'6 | 257.50 | 3.000 | 2.000 | 1.000 |
| | PK18_AMT | 18 | 23 | 2 3 5 | 257.50 | 3.000 | 1.000 | 2.000 |
| | PK19_AMT | 19 | 34, 54 | 2'3 5'; 2 2'6 6' | 267.90 | 3.300 | 1.900 | 1.400 |
| | PK20_AMT | 20 | 29 | 2 4 5 | 257.50 | 3.000 | 1.000 | 2.000 |
| | PK21_AMT | 21 | 26 | 2 3'5 | 257.50 | 3.000 | 1.000 | 2.000 |
| | PK22_AMT | 22 | 25 | 2 3'4 | 257.50 | 3.000 | 1.000 | 2.000 |
| | PK23_AMT | 23 | 31 | 2 4'5 | 257.50 | 3.000 | 1.000 | 2.000 |
| | PK24_AMT | 24 | 28, 50 | 2 4 4'; 2 2'4 6 | 257.50 | 3.000 | 1.000 | 2.000 |
| | PK25_AMT | 25 | 21, 33, 53 | 2 3 4; 2'3 4'; 2 2'5 6' | 259.50 | 3.056 | 1.112 | 1.944 |
| | PK26_AMT | 26 | 22, 51 | 2 3 4'; 2 2'4 6' | 258.70 | 3.034 | 1.068 | 1.966 |
| | PK27_AMT | 27 | 45 | 2 2'3 6 | 292.00 | 4.000 | 3.000 | 1.000 |
| | PK28_AMT | 28 | 36 | 3 3'5 | 257.50 | 3.000 | 1.000 | 2.000 |
| | PK29_AMT | 29 | 46 | 2 2'3 6' | 292.00 | 4.000 | 3.000 | 1.000 |
| | PK30_AMT | 30 | 39 | 3 4'5 | 257.50 | 3.000 | 1.000 | 2.000 |

**Table D-1(a). Congener-specific information for calculating total micromoles, average molecular weight, and chlorines per biphenyl (reference database MOL_WT.DBF)**

| | Database Peak Label | DB-1 Peak Number | Congener BZ Number | Molecular Structure of PCB Congener | DB-1 Peak Molecular Weight | DB-1 Peak Chlorines per Biphenyl Total | Ortho | Meta-Para |
|---|---|---|---|---|---|---|---|---|
| *Fields:* | *PEAKLABL* | *PEAK_NO* | *BZ_NO* | *MOL_STRU* | *MWT* | *CL_TOT* | *CL_ORTHO* | *CL_MP* |
| | PK31_AMT | 31 | 52, 73 | 2 2'5 5'; 2 3'5'6 | 292.00 | 4.000 | 2.000 | 2.000 |
| | PK32_AMT | 32 | 49 | 2 2'4 5' | 292.00 | 4.000 | 2.000 | 2.000 |
| | PK33_AMT | 33 | 47 | 2 2'4 4' | 292.00 | 4.000 | 2.000 | 2.000 |
| | PK34_AMT | 34 | 48, 75 | 2 2'4 5; 2 4 4'6 | 292.00 | 4.000 | 2.000 | 2.000 |
| | PK35_AMT | 35 | 62, 65 | 2 3 4 6; 2 3 5 6 | 292.00 | 4.000 | 2.000 | 2.000 |
| | PK36_AMT | 36 | 35 | 3 3'4 | 257.50 | 3.000 | 0.000 | 3.000 |
| | PK37_AMT | 37 | 44, 104 | 2 2'3 5'; 2 2'4 6 6' | 292.00 | 4.000 | 2.000 | 2.000 |
| | PK38_AMT | 38 | 37, 42, 59 | 3 4 4'; 2 2'3 4'; 2 3 3'6 | 272.40 | 3.430 | 0.860 | 2.570 |
| | PK39_AMT | 39 | 64, 71 | 2 3 4'6; 2 3'4'6 | 292.00 | 4.000 | 2.000 | 2.000 |
| | PK40_AMT | 40 | 68 | 2 3'4 5' | 292.00 | 4.000 | 1.000 | 3.000 |
| | PK41_AMT | 41 | 96 | 2 2'3 6 6' | 326.40 | 5.000 | 4.000 | 1.000 |
| | PK42_AMT | 42 | 40 | 2 2'3 3' | 292.00 | 4.000 | 2.000 | 2.000 |
| | PK43_AMT | 43 | 57, 103 | 2 3 3'5; 2 2'4 5'6 | 298.90 | 4.200 | 1.400 | 2.800 |
| | PK44_AMT | 44 | 67, 100 | 2 3'4 5; 2 2'4 4'6 | 298.90 | 4.200 | 1.400 | 2.800 |
| | PK45_AMT | 45 | 58, 63 | 2 3 3'5'; 2 3 4'5 | 292.00 | 4.000 | 1.000 | 3.000 |
| | PK46_AMT | 46 | 74, 94 | 2 4 4'5; 2 2'3 5 6' | 292.00 | 4.000 | 1.000 | 3.000 |
| | PK47_AMT | 47 | 61, 70, 76 | 2 3 4 5; 2 3'4'5; 2'3 4 5 | 292.00 | 4.000 | 1.000 | 3.000 |
| | PK48_AMT | 48 | 66, 93, 95 | 2 3'4 4'; 2 2'3 5 6; 2 2'3 5'6 | 293.50 | 4.045 | 1.090 | 2.955 |
| | PK49_AMT | 49 | 55, 91, 98 | 2 3 3'4; 2 2'3 4'6; 2 2'3'4 6 | 324.70 | 4.950 | 2.900 | 2.050 |
| | PK50_AMT | 50 | 56, 60 | 2 3 3'4'; 2 3 4 4' | 292.00 | 4.000 | 1.000 | 3.000 |
| | PK51_AMT | 51 | 84, 92, 155 | 2 2'3 3'6; 2 2'3 5 5'; 2 2'4 4'6 6' | 326.40 | 5.000 | 3.000 | 2.000 |
| | PK52_AMT | 52 | 89 | 2 2'3 4 6' | 326.40 | 5.000 | 3.000 | 2.000 |
| | PK53_AMT | 53 | 90, 101 | 2 2'3 4'5; 2 2'4 5 5' | 326.40 | 5.000 | 2.000 | 3.000 |
| | PK54_AMT | 54 | 99 | 2 2'4 4'5 | 326.40 | 5.000 | 2.000 | 3.000 |
| | PK55_AMT | 55 | 112, 119, 150 | 2 3 3'5 6; 2 3'4 4'6; 2 2'3 4'6 6' | 326.40 | 5.000 | 2.000 | 3.000 |
| | PK56_AMT | 56 | 83, 109 | 2 2'3 3'5; 2 3 3'4 6 | 326.40 | 5.000 | 2.000 | 3.000 |
| | PK57_AMT | 57 | 86, 97, 152 | 2 2'3 4 5; 2 2'3'4 5; 2 2'3 5 6 6' | 326.40 | 5.000 | 2.000 | 3.000 |
| | PK58_AMT | 58 | 87, 111, 115 | 2 2'3 4 5'; 2 3 3'5 5'; 2 3 4 4'6 | 326.40 | 5.000 | 2.000 | 3.000 |
| | PK59_AMT | 59 | 85, 116 | 2 2'3 4 4'; 2 3 4 5 6 | 326.40 | 5.000 | 2.000 | 3.000 |
| | PK60_AMT | 60 | 136 | 2 2'3 3'6 6' | 360.90 | 6.000 | 4.000 | 2.000 |



310531

**Table D-1(a). Congener-specific information for calculating total micromoles, average molecular weight, and chlorines per biphenyl (reference database MOL_WT.DBF)**

| | Database Peak Label | DB-1 Peak Number | Congener BZ Number | Molecular Structure of PCB Congener | DB-1 Peak Molecular Weight | DB-1 Peak Chlorines per Biphenyl Total | Ortho | Meta-Para |
|---|---|---|---|---|---|---|---|---|
| *Fields:* | *PEAKLABL* | *PEAK_NO* | *BZ_NO* | *MOL_STRU* | *MWT* | *CL_TOT* | *CL_ORTHO* | *CL_MP* |
| | PK61_AMT | 61 | 77, 110 | 3 3'4 4'; 2 3 3'4'6 | 315.80 | 5.000 | 2.000 | 3.000 |
| | PK62_AMT | 62 | 154 | 2 2'4 4'5 6' | 360.90 | 6.000 | 3.000 | 3.000 |
| | PK63_AMT | 63 | 82 | 2 2'3 3'4 | 326.40 | 5.000 | 2.000 | 3.000 |
| | PK64_AMT | 64 | 151 | 2 2'3 5 5'6 | 360.90 | 6.000 | 3.000 | 3.000 |
| | PK65_AMT | 65 | 124, 135 | 2'3 4 5 5'; 2 2'3 3'5 6' | 350.50 | 5.700 | 2.400 | 3.300 |
| | PK66_AMT | 66 | 144 | 2 2'3 4 5'6 | 360.90 | 6.000 | 3.000 | 3.000 |
| | PK67_AMT | 67 | 107, 108, 147 | 2 3 3'4'5; 2 3 3'4 5'; 2 2'3 4'5 6 | 336.80 | 5.300 | 1.600 | 3.700 |
| | PK68_AMT | 68 | 123 | 2'3 4 4'5 | 326.40 | 5.000 | 1.000 | 4.000 |
| | PK69_AMT | 69 | 106, 118, 149 | 2 3 3'4 5; 2 3'4 4'5; 2 2'3 4'5'6 | 337.50 | 5.320 | 1.640 | 3.680 |
| | PK70_AMT | 70 | 139, 140 | 2 2'3 4 4'6; 2 2'3 4 4'6' | 360.90 | 6.000 | 3.000 | 3.000 |
| | PK71_AMT | 71 | 114, 134, 143 | 2 3 4 4'5; 2 2'3 3'5 6; 2 2'3 4 5 6' | 347.80 | 5.620 | 2.240 | 3.380 |
| | PK72_AMT | 72 | 122, 131, 133 | 2'3 3'4 5; 2 2'3 3'4 6; 2 2'3 3'5 5' | 336.80 | 5.300 | 1.600 | 3.700 |
| | PK73_AMT | 73 | 146, 161 | 2 2'3 4'5 5'; 2 3 3'4 5'6 | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK74_AMT | 74 | 105, 132 | 2 3 3'4 4'; 2 2'3 3'4 6' | 347.80 | 5.620 | 2.240 | 3.380 |
| | PK75_AMT | 75 | 153 | 2 2'4 4'5 5' | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK76_AMT | 76 | 168 | 2 3'4 4'5'6 | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK77_AMT | 77 | 141 | 2 2'3 4 5 5' | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK78_AMT | 78 | 179 | 2 2'3 3'5 6 6' | 395.30 | 7.000 | 4.000 | 3.000 |
| | PK79_AMT | 79 | 130 | 2 2'3 3'4 5' | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK80_AMT | 80 | 137 | 2 2'3 4 4'5 | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK81_AMT | 81 | 176 | 2 2'3 3'4 6 6' | 395.30 | 7.000 | 4.000 | 3.000 |
| | PK82_AMT | 82 | 138, 163 | 2 2'3 4 4'5'; 2 3 3'4'5 6 | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK83_AMT | 83 | 158 | 2 3 3'4 4'6 | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK84_AMT | 84 | 129 | 2 2'3 3'4 5 | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK85_AMT | 85 | 178 | 2 2'3 3'5 5'6 | 395.30 | 7.000 | 3.000 | 4.000 |
| | PK86_AMT | 86 | 166 | 2 3 4 4'5 6 | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK87_AMT | 87 | 175 | 2 2'3 3'4 5'6 | 395.30 | 7.000 | 3.000 | 4.000 |
| | PK88_AMT | 88 | 182, 187 | 2 2'3 4 4'5 6'; 2 2'3 4'5 5'6 | 395.30 | 7.000 | 3.000 | 4.000 |
| | PK89_AMT | 89 | 128 | 2 2'3 3'4 4' | 360.90 | 6.000 | 2.000 | 4.000 |
| | PK90_AMT | 90 | 183 | 2 2'3 4 4'5'6 | 395.30 | 7.000 | 3.000 | 4.000 |

310532

**Table D-1(a).** **Congener-specific information for calculating total micromoles, average molecular weight, and chlorines per biphenyl (reference database MOL_WT.DBF)**

| | Database Peak Label | DB-1 Peak Number | Congener BZ Number | Molecular Structure of PCB Congener | DB-1 Peak Molecular Weight | DB-1 Peak Chlorines per Biphenyl | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | Total | Ortho | Meta-Para |
| *Fields:* | *PEAKLABL* | *PEAK_NO* | *BZ_NO* | *MOL_STRU* | *MWT* | *CL_TOT* | *CL_ORTHO* | *CL_MP* |
| | PK91_AMT | 91 | 167 | 2 3'4 4'5 5' | 360.90 | 6.000 | 1.000 | 5.000 |
| | PK92_AMT | 92 | 185 | 2 2'3 4 5 5'6 | 394.30 | 7.000 | 3.000 | 4.000 |
| | PK93_AMT | 93 | 174, 181 | 2 2'3 3'4 5 6'; 2 2'3 4 4'5 6 | 394.30 | 7.000 | 3.000 | 4.000 |
| | PK94_AMT | 94 | 177 | 2 2'3 3'4'5 6 | 394.30 | 7.000 | 3.000 | 4.000 |
| | PK95_AMT | 95 | 156, 171 | 2 3 3'4 4'5; 2 2'3 3'4 4'6 | 382.20 | 6.620 | 2.240 | 4.380 |
| | PK96_AMT | 96 | 202 | 2 2'3 3'5 5'6 6' | 429.80 | 8.000 | 4.000 | 4.000 |
| | PK97_AMT | 97 | 157 | 2 3 3'4 4'5' | 360.90 | 6.000 | 1.000 | 5.000 |
| | PK98_AMT | 98 | 173 | 2 2'3 3'4 5 6 | 395.30 | 7.000 | 3.000 | 4.000 |
| | PK99_AMT | 99 | 200, 204 | 2 2'3 3'4 5 6 6'; 2 2'3 4 4'5 6 6' | 429.80 | 8.000 | 4.000 | 4.000 |
| | PK100AMT | 100 | 172, 192 | 2 2'3 3'4 5 5'; 2 3 3'4 5 5'6 | 395.30 | 7.000 | 2.000 | 5.000 |
| | PK101AMT | 101 | 197 | 2 2'3 3'4 4'6 6' | 429.80 | 8.000 | 4.000 | 4.000 |
| | PK102AMT | 102 | 180 | 2 2'3 4 4'5 5' | 395.30 | 7.000 | 2.000 | 5.000 |
| | PK103AMT | 103 | 193 | 2 3 3'4'5 5'6 | 395.30 | 7.000 | 2.000 | 5.000 |
| | PK104AMT | 104 | 191 | 2 3 3'4 4'5'6 | 395.30 | 7.000 | 2.000 | 5.000 |
| | PK105AMT | 105 | 199 | 2 2'3 3'4 5 5'6' | 429.80 | 8.000 | 4.000 | 4.000 |
| | PK106AMT | 106 | 170 | 2 2'3 3'4 4'5 | 395.30 | 7.000 | 2.000 | 5.000 |
| | PK107AMT | 107 | 190 | 2 3 3'4 4'5 6 | 395.30 | 7.000 | 2.000 | 5.000 |
| | PK108AMT | 108 | 198 | 2 2'3 3'4 5 5'6 | 429.80 | 8.000 | 3.000 | 5.000 |
| | PK109AMT | 109 | 201 | 2 2'3 3'4 5'6 6' | 429.80 | 8.000 | 3.000 | 5.000 |
| | PK110AMT | 110 | 196, 203 | 2 2'3 3'4 4'5 6'; 2 2'3 4 4'5 5'6 | 429.80 | 8.000 | 3.000 | 5.000 |
| | PK111AMT | 111 | 189 | 2 3 3'4 4'5 5' | 395.30 | 7.000 | 1.000 | 6.000 |
| | PK112AMT | 112 | 195 | 2 2'3 3'4 4'5 6 | 429.80 | 8.000 | 3.000 | 5.000 |
| | PK113AMT | 113 | 208 | 2 2'3 3'4 5 5'6 6' | 464.20 | 9.000 | 4.000 | 5.000 |
| | PK114AMT | 114 | 207 | 2 2'3 3'4 4'5 6 6' | 464.20 | 9.000 | 4.000 | 5.000 |
| | PK115AMT | 115 | 194 | 2 2'3 3'4 4'5 5' | 429.80 | 8.000 | 2.000 | 6.000 |
| | PK116AMT | 116 | 205 | 2 3 3'4 4'5 5'6 | 429.80 | 8.000 | 2.000 | 6.000 |
| | PK117AMT | 117 | 206 | 2 2'3 3'4 4'5 5'6 | 464.20 | 9.000 | 3.000 | 6.000 |
| | PK118AMT | 118 | 209 | 2 2'3 3'4 4'5 5'6 6' | 498.60 | 10.000 | 4.000 | 6.000 |

*Sources:* Northeast Analytical, Inc.
HydroQual, Inc.

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**Table D-1(b). Congener-specific information for calculating homolog distributions (reference database MOL_WT.DBF)**

| | Database Peak Label | DB-1 Peak Number | Congener BZ Number | DB-1 Peak Homolog Group Distribution: Mono | Di | Tri | Tetra | Penta | Hexa | Hepta | Octa | Nona | Deca |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Fields:* | *PEAKLABL* | *PEAK_NO* | *BZ_NO* | *MONO* | *DI* | *TRI* | *TETRA* | *PENTA* | *HEXA* | *HEPTA* | *OCTA* | *NONA* | *DECA* |
| | PK1_AMT | 1 | 0 | | | | | | | | | | |
| | PK2_AMT | 2 | 1 | 1.000 | | | | | | | | | |
| | PK3_AMT | 3 | 2 | 1.000 | | | | | | | | | |
| | PK4_AMT | 4 | 3 | 1.000 | | | | | | | | | |
| | PK5_AMT | 5 | 4, 10 | | 1.000 | | | | | | | | |
| | PK6_AMT | 6 | 7, 9 | | 1.000 | | | | | | | | |
| | PK7_AMT | 7 | 6 | | 1.000 | | | | | | | | |
| | PK8_AMT | 8 | 5, 8 | | 1.000 | | | | | | | | |
| | PK9_AMT | 9 | 14 | | 1.000 | | | | | | | | |
| | PK10_AMT | 10 | 19 | | | 1.000 | | | | | | | |
| | PK11_AMT | 11 | 30 | | | 1.000 | | | | | | | |
| | PK12_AMT | 12 | 11 | | 1.000 | | | | | | | | |
| | PK13_AMT | 13 | 12, 13 | | 1.000 | | | | | | | | |
| | PK14_AMT | 14 | 15, 18 | | 0.248 | 0.752 | | | | | | | |
| | PK15_AMT | 15 | 17 | | | 1.000 | | | | | | | |
| | PK16_AMT | 16 | 24, 27 | | | 1.000 | | | | | | | |
| | PK17_AMT | 17 | 16, 32 | | | 1.000 | | | | | | | |
| | PK18_AMT | 18 | 23 | | | 1.000 | | | | | | | |
| | PK19_AMT | 19 | 34, 54 | | | 0.700 | 0.300 | | | | | | |
| | PK20_AMT | 20 | 29 | | | 1.000 | | | | | | | |
| | PK21_AMT | 21 | 26 | | | 1.000 | | | | | | | |
| | PK22_AMT | 22 | 25 | | | 1.000 | | | | | | | |
| | PK23_AMT | 23 | 31 | | | 1.000 | | | | | | | |
| | PK24_AMT | 24 | 28, 50 | | | 1.000 | | | | | | | |
| | PK25_AMT | 25 | 21, 33, 53 | | | 0.944 | 0.056 | | | | | | |
| | PK26_AMT | 26 | 22, 51 | | | 0.966 | 0.034 | | | | | | |
| | PK27_AMT | 27 | 45 | | | | 1.000 | | | | | | |
| | PK28_AMT | 28 | 36 | | | 1.000 | | | | | | | |
| | PK29_AMT | 29 | 46 | | | | 1.000 | | | | | | |
| | PK30_AMT | 30 | 39 | | | 1.000 | | | | | | | |

**Table D-1(b). Congener-specific information for calculating homolog distributions (reference database MOL_WT.DBF)**

| | Database Peak Label | DB-1 Peak Number | Congener BZ Number | DB-1 Peak Homolog Group Distribution | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Mono | Di | Tri | Tetra | Penta | Hexa | Hepta | Octa | Nona | Deca |
| *Fields:* | *PEAKLABL* | *PEAK_NO* | *BZ_NO* | *MONO* | *DI* | *TRI* | *TETRA* | *PENTA* | *HEXA* | *HEPTA* | *OCTA* | *NONA* | *DECA* |
| | PK31_AMT | 31 | 52, 73 | | | | 1.000 | | | | | | |
| | PK32_AMT | 32 | 49 | | | | 1.000 | | | | | | |
| | PK33_AMT | 33 | 47 | | | | 1.000 | | | | | | |
| | PK34_AMT | 34 | 48, 75 | | | | 1.000 | | | | | | |
| | PK35_AMT | 35 | 62, 65 | | | | 1.000 | | | | | | |
| | PK36_AMT | 36 | 35 | | | 1.000 | | | | | | | |
| | PK37_AMT | 37 | 44, 104 | | | | 1.000 | | | | | | |
| | PK38_AMT | 38 | 37, 42, 59 | | | 0.570 | 0.430 | | | | | | |
| | PK39_AMT | 39 | 64, 71 | | | | 1.000 | | | | | | |
| | PK40_AMT | 40 | 68 | | | | 1.000 | | | | | | |
| | PK41_AMT | 41 | 96 | | | | | 1.000 | | | | | |
| | PK42_AMT | 42 | 40 | | | | 1.000 | | | | | | |
| | PK43_AMT | 43 | 57, 103 | | | | 0.800 | 0.200 | | | | | |
| | PK44_AMT | 44 | 67, 100 | | | | 0.800 | 0.200 | | | | | |
| | PK45_AMT | 45 | 58, 63 | | | | 1.000 | | | | | | |
| | PK46_AMT | 46 | 74, 94 | | | | 1.000 | | | | | | |
| | PK47_AMT | 47 | 61, 70, 76 | | | | 1.000 | | | | | | |
| | PK48_AMT | 48 | 66, 93, 95 | | | | 0.955 | 0.045 | | | | | |
| | PK49_AMT | 49 | 55, 91, 98 | | | | 0.050 | 0.950 | | | | | |
| | PK50_AMT | 50 | 56, 60 | | | | 1.000 | | | | | | |
| | PK51_AMT | 51 | 84, 92, 155 | | | | | 1.000 | | | | | |
| | PK52_AMT | 52 | 89 | | | | | 1.000 | | | | | |
| | PK53_AMT | 53 | 90, 101 | | | | | 1.000 | | | | | |
| | PK54_AMT | 54 | 99 | | | | | 1.000 | | | | | |
| | PK55_AMT | 55 | 112, 119, 150 | | | | | 1.000 | | | | | |
| | PK56_AMT | 56 | 83, 109 | | | | | 1.000 | | | | | |
| | PK57_AMT | 57 | 86, 97, 152 | | | | | 1.000 | | | | | |
| | PK58_AMT | 58 | 87, 111, 115 | | | | | 1.000 | | | | | |
| | PK59_AMT | 59 | 85, 116 | | | | | 1.000 | | | | | |
| | PK60_AMT | 60 | 136 | | | | | | 1.000 | | | | |

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**Table D-1(b). Congener-specific information for calculating homolog distributions (reference database MOL_WT.DBF)**

| | Database Peak Label | DB-1 Peak Number | Congener BZ Number | DB-1 Peak Homolog Group Distribution | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Mono | Di | Tri | Tetra | Penta | Hexa | Hepta | Octa | Nona | Deca |
| *Fields:* | *PEAKLABL* | *PEAK_NO* | *BZ_NO* | *MONO* | *DI* | *TRI* | *TETRA* | *PENTA* | *HEXA* | *HEPTA* | *OCTA* | *NONA* | *DECA* |
| | PK61_AMT | 61 | 77, 110 | | | | | 1.000 | | | | | |
| | PK62_AMT | 62 | 154 | | | | | | 1.000 | | | | |
| | PK63_AMT | 63 | 82 | | | | | 1.000 | | | | | |
| | PK64_AMT | 64 | 151 | | | | | | 1.000 | | | | |
| | PK65_AMT | 65 | 124, 135 | | | | | 0.300 | 0.700 | | | | |
| | PK66_AMT | 66 | 144 | | | | | | 1.000 | | | | |
| | PK67_AMT | 67 | 107, 108, 147 | | | | | 0.700 | 0.300 | | | | |
| | PK68_AMT | 68 | 123 | | | | | 1.000 | | | | | |
| | PK69_AMT | 69 | 106, 118, 149 | | | | | 0.680 | 0.320 | | | | |
| | PK70_AMT | 70 | 139, 140 | | | | | | 1.000 | | | | |
| | PK71_AMT | 71 | 114, 134, 143 | | | | | 0.380 | 0.620 | | | | |
| | PK72_AMT | 72 | 122, 131, 133 | | | | | 0.700 | 0.300 | | | | |
| | PK73_AMT | 73 | 146, 161 | | | | | | 1.000 | | | | |
| | PK74_AMT | 74 | 105, 132 | | | | | 0.380 | 0.620 | | | | |
| | PK75_AMT | 75 | 153 | | | | | | 1.000 | | | | |
| | PK76_AMT | 76 | 168 | | | | | | 1.000 | | | | |
| | PK77_AMT | 77 | 141 | | | | | | 1.000 | | | | |
| | PK78_AMT | 78 | 179 | | | | | | | 1.000 | | | |
| | PK79_AMT | 79 | 130 | | | | | | 1.000 | | | | |
| | PK80_AMT | 80 | 137 | | | | | | 1.000 | | | | |
| | PK81_AMT | 81 | 176 | | | | | | | 1.000 | | | |
| | PK82_AMT | 82 | 138, 163 | | | | | | 1.000 | | | | |
| | PK83_AMT | 83 | 158 | | | | | | 1.000 | | | | |
| | PK84_AMT | 84 | 129 | | | | | | 1.000 | | | | |
| | PK85_AMT | 85 | 178 | | | | | | | 1.000 | | | |
| | PK86_AMT | 86 | 166 | | | | | | 1.000 | | | | |
| | PK87_AMT | 87 | 175 | | | | | | | 1.000 | | | |
| | PK88_AMT | 88 | 182, 187 | | | | | | | 1.000 | | | |
| | PK89_AMT | 89 | 128 | | | | | | 1.000 | | | | |
| | PK90_AMT | 90 | 183 | | | | | | | 1.000 | | | |

**Table D-1(b). Congener-specific information for calculating homolog distributions (reference database MOL_WT.DBF)**

| | Database Peak Label | DB-1 Peak Number | Congener BZ Number | DB-1 Peak Homolog Group Distribution | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | Mono | Di | Tri | Tetra | Penta | Hexa | Hepta | Octa | Nona | Deca |
| *Fields:* | *PEAKLABL* | *PEAK_NO* | *BZ_NO* | *MONO* | *DI* | *TRI* | *TETRA* | *PENTA* | *HEXA* | *HEPTA* | *OCTA* | *NONA* | *DECA* |
| | PK91_AMT | 91 | 167 | | | | | | 1.000 | | | | |
| | PK92_AMT | 92 | 185 | | | | | | | 1.000 | | | |
| | PK93_AMT | 93 | 174, 181 | | | | | | | 1.000 | | | |
| | PK94_AMT | 94 | 177 | | | | | | | 1.000 | | | |
| | PK95_AMT | 95 | 156, 171 | | | | | | 0.380 | 0.620 | | | |
| | PK96_AMT | 96 | 202 | | | | | | | | 1.000 | | |
| | PK97_AMT | 97 | 157 | | | | | | 1.000 | | | | |
| | PK98_AMT | 98 | 173 | | | | | | | 1.000 | | | |
| | PK99_AMT | 99 | 200, 204 | | | | | | | | 1.000 | | |
| | PK100AMT | 100 | 172, 192 | | | | | | | 1.000 | | | |
| | PK101AMT | 101 | 197 | | | | | | | | 1.000 | | |
| | PK102AMT | 102 | 180 | | | | | | | 1.000 | | | |
| | PK103AMT | 103 | 193 | | | | | | | 1.000 | | | |
| | PK104AMT | 104 | 191 | | | | | | | 1.000 | | | |
| | PK105AMT | 105 | 199 | | | | | | | | 1.000 | | |
| | PK106AMT | 106 | 170 | | | | | | | 1.000 | | | |
| | PK107AMT | 107 | 190 | | | | | | | 1.000 | | | |
| | PK108AMT | 108 | 198 | | | | | | | | 1.000 | | |
| | PK109AMT | 109 | 201 | | | | | | | | 1.000 | | |
| | PK110AMT | 110 | 196, 203 | | | | | | | | 1.000 | | |
| | PK111AMT | 111 | 189 | | | | | | | 1.000 | | | |
| | PK112AMT | 112 | 195 | | | | | | | | 1.000 | | |
| | PK113AMT | 113 | 208 | | | | | | | | | 1.000 | |
| | PK114AMT | 114 | 207 | | | | | | | | | 1.000 | |
| | PK115AMT | 115 | 194 | | | | | | | | 1.000 | | |
| | PK116AMT | 116 | 205 | | | | | | | | 1.000 | | |
| | PK117AMT | 117 | 206 | | | | | | | | | 1.000 | |
| | PK118AMT | 118 | 209 | | | | | | | | | | 1.000 |

*Sources:* Northeast Analytical, Inc.
HydroQual, Inc.

310537

**Table D-2. C18 column confirmation data (reference database C18_DATA.DBF).**

| Laboratory | Approx. | Date | Core Depth | | C18 Data (ppm) | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Sample ID | River Mile | Collected | Start | End | BZ4_AMT | BZ10_AMT | BZ5_AMT | BZ8_AMT | BZ18_AMT | BZ15_AMT |
| 911718F | 194.00 | 07/11/91 | 0.00 | 5.00 | 0.79 | 0.10 | 0.01 | 0.78 | 0.76 | 0.48 |
| 911719F | 194.00 | 07/11/91 | 5.00 | 10.00 | 0.82 | 0.09 | 0.01 | 0.83 | 0.72 | 0.49 |
| 911720F | 194.00 | 07/11/91 | 10.00 | 25.00 | 1.63 | 0.14 | 0.01 | 1.42 | 0.96 | 0.53 |
| 911778F | 194.00 | 07/15/91 | 0.00 | 5.00 | 24.80 | 4.12 | 0.01 | 1.95 | 0.88 | 0.95 |
| 911779F | 194.00 | 07/15/91 | 5.00 | 10.00 | 23.87 | 4.14 | 0.01 | 2.44 | 0.80 | 1.15 |
| 911780F | 194.00 | 07/15/91 | 10.00 | 25.00 | 16.63 | 2.98 | 0.00 | 3.04 | 0.55 | 0.94 |
| 911943F | 193.00 | 07/16/91 | 0.00 | 5.00 | 0.32 | 0.04 | 0.00 | 0.22 | 0.10 | 0.16 |
| 911944F | 193.00 | 07/16/91 | 5.00 | 10.00 | 0.11 | 0.02 | 0.00 | 0.10 | 0.03 | 0.07 |
| 911945F | 193.00 | 07/16/91 | 10.00 | 25.00 | 0.11 | 0.01 | 0.00 | 0.02 | 0.01 | 0.00 |
| 911924F | 193.00 | 07/17/91 | 0.00 | 5.00 | 1.39 | 0.32 | 0.00 | 0.54 | 0.25 | 0.53 |
| 911925F | 193.00 | 07/17/91 | 5.00 | 10.00 | 4.07 | 0.81 | 0.00 | 1.13 | 0.41 | 0.85 |
| 911926F | 193.00 | 07/17/91 | 10.00 | 25.00 | 30.92 | 4.95 | 0.01 | 4.61 | 0.95 | 1.63 |
| 912182F | 193.00 | 07/24/91 | 0.00 | 5.00 | 1.44 | 0.23 | 0.01 | 1.03 | 0.60 | 0.50 |
| 912333F | 193.00 | 07/26/91 | 0.00 | 5.00 | 2.24 | 0.52 | 0.00 | 1.61 | 0.49 | 0.86 |
| 912334F | 193.00 | 07/26/91 | 5.00 | 10.00 | 15.06 | 2.62 | 0.01 | 4.08 | 1.05 | 1.65 |
| 912335F | 193.00 | 07/26/91 | 10.00 | 25.00 | 54.34 | 8.56 | 0.02 | 8.53 | 1.83 | 2.93 |
| 912491F | 192.00 | 07/30/91 | 0.00 | 5.00 | 4.54 | 0.73 | 0.00 | 1.33 | 0.47 | 0.72 |
| 912492F | 192.00 | 07/30/91 | 5.00 | 10.00 | 15.29 | 2.44 | 0.01 | 2.17 | 0.71 | 1.08 |
| 912493F | 192.00 | 07/30/91 | 10.00 | 25.00 | 10.70 | 1.69 | 0.01 | 2.41 | 0.68 | 0.98 |
| 912676F | 192.00 | 07/31/91 | 0.00 | 5.00 | 2.10 | 0.32 | 0.00 | 1.99 | 0.38 | 1.00 |
| 912804F | 192.00 | 08/02/91 | 0.00 | 5.00 | 10.44 | 1.94 | 0.01 | 3.94 | 1.34 | 2.07 |
| 912805F | 192.00 | 08/02/91 | 5.00 | 10.00 | 27.09 | 4.39 | 0.02 | 6.59 | 1.59 | 2.62 |
| 912806F | 192.00 | 08/02/91 | 10.00 | 25.00 | 59.69 | 9.45 | 0.01 | 10.72 | 3.51 | 4.85 |
| 913273F | 191.00 | 08/07/91 | 0.00 | 5.00 | 40.55 | 5.97 | 0.01 | 5.65 | 1.23 | 1.68 |
| 913393F | 193.00 | 08/12/91 | 0.00 | 5.00 | 1.94 | 0.21 | 0.01 | 1.68 | 0.84 | 0.54 |
| 913680F | 191.00 | 08/15/91 | 0.00 | 5.00 | 0.99 | 0.15 | 0.00 | 0.98 | 0.35 | 0.40 |
| 913850F | 190.00 | 08/16/91 | 0.00 | 5.00 | 2.96 | 0.44 | 0.00 | 1.57 | 0.45 | 0.85 |
| 914118F | 190.00 | 08/21/91 | 0.00 | 5.00 | 9.95 | 1.61 | 0.01 | 3.74 | 0.98 | 1.78 |
| 914119F | 190.00 | 08/21/91 | 5.00 | 10.00 | 53.39 | 8.28 | 0.02 | 8.88 | 2.36 | 3.01 |
| 914120F | 190.00 | 08/21/91 | 10.00 | 25.00 | 103.23 | 14.45 | 0.03 | 18.71 | 3.18 | 3.48 |
| 914545F | 189.00 | 08/27/91 | 0.00 | 5.00 | 1.22 | 0.29 | 0.00 | 0.60 | 0.26 | 0.38 |
| 914546F | 189.00 | 08/27/91 | 5.00 | 10.00 | 13.85 | 2.16 | 0.01 | 3.27 | 0.94 | 1.31 |
| 914547F | 189.00 | 08/27/91 | 10.00 | 25.00 | 61.28 | 8.60 | 0.01 | 7.96 | 1.64 | 1.86 |
| 914559F | 189.00 | 08/28/91 | 0.00 | 5.00 | 4.78 | 0.79 | 0.00 | 1.58 | 0.60 | 0.87 |

**Table D-2. C18 column confirmation data (reference database C18_DATA.DBF).**

| Laboratory | Approx. | Date | Core Depth | | C18 Data (ppm) | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Sample ID | River Mile | Collected | Start | End | BZ4_AMT | BZ10_AMT | BZ5_AMT | BZ8_AMT | BZ18_AMT | BZ15_AMT |
| 914758F | 189.00 | 08/29/91 | 0.00 | 5.00 | 0.19 | 0.03 | 0.00 | 0.12 | 0.06 | 0.05 |
| 914812F | 189.00 | 08/30/91 | 0.00 | 5.00 | 3.63 | 0.51 | 0.00 | 1.93 | 0.69 | 1.02 |
| 950274F | 191.40 | 01/18/95 | | | 0.00 | 0.00 | 0.44 | 2.13 | 4.18 | 0.00 |
| 953879F | 192.40 | 05/11/95 | | | 0.00 | 0.00 | 0.38 | 1.30 | 3.00 | 0.00 |
| 955225F | 193.40 | 06/22/95 | | | 0.00 | 0.00 | 0.55 | 2.24 | 4.30 | 0.00 |
| 957979F | 194.40 | 10/03/95 | | | 0.95 | 0.46 | 0.37 | 1.31 | 5.27 | 0.00 |
| 9603897 | 196.90 | 07/17/96 | | | 20.70 | 1.76 | 1.86 | 46.70 | 78.70 | 6.46 |
| 9604293 | 196.90 | 08/07/96 | | | 1.93 | 1.10 | 0.44 | 2.74 | 5.61 | 0.00 |
| 9604954 | 196.90 | 09/10/96 | | | 20.40 | 1.44 | 1.02 | 38.10 | 105.50 | 19.10 |
| 9604179 | 194.40 | 07/31/96 | | | 0.00 | 0.00 | 0.00 | 0.36 | 2.07 | 0.00 |
| 961008F | 189.00 | 03/06/96 | | | 19.40 | 4.64 | 0.47 | 3.77 | 3.46 | 0.00 |
| 9601648 | 189.00 | 04/24/96 | | | 15.80 | 4.22 | 0.64 | 2.58 | 2.56 | 0.00 |
| 9603292 | 189.00 | 06/26/96 | | | 48.30 | 13.40 | 0.50 | 5.69 | 5.05 | 0.00 |
| 9603892 | 189.00 | 07/17/96 | | | 27.20 | 8.16 | 0.33 | 2.93 | 1.79 | 0.00 |
| 9605127 | 189.00 | 09/18/96 | | | 20.50 | 6.84 | 0.51 | 2.23 | 2.24 | 0.00 |
| 9605321 | 189.00 | 09/25/96 | | | 24.30 | 6.28 | 0.31 | 1.70 | 0.95 | 0.00 |
| 9605611 | 189.00 | 10/16/96 | | | 23.30 | 7.62 | 0.25 | 1.68 | 0.94 | 0.00 |
| 9605873 | 189.00 | 10/29/96 | | | 40.90 | 11.50 | 0.49 | 4.60 | 2.85 | 0.00 |
| 911287F | 194.40 | 06/07/91 | | | 6.02 | 1.20 | 0.71 | 2.26 | 2.17 | 0.00 |
| 911289F | 189.00 | 06/07/91 | | | 23.94 | 3.51 | 0.87 | 3.84 | 4.39 | 0.00 |
| 911682F | 194.40 | 07/11/91 | | | 5.33 | 1.20 | 1.06 | 3.85 | 5.16 | 0.00 |
| 911684F | 189.00 | 07/11/91 | | | 27.27 | 6.76 | 0.86 | 4.46 | 6.30 | 0.00 |
| 912162F | 194.40 | 07/25/91 | | | 5.65 | 1.16 | 0.93 | 2.11 | 3.46 | 0.00 |
| 912164F | 189.00 | 07/25/91 | | | 23.37 | 6.31 | 1.14 | 3.82 | 7.62 | 0.00 |
| 922022F | 194.40 | 06/04/92 | | | 4.29 | 0.78 | 0.64 | 3.62 | 5.54 | 0.00 |
| 922015F | 189.00 | 06/04/92 | | | 26.51 | 5.13 | 1.47 | 5.35 | 5.73 | 0.00 |
| 923464F | 194.40 | 08/19/92 | | | 35.43 | 2.97 | 1.11 | 34.31 | 34.29 | 6.88 |
| 923469F | 189.00 | 08/19/92 | | | 75.48 | 11.14 | 1.24 | 49.10 | 50.51 | 12.26 |
| 924687F | 194.40 | 10/15/92 | | | 5.95 | 1.66 | 0.79 | 6.03 | 8.24 | 0.00 |
| 924691F | 189.00 | 10/15/92 | | | 44.04 | 8.58 | 1.06 | 8.86 | 12.31 | 0.00 |
| 935526F | 194.40 | 09/29/93 | | | 0.00 | 0.00 | 0.56 | 2.32 | 3.82 | 0.00 |
| 935527F | 189.00 | 09/29/93 | | | 37.00 | 9.26 | 0.90 | 5.01 | 4.54 | 0.00 |
| 944734F | 194.40 | 08/24/94 | | | 0.00 | 0.00 | 0.00 | 0.00 | 2.34 | 0.00 |
| 944736F | 189.00 | 08/24/94 | | | 7.44 | 2.20 | 0.55 | 4.79 | 7.60 | 0.00 |

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Table D-2. C18 column confirmation data (reference database C18_DATA.DBF).

| Laboratory Sample ID | Approx. River Mile | Date Collected | Core Depth Start | Core Depth End | C18 Data (ppm) BZ4_AMT | BZ10_AMT | BZ5_AMT | BZ8_AMT | BZ18_AMT | BZ15_AMT |
|---|---|---|---|---|---|---|---|---|---|---|
| 945544F | 194.40 | 09/07/94 | | | 0.00 | 0.00 | 0.49 | 2.65 | 5.91 | 0.00 |
| 945547F | 189.00 | 09/07/94 | | | 12.46 | 2.61 | 0.76 | 9.35 | 16.60 | 4.07 |
| 954536F | 194.40 | 06/07/95 | | | 3.60 | 1.43 | 0.45 | 1.69 | 4.70 | 0.00 |
| 954537F | 189.00 | 06/07/95 | | | 52.40 | 12.87 | 0.46 | 5.29 | 7.08 | 0.00 |
| 957192F | 194.40 | 08/31/95 | | | 0.00 | 0.00 | 0.37 | 1.62 | 1.71 | 0.00 |
| 957193F | 189.00 | 08/31/95 | | | 29.21 | 8.32 | 0.49 | 3.17 | 5.37 | 0.00 |

*Source: HydroQual (1997)*

310540

Table D-3. Sediment and porewater records analyzed using Green Bay mixed Aroclor standard only (reference database GBS_ONLY.DBF).

| Database ID | Laboratory Sample ID | Approx. River Mile | Date Collected | Core Depth Start | Core Depth End | Sample Description | Total PCBs (ppm) |
|---|---|---|---|---|---|---|---|
| 1 | 911718 | 194.00 | 07/11/91 | 0.0 | 5.0 | 8A-C1-(0-5) | 16.11 |
| 2 | 911719 | 194.00 | 07/11/91 | 5.0 | 10.0 | 8A-C1-(5-10) | 15.35 |
| 3 | 911720 | 194.00 | 07/11/91 | 10.0 | 25.0 | 8A-C1-(10-25) | 15.16 |
| 7 | 911709 | 194.00 | 07/12/91 | 0.0 | 5.0 | 8A-C2-(0-5) | 15.61 |
| 8 | 911710 | 194.00 | 07/12/91 | 5.0 | 10.0 | 8A-C2-(5-10) | 28.08 |
| 9 | 911711 | 194.00 | 07/12/91 | 10.0 | 25.0 | 8A-C2-(10-25) | 13.86 |
| 13 | 911714 | 194.00 | 07/12/91 | 0.0 | 0.0 | 8A-C2-GRAB | 12.38 |
| 14 | 911778 | 194.00 | 07/15/91 | 0.0 | 5.0 | 8A-F1-(0-5) | 45.41 |
| 15 | 911779 | 194.00 | 07/15/91 | 5.0 | 10.0 | 8A-F1-(5-10) | 49.85 |
| 16 | 911780 | 194.00 | 07/15/91 | 10.0 | 25.0 | 8A-F1-(10-25) | 35.11 |
| 20 | 911787 | 194.00 | 07/16/91 | 0.0 | 5.0 | 8A-F2-(0-5) | 20.49 |
| 21 | 911788 | 194.00 | 07/16/91 | 5.0 | 10.0 | 8A-F2-(5-10) | 16.86 |
| 22 | 911789 | 194.00 | 07/16/91 | 10.0 | 25.0 | 8A-F2-(10-25) | 15.54 |
| 38 | 911943 | 193.00 | 07/16/91 | 0.0 | 5.0 | 8B-C1-(0-5) | 2.61 |
| 39 | 911944 | 193.00 | 07/16/91 | 5.0 | 10.0 | 8B-C1-(5-10) | 0.98 |
| 40 | 911945 | 193.00 | 07/16/91 | 10.0 | 25.0 | 8B-C1-(10-25) | 0.31 |
| 26 | 911871 | 193.00 | 07/17/91 | 0.0 | 5.0 | 8B-F1-(0-5) | 6.51 |
| 27 | 911872 | 193.00 | 07/17/91 | 5.0 | 10.0 | 8B-F1-(5-10) | 8.17 |
| 28 | 911873 | 193.00 | 07/17/91 | 10.0 | 25.0 | 8B-F1-(10-25) | 1.88 |
| 32 | 911937 | 193.00 | 07/17/91 | 0.0 | 5.0 | 8B-F2-(0-5) | 6.81 |
| 33 | 911938 | 193.00 | 07/17/91 | 5.0 | 10.0 | 8B-F2-(5-10) | 21.35 |
| 34 | 911939 | 193.00 | 07/17/91 | 10.0 | 25.0 | 8B-F2-(10-25) | 7.55 |
| 42 | 911924 | 193.00 | 07/17/91 | 0.0 | 5.0 | 8B-F3-(0-5) | 8.01 |
| 43 | 911925 | 193.00 | 07/17/91 | 5.0 | 10.0 | 8B-F3-(5-10) | 14.07 |
| 44 | 911926 | 193.00 | 07/17/91 | 10.0 | 25.0 | 8B-F3-(10-25) | 65.38 |
| 48 | 912060 | 193.00 | 07/18/91 | 0.0 | 5.0 | 8B-F4-(0-5) | 9.43 |
| 49 | 912061 | 193.00 | 07/18/91 | 5.0 | 10.0 | 8B-F4-(5-10) | 12.43 |
| 50 | 912062 | 193.00 | 07/18/91 | 10.0 | 25.0 | 8B-F4-(10-25) | 12.79 |
| 54 | 912182 | 193.00 | 07/24/91 | 0.0 | 5.0 | 8B-F5-(0-5) | 9.72 |
| 55 | 912183 | 193.00 | 07/24/91 | 5.0 | 10.0 | 8B-F5-(5-10) | 16.58 |
| 56 | 912184 | 193.00 | 07/24/91 | 10.0 | 25.0 | 8B-F5-(10-25) | 17.33 |
| 60 | 912231 | 193.00 | 07/25/91 | 0.0 | 5.0 | 8B-F6-(0-5) | 9.87 |
| 61 | 912232 | 193.00 | 07/25/91 | 5.0 | 10.0 | 8B-F6-(5-10) | 24.70 |
| 62 | 912233 | 193.00 | 07/25/91 | 10.0 | 25.0 | 8B-F6-(10-25) | 31.15 |
| 66 | 912239 | 193.00 | 07/25/91 | 0.0 | 5.0 | 8B-C2-(0-5) | 3.59 |
| 67 | 912240 | 193.00 | 07/25/91 | 5.0 | 10.0 | 8B-C2-(5-10) | 2.81 |
| 68 | 912241 | 193.00 | 07/25/91 | 10.0 | 25.0 | 8B-C2-(10-25) | 13.67 |
| 10 | 911715F | 194.00 | 07/12/91 | 0.0 | 5.0 | 8A-C2(0-5)PW | 1.57 |
| 17 | 911781F | 194.00 | 07/15/91 | 0.0 | 5.0 | 8A-F1-(0-5)PW | 11.99 |
| 18 | 911782F | 194.00 | 07/15/91 | 5.0 | 10.0 | 8A-F1-(5-10)PW | 10.25 |
| 19 | 911783F | 194.00 | 07/15/91 | 10.0 | 25.0 | 8A-F1-(10-25)PW | 43.79 |
| 23 | 911790F | 194.00 | 07/16/91 | 0.0 | 5.0 | 8A-F2-(0-5)PW | 6.13 |
| 24 | 911791F | 194.00 | 07/16/91 | 5.0 | 10.0 | 8A-F2-(5-10)PW | 5.71 |
| 25 | 911792F | 194.00 | 07/16/91 | 10.0 | 25.0 | 8A-F2-(10-25)PW | 4.68 |
| 29 | 911874F | 193.00 | 07/17/91 | 0.0 | 5.0 | 8B-F1-(0-5)PW | 3.82 |
| 35 | 911940F | 193.00 | 07/18/91 | 0.0 | 5.0 | 8B-F2(0-5)PW | 5.29 |
| 37 | 911942F | 193.00 | 07/18/91 | 10.0 | 25.0 | 8B-F2(10-25)PW | 9.03 |
| 41 | 911946F | 193.00 | 07/18/91 | 0.0 | 5.0 | 8B-C1(0-5)PW | 4.55 |
| 45 | 911927F | 193.00 | 07/19/91 | 0.0 | 5.0 | 8B-F3-(0-5)PW | 2.97 |
| 46 | 911928F | 193.00 | 07/19/91 | 5.0 | 10.0 | 8B-F3-(5-10)PW | 3.60 |

**Table D-3. Sediment and porewater records analyzed using Green Bay mixed Aroclor standard only (reference database GBS_ONLY.DBF).**

| Database ID | Laboratory Sample ID | Approx. River Mile | Date Collected | Core Depth Start | Core Depth End | Sample Description | Total PCBs (ppm) |
|---|---|---|---|---|---|---|---|
| 47 | 911929F | 193.00 | 07/19/91 | 10.0 | 25.0 | 8B-F3(10-25)PW | 48.03 |
| 51 | 912063F | 193.00 | 07/22/91 | 0.0 | 5.0 | 8B-F4(0-5)PW | 3.32 |
| 52 | 912064F | 193.00 | 07/22/91 | 5.0 | 10.0 | 8B-F4(5-10)PW | 8.30 |
| 53 | 912065F | 193.00 | 07/22/91 | 10.0 | 25.0 | 8B-F4(10-25)PW | 5.16 |
| 57 | 912185F | 193.00 | 07/24/91 | 0.0 | 5.0 | 8B-F5(0-5)PW | 4.39 |
| 59 | 912187F | 193.00 | 07/24/91 | 10.0 | 25.0 | 8B-F5(10-25)PW | 3.15 |
| 63 | 912234F | 193.00 | 07/25/91 | 0.0 | 5.0 | 8B-F6(0-5)PW | 4.99 |
| 64 | 912235F | 193.00 | 07/25/91 | 5.0 | 10.0 | 8B-F6(5-10)PW | 12.61 |
| 65 | 912236F | 193.00 | 07/25/91 | 10.0 | 25.0 | 8B-F6(10-25)PW | 21.59 |
| 69 | 912243F | 193.00 | 07/25/91 | 0.0 | 5.0 | 8B-C2(0-5)PW | 9.27 |
| 71 | 912245F | 193.00 | 07/25/91 | 10.0 | 25.0 | 8B-C2(10-25)PW | 20.16 |
| 75 | 912336F | 193.00 | 07/26/91 | 0.0 | 5.0 | 8B-F7(0-5)PW | 4.32 |
| 76 | 912337F | 193.00 | 07/26/91 | 5.0 | 10.0 | 8B-F7(5-10)PW | 26.60 |
| 77 | 912338F | 193.00 | 07/26/91 | 10.0 | 25.0 | 8B-F7(10-25)PW | 0.87 |
| 81 | 912348F | 193.00 | 07/29/91 | 0.0 | 5.0 | 8B-C3(0-5)PW | 0.70 |
| 83 | 912350F | 193.00 | 07/29/91 | 10.0 | 25.0 | 8B-C3(10-25)PW | 5.32 |
| 88 | 912500F | 192.00 | 07/30/91 | 0.0 | 5.0 | 8C-F1-(0-5)PW | 11.83 |
| 94 | 912486F | 192.00 | 07/31/91 | 0.0 | 5.0 | 8C-F2(0-5)PW | 5.47 |
| 95 | 912487F | 192.00 | 07/31/91 | 5.0 | 10.0 | 8C-F2(5-10)PW | 5.22 |
| 96 | 912488F | 192.00 | 07/31/91 | 10.0 | 25.0 | 8C-F2(10-25)PW | 19.56 |
| 100 | 912494F | 192.00 | 07/31/91 | 0.0 | 5.0 | 8C-C1(0-5)PW | 5.15 |
| 120 | 912673F | 192.00 | 08/02/91 | 0.0 | 5.0 | 8C-F5(0-5)PW | 15.31 |
| 121 | 912674F | 192.00 | 08/02/91 | 5.0 | 10.0 | 8C-F5(5-10)PW | 21.59 |
| 122 | 912675F | 192.00 | 08/02/91 | 10.0 | 25.0 | 8C-F5(10-25)PW | 41.01 |
| 120.1 | 912773F | 192.00 | 08/02/91 | 0.0 | 5.0 | 8C-F5-(0-5) PW #120 | 5.21 |
| 122.1 | 912775F | 192.00 | 08/02/91 | 10.0 | 25.0 | 8C-F5-(10-25)PW #122 | 10.01 |
| 126 | 912807F | 192.00 | 08/05/91 | 0.0 | 5.0 | 8C-F6-(0-5)PW #126 | 4.79 |
| 139 | 913116F | 191.00 | 08/07/91 | 5.0 | 10.0 | 8D-F1-(5-10)PW #139 | 14.49 |
| 147 | 913278F | 191.00 | 08/08/91 | 10.0 | 25.0 | 8D-F2-(10-25)PW #147 | 38.48 |
| 330 | 915402F | 184.80 | 09/12/91 | 0.0 | 5.0 | 6B-F2(0-5)-330 | 19.58 |
| 331 | 915403F | 184.80 | 09/12/91 | 5.0 | 10.0 | 6B-F2(5-10)-331 | 23.21 |
| 332 | 915404F | 184.80 | 09/12/91 | 10.0 | 25.0 | 6B-F2(10-25)332 | 25.72 |
| 358 | 915760F | 178.50 | 09/20/91 | 0.0 | 5.0 | 5EF-F1(0-5)358 | 2.53 |
| 359 | 915761F | 178.50 | 09/20/91 | 5.0 | 10.0 | 5EF-F1(5-10)359 | 8.33 |
| 360 | 915762F | 178.50 | 09/20/91 | 10.0 | 25.0 | 5EFF1(10-25)360 | 9.77 |
| 377 | 915958F | 176.50 | 09/24/91 | 0.0 | 5.0 | 5GH-F1(0-5)-377 | 1.32 |
| 378 | 915959F | 176.50 | 09/24/91 | 5.0 | 10.0 | 5GH-F1(5-10)378 | 1.83 |
| 379 | 915960F | 176.50 | 09/24/91 | 10.0 | 25.0 | 5GHF1(10-25)379 | 10.35 |
| 390 | 916129F | 174.50 | 09/26/91 | 0.0 | 5.0 | 5IJ-F1(0-5)390 | 2.75 |
| 391 | 916130F | 174.50 | 09/26/91 | 5.0 | 10.0 | 5IJ-F1(5-10)391 | 4.97 |
| 392 | 916131F | 174.50 | 09/26/91 | 10.0 | 25.0 | 5IJF1(10-25)392 | 18.17 |
| 81791 | 9605675 | 194.90 | 09/18/96 | 0.0 | 0.0 | 1 | 2.50 |
| 81792 | 9605676 | 194.90 | 09/18/96 | 0.0 | 0.0 | 2 | 3.46 |
| 81793 | 9605677 | 194.90 | 09/18/96 | 0.0 | 0.0 | 3 | 2.16 |
| 81794 | 9605678 | 194.90 | 09/18/96 | 0.0 | 0.0 | 4 | 4.49 |
| 81795 | 9605679 | 194.90 | 09/18/96 | 0.0 | 0.0 | 5 | 6.05 |
| 81796 | 9605680 | 194.90 | 09/19/96 | 0.0 | 0.0 | 6 | 2.83 |
| 81797 | 9605681 | 194.90 | 09/19/96 | 0.0 | 0.0 | 7 | 5.34 |
| 81798 | 9605682 | 194.90 | 09/19/96 | 0.0 | 0.0 | 8 | 2.55 |
| 81799 | 9605683 | 194.90 | 09/19/96 | 0.0 | 0.0 | 9 | 8.68 |

**Table D-3. Sediment and porewater records analyzed using Green Bay mixed Aroclor standard only (reference database GBS_ONLY.DBF).**

| Database ID | Laboratory Sample ID | Approx. River Mile | Date Collected | Core Depth Start | Core Depth End | Sample Description | Total PCBs (ppm) |
|---|---|---|---|---|---|---|---|
| 81800 | 9605684 | 194.90 | 09/19/96 | 0.0 | 0.0 | 10 | 6.58 |
| 81801 | 9605685 | 194.90 | 09/19/96 | 0.0 | 0.0 | 11 | 2.85 |
| 81802 | 9605686 | 194.90 | 09/20/96 | 0.0 | 0.0 | 12 | 3.22 |
| 81803 | 9605687 | 194.90 | 09/20/96 | 0.0 | 0.0 | 13 | 3.38 |
| 81804 | 9605688 | 194.90 | 09/20/96 | 0.0 | 0.0 | 14 | 1.77 |
| 81805 | 9605689 | 194.90 | 09/20/96 | 0.0 | 0.0 | 15 | 4.24 |
| 81806 | 9605690 | 194.90 | 09/20/96 | 0.0 | 0.0 | 16 | 3.74 |
| 81807 | 9605691 | 194.90 | 09/20/96 | 0.0 | 0.0 | 17 | 4.89 |
| 81808 | 9605692 | 194.20 | 09/18/96 | 0.0 | 0.0 | 18 | 2.67 |
| 81809 | 9605693 | 194.20 | 09/18/96 | 0.0 | 0.0 | 19 | 5.04 |
| 81810 | 9605694 | 194.20 | 09/18/96 | 0.0 | 0.0 | 20 | 3.19 |
| 81811 | 9605695 | 194.20 | 09/18/96 | 0.0 | 0.0 | 21 | 2.71 |
| 81812 | 9605696 | 194.20 | 09/18/96 | 0.0 | 0.0 | 22 | 4.48 |
| 81813 | 9605697 | 194.20 | 09/18/96 | 0.0 | 0.0 | 23 | 5.15 |
| 81814 | 9605698 | 194.20 | 09/19/96 | 0.0 | 0.0 | 24 | 2.96 |
| 81815 | 9605699 | 194.20 | 09/19/96 | 0.0 | 0.0 | 25 | 3.54 |
| 81816 | 9605700 | 194.20 | 09/19/96 | 0.0 | 0.0 | 26 | 4.70 |
| 81817 | 9605701 | 194.20 | 09/19/96 | 0.0 | 0.0 | 27 | 18.60 |
| 81818 | 9605702 | 194.20 | 09/19/96 | 0.0 | 0.0 | 28 | 4.72 |
| 81819 | 9605703 | 194.20 | 09/19/96 | 0.0 | 0.0 | 29 | 4.46 |
| 81820 | 9605704 | 194.20 | 09/20/96 | 0.0 | 0.0 | 30 | 2.44 |
| 81821 | 9605705 | 194.20 | 09/20/96 | 0.0 | 0.0 | 31 | 2.30 |
| 81822 | 9605706 | 194.20 | 09/20/96 | 0.0 | 0.0 | 32 | 2.37 |
| 81823 | 9605707 | 194.20 | 09/20/96 | 0.0 | 0.0 | 33 | 2.56 |
| 81824 | 9605708 | 194.20 | 09/20/96 | 0.0 | 0.0 | 34 | 2.87 |
| 81850 | 9605709 | 194.20 | 09/20/96 | 0.0 | 0.0 | 35 | 7.40 |
| 81851 | 9605710 | 0.00 | 09/23/96 | 0.0 | 0.0 | 38 | 6.44 |
| 81852 | 9605711 | 0.00 | 09/23/96 | 0.0 | 0.0 | 39 | 2.34 |
| 81853 | 9605712 | 0.00 | 09/23/96 | 0.0 | 0.0 | 40 | 2.41 |
| 81854 | 9605713 | 0.00 | 09/23/96 | 0.0 | 0.0 | 41 | 31.95 |
| 81855 | 9605714 | 0.00 | 09/23/96 | 0.0 | 0.0 | 42 | 27.15 |
| 81856 | 9605715 | 0.00 | 09/23/96 | 0.0 | 0.0 | 43 | 12.62 |
| 81857 | 9605716 | 0.00 | 09/23/96 | 0.0 | 0.0 | 44 | 6.89 |
| 81858 | 9605717 | 0.00 | 09/23/96 | 0.0 | 0.0 | 45 | 8.72 |
| 81859 | 9605718 | 0.00 | 09/23/96 | 0.0 | 0.0 | 46 | 6.07 |
| 81860 | 9605719 | 0.00 | 09/23/96 | 0.0 | 0.0 | 47 | 2.80 |
| 81861 | 9605720 | 0.00 | 09/23/96 | 0.0 | 0.0 | 48 | 3.79 |
| 81862 | 9605721 | 0.00 | 09/23/96 | 0.0 | 0.0 | 50 | 5.74 |
| 81863 | 9605722 | 0.00 | 09/23/96 | 0.0 | 0.0 | 51 | 5.97 |
| 81864 | 9605723 | 0.00 | 09/23/96 | 0.0 | 0.0 | 52 | 5.73 |
| 81865 | 9605724 | 194.90 | 09/18/96 | 0.0 | 0.0 | 53 | 3.06 |
| 81866 | 9605725 | 194.90 | 09/18/96 | 0.0 | 0.0 | 54 | 2.98 |
| 81867 | 9605726 | 194.90 | 09/19/96 | 0.0 | 0.0 | 55 | 1.37 |
| 81868 | 9605727 | 194.90 | 09/20/96 | 0.0 | 0.0 | 56 | 2.81 |
| 81869 | 9605728 | 194.20 | 09/18/96 | 0.0 | 0.0 | 57 | 2.58 |
| 81870 | 9605729 | 194.20 | 09/20/96 | 0.0 | 0.0 | 58 | 6.95 |
| 81871 | 9605730 | 0.00 | 09/23/96 | 0.0 | 0.0 | 59 | 2.42 |
| 81872 | 9605731 | 0.00 | 09/23/96 | 0.0 | 0.0 | 60 | 5.84 |
| 81992 | 9701419 | 194.20 | 04/08/97 | 0.0 | 0.0 | R.I. EAST CHANN | 1.29 |
| 81993 | 9701420 | 194.20 | 04/08/97 | 0.0 | 0.0 | R.I. WEST CHANN | 11.90 |

**Table D-3. Sediment and porewater records analyzed using Green Bay mixed Aroclor standard only (reference database GBS_ONLY.DBF).**

| Database ID | Laboratory Sample ID | Approx. River Mile | Date Collected | Core Depth Start | Core Depth End | Sample Description | Total PCBs (ppm) |
|---|---|---|---|---|---|---|---|
| 81994 | 9701421 | 194.20 | 04/09/97 | 0.0 | 0.0 | R.I. WEST CHANN | 4.53 |
| 81995 | 9701071 | 0.00 | 03/20/97 | 0.0 | 0.0 | 36 | 5.47 |
| 81996 | 9701072 | 0.00 | 03/20/97 | 0.0 | 0.0 | 37 | 5.14 |
| 90181 | 935214F | 0.00 | 08/20/93 | 0.0 | 0.0 | HR-2 | 1856.84 |
| 91006 | 923483F | 0.00 | 08/19/92 | 0.0 | 0.0 | 002 OUTFALL BEDDING | 2843.20 |

Note:

Sample descriptions for 1991 Sediment Survey samples indicate river reach (5 through 8), subsection of reach (A-J), sediment texture (F=fine, C=coarse), sample depth, and PW if sample is porewater. Samples numbered 1 through 60 were collected for the 1996 Particle Transport Study. Samples R.I. EAST CHANN and R.I. WEST CHANN are bedload samples collected during the 1997 High Flow Monitoring. Samples HR-2 and 002 OUTFALL BEDDING were collected in the Bakers Falls area.

*Source: HydroQual (1997)*

# Northeast Analytical Laboratories letter of August 27, 1997

# NORTHEAST ANALYTICAL

ENVIRONMENTAL LAB SERVICES

301 Nott Street, Schenectady, NY 12305

(518) 346-4592 • FAX (518) 381-6055


August 27, 1997

Mr. William Ayling
O'Brien & Gere Engineers
5000 Brittonfield Parkway
P.O. Box 4873, Suite 300
Syracuse, NY 13221

Re: Update of Weight Percent Distribution for Congener Specific PCB Analysis associated with General Electric's Hudson River Program. Corrections to PCB weight percent distributions as reported in "Development of Corrections for Analytical Biases in the 1991-1997 GE Hudson River PCB Database," June 1997, by HydroQual, Inc.

Mr. Ayling:

Starting on September 1, 1997, Northeast Analytical, Inc. will be using a new set of weight percent values for all congener specific PCB measurements performed by the Green Bay Mass Balance Study Protocol (EPA 1987) covered by Northeast Analytical, Inc.'s Standard Operating Procedures NEA-608CAP. This will entail changing the PCB mixed Aroclor calibration standard values for each reported DB-1 peak with new updated concentration values.

The new weight percent values to be used were issued by Dr. Michael D. Mullin (USEPA) in a letter dated November 21, 1994 to Dr. George Frame (General Electric Corporate R&D), which supplied values for a commercially available Aroclor source.

Attached is a listing of currently used weight percent values and the new weight percent values based on the DB-1 capillary peak number assignment. Also listed are concentration values for each reportable peak and the new peak amounts calculated from the new weight % values (Mullin 1994).

All samples received at the laboratory for PCB analysis by the above referenced method after September 1, 1997 will be quantified by the new calibration values. If you have any questions concerning this change in the PCB quantitation profile, please contact me to discuss them.

Sincerely,

Northeast Analytical, Inc.

Robert E. Wagner
Laboratory Director

S:\TEXT\CORR\REW\970825A.OBG
REW\JMP

cc: Dr. Jim Rhea, Ph.D., HydroQual, Inc.
Dr. John Haggard, Ph.D., General Electric

# WEIGHT PERCENT DISTRIBUTIONS FOR "GREEN BAY STANDARD" COMPRISING PCB FROM AROCLORS 1232, 1248, 1262 IN THE RATIO OF 25:18:18

**August 25, 1997 RE Wagner**

**Provided by:** Northeast Analytical, Inc. 301 Nott St., Schenectady, NY 12305
Phone:(518) 346-4592 Fax:(518) 381-6055 E-mail: nelab@aol.com

FILE ; S:\FORMS\DB1WT%97.WK4

| DB-1 PEAK # ASSIGNMENT | CURRENT PEAK AMOUNT SWACKHAMER 1987 (1) (ng/mL) | CURRENT WEIGHT % SWACKHAMER 1987 (1) | NEW PEAK AMOUNT MULLIN 1994 (2) (ug/mL) | NEW WEIGHT % MULLIN 1994 (2) (commercial Aroclors) | NEW PEAK AMOUNT NORTHEAST ANALYTICAL (EFFECTIVE 09/1/97) (ng/mL) |
|---|---|---|---|---|---|
| 001 | | | | | |
| 002 | 430 | 6.76 | 12 | 6.99 | 445.14 |
| 003 | | | | | |
| 004 | 260 | 4.09 | 7.0 | 4.08 | 259.67 |
| 005 | 28 | 0.44 | 3.4 | 1.98 | 126.12 |
| 006 | 22 | 0.35 | 1.2 | 0.70 | 44.51 |
| 007 | 42 | 0.66 | 1.9 | 1.11 | 70.48 |
| 008 | 500 | 7.86 | 14.0 | 8.16 | 519.33 |
| 009 | | | | | |
| 010 | 10 | 0.16 | 0.28 | 0.16 | 10.39 |
| 011 | | | | | |
| 012 | | | | | |
| 013 | 9.2 | 0.14 | 0.267 | 0.16 | 9.90 |
| 014 | 130 | 2.04 | 3.7 | 2.16 | 137.25 |
| 015 | 74 | 1.16 | 3.7 | 2.16 | 137.25 |
| 016 | 8.8 | 0.14 | 0.26 | 0.15 | 9.64 |
| 017 | 131 | 2.06 | 3.9 | 2.27 | 144.67 |
| 018 | | | | | |
| 019 | | | | | |
| 020 | 1.8 | 0.03 | 0.053 | 0.03 | 1.97 |
| 021 | 23 | 0.36 | 0.72 | 0.42 | 26.71 |
| 022 | 10 | 0.16 | 0.32 | 0.19 | 11.87 |
| 023 | 166 | 2.61 | 4.123 | 2.40 | 152.94 |
| 024 | 214 | 3.36 | 5.277 | 3.08 | 195.75 |
| 025 | 168.5 | 2.65 | 3.972 | 2.32 | 147.34 |
| 026 | 116.7 | 1.83 | 2.9 | 1.69 | 107.58 |
| 027 | 27 | 0.42 | 0.89 | 0.52 | 33.01 |
| 028 | | | | | |
| 029 | 14 | 0.22 | 0.40 | 0.23 | 14.84 |
| 030 | | | | | |
| 031 | 129.1 | 2.03 | 4.77 | 2.78 | 176.94 |
| 032 | 90 | 1.41 | 2.3 | 1.34 | 85.32 |
| 033 | 50 | 0.79 | 1.0 | 0.58 | 37.10 |
| 034 | 40 | 0.63 | 1.0 | 0.58 | 37.10 |
| 035 | | | | | |
| 036 | | | | | |
| 037 | 150 | 2.36 | 4.3 | 2.51 | 159.51 |
| 038 | 88 | 1.38 | 2.6 | 1.52 | 96.45 |
| 039 | 163 | 2.56 | 4.1 | 2.39 | 152.09 |

| DB-1 PEAK # ASSIGNMENT | CURRENT PEAK AMOUNT SWACKHAMER 1987 (1) (ng/mL) | CURRENT WEIGHT % SWACKHAMER 1987 (1) | NEW PEAK AMOUNT MULLIN 1994 (2) (ug/mL) | NEW WEIGHT % MULLIN 1994 (2) (commercial Aroclors) | NEW PEAK AMOUNT NORTHEAST ANALYTICAL (EFFECTIVE 09/1/97) (ng/mL) |
|---|---|---|---|---|---|
| 040 | | | | | |
| 041 | | | | | |
| 042 | 33 | 0.52 | 0.94 | 0.55 | 34.87 |
| 043 | | | | | |
| 044 | 5 | 0.08 | 0.11 | 0.06 | 4.08 |
| 045 | 7.4 | 0.12 | 0.21 | 0.12 | 7.79 |
| 046 | 81 | 1.27 | 1.9 | 1.11 | 70.48 |
| 047 | 210 | 3.30 | 3.4 | 1.98 | 126.12 |
| 048 | 272 | 4.27 | 7.2 | 4.20 | 267.08 |
| 049 | 14 | 0.22 | 0.51 | 0.30 | 18.92 |
| 050 | 180 | 2.83 | 3.5 | 2.04 | 129.83 |
| 051 | 43 | 0.68 | 1.8 | 1.05 | 66.77 |
| 052 | 3 | 0.05 | 0.10 | 0.06 | 3.71 |
| 053 | 48 | 0.75 | 1.8 | 1.05 | 66.77 |
| 054 | 23 | 0.36 | 0.74 | 0.43 | 27.45 |
| 055 | 1.8 | 0.03 | 0.028 | 0.02 | 1.04 |
| 056 | 3.6 | 0.06 | 0.15 | 0.09 | 5.56 |
| 057 | 19 | 0.30 | 0.56 | 0.33 | 20.77 |
| 058 | 33.2 | 0.52 | 1.16 | 0.68 | 43.03 |
| 059 | 21 | 0.33 | 0.70 | 0.41 | 25.97 |
| 060 | 14 | 0.22 | 0.75 | 0.44 | 27.82 |
| 061 | 71 | 1.12 | 2.13 | 1.24 | 79.01 |
| 062 | | | | | |
| 063 | 13 | 0.20 | 0.44 | 0.26 | 16.32 |
| 064 | 57 | 0.90 | 1.7 | 0.99 | 63.06 |
| 065 | 22 | 0.35 | 0.29 | 0.17 | 10.76 |
| 066 | 2.23 | 0.04 | 0.60 | 0.35 | 22.26 |
| 067 | 3.3 | 0.05 | 0.13 | 0.08 | 4.82 |
| 068 | | | | | |
| 069 | 145 | 2.28 | 4.0 | 2.33 | 148.38 |
| 070 | | | | | |
| 071 | 8.5 | 0.13 | 0.202 | 0.12 | 7.49 |
| 072 | 0.91 | 0.01 | 0.029 | 0.02 | 1.08 |
| 073 | 16 | 0.25 | 0.39 | 0.23 | 14.47 |
| 074 | 68.04 | 1.07 | 1.355 | 0.79 | 50.26 |
| 075 | 147.96 | 2.32 | 2.945 | 1.72 | 109.25 |
| 076 | | | | | |
| 077 | 52 | 0.82 | 1.7 | 0.99 | 63.06 |
| 078 (3) | 54.6 | 0.86 | 1.46 | 0.85 | 54.16 |
| 079 | 2.5 | 0.04 | 0.075 | 0.04 | 2.78 |
| 080 | 13.88 | 0.22 | 0.26 | 0.15 | 9.64 |
| 081 | no peak 81, combined and reported with peak 80 | | | | |
| 082 | 98 | 1.54 | 2.7 | 1.57 | 100.16 |
| 083 | 12 | 0.19 | 0.25 | 0.15 | 9.27 |
| 084 | 3 | 0.05 | 0.013 | 0.01 | 0.48 |

| DB-1 PEAK # ASSIGNMENT | CURRENT PEAK AMOUNT SWACKHAMER 1987 (1) (ng/mL) | CURRENT WEIGHT % SWACKHAMER 1987 (1) | NEW PEAK AMOUNT MULLIN 1994 (2) (ug/mL) | NEW WEIGHT % MULLIN 1994 (2) (commercial Aroclors) | NEW PEAK AMOUNT NORTHEAST ANALYTICAL (EFFECTIVE 09/1/97) (ng/mL) |
|---|---|---|---|---|---|
| 085 | 34 | 0.53 | 1.1 | 0.64 | 40.80 |
| 086 | | | | | |
| 087 | 6 | 0.09 | 0.2 | 0.12 | 7.42 |
| 088 | 150 | 2.36 | 3.6 | 2.10 | 133.54 |
| 089 | 4.7 | 0.07 | 0.10 | 0.06 | 3.71 |
| 090 | 77 | 1.21 | 1.7 | 0.99 | 63.06 |
| 091 | 1.1 | 0.02 | 0.049 | 0.03 | 1.82 |
| 092 | 22 | 0.35 | 0.47 | 0.27 | 17.43 |
| 093 | 110 | 1.73 | 3.2 | 1.87 | 118.70 |
| 094 | 57 | 0.90 | 1.7 | 0.99 | 63.06 |
| 095 | 36.9 | 0.58 | 0.79 | 0.46 | 29.31 |
| 096 | 3.31 | 0.05 | 0.066 | 0.04 | 2.45 |
| 097 | | | | | |
| 098 | 1.273 | 0.02 | 0.038 | 0.02 | 1.41 |
| 099 | 20.697 | 0.33 | 0.39 | 0.23 | 14.47 |
| 100 | 19.2 | 0.30 | 0.56 | 0.33 | 20.77 |
| 101 | 2.18 | 0.03 | 0.11 | 0.06 | 4.08 |
| 102 | 240 | 3.77 | 6.1 | 3.56 | 226.28 |
| 103 | 14 | 0.22 | 0.42 | 0.24 | 15.58 |
| 104 | 4.5 | 0.07 | 0.12 | 0.07 | 4.45 |
| 105 | 10 | 0.16 | 0.43 | 0.25 | 15.95 |
| 106 | 91.1 | 1.43 | 1.280 | 0.75 | 47.48 |
| 107 | 29.9 | 0.47 | 0.420 | 0.24 | 15.58 |
| 108 | 6.7 | 0.11 | 0.12 | 0.07 | 4.45 |
| 109 | 150 | 2.36 | 4.2 | 2.45 | 155.80 |
| 110 | 170 | 2.67 | 4.3 | 2.51 | 159.51 |
| 111 | 1.8 | 0.03 | 0.040 | 0.02 | 1.48 |
| 112 | 55.9 | 0.88 | 0.553 | 0.32 | 20.51 |
| 113 | 24.9 | 0.39 | 0.247 | 0.14 | 9.16 |
| 114 | 4.8 | 0.08 | 0.093 | 0.05 | 3.45 |
| 115 | 69 | 1.08 | 1.8 | 1.05 | 66.77 |
| 116 | 4 | 0.06 | 0.11 | 0.06 | 4.08 |
| 117 | 42 | 0.66 | 0.68 | 0.40 | 25.22 |
| 118 | 0.95 | 0.01 | 0.012 | 0.01 | 0.45 |
| TOTAL | 6363.93 | 100 | 171.557 | 100 | 6363.93 |

(1) Weight percent distributions obtained from " Deborah L. Swackhamer, Quality Assurance Plan, Green Bay Mass Balance Study, I. PCBs and Dieldrin U.S. EPA Great Lakes National Program Office, Final Draft, Quality Assurance Coordinator, Field and Analytical Methods Committee, December 11, 19

(2) Weight percent disributions provided by Michael D. Mullin/LLRS to George M. Frame/GE CRD in a letter dated November 21, 1994. New reference standard solution prepared from a commercial source.

(3) Peak #78, which contains PCB congener IUPAC 179 was not reported by Mullins in either the 1987 or 1994 weight percent listing. The weignt perce used for peak #78 is from data published in "Comprehensive, Quantitative, Congener-Specific Analysis of Eight Aroclors and Complete PCB Congener on DB-1 Capillary GC Columns." George M. Frame et. al., Chemosphere, Vol. 33, No. 4, pp. 603-623, 1996.