28.1 Purpose:

Processing Convicted Offender samples submitted for inclusion in the DNA database; comprehensively from set up of worksheets and plates/tubes, amplification of samples, interpretation of data/results and import into CODIS.

28.2 Responsibility:

Forensic Science Examiners 1, 2, and 3, Laboratory Assistants 2 and Connecticut Career Trainees in the DNA Unit.

28.3 Database plate sample list preparation (of consecutive database samples):

28.3.1 Use #1-1 database cards for all samples, except QC samples which can be either #1-1 or #1-2.

28.3.2 Determine the range of samples to be tested (all must be consecutive, except QC samples). Two samples must be QC samples. Take the QC sample cards with you to the LIMS computer.

28.3.3 In LIMS, select the "Crystal Reports" icon.

28.3.4 Choose "DNA Database Plate Sample List", then Print, and Screen.

28.3.5 With 'Starting Sample' highlighted, enter the first sample number in the format specified. Next highlight 'Ending Sample' and enter the last sample number in the same way. Select OK.

28.3.6 Select the 'Export Report' icon in the upper left. For 'Format', choose tab-separated text; for 'Destination', choose Disk File. Select OK. Name the file and save.

28.3.7 Open the file just saved using Notepad. To do this:

28.3.7.1 Select the file. At the first screen, choose to select the program to use from a list. Do not use the web service.

28.3.7.2 At the second screen, uncheck the box next to "always use the selected program to open this kind of file."

28.3.7.3 Select Notepad from the list and OK.

28.3.8 At two distant positions from each other in the list, add a line for each QC sample. At each position type the QC sample number, hit tab, and scan the barcode.

28.3.9 Save the file on a removable disk or shared drive.

28.3.10 On a computer with U: Drive access, open the file using Microsoft Excel. Copy all the data in the two columns.

28.3.11 Open the GlobalFiler Express Amplification Worksheet (DNA QR-326). In the LIMS tab, paste into cell A2 all the data copied in 28.3.10. Continue to 28.6.

28.4 Database plate sample list preparation (of non-consecutive database samples):

28.4.1 Collect all the database cards to be tested (#1-1 and/or #1-2). Swabs may be run on the database plates, but must be manually entered onto DNA QR-326 (GlobalFiler Express Amplification Worksheet).

28.4.2 Bring the cards to a computer with a barcode scanner. Open Microsoft Excel. Type the number of the first database sample in cell A01, in DB-XX-XXXXXX format. In cell B1, scan the barcode on this card.

28.4.3 Continue to enter the database numbers into column A and the corresponding barcodes into column B, for all samples including QC samples, in the order of testing. Note: If the plate includes Database Hit Confirmations, no QC samples are required.

28.4.4 Save the file on a removable disk or shared drive.

28.4.5 On a computer with U: Drive access, open the file using Microsoft Excel. Copy all data in the two columns.

28.4.6 Open the Globalfiler Express Amplification Worksheet (DNA QR-326). In the LIMS tab, paste into cell A2 all the data copied in 28.4.5. Continue to 28.6.

28.5 Plate workbook setup:

28.5.1 **Note: Detailed instructions on plate workbook setup (full and partial plates for database and casework samples) can be found in the Database and Known casework sample worksheets: DNA QR-326.**

28.5.2 Naming of Database Plates:

28.5.2.1 Every plate will have a letter and numerical designation. The letter will be indicative of the type of lab work completed on the plate, and the numerical designation will be indicative of when the testing took place, whether it is a date or a consecutive counting.

28.5.2.2 Letter Designation:

i. **E**: First Amplification
ii. **E2**: 2nd Amplification
iii. **A**: Swab Amplification
iv. **R**: Reinjection
v. **AR**: Plate containing both reamplifications and reinjections
vi. **HC**: CODIS hit confirmations
vii. **HC-E2**: Plate containing both CODIS hit confirmations and 2nd extractions
viii. **PT**: for Proficiency Tests

28.5.2.3 Numerical Designation:

i. **For E plates only**: the plates will be numbered in order based on the year and sequence the samples were received at the laboratory. For example, the 50th plate of samples that came into the laboratory in 2010 would be named E-2010-50.
ii. **For all other plates**: the numerical designation will be a 6 digit number corresponding to the date that lab work was **started** on those samples. For example, for an A plate, if the amplification was conducted on September 2nd, 2011, and the injection on September 5th, 2011, the plate name will be A-090211.

28.5.2.4 This unique identifier must be written on the top right of every paper associated with the lab work completed for this plate, and will be considered a means of batching a group of database samples with one specified name.

28.5.2.5 If a situation presents itself that is not listed, please follow the logic behind the protocols in keeping the naming consistent.

28.6 Punching a plate using the BSD Duet:

Detailed instructions can be found in DNA SOP-36 and DNA QR-326.

28.7 Manual Punching of FTA Cards:

28.7.1 FTA cards may be punched manually; this is generally only appropriate if the number of cards to be tested is small. Detailed instructions can be found in DNA SOP-36.

28.8 Amplification of Database Samples Using GlobalFiler Express:

See DNA SOP-36.

28.9 Detection of Data for Database Samples

See DNA SOP-38.

28.10 Analysis of database samples:

28.10.1 After injecting a set of samples on a 3500xL per DNA SOP-38, create a folder in "U:\Database \convicted offender data\being analyzed" with your plate name. Copy the Data Set run folders from the 3500xL computer to the folder just created.

28.10.2 The analyst shall analyze the data according to the GlobalFiler Express analysis method described in DNA SOP-39. Routine click-offs do not need to be noted on the analysis worksheets. The positive control(s) DNA profile(s) are checked using DNA QR-37 (Concordance Check). Allele changes and sizes of peaks out of ladder ranges should be noted in the comment section of the comment chart (DNA QR-327 GlobalFiler Injection/Analysis Worksheet - Database), as should any low peak height ratios and possible tri-alleles. Change out of bin (OB) alleles to their true allele designations as appropriate, making sure the allele is accepted at CODIS. Any alleles that are not accepted at CODIS should be changed to a <# or # >. The # indicates the minimum/maximum allele acceptable at CODIS for that locus (i.e. FGA 31.2 is changed to >30). The Known PHR Filter Macro is used to assist analysts in identifying any results warranting further review or documentation.

28.10.3 For incomplete or unacceptable profiles, determine if the sample needs to be reamplified, or reinjected. If applicable, check the appropriate box on the comment chart. If a partial profile is obtained, print out this profile (for comparison purposes to the full profile (when obtained)). Disable these incomplete or unacceptable profiles from the project. Fill out the "Database Quant and Reinject" spreadsheet located on the U: Drive. Include the sample name, well number, reason for re-do, and all appropriate controls to be redone with the sample.

28.10.4 For database known processing, the RB and the Neg must be amplified and injected to reflect the largest amplification volume and the longest injection times for the samples associated with them.

28.10.5 If called peaks arise in the RB or the Neg on database plates, interpret with caution, and see DNA Technical Leader for approval/documentation of the control. If the CODIS administrator does not approve the control it will be necessary to re-amplify affected samples.

28.10.6 If after re-injection, and/or re-amplification, a complete DNA profile has not been generated, the applicator sponge/swab should be used for Amplification. This envelope containing the sponges has a temporary seal (as per DNA SOP-11) and will be disposed after a complete DNA profile has been generated. If the sponge fails to generate a full DNA profile, a copy of the identifying information for the offender sample will be made and delivered to the CODIS Administrator. The CODIS Administrator will notify the submitting agency that a new sample needs to be collected from the offender.

28.10.7 For acceptable profiles, on the comment chart (DNA QR-327), check the box for good profile (if applicable). Save and export the project to the folder created in step 28.10.1. The SGF file and the plate name should be the same.

28.10.8 The Technical Reviewer shall import the GeneMarker project (.SGF) into GeneMarker. The Technical Reviewer should review the data, but not make any changes. Comments or questions should be noted and given to the primary examiner to address and maintain on the appropriate QR worksheet. The Technical Reviewer will not save any changes made or export this project.

28.10.9 The 1st analyst shall review the comments made by the Technical Reviewer and make changes and annotations where appropriate. If changes were made, save and export the file again, overwriting the original SGF file.

28.10.10 The Technical Reviewer shall technically review all paperwork associated with analyzed samples. These checks will be noted on DNA QR-327.

28.11 Export and Import of Profiles:

28.11.1 **Export of Offender profiles from GeneMarker:** Move file folder created in step 28.10.1 to U:\Database\Convicted offender data\completed folder.

28.11.2 Insert a removable disk into the computer.

28.11.3 Open GeneMarker and the project to be imported into CODIS. Select Application and Export CODIS.

28.11.4 Change Source ORI and Destination ORI to CTCSP3500.

28.11.5 Select GlobalFiler Express as PCR kit.

28.11.6 Enter CODIS User ID into the Submit User ID blank.

28.11.7 Select CMF 3.2 (.xml) file.

28.11.8 The default setting is to have the check box selected for export. Verify that controls, ladders, and samples not to be exported are not selected. Deselect any specimens as necessary.

28.11.9 The default setting for Specimen Category is Convicted Offender. Verify the Specimen Category is set to Convicted Offender for each sample to be exported.

28.11.10 Click OK.

28.11.11 Save and export the file to a removable disk. The export file name should contain the plate/project name for traceability.

28.11.12 **Import of profiles into CODIS:** On a CODIS workstation, insert the removable disk, then open the Analyst Workbench.

28.11.13 Select/open Specimen Manager.

28.11.14 On the tool bar, select Specimen Manger and Import. Alternatively, select the Import icon.

28.11.15 Browse for the file created in step 28.11.11.

28.11.16 Verify 'Import Type' is set to 'Data Import' and 'Assign to User' is correct, then select OK.

28.11.17 Observe the confirmation message says the input file was successfully sent to the message center, select OK.

28.11.18 Select/open Message Center. New Import STR Files should be in bold face. This indicates the file was sent successfully to the message center.

28.11.19 Select Import STR Files. The newly imported file should be in boldface in the larger window. Double-click on that file to execute.

28.11.20 When the file has finished importing, Import Reports will be in boldface.

28.11.21 Select Import Reports and choose the file that was just created. An SDIS Import Reconciliation Report should appear on the screen. Review all the pages of this report to ensure the samples have been imported and assigned the correct CODIS specimen category.

28.11.22 Verify that the correct QC samples were imported and concordant with previous entries. Verify that the number of new database samples being imported is correct. Verify that all newly imported samples are assigned the correct specimen category. Document the verification on DNA QR-327.

28.11.23 Print out the first page of the import reconciliation report and attach it to DNA QR-327.

28.11.24 Any problems listed on the SDIS Import Reconciliation Report must be rectified.

28.11.25 File away with appropriate database paperwork.

28.11.26 Update the In-House Database Post-Processing spreadsheet for each sample that a good profile was obtained. Fill in the CT Plate Name and Date Sample Uploaded to CODIS columns.

28.12 Searching for duplicate specimens:

28.12.1 On a CODIS workstation, open Analyst Workbench and click on AutoSearcher.

28.12.2 Under Identity Search, click on Duplicate Offenders. Perform the search by clicking on the Perform Search icon or through the pull-down menu. A new Duplicate Offender tab should open and show the progress of the search. The Message Text will indicate when the search is completed. Close this window and the AutoSearch window.

28.12.3 To view the results of the Duplicate Offender search either: 1) Click on Match Manager and the new matches will be listed in red at the top of the default view. Highlight the matches, click the Print icon, and Match Inventory Report. Or 2) Open Message center,

click on AutoSearcher Reports and execute the appropriate file. Print the matches usually found on the second page of the report.

28.12.4 Find the offender information cards for both the target specimen and candidate specimen, and assure the sample is in fact a duplicate through comparison of the identifying information. If the sample is a duplicate, proceed to 28.13. If the sample is not a duplicate, identify the issue(s) that has caused the sample to be matched as duplicates. Notify the CODIS Administrator for appropriate match disposition and specimen category assignment. If ambiguities continue to exist the CODIS Administrator will forward the match/information to the DNA Data Bank Oversight Panel for resolution.

28.13 Disposition of duplicate samples in CODIS:

28.13.1 On a CODIS workstation, open Analyst Workbench and click on Match Manager.

28.13.2 Find the match(es) that you have determined to be duplicate sample(s)from the same individual. Highlight one or all the matches. Right click, scroll down to Set Disposition then Set Own State's Specimen Disposition as Offender Duplicate.

28.13.3 From each Match determined to be an Offender Duplicate, determine which specimen will be considered the CO Duplicate. Generally, the new specimen or the specimen that has data at the least number of loci will be the CO Duplicate. If any of the specimens have previously associated matches, notify one of the CODIS Administrators. The specimen category of those samples determined to be a CO Duplicate can be changed by finding and highlighting the samples in Specimen Manager, right click, scroll down to Set Specimen Properties then Specimen Category. From the drop-down menu, choose CO Duplicate and click OK.

28.13.4 Close out of the Analyst Workbench. There is no need to save anything.