13.1 PURPOSE:

13.1.1 To ensure that all forensic STR DNA records are entered and searched in the State level of CODIS (SDIS) by the CT DSS DNA Unit as set forth in PA 15-207, CT State Statute 29-7b, and Quality Assurance Standards for Forensic DNA Testing Laboratories.

To ensure that all forensic STR DNA records are entered and searched in the National level of CODIS (NDIS) by the CT DSS DNA Unit as set forth in PA 15-207, CT State Statute 29-7b, NDIS Acceptance Standards (Chapter 4.0) and NDIS Searches (Chapter 5.0) of the NDIS Operational Procedures Manual and Quality Assurance Standards for Forensic DNA Testing Laboratories.

To ensure the reliability, accuracy and compatibility of DNA records uploaded to NDIS. To define the search parameters and guidelines for conducting searches at the CT laboratory (SDIS).

13.2 RESPONSIBILITY:

13.2.1 DNA Section Personnel.

13.3 DNA Records

13.3.1 A DNA record includes the following information: the DNA profile, the Laboratory ORI, the specimen identification number and the DNA personnel associated with or assigned to the DNA analysis. DNA records will not contain any identifiable information relating to the source/donor of the sample nor will it contain or be linked to any criminal history information.

13.3.1.1 The only categories of DNA records that may be maintained in CODIS are: DNA profiles from individuals convicted of a crime as specified in Connecticut General Statute 54-102g through 54-102m, misdemeanors with enhanced felony penalties as established by McCoy v. Commissioner of Public Safety, 300 Conn. 144 (2011) (see listed offenses in section 13.11) or so ordered by the court; DNA samples recovered from crime scenes; DNA samples from unidentified human remains; deduced knowns from missing persons; DNA samples voluntarily contributed from relatives of missing persons; staff samples, and research/validation samples volunteered for the duration of the research. No sample submitted solely for elimination purposes shall be entered into SDIS, nor shall it be uploaded to NDIS.

13.3.1.2 The laboratory will only upload the categories of DNA records that are acceptable at NDIS. These categories include Arrestee, Convicted Offender, Forensic Mixture, Multiallelic Offender, Forensic Partial, Forensic Unknown, Biological Child, Biological Father, Biological

Mother, Biological Sibling, Deduced Missing Person, Maternal Relative, Missing Person, Paternal Relative, Spouse and Unidentified Person.

13.4 Forensic DNA Record Eligibility for CODIS Entry:

13.4.1 All forensic STR DNA profiles being considered for entry into CODIS will be generated in adherence to the current Standard Operating Procedures for the DNA Unit of the CT Division of Scientific Services such that all DNA records to be submitted to NDIS are in accordance with Standard 9 of the QAS. Only NDIS accepted PCR testing kits will be used to generate these profiles.

13.4.2 All STR DNA results obtained from the analysis of forensic samples being considered for entry into CODIS will be analyzed by a second qualified analyst according to standard DNA protocols prior to entry into CODIS. This independent analysis will include the verification of all extraction and amplification controls, allelic ladders and internal lane standards.

13.4.3 (NDIS Upload) The CT Division of Scientific Services generally follows the principles described in ‘A Guide to Determining What is Allowable in the Forensic Index at NDIS” (DNA SOP 13.10) in determining the eligibility of a forensic STR DNA profile for upload to NDIS.

13.4.3.1 The analyst will review the case documentation to determine that a crime has been reported. If the analyst cannot ascertain that a crime was reported, the profile is not eligible for entry into NDIS unless additional information indicates a crime was committed.

13.4.3.2 If a crime has been reported, then the analyst will determine if the STR DNA profile was developed from a piece of evidence/biological material collected from a crime scene. If the evidence/biological material was not collected from a crime scene, then the forensic STR DNA profile shall not be uploaded to NDIS.

13.4.3.3 If the evidence/biological material was collected from a crime scene, then the analyst will establish that the forensic STR DNA profile to be entered into NDIS is attributable to the putative perpetrator. A good faith effort will be made and documented in the case file to obtain known samples from victims, consensual partners and other individuals for elimination purposes. If all other eligibility requirements are met, the profile may be entered into NDIS immediately following the documented attempt to obtain the elimination known. If the forensic STR DNA profile or unambiguous alleles are attributable to the victim or another individual other than the putative perpetrator, then the profile or unambiguous alleles shall not be uploaded to NDIS.

13.4.3.4 If the forensic STR DNA profile or unambiguous alleles are attributable to the putative perpetrator, then the analyst will review the case documentation and/or contact the submitting agency to determine if there is a suspect in the case. If there is no suspect in the case or no arrest has been made, the forensic STR DNA profile is eligible to be uploaded to NDIS.

13.4.3.5 If there is a suspect in the case, the analyst will ascertain whether the item from which the forensic STR DNA profile was developed was seized from the suspect's person or in the suspect's possession at the time of collection. Any forensic STR DNA profile generated from an item taken from the suspect's person or possession shall not be considered a forensic unknown nor shall it be eligible for entry into NDIS. If the item was not collected from the suspect's person or possession, the STR DNA profile is eligible for upload to NDIS.

13.4.3.6 Documentation of the eligibility of the forensic STR DNA profile will be recorded on DNA QR-13: CODIS Profile Entry Worksheet.

13.4.3.7 If information that indicates a profile is no longer eligible to be in the database is obtained after NDIS entry and/or searching, the profile shall be deleted from NDIS. If it is determined by the State's Attorney that no crime has been committed, the profile will be deleted from NDIS. If the profile is deleted after a report has already been issued, a "CODIS Change in Profile Status" memo will be completed.

13.4.3.8 When an analyst is uncertain whether an unknown profile is eligible for NDIS entry based on the information or lack of information available in the case jacket, the profile will be brought to the CODIS Administrator or designee(s) for review. Any mixture profile that has sufficient data but the intended profile entry does not meet the national moderate match estimation (MME) threshold will be brought to the CODIS Administrator. The CODIS Administrator or designee(s), will initial and date the statement of no CODIS entry for the sample in the Draft Report. In the event the CODIS State Administrator (or designee(s)) has verified the DNA record to be a State Forensic Mixture and not eliglible to be a Forensic Mixture on DNA-QR-13 (see DNA SOP 13.7.2), this documentation is sufficient and does not require further documentation of the Draft Report. The CODIS Administrator is responsible to ensure the quality of the data in the database and will make the final decision regarding profile eligibility.

13.4.4 (SDIS Entry) The CT Division of Scientific Services follows the DSS policies and procedures in determining the eligibility of a forensic STR DNA profile for entry at SDIS (DNA SOP 13.5, GL 1.2, PA 15-207).

13.4.4.1 Any DNA profile obtained from forensic unknown evidentiary samples submitted in accordance with DSS requirements (PA 15-207, GL 1.2, CT Statute 29-7b) may be entered into SDIS as discussed in 13.4.4.2-5 in accordance with the standards discussed in DNA SOP 13.5.

13.4.4.2 A good faith effort will be made and documented in the case file to obtain known samples from victims, consensual partners and other individuals for elimination purposes. If all other eligibility requirements are met, the profile should be entered into SDIS immediately following the documented attempt to obtain the elimination known. If the forensic STR DNA profile or unambiguous alleles are attributable to the victim or another elimination sample, then the profile or unambiguous alleles shall not be entered into SDIS.

13.4.4.3 Documentation of the eligibility of the forensic STR DNA profile will be recorded on DNA QR-13: CODIS Profile Entry Worksheet. Should circumstances warrant an exception to these eligibility requirements and the State Administrator allows an STR DNA profile to be entered at SDIS, the event will be documented on DNA-QR-13, “Describe why sample is eligible for SDIS CODIS entry” field. The State Administrator will initial and date the documentation.

13.4.4.4 If information that indicates a profile is no longer eligible to be in the database is obtained after SDIS entry and/or searching, the profile shall be deleted from SDIS. If it is determined by the State’s Attorney that no crime has been committed, the profile will be deleted from SDIS. If the profile is deleted after a report has already been issued, a “CODIS Change in Profile Status” memo will be completed.

13.4.4.5 When an analyst determines an unknown profile is not eligible for SDIS entry based on the information or lack of information available in the case jacket (or is uncertain of eligibility), the profile will be brought to the CODIS Administrator or designee(s) for review. Any profile that has sufficient data but the intended profile entry does not meet the state match estimation threshold will be brought to the CODIS Administrator. The CODIS Administrator or designee(s), will initial and date the statement of no CODIS entry for the sample in the Draft Report. The CODIS Administrator is responsible to ensure the quality of the data in the database and will make the final decision regarding profile eligibility.

13.5 Standards for Entering a Forensic STR DNA Profile into CODIS

13.5.1 All forensic STR DNA profiles to be entered into CODIS shall be interpretable such that the data can be used to make an exclusion. A good faith effort will be made to obtain complete and accurate results for each locus and enter all probative data from the STR DNA profile.

Additionally, the profile must be of sufficient quality to apply a statistical calculation to at least one locus in the event of a match. The locus/loci being used for statistical analysis and the type of statistical calculation to be applied will be documented on DNA QR-13.

13.5.1.1 Peaks between 50 and 74 rfu (* peaks) can be entered into CODIS keeping in mind the utility of the STR DNA profile after a database hit has occurred (i.e. without the use of * peaks a RMP, CPI or database match probability can still be generated). Only those alleles attributable to the putative perpetrator(s) shall be entered into NDIS. However if an ambiguity exists as to whether an allele(s) is attributable to the putative perpetrator and another individual (e.g. victim), the allele(s) is not precluded from being entered into NDIS (refer to 13.4.3.3).

13.5.1.2 Single source profiles: The analyst will determine which locus/loci a statistical calculation can be performed prior to making a CODIS entry. The profile entered will include all available data necessary to meet CODIS requirements (e.g. 13 CODIS core loci, minimum number of loci, maximum number of alleles per locus, MME, etc.).

13.5.2 Mixtures Not Deconvoluted: When the entire profile is above the stochastic threshold and an unrestricted CPI can be applied to the entire profile, the analyst may select the appropriate subset of alleles necessary to meet CODIS entry requirements (e.g. MME, maximum number of alleles per locus, minimum number of required loci etc). The analyst will evaluate the following profile features; peak height imbalance, potential stochastic fluctuation, and the discriminating power associated with including different loci or alleles. If unambiguous allele selection for CODIS entry is not possible, the analyst may generally enter more than one STR DNA profile into CODIS for a single forensic sample. The case analyst and the analyst verifying the profile(s) entry should discuss the possibility of entering more than one profile for a contributor, with the goal of maximizing the chance of generating an investigative lead following a database search. The match estimation function in PopStats or an in-house match estimation tool may be used to assist in determining which deconvoluted profile(s) should be entered to SDIS.

13.5.2.1 When the entire profile is not above the stochastic threshold and deconvolution of a major and or minor is not an option, the analyst will determine which locus/loci a statistical calculation can be performed prior to making a CODIS entry. The CODIS entry will be made as in 13.5.2 keeping in mind the locus/loci selected for statistical comparison.

13.5.3 Mixture to be Deconvoluted: In general, when a forensic STR DNA profile appears to be suitable for deconvolution into a major and or major/minor contributor or when circumstances permit use of a known profile to deduce the profile of another component to a DNA mixture, mixture deconvolution is performed as specified in DNA SOP-5 Section 5.4.8. The analyst will determine which locus/loci a statistical calculation can be performed prior to making a CODIS entry. However, since the purpose of CODIS entry is to elucidate sufficient components of a contributor to a mixture to enter a searchable profile, when otherwise the entire profile would not be suitable for a CODIS search, the requirements for CODIS entry deconvolutions may be less stringent than those for statistical purposes, report writing, and court testimony. Therefore, all the alleles or the appropriate subset of alleles may be entered into CODIS when a locus is determined to be indistinguishable through the deconvolution pathway.

13.5.4 Specimen categories for forensic samples are Forensic Unknown, State Forensic Unknown, Forensic Partial, State Forensic Partial, Forensic Mixture, and State Forensic Mixture.

13.5.4.1 A forensic STR DNA record shall be categorized as a Forensic Unkown or a State Forensic Unknown when the DNA profile originates from a single source forensic sample (or a fully deduced profile originating from a mixture) having apparent complete genotypes at all 13 core CODIS loci for NDIS and all 15 loci for SDIS, and shall not have more than 3 alleles at one locus while the remaining loci can have up to 2 alleles. If the profile to be entered was deconvoluted from a mixture the analyst should be confident that the profile being entered into the Forensic Unknown specimen category is a complete single source profile.

Note: If a profile has a locus with an apparent mutation resulting in a lower peak, it should be entered as a mixture even if it appears to be single-source, so that it will search at Moderate Stringency.

13.5.4.2 A forensic STR DNA record shall be categorized as a Forensic Partial when the DNA profile originates from a single source forensic sample (or a fully deduced profile originating from a mixture) in which either locus or allelic dropout has occurred at any of the 13 core CODIS loci. The DNA profle entered as a Forensic Partial must include data from at least 8 of the core CODIS loci. A Forensic Partial DNA record shall not have more than 3 alleles at one locus while the remaining loci can have up to 2 alleles.

13.5.4.2.1 A forensic STR DNA record shall be categorized as a State Forensic Partial when the DNA profile originates from a single source forensic sample (or a deduced profile originating from a mixture) in which either locus or allelic dropout has occurred. The DNA profle entered as a State Forensic Partial must include complete data from at least 6 loci. A State Forensic Partial DNA record shall not have more than 3 alleles at one locus while the remaining loci can have up to 2 alleles.

13.5.4.3 A forensic STR DNA record shall be categorized as Forensic Mixture when the DNA profile originates from a forensic sample comprised of DNA potentially contributed from more than one source and contains data from at least 8 of the core CODIS loci. A Forensic Mixture DNA record will have no more than four (4) alleles entered at any locus.

13.5.4.3.1 A forensic STR DNA record shall be categorized as State Forensic Mixture when the DNA profile originates from a forensic sample comprised of DNA contributed from more than one source and contains data from at least 8 loci. A State Forensic Mixture DNA record should have no more than four (4) alleles entered at any locus. The CODIS Administrator may give approval to exceed the four allele limit for SDIS only. The CODIS Administrator will document the exception to the rule on QR-13 or the Specimen Detail Report.

13.5.5 All Forensic Mixture and Forensic Partial DNA records will be evaluated to ensure the DNA record will satisfy a statistical threshold for MME in CODIS of 10^7. Data from the 13 core loci will be used to calculate the MME for NDIS.

All State Forensic Mixture and State Forensic Partial DNA records will be evaluated to ensure the DNA record will satisfy a statistical threshold for an average number of matches of approximately five (5) matches in the size of the State DNA database with one (1) mismatch when data at 10 or more loci are entered and zero (0) mismatches when data at 9 or less loci are entered.

For profiles entered at SDIS only, the match estimation function in PopStats or an in-house match estimation tool may be used to assist in determining the statistical threshold for profile(s) entered into CODIS.

13.5.5.1 The CODIS State Administrator may approve exceptions to the above rule for records entered at SDIS only. Approval of the CODIS Administrator, initials and date, will be documented on the specimen detail report or on DNA-QR-13.

13.5.6 Composite STR DNA profiles may be submitted to SDIS and NDIS. The CT Division of Scientific Services defines a composite STR DNA profile as a profile generated from combining the allelic data obtained from the amplification(s) of a single extracted evidentiary sample by more than one PCR kit (e.g. ABI AmpF*l*STR Identifiler/Identifiler Plus and Minifiler kits) and/or multiple amplifications of the same extact using a single PCR kit, or by combining data from more than one injection from a single amplification from a single kit.

13.5.7 Generally, a manual keyboard search compares a DNA profile against DNA records contained in SDIS without the searched DNA profile being entered as a DNA record into SDIS or uploaded into NDIS. Keyboard searches are not intended to be a replacement for scheduled searches, however in the event of exigent circumstances, a DNA record may be keyboard searched with the permission of the State Administrator. Discretion will be used in making such decisions, keeping in mind the investigative usefulness of the information gained from the search, state laws and other legal considerations. Approval of the CODIS Administrator for all keyboard searches (initials and date) will be documented on the match detail report or QR-13 (in the event of no matches).

13.5.7.1 Configuration Data for a Keyboard Search

✓ Return All Candidates
✓ STR
Minimum # of loci to report a match = **6**
Include Specimen Candidates that Match at all but **0** loci
✓ Use as Match Filter
Index(es) to Search In = Forensic, Forensic Partial, Forensic Mixture, Offender, Multiallelic Offender
Candidate View = Default
Stringency = **M** (Moderate)*

If data from 10 or more loci are entered a second keyboard search should be conducted with the same parameters as above except the following:

Minimum # of loci to report a match = **9**
Include Specimen Candidates that Match at all but **1** loci

13.5.7.2 A request to the NDIS Custodian can be made for a keyboard search of a DNA profile at NDIS in exigent circumstances as defined in the NDIS Procedures or if the DNA profile generated from a serious violent crime does not meet the minimum required loci but does satisfy the statistical threshold for match rarity of one (1) in the size of the National DNA database.

Note: If the statistical threshold is not satisfied but the exact genotype can be determined for one or more loci, the request to search the profile may be submitted to NDIS along with this list of loci that can be searched at high stringency to improve the match rarity statistic. Only core loci are used in the match rarity estimate.

13.5.7.3 STR DNA profiles that have been keyboard searched may be saved to an appropriate Batch Target file in order to be searched periodically at SDIS. A Batch Target file is a single file containing several DNA profiles that may be used as target profiles during a search.

13.5.7.4 In instances where it is highly likely that the source of the profile is the listed victim and a known reference sample from the victim has not been submitted, following the request and documentation of a known reference sample, the CODIS Administrator may conduct a keyboard search using the parameters listed in 13.5.7.1 except the following:

Index(es) to Search In = Offender, Multiallelic Offender

If this keyboard search generates a match and it is determined that the matching Offender is the listed victim, the match will be saved. The profile will not be entered into SDIS or NDIS. The disposition for this match will be Investigative Information. The submitting agency will be notified of this information either the DNA report, by the CIPS form, or by the CODIS unit.

If this keyboard search generates a match and it is determined that the matching Offender is not the listed victim, the match will be saved and confirmed according to SOP 15. The profile should be entered into SDIS and/or NDIS as appropriate.

If this keyboard search does not generate any matches, the profile should be entered into SDIS and/or NDIS as appropriate. If at any time it is determined that this profile is attributable to the victim, it will be deleted from CODIS.

13.5.8 Low template and low copy DNA analyses are not conducted by the DNA Section of the CT Division of Scientific Services, therefore no profiles of this nature will be submitted to SDIS or NDIS.

13.6 Entering a Forensic STR DNA Profile into CODIS (Creating a DNA Record)

13.6.1 A qualified DNA analyst will establish a unique DNA record for each profile to be entered into CODIS. A second qualified DNA analyst will verify the accuracy and eligibility of the DNA record. The first qualified DNA analyst will document the establishment of a unique DNA record on DNA-QR-13 by recording the case #, the submission/item #, item description and the intended specimen category for the profile to be entered into CODIS.

13.6.1.1 If the final specimen category for the DNA record is intended to be Forensic Unknown, establish a DNA record by opening Analyst Workbench. Click on the STR/Y-STR Data Entry icon (red notebook and pencil icon).

13.6.1.2 Enter the Specimen ID # in the STR/Y-STR Data Entry window. The specimen ID # is the laboratory case # followed by a space then the submission/item # (e.g. 11-4444 1CB). If this is an SDIS-only profile because of case scenario, the letters CT will precede the specimen ID# (e.g. CT 11-4444 1CB). For ease in querying DNA records, the laboratory case # should be entered with at least four digits after the year (e.g. 12-**00**xx 1S1 rather than 12-xx 1S1). If more than one DNA record will be established for a DNA profile, then a suffix should be added to the Specimen ID # (e.g. 11-4444 1CB-MAJ or 11-4444 1CB-major).

13.6.1.3 Click on the pull down arrow for Specimen Category and select OTHER. OTHER has been defined as a nonsearchable specimen category.

13.6.1.4 If the profile to be entered has been associated with a known sample, using the pulldown menu for Source Identified?, select YES. Otherwise, select NO.

13.6.1.5 Enter the probative alleles/*peaks for each locus under Reading #1. Enter the probative alleles/*peaks for each locus under Reading #2. Check to make sure that both readings are concordant.

13.6.1.6 If the final specimen category for the DNA record is intended to be State Forensic Partial, State Forensic Mixture, Forensic Partial or Forensic Mixture and there are potentially additional probative alleles/*peaks that have not been entered, using the pulldown menu change Partial Profile to Yes.

13.6.2 If the final specimen category for the DNA record is intended to be State Forensic Partial or State Forensic Mixture, open Popstats and access Match Estimation. Enter the probative alleles/*peaks for each locus. Change the Database Specimen Count to the size of the appropriate database. Change the number of mismatches as appropriate for the database and number of loci entered. Click calculate and observe the average number of moderate matches to verify the match rarity estimation meets the appropriate statistical threshold. Document that the average number of matches satisfies the statisical threshold on DNA-QR-13.

13.6.2.1 If necessary, the entered alleles/*peaks may be modified appropriately to attain the statistical threshold. The State Administrator may approve the entry of a DNA record that does not meet the statistical threshold for SDIS. Discretion will be used in making such decisions, keeping in the mind the circumstances of the particular case, the ability to verify any matches with a second technology and other legal considerations. The State Administrator will document his/her approval on DNA-QR-13. The CODIS software will automatically reject any profile uploaded to NDIS that does not have an MME of 10^7 or greater.

13.7 Verification of a Forensic STR DNA Record.

13.7.1 A second qualified DNA analyst will verify the eligibility of the DNA record to be entered into CODIS. To verify the eligibility of the DNA record, confirm that the forensic STR DNA profile meets the requirements stated in section 13.4. Document verification of eligibility on DNA-QR-13.

13.7.2 Any qualified DNA analyst may verify the accuracy of the DNA record intended to be a State Forensic Unknown, State Forensic Partial, Forensic Unknown or Forensic Partial. The

CODIS State Administrator (or designee(s)) will verify the accuracy of the DNA record for any State Forensic Mixture or Forensic Mixture. Open Analyst Workbench. Click on Specimen Manager. Click on the EDIT icon and query the DNA record. Click on the STR/Y-STR Data entry icon.

13.7.2.1 Confirm that the correct alleles have been entered at each locus. To document this verification, under the Verified By column, click on the blank box for the first locus with entered data and select username from the pulldown menu. The Verified Date will automatically be populated. Repeat this step for every locus that has entered data.

13.7.2.2 If the appropriate specimen category is Forensic Partial, Forensic Mixture, State Forensic Partial or State Forensic Mixture, then the verifying DNA analyst will validate the compatibility of the DNA record for entry into State DNA database and/or upload to NDIS by checking the appropriate statistic. For state-only profiles this is done using Match Estimation in PopStats. Open Popstats and access Match Estimation. Enter the Specimen ID and click Retrieve. Change the Database Specimen Count to the size of the appropriate database. Change the number of mismatches as appropriate for the database and number of loci entered. Click Calculate and observe the Average Number of Moderate Matches to verify the match rarity Threshold. Document that the estimation satisfies the appropriate statistical threshold on DNA-QR-13.

13.7.2.3 Change the specimen category from OTHER to the appropriate FORENSIC specimen category. (Refer to section13.5.4.1 through13.5.4.3.1). CLOSE the Specimen Detail Report window.

13.7.3 A verifying DNA analyst will mark an eligible DNA record for upload to NDIS. The DNA record is “marked” for upload to NDIS when the column called “Marked Date” is populated. If the DNA record should be uploaded to NDIS and ‘Marked Date” column is unpopulated, click on the” Mark Specimen for Upload” icon. Document whether the DNA record is marked for upload to NDIS on DNA-QR-13.

13.7.3.1 If the DNA record is not eligible for upload to NDIS, the column called “Marked Date” should be unpopulated. If necessary, click on the “Unmark Specimen for Upload” icon. The reason for unmarking a specimen for upload to NDIS should be recorded on DNA QR-13 and in the comments section of STR data entry.

13.7.3.2 PRINT the Specimen Detail report.

13.7.4 The first qualified DNA analyst will confirm that the correct specimen category was selected and indicate this by initialling and dating the Specimen Detail report prior to the next Autosearch.

13.8 Conducting Searches and Search Parameters

13.8.1 Search of Forensic Profiles to the Staff Index

13.8.1.1 All forensic profiles (single source profiles and mixtures of no more than 3 individuals) shall be searched against the staff index unless the profile can be unambiguously attributed to elimination, suspect, or victim known(s) or insufficient data was generated to conduct such a search. DNA mixtures of 4 or more individuals will be searched only against the persons who processed the item. This search may be conducted against the staff index contained within the Cross-Comparison & Staff Search tool manually or aided by macros in the file, or in CODIS against the staff index. Document the staff search results on QR-20.

13.8.1.1.2 Mixtures to be searched against the staff index should be treated in the same manner as if being entered into CODIS. If the alleles from an unknown source can be separated from those attributable to a known, then only the alleles and *peaks from the unknown source need to be searched. Refer to section 13.5.3. If the source of the alleles in a mixture cannot be determined, then all of the detected alleles and * peaks are searched.

13.8.1.2 To search a forensic profile against the staff index using CODIS, open Analyst Workbench, click on Searcher and select Staff under Identity Search.

13.8.1.2.1 Enter a Specimen ID. If the full profile (all alleles and * peaks) has already been entered into CODIS, click the Retrieve button. If the full profile is not in CODIS, enter the additional alleles detected in the profile. It may be necessary to enter and search various combinations and numbers of alleles/loci (e.g. all called alleles vs. only low level alleles) to ensure that a staff profile is not present. The search configuration may also be set to allow for a no match at one or two loci, stringency at high or moderate and, the minimum number of loci required to report a match may be modified. The search configuration can be modified in the Searcher program, select the Tools drop down, then select Identity Search Configuration. Modify the configuration as needed to perform an appropriate search.

13.8.1.2.2 Perform the search by clicking the Search button. When the search is completed the Match Detail window will appear.

13.8.1.2.3 If no matches to the staff index were made, the column next to the Target (searched) profile will display "No matches found on *DATE, TIME*). Click File then Exit to close Searcher or click Staff under Identity Search to conduct another search. When the small Match Details window appears, click OK to continue without saving the match. If the search configuration was changed a small window will appear, click OK to continue without saving the configuration.

13.8.1.2.4 If potential matches to the staff index were made, the column(s) next to the Target profile will display the Candidate profile(s). Review the forensic profile including the electropherograms, peak height intensities and other relevant information to determine whether the match(es) is coincidental or confirmed.

13.8.1.2.5 If the match is not valid, click File then Exit to close Searcher. When the small Match Details window appears, click OK to continue without saving the match. If the search configuration was changed a small window will appear, click OK to continue without saving the configuration.

13.8.1.2.6 If a match to the staff index is confirmed (including coincidental matches), print and save the match. Select the matching Candidate Specimen from the list then right click on the Candidate Specimen. Select Print Reports then click Print to print the Match Detail Report. Right click again on the matching Candidate Specimen and select Save Results to Match Manager to save the match. Inform the Technical Leader of the DNA section as soon as possible. Any staff match will be given the disposition Investigative Information. For those deemed to be coincidental matches, a note will be added to the comments section indicating this information.

13.8.1.2.8 Record the results of the staff search on DNA QR-20. Any positive matches require TL approval.

13.8.1.2.9 Default Configuration Data for a Staff Search:
√ Return All Candidates
√ STR
Minimum # of loci to report a match = **3***
Include Specimen Candidates that Match at all but **1*** loci
√ Use as Match Filter
Index(es) to Search In = Staff and/or Staff-Archived** as appropriate
Candidate View = Default
Stringency = **M** (Moderate)*

*These numbers can be modified to better evaluate the possibility of a staff match.
**Staff = currently/recently employed lab personnel and current/recent interns and visitors
Staff- Archived = previously employed personnel and past interns and visitors, currently employed non-laboratory staff, and OCME staff and outsource lab staff

13.8.2 Scheduled AutoSearches at SDIS

13.8.2.1 An Autosearch is a set of parameters that is established to automatically search all DNA profiles in a specified index against all profiles in other specified indexes. Autosearches are conducted at SDIS at a time determined by the State Administrator. The six autosearches outlined in 13.8.2.1.1 through 13.8.2.1.6 shall be scheduled to occur at least once weekly. The one autosearch outlined in 13.8.2.1.7 shall be scheduled to occur at least once monthly.

13.8.2.1.1 Configuration Data for High Stringency 6 Loci 0 loci no match

✓ Return All Candidates
✓ STR
Minimum # of loci to report a match = **6**
Include Specimen Candidiates that Match at all but **0** loci
✓ Use as Match Filter
✓ Required to report a Match
AutoSearcher Mode = Standard
Specimens to Search = Specimens Not Previously Searched
Index(es) to Search In =
Forensic vs. Forensic
Forensic vs. Forensic Mixture
Forensic vs. Offender
Forensic Mixture vs. Forensic
Forensic Mixture vs. Forensic Mixture
Forensic Mixture vs. Offender
Offender vs. Forensic
Offender vs. Forensic Mixture
Forensic Partial vs. Forensic
Forensic Partial vs. Forensic Partial
Forensic Partial vs. Forensic Mixture
Forensic Partial vs. Offender
Forensic vs. Forensic Partial
Forensic Mixture vs. Forensic Partial
Offender vs. Forensic Partial
Match Reports = Automatically send Match Reports to Remote Labs
Stringency = **H** (High)

13.8.2.1.2 Configuration Data for High Stringency 8 Loci 1 locus no match

✓ Return All Candidates
✓ STR
Minimum # of loci to report a match = **7**
Include Specimen Candidiates that Match at all but **1** loci
✓ Use as Match Filter
✓ Required to report a Match
AutoSearcher Mode = Standard
Specimens to Search = Specimens Not Previously Searched

Index(es) to Search In =
Forensic vs. Forensic
Forensic vs. Forensic Mixture
Forensic vs. Offender
Forensic Mixture vs. Forensic
Forensic Mixture vs. Forensic Mixture
Forensic Mixture vs. Offender
Offender vs. Forensic
Offender vs. Forensic Mixture
Forensic Partial vs. Forensic
Forensic Partial vs. Forensic Partial
Forensic Partial vs. Forensic Mixture
Forensic Partial vs. Offender
Forensic vs. Forensic Partial
Forensic Mixture vs. Forensic Partial
Offender vs. Forensic Partial
Match Reports = Automatically send Match Reports to Remote Labs
Stringency = **H (**High)

13.8.2.1.3 Configuration Data for Mod Stringency 10 Loci 1 locus no match

√ Return All Candidates
√ STR
Minimum # of loci to report a match = **9**
Include Specimen Candidiates that Match at all but **1** loci
√ Use as Match Filter
√ Required to report a Match
AutoSearcher Mode = Standard
Specimens to Search = Specimens Not Previously Searched
Index(es) to Search In =
Forensic vs. Forensic
Forensic vs. Forensic Mixture
Forensic vs. Offender
Forensic Mixture vs. Forensic
Forensic Mixture vs. Forensic Mixture
Forensic Mixture vs. Offender
Offender vs. Forensic
Offender vs. Forensic Mixture
Forensic Partial vs. Forensic
Forensic Partial vs. Forensic Partial
Forensic Partial vs. Forensic Mixture
Forensic Partial vs. Offender
Forensic vs. Forensic Partial
Forensic Mixture vs. Forensic Partial
Offender vs. Forensic Partial
Match Reports = Automatically send Match Reports to Remote Labs
Stringency = **M** (Moderate)

13.8.2.1.4 Configuration Data for Mod Stringency 8 Loci 0 loci no match

√ Return All Candidates
√ STR
Minimum # of loci to report a match = **8**
Include Specimen Candidiates that Match at all but **0** loci
√

Use as Match Filter
√ Required to report a Match
AutoSearcher Mode = Standard
Specimens to Search = Specimens Not Previously Searched
Index(es) to Search In =

- Forensic vs. Forensic
- Forensic vs. Forensic Mixture
- Forensic vs. Offender
- Forensic Mixture vs. Forensic
- Forensic Mixture vs. Forensic Mixture
- Forensic Mixture vs. Offender
- Offender vs. Forensic
- Offender vs. Forensic Mixture
- Forensic Partial vs. Forensic
- Forensic Partial vs. Forensic Partial
- Forensic Partial vs. Forensic Mixture
- Forensic Partial vs. Offender
- Forensic vs. Forensic Partial
- Forensic Mixture vs. Forensic Partial
- Offender vs. Forensic Partial

Match Reports = Automatically send Match Reports to Remote Labs
Stringency = **M** (Moderate)

13.8.2.1.5 Configuration Data for Mod Stringency 6 Loci 0 loci no match

√Return All Candidates
√STR
Minimum # of loci to report a match = **6**
Include Specimen Candidiates that Match at all but **0** loci
√Use as Match Filter
√Required to report a Match
AutoSearcher Mode = Standard
Specimens to Search = Specimens Not Previously Searched
Index(es) to Search In =

- Forensic vs. Unidentified Human Remains (UHR)
- Forensic Mixture vs. UHR
- Missing Person vs. UHR
- Offender vs. UHR
- Forensic vs. Missing Person
- Forensic Mixture vs. Missing Person
- Offender vs. Missing Person
- UHR vs. Forensic
- UHR vs. Forensic Mixture
- UHR vs. Missing Person
- Forensic Partial vs. UHR
- Forensic Partial vs. Missing Person
- UHR vs. Forensic Partial
- Missing Person vs. Forensic Partial
- Missing Person vs. Forensic
- Missing Person vs. Forensic Mixture
- Missing Person vs.Offender
- UHR vs. UHR
- UHR vs. Offender

Match Reports = Automatically send Match Reports to Remote Labs
Stringency = **M** (Moderate)

13.8.2.1.6 Configuration Data for Low Stringency 6 Loci 0 loci no match

√Return All Candidates
√STR
Minimum # of loci to report a match = **6**
Include Specimen Candidiates that Match at all but **0** loci
√ Use as Match Filter
√ Required to report a Match
AutoSearcher Mode = Standard
Specimens to Search = Specimens Not Previously Searched
Index(es) to Search In =
UHR vs. Relatives of Missing Person
UHR vs. UHR
Relatives of Missing Persons vs. UHR
Missing Person vs. Relatives of Missing Person
Relatives of Missing Person vs. Missing Person
Match Reports = Automatically send Match Reports to Remote Labs
Stringency = **L**(Low)

13.8.2.1.7 Configuration for Mitochondrial DNA Search
√Return All Candidates
√ Mito
Minimum # of Overlapping Base Pairs to report a Match = **400**
√ Use as Match Filter
√ Required to Report a Match
AutoSearcher Mode = Standard
Specimens to Search = Specimens Not Previously Searched
Index(es) to Search In =
UHR vs. Relatives of Missing Person
UHR vs. UHR
Missing Person vs. UHR
UHR vs. Missing Person
Relatives of Missing Persons vs. UHR
Missing Person vs. Relatives of Missing Person
Relatives of Missing Person vs. Missing Person
Match Reports = Automatically send Match Reports to Remote Labs

13.8.3 Manual AutoSearch

13.8.3.1 Configuration Data for Duplicate Offenders

✓ Return All Candidates
✓ STR
Minimum # of loci to report a match = **12**
Include Specimen Candidiates that Match at all but **1** loci
✓ Use as Match Filter
✓ Required to report a Match
AutoSearcher Mode = Standard
Specimens to Search = Specimens Not Previously Searched
Index(es) to Search In = Offender vs.Offender
Match Reports = Automatically send Match Reports to Remote Labs
Stringency = **H** (High)

13.8.3.2 Additonal manual Autosearch configurations and searches may be authorized by the CODIS Administrator.

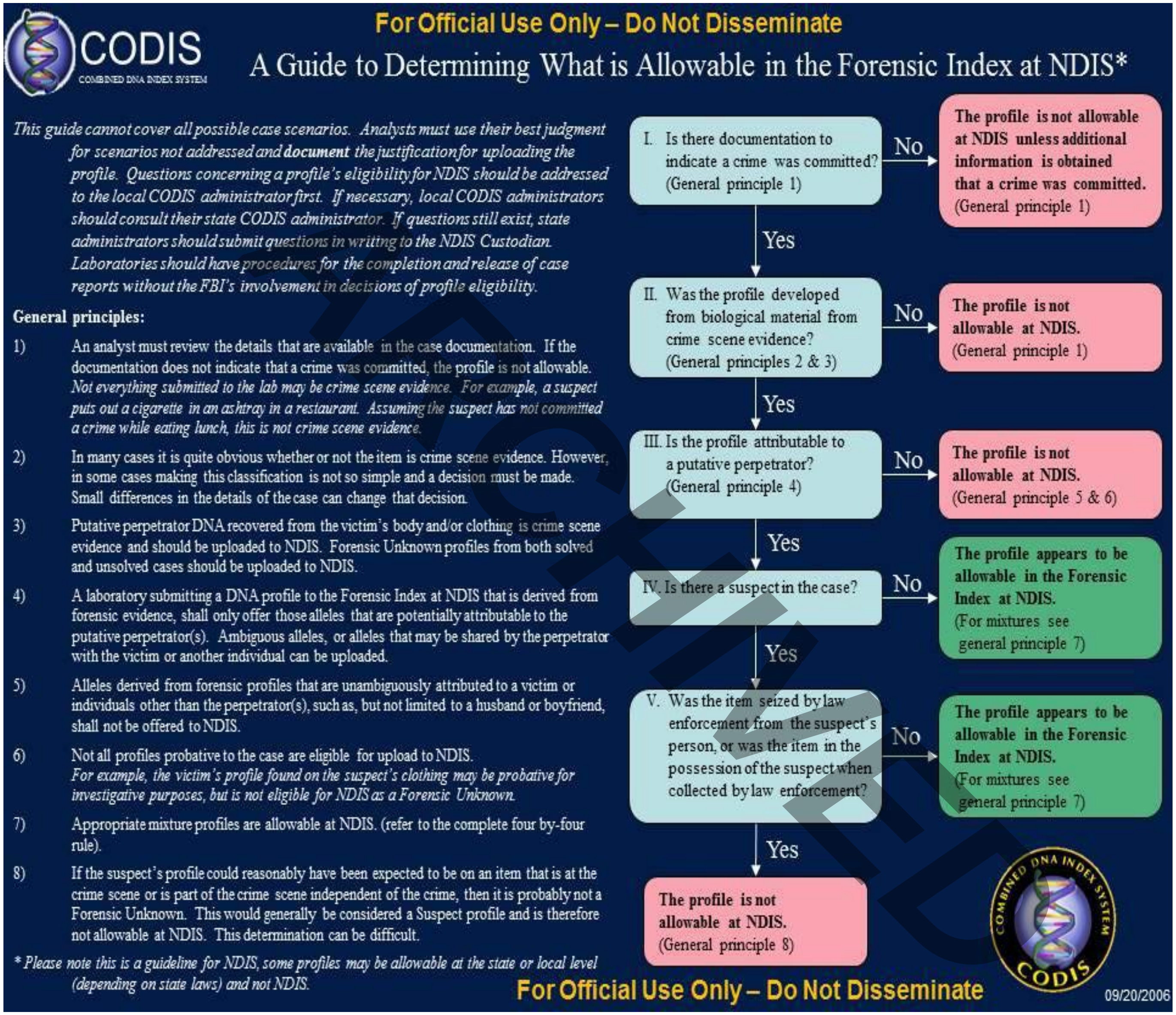
13.8.4 **Familial Searching**

13.8.4.1 The CT Division of Scientific Services does not conduct Familial Searches at this time.

13.9 **Upload of DNA records to NDIS**

13.9.1 An incremental upload of DNA records will be sent to NDIS at least once weekly at a time determined by the State Administrator. Full uploads of DNA records to NDIS will be scheduled with the permission of the NDIS custodian. A full upload should occur at least once annually.

13.10 A Guide to Determining What is Allowable for NDIS Entry



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CODIS
COMBINED DNA INDEX SYSTEM

A Guide to Determining What is Allowable in the Forensic Index at NDIS*

This guide cannot cover all possible case scenarios. Analysts must use their best judgment for scenarios not addressed and ***document*** *the justification for uploading the profile. Questions concerning a profile's eligibility for NDIS should be addressed to the local CODIS administrator first. If necessary, local CODIS administrators should consult their state CODIS administrator. If questions still exist, state administrators should submit questions in writing to the NDIS Custodian. Laboratories should have procedures for the completion and release of case reports without the FBI's involvement in decisions of profile eligibility.*

General principles:

1) An analyst must review the details that are available in the case documentation. If the documentation does not indicate that a crime was committed, the profile is not allowable. *Not everything submitted to the lab may be crime scene evidence. For example, a suspect puts out a cigarette in an ashtray in a restaurant. Assuming the suspect has not committed a crime while eating lunch, this is not crime scene evidence.*
2) In many cases it is quite obvious whether or not the item is crime scene evidence. However, in some cases making this classification is not so simple and a decision must be made. Small differences in the details of the case can change that decision.
3) Putative perpetrator DNA recovered from the victim's body and/or clothing is crime scene evidence and should be uploaded to NDIS. Forensic Unknown profiles from both solved and unsolved cases should be uploaded to NDIS.
4) A laboratory submitting a DNA profile to the Forensic Index at NDIS that is derived from forensic evidence, shall only offer those alleles that are potentially attributable to the putative perpetrator(s). Ambiguous alleles, or alleles that may be shared by the perpetrator with the victim or another individual can be uploaded.
5) Alleles derived from forensic profiles that are unambiguously attributed to a victim or individuals other than the perpetrator(s), such as, but not limited to a husband or boyfriend, shall not be offered to NDIS.
6) Not all profiles probative to the case are eligible for upload to NDIS. *For example, the victim's profile found on the suspect's clothing may be probative for investigative purposes, but is not eligible for NDIS as a Forensic Unknown.*
7) Appropriate mixture profiles are allowable at NDIS. (refer to the complete four by-four rule).
8) If the suspect's profile could reasonably have been expected to be on an item that is at the crime scene or is part of the crime scene independent of the crime, then it is probably not a Forensic Unknown. This would generally be considered a Suspect profile and is therefore not allowable at NDIS. This determination can be difficult.

** Please note this is a guideline for NDIS, some profiles may be allowable at the state or local level (depending on state laws) and not NDIS.*

I. Is there documentation to indicate a crime was committed? (General principle 1)
No → **The profile is not allowable at NDIS unless additional information is obtained that a crime was committed.** (General principle 1)
Yes ↓

II. Was the profile developed from biological material from crime scene evidence? (General principles 2 & 3)
No → **The profile is not allowable at NDIS.** (General principle 1)
Yes ↓

III. Is the profile attributable to a putative perpetrator? (General principle 4)
No → **The profile is not allowable at NDIS.** (General principle 5 & 6)
Yes ↓

IV. Is there a suspect in the case?
No → **The profile appears to be allowable in the Forensic Index at NDIS.** (For mixtures see general principle 7)
Yes ↓

V. Was the item seized by law enforcement from the suspect's person, or was the item in the possession of the suspect when collected by law enforcement?
No → **The profile appears to be allowable in the Forensic Index at NDIS.** (For mixtures see general principle 7)
Yes ↓

The profile is not allowable at NDIS. (General principle 8)

COMBINED DNA INDEX SYSTEM CODIS

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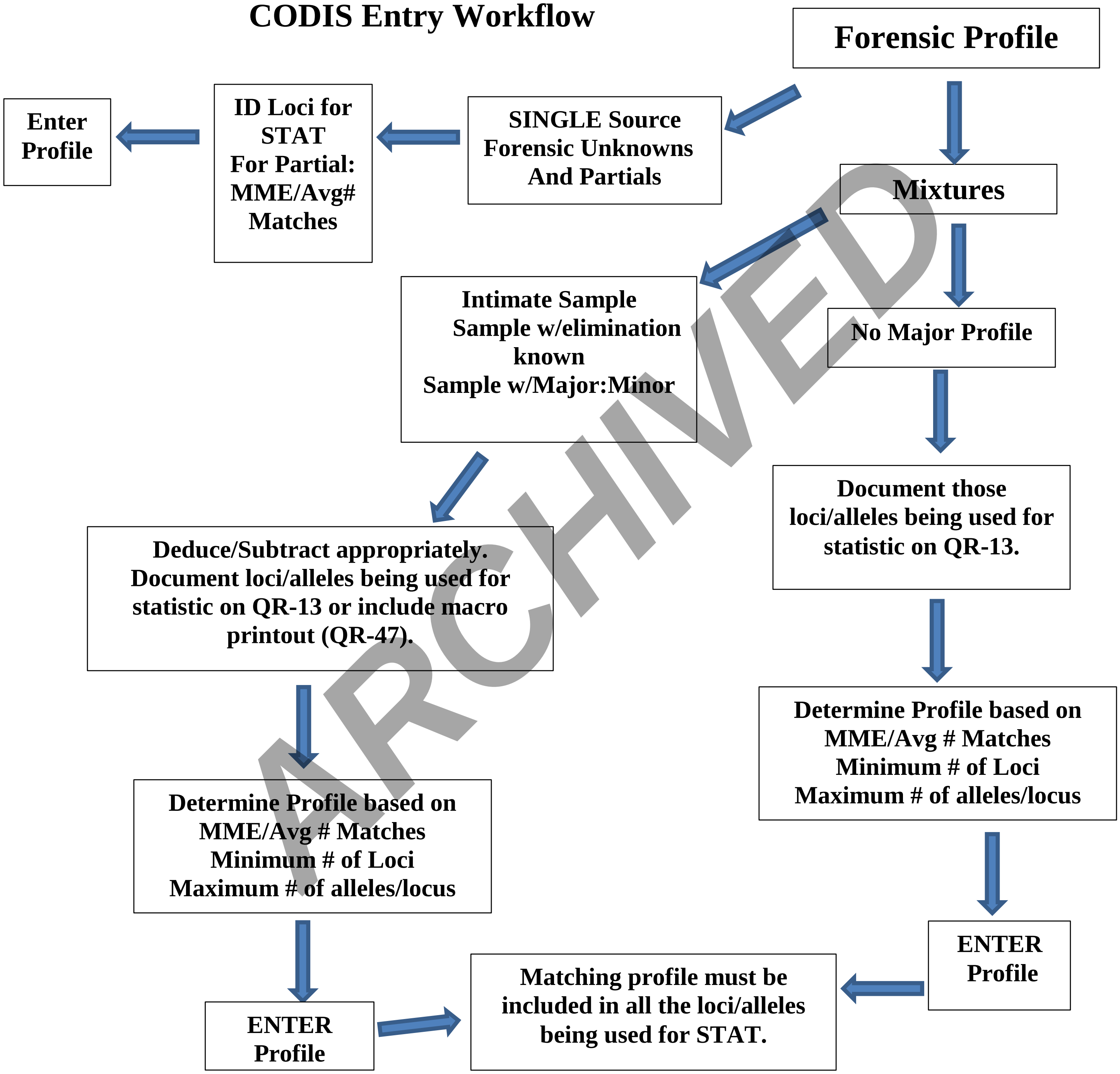
13.11 Misdemeanors with Enhanced Felony Penalties

53a-40(e)/53a-125	Larceny 4th degree
53a-40(e)/53a-125a	Larceny 5th degree
53a-40(e)/53a-125b	Larceny 6th degree
53a-40a/46a-58(a)	Deprivation of Rights
53a-40a/46a-58(b)	Desecration of Property
53a-40a/46a-58(c)	Cross Burning
53a-40a/53a-1811	Intimidate due to Bias 3rd degree
53a-40b	Criminal Act (Misdemeanor) While on Bond
53a-40d/53a-61	Assault 3rd degree
53a-40d/53a-61(a)(1)	Assault 3rd degree - Physical Injury
53a-40d/53a-61(a)(2)	Assault 3rd degree - Reckless Serious Injury
53a-40d/53a-61(a)(3)	Assault 3rd degree - Negligent Injury-Weapon
53a-40d/53a-61a	Victim Assault 3rd degree-Victim Elderly or Other
53a-40d/53a-181d	Stalking 2nd degree
53a-40d/53a-62	Threatening 2nd degree
53a-40d/53a-183b	Interfering with an Emergency Call
53a-40d/53a-183c	Disruption of a Funeral
53a-40d/53a-107	Criminal Trespass 1st degree
53a-40d/53a-107(a)(4)	Criminal Trespass 1st degree-Public Land
53a-217e(f)/53a-217e(c)	Negligent Hunting 2nd degree

CODIS Entry Workflow



Forensic Profile

SINGLE Source Forensic Unknowns And Partials

ID Loci for STAT For Partial: MME/Avg# Matches

Enter Profile

Mixtures

Intimate Sample
Sample w/elimination known
Sample w/Major:Minor

Deduce/Subtract appropriately. Document loci/alleles being used for statistic on QR-13 or include macro printout (QR-47).

Determine Profile based on
MME/Avg # Matches
Minimum # of Loci
Maximum # of alleles/locus

ENTER Profile

Matching profile must be included in all the loci/alleles being used for STAT.

No Major Profile

Document those loci/alleles being used for statistic on QR-13.

Determine Profile based on
MME/Avg # Matches
Minimum # of Loci
Maximum # of alleles/locus

ENTER Profile