



Forensic Biology Section

CODIS Entering Uploading and Searching Casework DNA Profiles

1. **Scope**

- 1.1. Guidelines and instructions for entering, uploading, and searching casework DNA profiles in the State DNA Index System (SDIS) and National DNA Index System (NDIS), collectively known as the Combined DNA Index System (CODIS), comprised of DNA profiles from all 50 states, the District of Columbia, the federal government, the U.S. Army Criminal Investigation Laboratory, and Puerto Rico.
- 1.2. This protocol applies to casework profiles (Forensic, Forensic Mixture, Forensic Mixture-SDIS, Forensic Partial, Forensic Partial-SDIS, and Forensic Targeted) and to missing or unknown individuals (Missing Person, Unidentified Human Remains, Relatives of Missing Persons).
- 1.3. This protocol does not apply to convicted offenders (Offender and Multi-allelic Offenders). There is separate protocol for those types of samples.

2. **Requirements**

- 2.1. All individuals involved in reading or entering data in CODIS must be entered as a "User" in the state CODIS system and approved by the FBI as qualifying for CODIS access. The FBI must be notified in writing about the addition or deletion of any users. Refer to the FBI's NDIS Operational Procedures Manual for appropriate forms and fingerprint cards.
- 2.2. DNA Analysts involved in reading and entering/deleting/modifying DNA profiles in CODIS must be authorized by NDIS, meet the FBI Quality Assurance Standards for a DNA Analyst, and complete any annual online training required by NDIS.
- 2.3. If the CODIS Administrator position is unoccupied and there is no backup CODIS Admin, profiles cannot be uploaded to NDIS.
- 2.4. Technicians involved in reading but NOT entering/deleting/modifying DNA profiles in CODIS must be authorized by NDIS and complete any annual online training required by NDIS.
- 2.5. State of Maine computer technicians who have login access to the CODIS computers must be authorized by NDIS.

3. **Procedural Notes**

- 3.1. Only DNA profiles originating from and/or associated with a crime scene relevant to a criminal investigation and attributable to a putative perpetrator may be considered for database entry. If there is strong doubt as to whether a sample is from a crime scene, an attempt to contact the investigator(s) should be made and documented in an attempt to clarify the origin of the item (e.g. whether an item is from a crime scene or is simply a secondary known).
- 3.2. DNA profiles must potentially be from a putative perpetrator. DNA profiles that are unambiguously attributable to a victim, non-involved party, or from a random collection of biological materials, are not allowed in NDIS. Ambiguous or shared alleles may be entered if they meet the other criteria in this section.
- 3.3. DNA profiles entered into CODIS that do not meet the NDIS requirements for number of loci or match probability may still be entered into the local database under the "-SDIS" categories (e.g. Forensic Mixture-SDIS or Forensic Partial-SDIS) because they are not uploaded to NDIS.



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- 3.4. Other than Missing Person cases, the State of Maine does NOT enter or search DNA profiles for the purpose of finding individuals closely related to the DNA profile being searched (i.e. “familial” or “partial match” searches), nor will these types of searches be performed at the request of agencies from outside the state of Maine.
- 3.5. Matches from CODIS which result from an error made in good faith will still be reported to the investigating agency (and prosecutor’s office if possible). The nature of the error should be included in the report or communications. It is up to the court to decide whether suppression or exclusion of the evidence is warranted under the circumstances.
- 3.6. The State CODIS Admin (or designee) will regularly check profiles in database (approximately once a year) to ensure the proper category designations have been marked for upload. If profiles were not marked properly, the DNA Analysts will be notified that they need to edit or mark those profiles.

4. Criteria for Casework DNA Profiles Allowed in the Maine Database (SDIS)

- 4.1. Casework DNA profiles to be entered into SDIS include Forensic Unknown, Forensic Mixture, Forensic Mixture-SDIS, Forensic Partial, Forensic Partial-SDIS, Forensic Targeted, Population, Unidentified Human (Remains), Missing Person, and Relatives of Missing Person profiles. These profiles are then uploaded to NDIS if they meet any statistical match probabilities and required number of loci as required by NDIS.
- 4.2. “Forensic Mixture-SDIS” and “Forensic Partial-SDIS” are for mixtures and partial profiles that do not qualify for NDIS but can be stored and searched in SDIS. These SDIS-specific profiles will only be searched against the Maine database and are blocked from uploading to NDIS. If too many non-specific/spurious matches occur with a given SDIS-specific profile, that profile may need to be deleted from the database.
- 4.3. The “Population” index exists in SDIS and is not uploaded to NDIS. The DNA profiles in the Population index help monitor for contamination from Staff in any of the profiles entered into the database. Staff includes but is not limited to: Crime Lab staff, Law Enforcement officers, and staff at the Medical Examiner’s Office.
- 4.4. Composite DNA profiles may be entered into SDIS. These are combined DNA profiles created from multiple injections and/or amplifications from the same DNA extract. In certain cases, multiple extractions may also be considered a composite DNA profile if there is a reasonable expectation that the sample originated from a common source (e.g. duplicate vaginal swabs, known reference samples, bone, and contiguous cuttings from a single visible stain).
- 4.5. Low Template or Low Copy Number DNA profiles may not be entered into SDIS. These are profiles generated from extremely limited quantity and/or quality of DNA that exhibit drastic stochastic effect at every locus (e.g. a profile with peaks below the dropout stochastic threshold at every locus). A DNA Analyst’s experience is crucial to assessing whether a DNA profile is suitable for database entry.

5. Criteria for Casework DNA Profiles Allowed in the National Database (NDIS)

- 5.1. Casework profiles to be entered into NDIS include DNA profiles from Forensic Unknown, Forensic Mixture, Forensic Partial, Forensic Targeted, Unidentified Persos, Missing Person, and Relatives of Missing Person profiles.



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- 5.2. Forensic samples must be tested with all of the expanded CODIS core loci (although there may not be results for all of these loci). If a sample has not been tested with all of the expanded CODIS core loci, it should not be uploaded to NDIS.
- 5.3. DNA profiles of suspects from evidence items are not suitable for upload to NDIS if the biological material was recovered from an item taken directly from the suspect and could reasonably be expected to have that suspect's biological material on it (e.g. Suspect's DNA profile obtained from a weapon or object taken directly from that suspect's possession, home, or car, or the suspect's DNA profile obtained from clothing taken off that suspect).
- 5.4. Forensic Mixtures and Forensic Partial DNA profiles may be uploaded to NDIS if they meet the requisite number of original CODIS core loci and exceed the Moderate Match Estimation threshold (calculated from the original CODIS core loci).
- 5.5. If there are numerous matches to a profile after it is uploaded to NDIS, the NDIS Custodian may request the DNA profile be re-categorized (e.g. change from "Forensic Partial" to "Forensic Partial-SDIS") so that the profile is deleted from NDIS.
6. **Criteria for DNA Profiles to be Keyboard Searched in the Maine Database (SDIS)**
 - 6.1. Known reference samples from suspects submitted under a law enforcement investigation (regardless of whether other evidence items are submitted or not) should only be **keyboard searched** in SDIS. This is a one-time search. Known reference samples from suspects cannot be entered into SDIS and cannot be uploaded to NDIS.
 - 6.2. For all other samples, it is optional to perform a keyboard search of a profile before entering it into CODIS, but this should only be performed with profiles that qualify for entry into SDIS and/or NDIS.
 - 6.3. Before entering a DNA profile into SDIS, it is optional to keyboard search the DNA profile to see if too many hits might occur (e.g. a partial profile with very few loci, or a mixture with several contributors, that matches to 100 or more candidates). This can help determine if a profile should even be entered into SDIS or not.
 - 6.4. Known reference samples from victims or any individual other than suspects or Missing Person categories should not be keyboard searched in SDIS.
7. **Match Estimation**
 - 7.1. Match Estimations are approximations for how many matches would occur if a Forensic Partial or Forensic Mixture profile were to be compared to a specified number of unrelated, single-source profiles.
 - 7.2. Match estimations are not calculated for single-source profiles that contain all of the original CODIS core loci.
 - 7.3. In order to qualify for upload to NDIS, Forensic Mixture profiles and Forensic Partial profiles must have an MME of 1 in 10 million or greater (i.e. $MME \geq 1.000E+007$) AND have at least 8 of the original CODIS Core Loci.



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- 7.4. The match estimations are expressed in scientific notation. A match estimation of 10 million is displayed as 1.0000E+07 (i.e. $1.0000 \times 10^7 = 10,000,000$). This would be expressed as “an MME of 1 in 10 million”.
- 7.5. As a Forensic Mixture or Forensic Partial profile is entered into SDIS, the program automatically calculates the Moderate Match Estimation (MME) and Match Rarity Estimation (MRE) for the profile.
- 7.6. When a partial or mixture profile is entered into CODIS, the MME and MRE are printed in the top part of the specimen report. At that point, the decision to enter the profile into SDIS and NDIS (as a ‘Forensic Partial’ or ‘Forensic Mixture’ or ‘Forensic Targeted’) or just SDIS (as a ‘Forensic Partial-SDIS’ or ‘Forensic Mixture-SDIS’) can be made. The specimen category can be changed after it is Tech Reviewed, depending on the MME.

8. Completeness Definitions

- 8.1. There are minimum thresholds for # of loci and match estimation that must be met in order to have a profile upload to NDIS:

Specimen Category	Minimum # of Loci	Match estimation	Additional
Forensic Unknown	≥ 13 Original Core loci	Not calculated	Single-source
Forensic Mixture	≥ 8 Original Core loci	MME ≥ 1.000E+007	Max. 4 alleles per locus
Forensic Mixture-SDIS	No min. # Core loci	MME < 1.000E+007	No max. # of 4 alleles
Forensic Partial	≥ 8 Original Core loci	MME ≥ 1.000E+007	Single-source
Forensic Partial-SDIS	No min. # Core loci	MME < 1.000E+007	Single-source
Forensic Targeted	≥ 8 Original Core loci	MRE ≥ 1.000E+007	

9. Entering Profiles into CODIS

- 9.1. Enter profiles as “unreviewed forensic” and then change the Specimen Category to the appropriate Category after Tech Review is complete. All profiles must be technically reviewed before being saved in any category OTHER THAN “unreviewed forensic”.
- 9.2. Open the Analyst Workbench.
- 9.3. Click on the “STR Data Entry” or select “STR/Y-STR Data Entry” under the Tools tab.
- 9.4. Enter the following:
 - 9.4.1. Specimen ID = consisting of case # and item #.
 - 9.4.2. Specimen Category (type of sample) = choose “Unreviewed Forensic” if profile has not been Tech Reviewed yet.
 - 9.4.3. Source Identified = ‘yes’ if DNA profile has been matched to a known reference.
 - 9.4.4. Partial Profile = ‘yes’ if DNA profile does not have all of the 13 Original Core loci.
 - 9.4.5. Comments = notes specific to the profile or case.
 - 9.4.6. Alleles = the DNA profile, entered as #,# for hetero. loci, and # for homoz. loci. Each locus is entered twice to ensure accuracy in the data entry.



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- The MME and MRE will be calculated and updated as each locus is added.

9.4.7. Click 'Save'.

- 9.5. Print the 'Inventory Report with Readings' (includes alleles and match estimation) and **write a note about which Specimen Category the 'unreviewed forensic' profile will be changed to once reviewed.**
- 9.6. Place the printed report in the case folder for verification of data entry, Specimen ID, and which Specimen Category it should be assigned to depending on the profile and the match estimation.
- 9.7. After Tech Reviewer signs off on data entry and proposed specimen category, go back into Analyst Workbench, change the specimen to the agreed upon category, mark the profile for upload to NDIS (if eligible), then right-click and print the Audit Trail to show the category change and that it is marked for upload (if eligible) and place it in the case folder so Admin Reviewer can verify the correct specimen category and marked for upload if eligible. It is optional to print a new 'Inventory Report with Readings' instead of the audit trail.

10. Uploading from SDIS to NDIS

- 10.1. All DNA profiles saved in NDIS-qualifying categories will try to upload to NDIS, but NDIS will reject any profiles that don't meet their requirements for number of loci or statistical probability. A "recon code" will accompany the rejected profile to explain why it was rejected.
- 10.2. An Incremental upload will be performed at least once a week:
- 10.2.1. Open Specimen Manager within the Analyst Workbench.
 - 10.2.2. Under the Tools tab, select Incremental Upload and Generate Upload.
- 10.3. A Full Upload is sent to NDIS when the FBI requests one (e.g. after installing software):
- 10.3.1. Open Specimen Manager within the Analyst Workbench.
 - 10.3.2. Under the Tools tab, select Full Upload and Generate Upload.
- 10.4. Open Message Center, locate and click on the upload report (new uploads are red) and print the following reports: Summary, Detail, and User. Upload reports are archived in Message Center.
- 10.5. After the upload is sent to NDIS, the DNA profiles will be searched, and any possible matches will be reported to the laboratory by a Match Message in the Message Center.

11. Local Database – Automatic Searches

- 11.1. Autosearcher compares DNA profiles between categories.
- 11.2. Run Autosearcher once a week, preferably before the NDIS upload:
- 11.2.1. Double click on the Autosearcher tab within the Analyst Workbench.
 - 11.2.2. Under the Autosearcher tab at the top, click on Perform Search.
 - 11.2.3. Results from Autosearcher are available by clicking the Message Center icon.
 - 11.2.4. Evaluate the appropriate search results under the Autosearcher Reports tab.



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- 11.2.5. Matches are viewed in Match Manager (new matches are red). Open each match by double-clicking.
- 11.2.6. Print the State Match Detail Report.
- 11.3. Hits should be evaluated per the “CODIS Match Confirmation” protocol.
- 12. Local Database – Manual Searches**
 - 12.1. Click on Searcher in the Analyst Workbench and enter the case number, item number, and allele designations for the relevant loci.
 - 12.2. To change the Stringency of the locus in the search from “HIGH” to “MODERATE” or “LOW”, double-click the letter to toggle through the choices of “H”, “M”, or “L”. To change all of the loci at once, right-click on the column header and choose a stringency.
 - 12.2.1. **A low stringency match** requires at least ONE allele at a locus to match/overlap between the searched profile and the candidate profile.
 - 12.2.2. **A moderate stringency match** requires ALL of the alleles in one profile’s locus that has the lower # of alleles to be present in the other profile’s locus that has the higher # of alleles. For example, if a locus in one profile has two alleles, both of those alleles must be a subset of (i.e. match/overlap) another profile’s locus that has two or more alleles.
 - 12.2.3. **A high stringency match** requires ALL of the alleles at a locus to match/overlap between the searched profile and the candidate profile.
 - 12.3. For DNA mixtures, set the Stringency to MODERATE for any locus that the person-of-interest’s alleles cannot be deduced. If a locus with more than two alleles is searched with a HIGH stringency, it will only produce matches to loci that have ALL of those same alleles.
 - 12.4. Click the Search button. A disposition box will display any potential hits.
 - 12.5. Print the Match Report (even if there are no matches) and place the report in the case folder for data entry review and verification of any matches or exclusions.
 - 12.6. Any matches should be saved in Match Manager if the match is to be reported, or the profile can be entered and a CODIS Hit report will be initiated after Autosearcher is run.
 - 12.6.1. Choose ‘File – Save Results – To Match Manager’ to save the match so it will be included in hit counting reports.
- 13. National Database Searches**
 - 13.1. DNA profiles uploaded from SDIS to NDIS are searched by the FBI at least once a week.
 - 13.2. Open Message Center in the Analyst Workbench and click on Match Messages to check for any new match messages (will appear in red).
 - 13.3. Double-click each red match message to execute (run) the message.
 - 13.4. Several reports will appear. View and/or print the National Match Detail Reports.
 - 13.5. Hits should be evaluated per the “CODIS Match Confirmation” method.



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Glossary

- 13.6. Autosomal loci = the loci in a DNA profile from locations NOT on the X- or Y-chromosomes (i.e. all loci except Amelogenin and DYS391 in Promega's PowerPlex Fusion kit).
- 13.7. Expanded CODIS core loci = the loci with which all forensic samples must be tested: D3s1358, D1s1656, D2s441, D10s1248, D13s317, D16s539, D18s51, D2s1338, CSF1PO, TH01, vWA, D21s11, D7s820, D5s818, TPOX, D8s1179, D12s391, D19s433, FGA, and D22s1045 (Fusion has these loci and Penta D, Penta E, and DYS391). Effective Jan. 1, 2017.
- 13.8. Original CODIS core loci = the loci D3s1358, D13s317, D16s539, D18s51, CSF1PO, TH01, vWA, D21s11, D7s820, D5s818, TPOX, D8s1179, and FGA.
- 13.9. Complete DNA profile = when a single-source profile (or deduced profile) has comparable data for the minimum # of loci at the required CODIS core loci for its specific Specimen Category. It is assumed that all of the expanded CODIS Core loci will have been attempted on the sample.
- 13.10. Forensic Partial DNA profile = when a single-source profile (or deduced profile) has missing or inconclusive data at any of the **Original** CODIS core loci. At NDIS, a partial profile must also have at least 8 of the **Original** CODIS core loci, have no more than 4 alleles at any locus, and meet the requisite MME or MRE for the partial, mixed, or targeted categories. *This definition is different than a "partial profile" in the interpretation and reporting of a DNA profile (see 'PowerPlex Fusion Casework Amplification and Detection' method).*
- 13.11. Forensic Mixture DNA profile = when a profile appears to have DNA from two or more contributors, it is called a "mixture" or "mixed DNA profile". It is sometimes possible to deduce a single-source profile from a major/minor mixture or from a mixture on an intimate body swab. It is possible to DEDUCE a single-source profile from a mixed DNA profile.
- 13.12. Forensic Targeted DNA profile = a partial profile or mixed profile with MME less than 1 in 10 million (i.e. $MME < 1.000E+007$) but has an MRE (stringency by locus) equal to or greater than 1 in 10 million (i.e. $MRE \geq 1.000E+007$). Loci marked partial and loci with more than 2 alleles are searched at Moderate stringency and all other loci are searched at High stringency. **This is a category of last resort since obtaining matches is better with Forensic Partial and Forensic Mixture categories.**