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4.0 PROFILE MANAGEMENT

4.1   CODIS Identification Number (Specimen ID Number)

4.1.1   Each profile entered into CODIS will have a unique identifier. Only uppercase letters (due to LIMS ramifications) and numbers will be used in the body of the description. Do not use any other spaces or any other characters, except a dash (-), period, or grant-tracking special characters (# or $) when indicated below. The standardized format for entering specimen information into CODIS is as follows:

4.1.1.1   The first eight to ten characters will encompass the Forensic Biology laboratory number (last two digits of the year, followed by a dash, followed by a four digit number if the case is from 2006 or earlier, or a five digit number if the case if from 2007 or later) followed by a dash. If the specimen is from a contract laboratory the year will be preceded by a laboratory abbreviation (Bode Technologies (BT or BTB), Cellmark Diagnostics (CD) or Genescreen (GS).

4.1.1.2   Vouchered items: add the last three digits of the voucher followed by a dash.

4.1.1.3   Post mortem items: add PM followed by the item number followed by a dash, in place of the voucher number.

4.1.1.4   Out-of-jurisdiction cases: add "OOJ" followed by a dash, in place of the voucher number.

4.1.1.5   The final set of characters will be reserved for sample type and identification.

4.1.1.6   Stained items (sheets, clothing, etc.): add a few (2 to 6) letters and/or numbers that describe the item, the item number, and the stain designation followed by a dash. If there is only one item of that type in the case (e.g. one pair of jeans, one beer bottle, or one baseball cap) the specimen ID need not contain the item or stain number. This segment may need to be shortened to help the Specimen ID comply with the 24-character upper limit. When a case has multiple CODIS profiles, attempt to create specimen ID's that are easily told apart, e.g. REDCAP and BLUCAP rather than CAP1A and CAP1B. This can help make subsequent match review and notification easier to perform. For stains with differential extractions the designations below will apply to the fractions.

4.1.1.7   **Sexual assault kit items:** the abbreviated descriptions for source and differential extraction fraction (if appropriate) below must be used. For kit samples processed with Zygem, use the swab designation (e.g. VS) but no fraction. Stain designations or the dried secretion swab numbers should NOT be used unless there are multiple DNA

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contributors from the same case on the same sample type, and samples need to be distinguished from one another:

>   **Dried secretions swabs** described as **DS**
>   **Oral swabs or smears** described as **OS**
>   **Vaginal swabs or smears** described as **VS**
>   **Vulvar swabs or smears** described as **VU**
>   **Cervical swabs or smears** described as **CS**
>   **Anal swabs or smears** described as **AS**
>   **Perianal swabs or smears** described as **PA**
>   **Perianal/anal swabs or smears**, (no information whether one or both) should be described as PAA
>   **Penile swabs or smears** described as **PS**
>   **Underwear** described as **UW**
>   **Sperm fraction** described as **SF**
>   **Epithelial fraction** described as **EF**
>   **Substrate/swab remains fraction** described as **SR**

4.1.1.8   **Missing and Unidentified Persons Cases:** the specimen ID will follow the same general format as other casework:

- Case number followed by a dash**.**

- For vouchered items, add last three digits of the voucher followed by a dash.

- For cases worked on behalf of other labs, use –OOJ instead of the voucher information.

- To differentiate between sample types, use **R** for Relatives of Missing Persons, **M** for Missing Persons (or Deduced Missing Persons) samples, and **U** for Unidentified Human Remains.

- **$ -** for cases worked with grant-funded supplies

4.1.1.9   **Relatives of Missing Persons:** the abbreviated descriptions below will be used for samples from relatives. If more than one sibling, other maternal relative or other paternal relative is submitted, designate each with a number after the abbreviated description:

- Mother described as **M**

- Father described as **F**

- Biological Sibling (brother or sister) described as **S**

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- Other Maternal Relative described as **OM**

- Other Paternal Relative described as **OP**

- Spouse (other parent of child(ren) in common) described as **SP**

4.1.1.10 **Missing Persons:** add 4-5 letters describing the item, item number, and/or cutting followed by a dash. This segment may need to be shortened to help the specimen ID comply with the 24-character upper limit.

4.1.1.11 **Unidentified Human Remains**: utilize "PM" followed by a dash

4.1.1.12 **Pedigree Trees**: case number followed by a dash; four numerals for month and day created, followed by a dash; and the letters "PT". For a pedigree tree for case FB14-06802, created January 23, the pedigree tree ID would be 14-06802-0123-PT.

4.1.1.13 **Grant-Funded cases**: add the special character followed by a dash. This segment should be omitted from the specimen ID if neither condition applies. The first instance of grant assistance determines which symbol is used, it cannot be both.

- **#** - for cases worked on weekend overtime grant money

- **$** - for cases worked with grant-funded supplies

4.1.1.14 **Case type indicator**: the last notation is a pair of letters indicating the case type. Do not add segments after this segment. This allows management or CODIS staff to query by crime type in the database.

AS	assault, attempted homicide, and related cases
BU	burglary and related cases
DR	drug possession and related cases
HO	homicide cases
MP	missing and unidentified persons cases
RO	robbery, attempted robbery, and related cases
SA	sexual assault and related cases
WE	weapons possession and related cases
AU	auto theft (grand larceny auto), unauthorized use of vehicle, and related cases
OT	use for any case type not covered above

4.1.2 Examples

- Example 1: case no: FB07-00022, voucher N123456, item #1: purple shirt, stain 1B; assault. Specimen ID number will be: *07-00022-456-PS1B-AS*

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- Example 2: case no: FB00-1257, post mortem kit item PM 2F, vaginal swab, sperm cell fraction, homicide. Specimen ID number will be: *00-1257-PM2F-VSSF-HO*

- Example 3: case no: FB08-01034, voucher P124589, item #1B: glove, scrapings, burglary, examined on a weekend. Specimen ID number will be: *08-01034-589-GLSCR-#-BU*

- Example 4: case no: FB11-05500, voucher 1000099832, item #1, auto theft case, cigar butt, sample amped using primers purchased on grant. Specimen ID number will be *11-05500-832-CB1-$-AU*.

- Example 5: Cellmark Diagnostics backlog case CD01-0001, voucher K321123, sexual assault kit underwear stain, sperm cell fraction, sexual assault. Specimen ID number will be: *CD01-0001-123-UWSF-SA*

- Example 6: case no: FB11-01234, bone, PM1, unidentified human remains. Specimen ID number will be: *11-01234-PM1-U-MP*

- Example 7: case no: FB04-1234, voucher number K123456 , brother and sister of Missing Person. Specimen ID numbers will be: *04-1234-456-S1-R-MP* and *04-1234-456-S2-R-MP*

4.1.3   There is a maximum limit of 24 characters for the specimen identification number in CODIS. The above specimen identification system should not be deviated from unless it is necessary to distinguish two samples, or under unusual case situations.

4.1.4   Suspect profiles entered into LDIS will have specimen IDs of the form XXX-18-S00000 for suspect files from 2018 and later (suspects from 2006 and earlier will have specimen IDs of the form XXX-00-S000 or XXX-07-S0000). This special format is intended to prevent the CODIS team and analysts from placing the suspect in the wrong index where it might be accidentally uploaded.

4.1.5   **LDIS Only profiles entered into LDIS will have specimen IDs of the form LLL-13-00000.** This special format is intended to prevent the CODIS team and analysts from placing an evidence profile which is ineligible for NDIS, into an index where it might be accidentally uploaded past SDIS. Extensions such as –MDA or –FDA may be added when there is more than one LDIS Only profile for a case, to aid in distinguishing between the two. The specimen category for LDIS Only profiles is "LDIS Only".

4.1.6   **LabTypes profiles entered into LDIS will have specimen IDs of the form 12345.** This format is intended to prevent the CODIS team and others from placing these known profiles in the wrong index where they might be accidentally uploaded; and preserves the anonymity of the personnel whose profiles these are.

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4.2   **General Guidelines for Entering STR Profiles into CODIS** (see also table at the end of this section)

4.2.1   Procedures for determining STR typing results are detailed in the current Forensic Biology STR manual.

4.2.2   All STR profiles and mtDNA sequences that are CODIS eligible must undergo technical review prior to entry into LDIS. The technical review includes evaluation of associated positive and negative controls, the eligibility of the DNA profile for CODIS, as well as ensuring that appropriate exemplars and/or elimination samples have been requested at least once.

4.2.3   All core CODIS STR loci (prior to 1/1/2017, the original core 13; after 1/1/2017, the expanded core 20) and appropriate additional technologies as needed must be attempted on appropriate samples in order for that sample's data to be eligible for CODIS.

4.2.4   **Eligibility for entry and upload**

4.2.4.1   **LDIS:** A minimum of 6 fully deconvoluted loci are necessary for search of, or entry into LDIS. All partial or mixed evidence profiles must satisfy a statistical threshold for match rarity on order to be uploaded into LDIS. This calculation must also be performed for all partial suspect profiles with information at 10 or fewer loci. This is determined by the case analyst using the CODIS Match Estimation Utility and setting the database of size N to the current database size rounded up to the next ten thousand. If the match rarity (i.e. "Combined Expected Number of Matches") is greater than one (i.e. Combined Inverse MRE value is less than or equal to the database threshold), the profile should only be searched against Lab Types (refer to **4.6.1.2**) and should not be entered into LDIS. Alternatively, calculate the Moderate Match Estimate for the profile using the COSTaR MME Calculator. Confirm the LDIS MME threshold is set to the current database size rounded up to the next ten thousand. If the MME value is less than the LDIS MME threshold the profile should only be searched against Lab Types (refer to **4.6.1.2**) or entered into LDIS.

4.2.4.1.1   NOTE: Without data for at least 6 original CODIS core loci, LDIS-only samples may not be searched against samples with non-Fusion loci (e.g. samples only typed in Cofiler, or partial profiles typed in Identifiler).

4.2.4.2   **SDIS: To be eligible for upload into SDIS, in addition to fulfilling all of the LDIS requirements; the profile must have data (i.e. fully deduced, mixed, or partial locus) at a minimum of 6 of the original 13 CODIS core loci.** All profiles intended for the Forensic Mixture and Forensic Partial indexes must satisfy a statistical threshold for match rarity. This is determined by the case analyst using the CODIS Match Estimation Utility and setting the database of size N to the current database size rounded up to the next hundred thousand. If the match rarity (i.e. "Combined Expected Number of Matches") is greater than one (i.e. Combined Inverse MRE value is less than or equal

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to the database threshold), the profile is eligible for LDIS only. Alternatively, calculate the Moderate Match Estimate for the profile using the COSTaR MME Calculator. Confirm the SDIS MME threshold is set to the current database size rounded up to the next hundred thousand. If the MME value is less than the SDIS threshold the profile is eligible for LDIS only.

4.2.4.3   **NDIS: To be eligible for upload into NDIS, in addition to fulfilling all of the LDIS requirements; the profile must have data (i.e. fully deduced, mixed, or partial locus) at a minimum of <u>8</u> of the original 13 CODIS core loci.** All profiles intended for the Forensic Mixture and Forensic Partial indexes must satisfy a statistical threshold for match rarity. This is determined by the case analyst using the CODIS Match Estimation Utility and setting the database of size N to 10,000,000 (1E7). If the "Combined Expected Number of Matches" is greater than one (i.e. Combined Inverse MRE value is less than or equal to 10,000,000), the profile is eligible for SDIS only. Alternatively, calculate the Moderate Match Estimate for the profile using the COSTaR MME Calculator. Confirm the NDIS MME threshold is set to 10,000,000 (1E7). If the MME value is less than the NDIS MME threshold the profile is eligible for SDIS only.

NOTE: When using the CODIS Match Estimation Utility, the MME should be calculated using only the Combined population. The Caucasian, African American, Hispanic, and Asian populations may be clicked off in the Configuration Summary to the right of the Target Profile input panel.

4.2.5   For Missing Persons and Unidentified Human Remains cases, the following minimum core loci plus Amelogenin are necessary for upload into CODIS:

- Unidentified Human Remains: 6 for SDIS, 7 for NDIS

- Missing Persons and Deduced Missing Persons: 8 for SDIS and NDIS

- Relatives of Missing Persons: 13 for SDIS and NDIS

4.2.6   The DNA result from each locus will be entered on the DB Profile documentation in the form p, q for heterozygotes (in ascending order) and p, p for homozygotes (for example, TH01 6, 7 or 6, 6).

4.2.7   In certain circumstances, a single obligate allele may be entered as p+. For single-source DNA profiles, this is allowable only as described in section 4.3.6. If this option is used, the profile must be placed in the Forensic Partial, Forensic Mixture, Forensic SDIS Only or LDIS Only index. Do not enter single obligate alleles (p+) for Suspect profiles. Loci entered into LDIS Suspect Known Category must be full or INC.

4.2.7.1   This convention may not be used for any known/exemplar samples entered into the CODIS database, whether they are LDIS categories such as Suspects or LabTypes, or

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samples uploaded to SDIS/NDIS, including Missing Persons, Relatives of Missing Persons, and Unidentified Human Remains samples.

4.2.8   Forensic mixture profiles shall not have more than 4 alleles at any locus.

4.2.8.1   No more than two alleles per locus (with the exception of one tri-allelic pattern to allow for genuine trisomy) may be used for DNA profiles in the specimen categories: Forensic Unknown, Forensic Partial, Missing Persons, Relatives of Missing Persons, Suspects, Lab Types, and Unidentified Human Remains.

4.2.9   Only DNA data derived from analysis of NDIS accepted PCR loci/systems shall be entered into CODIS. NDIS accepted PCR loci/systems are referenced in the *FBI NDIS Standards for Acceptance of DNA Data.*

4.2.10   Forensic Biology Laboratory reports that contain results eligible for entry into CODIS contain a statement indicating that this information has been added to and will be maintained in the CODIS system.

4.2.11   Currently, profiles developed using Low Copy Number amplification techniques are not eligible for entry into NDIS. They were, however, uploaded to NY-SDIS for searching, via the Low Copy Number specimen category of the Forensic SDIS Only Index. Samples in this SDIS Index are unmarked for any further upload (i.e. to NDIS).

4.3   **Guidelines for Entering STR Profiles Derived from Mixed Samples into CODIS (see also table at the end of this section)**

4.3.1   Mixtures refer to the situation where the DNA profile from the evidence is composed of alleles from more than one individual.

4.3.2   As many loci and alleles as possible should be included in the profile submitted to the database.

4.3.3   When a locus can be only partially deconvoluted, use of the obligate allele designator, a "+", aids in moderate stringency searches by preventing some of the spurious moderate matches possible at mixed loci. Use of required alleles limits the possible matches that are returned in a search. For example, a 13, 14, 15 would match 13; 14; 15; 13, 14; 13, 15; and 14, 15. If the mixture were entered as 13, 14+, 15, then a 14 would be required to appear in the other profile: a 14; a 13, 14; or a 14, 15.

NOTE: SPECIAL NOTE REGARDING OBLIGATES: a 13, 14+, 15 will not match a 13+, 15 at moderate stringency because the 14 does not appear in the second sample; even though the 13 and 15 are in both samples. Assuming one non-matching locus is allowed in the search configuration, one such instance as described would not prevent a match from being detected, however two such instances in the same pair of samples, would prevent the match from being detected.

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4.3.4   A locus may be designated inconclusive ("INC") on the DNA Profile Evaluation form at the discretion of the interpreting analyst and the technical reviewer(s) if an ambiguity exists at that locus (see section for Type II mixtures below). This locus, however, can and should still be used in the confirmation process once a candidate match is made.

4.3.5   **Type I mixture** - the results are such that it is possible to determine/deduce a complete profile of a contributor at 6 or more loci. The deduced profile of the major contributor or the major component will be entered into LDIS. If the profile is partial or a mixture, it must meet the Moderate Match Estimation threshold.

4.3.5.1   Only if the allele intensities are such that the minor component can clearly be deduced at six or more loci will the deduced DNA profile of the minor component be entered into LDIS. If the profile is partial or a mixture, it must meet the Moderate Match Estimation threshold.

4.3.6   **Type II mixture** - the results are such that it is not possible to determine/deduce a complete profile of a contributor at all loci; the allele intensities are such that the contributor can be deduced at some loci but not at other loci. Enter the deduced alleles at all deconvoluted loci. Any loci that cannot be deconvoluted can be entered as a mixture with the obligate allele indicated on the DNA Profile Evaluation Form with a "+". Because of possible allele sharing, include any alleles that might be attributable to the perpetrator, even if the victim also has those alleles.

4.3.6.1   There are two options for entering partially known loci when not all of the possible alleles at that locus are confirmed.

Type II mixture – **option one** for entry of a mixture locus: Enter the locus as "INC". This may be the method of choice when your profile contains good data at most of the loci, and the loss of one or two loci still leaves a profile which meets the Match Estimation or Moderate Match Estimation thresholds.

Type II mixture – **option two** for entry of a mixture locus: If only one of the potentially two alleles of the profile at that locus can be determined (due to interpretation rules) or after all attempts to get results for a clearly visible but below threshold peak have failed, enter the one known allele with a "+". This is a CODIS method of designating that "another allele may be present at this locus." The advantage of listing one known allele over none or "INC" is that a match might be found at moderate stringency, but will prevent at least most of the spurious candidate matches which might occur if nothing at all is entered for that locus.

For example, a 10+ would match 9, 10; 10, 10; 10, 11… but would preclude anything that contained no 10 allele, for example, 9, 9; 9, 11; 9, 12… would not match, in contrast to an "INC", or no entry at that locus, which would allow any allele to appear at that locus and not be a mismatch.

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This option is only meant to enhance a limited number of loci in a profile, for instance to enable a profile with 7 loci to meet the minimum amount (8 loci) needed in order to be searched at NDIS instead of being stopped at SDIS. Certain criteria must be met and documented in the case record in order to justify using this method:

- Documentation that the profile meets the eligibility requirements as stated in section 4.2.4.

- This is the one and only instance on a DNA Profile Evaluation Form when a single allele is entered in the box for that locus. The "+" must also be present.

- The interpreting analyst and/or technical reviewer(s) submitting such a profile may be called upon to evaluate all candidate matches found when the profile is searched.

4.4   Entering STR Profiles into LDIS

4.4.1   CODIS eligible profiles will be entered into LDIS by CODIS software-trained staff only. The profiles entered and/or imported into LDIS must fall into one of the following CODIS categories: Forensic Unknown; Forensic Mixture; Forensic Partial; Forensic SDIS Only; Low Copy Number; Suspect, Known; Missing Persons Index; the Relatives of Missing Persons Index or the Unidentified Human (Remains) Index) (see section 1.0 - CODIS Terms and Abbreviations for definitions; for procedural guidelines on how to enter a profile into LDIS, see the *FBI CODIS Training Manual or the relevant module in the online LMS*). For a list of NDIS-approved STR PCR kits, consult the current version of *NDIS Operational Procedures Manual*.

4.4.2   Profiles matching the victim or elimination samples (for example, a family member or a consensual sex partner) unambiguously will not be entered into CODIS. For a profile to be unambiguously attributed to the victim or elimination sample, an exemplar must be tested and compared to the profile in question. *It is not sufficient to make an assumption based on case information that the profile in question matches the victim or consensual sex partner*.

4.4.3   Evidence profiles that are clearly unrelated to a case or crime will not be entered into CODIS. For example, a semen profile from a condom from which a female profile was determined and the victim is excluded as the female contributor of DNA. This will be at the discretion of the appropriate Assistant Director and the CODIS Program Manager. The determination can be aided using the CODIS *Guide to Determining What is Allowable for Entry into the Forensic Index at NDIS*.

4.4.4   Local suspect profiles reside in LDIS. They are not eligible for upload to higher levels of CODIS, nor are they eligible to be shared with any other laboratories through or outside of CODIS.

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4.4.4.1   Suspect files may be created from decedents of OCME cases who are also documented suspects in one or more criminal cases (with case contacts from NYPD or DAO). The resulting profiles will be entered into LDIS' Suspect, Known Index under the usual nomenclature and search conditions.

4.4.4.2   Local suspect profiles will be entered into LDIS (Suspect, Known Index), unless:

- A properly executed court order dictates otherwise concerning a specific sample. When any court order or similar paperwork is received, the OCME Legal Department must be consulted and provided a copy of the paperwork. The court order will be attached to the case record in LIMS.

- The exemplar was submitted subsequent to a partial match notification and does not match the case for which it was submitted.

4.4.5   Entry of a profile into LDIS will be documented on the DB Profile documentation in the case record.

4.4.6   Upload of a profile to SDIS will be documented by including a copy of the CODIS Specimen Detail Report in the case record.

4.4.7   Non-victim DNA profiles derived from evidence that are not eligible for SDIS/NDIS entry will be entered into the LDIS Only CODIS category (for example, a profile obtained from the clothing of a suspect, or a weapon taken directly from an arrestee).

4.4.8   Off ladder alleles above or below the allelic ladder are entered as < (lowest allele at that locus) or > (highest allele), respectively. The official standardized NDIS allelic ladder is as listed. The original 13 CODIS core loci are marked with an asterisk. The expanded 20 CODIS core loci are marked with 2 asterisks. The remainder of the listed loci are accepted but not required.

> *** CSF1PO** <6, 6-15, >15
> *** D13S317** <8, 8-15, >15
> *** D16S539** <5, 5-15, >15
> *** D18S51** <9, 9-26, >26
> *** D21S11** <24.2, 24.2-38, >38
> *** D3S1358** <12, 12-19, >19
> *** D5S818** <7, 7-16, >16
> *** D7S820** <6, 6-14, >14
> *** D8S1179** <8, 8-18, >18
> *** FGA** <18, 18-30, >30
> *** TH01** <5, 5-10, >10
> *** TPOX** <6, 6-13, >13
> *** vWA** <11, 11-21, >21
> **Amelogenin** X,Y

**D19S433 <9, 9-17.2, >17.2
**D2S1338 <15, 15-28, >28
Penta E <6 6-24, >24
Penta D <2.2, 2.2-17, >17
**D1S1656 <9, 9-20.3, >20.3
**D2S441 <9, 9-16, >16
**D10S1248 <8, 8-18, >18
**D12S391 <14, 14-27, >27
**D22S1045 <8, 8-19, >19
SE33 <4.2, 4.2-37, >37

4.4.9   Y STR loci are accepted in CODIS but are not routinely entered into LDIS.

4.4.9.1   Y STR data is occasionally entered for missing/unidentified persons, for casework samples involved in partial match resolution, and for cases involved in familial search requests.

4.4.9.2   The Y STR standardized NDIS allelic ladder with loci currently used in Forensic Biology is as listed:

DYS19 <10, 10-19, >19
DYS385 <7, 7-25, >25
DYS389 I <10, 10-15, >15
DYS389 II <24, 24-34, >34
DYS390 <18, 18-27, >27
DYS391 <8, 8-13, >13
DYS392 <7, 7-18, >18
DYS393 <8, 8-16, >16
DYS438 <8, 8-12, >12
DYS439 <8, 8-15, >15
DYS448 <17, 17-24, >24
DYS456 <13, 13-18,>18
DYS458 <14, 14-20, >20
DYS635 <20, 20-26, >26
YGATAH4 <8, 8-13, >13

4.4.10   Off ladder alleles which fall within the lower and upper limits at each locus should be entered as determined by the analysis software (e.g. an allele called as 9.1 should be entered as 9.1, not 9.x).

4.4.11   If a discrepancy exists on the DB Profile documentation (for example, the wrong specimen category is used, the reviewer's initials are missing, the specimen ID appears incorrect or is too long) the Interpreting Analyst (IA) and the technical reviewer(s) for that profile must resolve the discrepancy **before** the data from that profile is entered. If

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the discrepancy is discovered once the profile has already been entered, a modification or deletion/re-import may be needed (case by case determination). Interpretation issues should be discussed with the appropriate Assistant Director.

4.5 Modifying or Deleting an STR Profile from CODIS

4.5.1   Modification of data already entered into CODIS may be due to several reasons:

- Additional testing has been completed on the sample.

- An interpretation error was discovered regarding the profile.

- The specimen ID has an error such that the sample needs to be renamed, and the sample has not yet been sent to SDIS/NDIS.

- The profile could be improved by the addition of the obligate allele designator "+".

4.5.2   Once it has been determined that a profile must be modified in CODIS, a Profile Modification form should be filled out and submitted to the CODIS staff for processing. The original Profile Modification form will be maintained in the Profile Modification form binder and a copy will be added to the case record.

4.5.3   The format the modification request takes depends on the era from which the case comes originally.

4.5.3.1   Profile modifications for paper-only files should be submitted on the traditional paper form. This includes all Backlog and Biotracks cases, Forensic Biology cases FB12-03799 and earlier, and Forensic Biology suspect cases FB12-S0949 and earlier; with NO TESTING DONE WITHIN LIMS. An example would be the correction of a typographical error that is newly identified, or a further deduction of one or more loci using the original data, such as updating FGA from "24, 25.2, 29" to "24+, 25.2, 29", or a TPOX "7, uncalled blip" to "7+".

4.5.3.2   Profile modifications for LIMS-era files (FB12-03800 and later, and suspect files FBS12-00950 and later) must be submitted via the LIMS profile modification procedure, and a new dataset submitted for importing by the CODIS staff. The desired interpretation/dataset should include all loci desired in the final version in CODIS, even those not being changed.

NOTE: **NOTE OF CAUTION IF YOU ARE MAKING AN EXISTING LOCUS "INC":** Sending a locus as "INC" (blank) in a new dataset from LIMS, where there was previously one or more alleles present in the previous dataset(s), will NOT result in that locus being over-written to be "INC". The technical reviewer who submits the

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modification MUST notify CODIS staff by email to ensure that the locus/loci in question are modified by hand in CODIS. The email does NOT replace the need for the modification form.

4.5.3.3   Cases from the paper-only era that are being modified due to additional testing done during the LIMS era, should be treated as LIMS-era cases. The specimen ID must be **identical** to that already present in CODIS, to ensure the profile is updated and not present as two separate versions in the database. An example would be FB03-S567, with only Cofiler data, being updated using Fusion; name as XXX-03-S567 and submit all loci obtained. The technical reviewer will notify CODIS staff that the profile being sent is an update to a previously-existing specimen. CODIS staff should document in LIMS and CODIS that although this is Dataset 1 from LIMS, that it is an update to a previously-existing specimen.

4.5.4   Any modification to a DNA profile once it has been entered into LDIS will be documented in the appropriate profile modification log.

4.5.5   Reasons for administrative removal/expungement might include:

- A profile entered is later determined to be from a victim, witness, consensual partner, family member, etc.

- Documentation is provided for legal expungement.

- The specimen ID has an error such that the sample needs to be renamed, and the sample has already been sent to SDIS/NDIS.

- A determination was made that the profile should not have been entered into CODIS due to a user problem (for example, the IA has failed a proficiency test during the time the data was generated) or a systemic laboratory problem.

- Profiles from missing persons and/or relatives of missing persons are removed once a person is identified unless they will be needed to assist in identification of possible further remains and the data for the first-identified remain is not complete. Profiles from unidentified human remains will be removed only if the body recovered is intact.

4.5.5.1   Once it has been determined that a profile must be deleted from CODIS, a Profile Removal/Expungement Form must be filled out and submitted to the CODIS staff for processing. Unless there are time restraints surrounding the deletion (for example, in response to a court order requiring it before the next local upload; if so, an Expungement Request letter will be sent to the SDIS custodian), the deletion will be processed with the next upload to SDIS.

4.5.5.2   The original form will be maintained in the Case Deletion/Expungement form binder and a copy will be added to the case record. The deletion will also be recorded in the

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Upload Deletion/Expungement log at the time it is processed. The deletion portion of the reconciliation report from the upload will also be printed and placed in the Case Deletion/Expungement form binder confirming that the deletion was completed.

4.6   **Routine Searches of LINKAGE and LDIS**

4.6.1   Interpreting analysts and their technical reviewers will routinely compare appropriate preliminary DNA profiles to those in LINKAGE and LDIS, and document the results as an event on the DB Profile page in LIMS. Indexes to be searched include Forensic Unknowns, Forensic Mixtures, Forensic Partial, Forensic SDIS Only, LDIS Only, Other (patterns), Unidentified Human Remains, Suspect Knowns, and Lab Types.

4.6.1.1   **Regular Searcher settings should be as follows** (click yellow wrench icon to get to configuration menu):

- General: check box for "return all candidates"

   Use metadata sex as match filter: check box

- STR: check box

   Minimum # of loci required to report a match: 6

   Include Candidate Specimens that Match on All but __ Loci: 1

   Use as Match Filter: check box

- mtDNA: don't check box

- Y-STR: don't check box

- Indexes to Search in:

   Forensic

   Forensic LDIS Only

   Forensic Mixture

   Forensic Partial

   Forensic SDIS Only

   Lab Types

Pattern

Subject

Unidentified Human (Remains)

- Candidate View: [None]

- STR Locus Display Order: drag and drop so that loci are in the order you'll be entering them, i.e. Fusion order starting with Amelogenin and ending with D22S1045.

- Check the boxes for all Fusion loci (original CODIS core 13 plus the additional 9). Leave Amelogenin and SE33 unchecked.

- Ensure Stringency for all checked loci is set to "M" (moderate). If you need to change it from H or L, right-click.

- Click OK to exit setup mode.

- Do "Save-as" for this Searcher configuration and name appropriately (e.g. "Local Forensic Search (use me)".

4.6.1.2 **Searcher settings for Lab Types Only searches** (click yellow wrench icon to get to configuration menu):

4.6.1.2.1 This search is for when you have a sample under a protective order, or for some other reason only will be searching against Lab Types samples, for QA/QC purposes.

- Settings: open the regular search you have saved in your profile

- Click off: all indexes EXCEPT Lab Types

- Click: OK

- Save-As: Lab Types Only Search (or something else obvious to yourself)

4.6.2 LDIS autosearches will be conducted after the addition of new profiles into LDIS and before an upload to SDIS. This search will serve to ensure that no intra-laboratory DNA matches were overlooked, and to track local DNA hits using the CODIS system. LDIS autosearches will be performed by the CODIS staff only.

4.6.3 All LDIS autosearches will be conducted at moderate or high stringency using a minimum of six core loci. The default setting is moderate.

4.6.4 Samples with 10 or more loci will also be searched, allowing one locus to have either low-stringency or non-matching results ("one-mismatch search").

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4.6.5   All LDIS candidate matches will be examined. The CODIS staff will investigate any matches not already documented and ensure that all proper notifications are prepared, reviewed and made expeditiously. The CODIS group may return such matches to the analyst and technical reviewers who submitted the specimen, and delegate the match notifications to them.

4.7   Uploading Profiles to SDIS/NDIS and Search Policies

4.7.1   All appropriate LDIS profiles will be uploaded to SDIS by the CODIS staff. Currently, New York State local DNA laboratories upload to SDIS twice weekly, with the SDIS search performed shortly thereafter. Forensic STR Index, Unidentified Human (Remains) Index and Missing Person Index profiles containing 8 or more loci are searched at both high and moderate stringency provided they meet the MME threshold to be enrolled in NDIS. Profiles with too few loci or having MME values below the NDIS threshold are placed in the "Forensic SDIS Only" index.

4.7.2   LDIS profiles for upload to SDIS will be from evidentiary samples only. Under no circumstances will known human reference samples be uploaded to SDIS forensic indexes. Such profiles may be entered into the Missing Persons Index, the Relatives of Missing Persons Index or the Unidentified Human Remains Index if appropriate. Suspect or LabTypes samples are not eligible for any SDIS indexes and reside in LDIS indexes only.

4.7.3   All putative perpetrator profiles in a Forensic Biology DNA pattern will be uploaded to SDIS.

NOTE: Additional profiles from patterns will no longer be placed in the Other (pattern) Index in LDIS. Confirmed additional matches to the same offender are dispositioned as State Defined #1.

4.7.4   Uploads to NDIS will take place as scheduled by the SDIS custodian.

4.8   Other Searches

4.8.1   Only DNA profiles developed by the Department of Forensic Biology may be compared to suspects in LINKAGE or LDIS. Requests to compare other labs' DNA profiles to LINKAGE or the Suspect Known specimen category in LDIS will not be approved and are not allowed.

4.8.2   External keyboard search requests of LDIS, SDIS, and NDIS are only allowed of DNA profiles derived from evidence. Keyboard searches of DNA profiles from known individuals are not allowed.

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4.8.2.1   Keyboard search requests of SDIS/NDIS are addressed to the Databank coordinator. This search is requested through the DCJS Databank coordinator and is executed at the discretion of the SDIS custodian.

4.8.2.2   Keyboard search requests of LDIS are addressed to the CODIS custodian, CODIS Program Manager, or the laboratory director.

4.8.3   There are assorted reasons a keyboard search would be requested by a laboratory. All requests must be accompanied by a Justification for Keyboard Search Request form.

4.8.3.1   **Reason #1:** The requesting laboratory wants to search a profile that does not meet the minimum loci requirements for SDIS or NDIS entry or would not be searched based upon SDIS or NDIS current search policy. Keyboard searches for this reason must be, accompanied with a documented scientific reason justifying the search (for example, apparent presence of mixtures, sample degradation or limited sample availability). Scientific justification must include but is not limited to a statistical significance of the profile (or deduced loci) that meets the NDIS Moderate Match Estimation requirements of 10 million, and has at least 7 CODIS core loci. NDIS does allow keyboard searches of profiles with fewer than 8 loci, if this required MME threshold can be met. A copy of the Match Estimation calculation printout must be provided to the CODIS group with a justification of this type, and the CODIS staff will check the MME prior to requesting an NDIS keyboard search

4.8.3.2   **Reason #2:** - The requesting agency wants to search a profile before the next search in a situation where a known convicted offender is a suspect in a particular case and there is a need for an expedited search. The initial request from a Bureau Chief from one of the District Attorney's Offices must be submitted in written form, **must be accompanied with a valid justification for the urgency,** and **it must be confirmed that the suspect in question is, in fact, in the databank. This confirmation is the responsibility of the requesting agency.** There must also be a documented conversation with an Assistant Director and appropriate case information. **Case information from the DAO must include:** the suspect's full name, NYSID number, social security number, and any known aliases.

4.8.3.3   The following reasons are considered valid urgency justifications by the Department of Forensic Biology to request a keyboard search to expedite a CODIS search at SDIS or NDIS:

- A suspect has been arrested for a particular case and will be released without the search. Additionally, there is no other evidence (eyewitness, fingerprints, etc.) to hold the suspect and attempts to obtain a DNA sample from the suspect have been exhausted.

- A strong investigative lead has developed a suspect in a particular case and the search will lead to an arrest. Additionally, there is no other evidence (eyewitness, prints, etc.)

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to arrest the suspect and attempts to obtain a DNA sample from the suspect have been exhausted.

NOTE: Even if the DAO or NYPD can confirm a potential suspect has qualified for entry in the convicted offender databank this does not insure the sample has been collected, processed, or entered into the offender databank. Expedition of a convicted offender sample by DCJS does not have to be in response to a keyboard request. If the suspect is based on a strong investigative lead and the investigator wants to insure the corresponding convicted offender sample is in the offender databank before the next routine search they should be referred to DCJS. Investigators should always be advised to attempt to obtain a DNA sample from the suspect and submit it directly to Forensic Biology.

4.8.3.4   **Reason #3:** - The requesting agency and/or the Department of Forensic Biology wants to search a profile before the next search in a situation where there is an urgency for an expedited search to attempt to identify an offender in a serious or serial crime, for public safety reasons.

4.8.4   Both the CODIS Custodian/Supervisor and the CODIS Program Manager must approve keyboard search requests. Disagreements between the CODIS Program Manager and the analyst, technical reviewer(s), or manager requesting a keyboard search will be resolved by the laboratory director.

4.8.4.1   Once a keyboard search request has been approved, the interpreting analyst will fill out a Forensic Biology Keyboard Search Request form and forward it to the CODIS staff for processing. All keyboard search requests will be processed by the CODIS staff. If the keyboard search request is for SDIS, the CODIS supervisor will discuss the request and case information with the DCJS Databank coordinator via telephone and fax the request form accordingly. Documentation of the request and search results will be added to the case record. Keyboard search requests from outside laboratories are kept in the Keyboard Search requests binder. **The interpreting analyst requesting the keyboard search will be responsible for evaluating all candidate match results from the search *within 15 days* of receiving the results from the CODIS staff.**

NOTE: Prior to sending a Keyboard Search Request form to SDIS, the CODIS staff will first perform a local keyboard search to identify any local candidate matches.

4.8.5   A forensic profile may be searched at a non-CODIS databank (for example, via Interpol). See the NDIS Procedures for further information.

4.8.6   A non-US forensic profile may be searched at NDIS upon request to the FBI and at their discretion. Such a profile may NOT be searched at LDIS.

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4.8.7

STR result	Interpretation	DNA Profile Evaluation Form	Will match
7, 8, 9	deduced contributor is 9, 9	9, 9	9, 9 (high stringency)
7, 8, 9	deduced contributor is 8, 9	8, 9	8, 9 (high stringency)
7, 8, 9	deduced contributor is 9, Z (where Z is either a 7 or 8 or 9)	7, 8, 9+	7, 9 or 8, 9 or 9, 9 (moderate stringency)
7, 8, 9	deduced contributor is 9, Z	INC or 9+	anything 9 plus any other allele (moderate stringency)