PROFILE MANAGEMENT

Table of Contents

1 CODIS Identification Number (Specimen ID Number)

Each profile entered into CODIS will have a unique identifier (specimen ID) with a maximum of 24 characters. These characters can only be uppercase letters, numbers, dashes (-), periods, or grant-tracking special characters (#, $, or +) as indicated below. The below specimen identification system should not be deviated from unless it is necessary to distinguish two samples, or under unusual case situations. Even when you are using "MDA" or "MDB" as part of the 6-letter sample description segment, always end the specimen ID with the two-letter case type indicator if the sample is eligible for SDIS/NDIS.

1.1 SDIS/NDIS Specimens

For all LabVantage (LV) LIMS cases and BEAST LIMS cases starting with F26- and beyond, the standardized format for specimens eligible for SDIS/NDIS is as follows:

Case Number Ex. 21-12345 (no "FB")	-	Last 3 Digits of Voucher or PM[item number] or OOJ	-	Sample Description (2-6 letters)	-	OT/Grant Code	-	Case Type Identifier

For BEAST LIMS cases starting with F25-, the standardized format for specimens eligible for SDIS/NDIS is as follows:

Case Number (with F) Ex. F25-01234	-	Last 3 Digits of Voucher or PM[item number] or OOJ	-	Sample Description (2-6 letters)	-	OT/Grant Code	-	Case Type Identifier

1.1.1 Case Number:

1.1.1 Case Number: 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 unique identifier, followed by a dash). If the case is from 2006 or earlier: the unique identifier is a four-digit number. If the case is from 2007 or later: the unique identifier is a five-digit number.

1.1.1.1 Specimens eligible for SDIS and NDIS in BEAST LIMS cases starting with F25 will have an F at the beginning of the specimen ID. Ex. F25-01234-123-SAMPL-#-OT. Be mindful of the 24-character limit if the specimen ID contains a grant-funding code; in that instance, the sample description must be capped at five characters.

1.1.1.2 Specimens eligible for SDIS and NDIS in BEAST LIMS cases starting with F26 and later will utilize the standard naming structure, i.e., without an F at the beginning.

1.1.1.3 If the specimen is from a contract laboratory, the year will be preceded by a laboratory abbreviation, i.e., Bode Technologies (BT or BTB), Cellmark Diagnostics (CD) or Genescreen (GS).

1.1.2 Voucher/Post Mortem/Out-Of-Jurisdiction (OOJ):

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

1.1.2.2 **Postmortem items (no voucher number):** add “PM” followed by the item number followed by a dash, in place of the voucher number.

1.1.2.3 **Out-of-jurisdiction cases (no voucher number):** add “OOJ” followed by a dash, in place of the voucher number.

1.1.3 Sample Description: The next set of characters will be reserved for sample type and identification. Sample description may be shortened to comply with the 24-character limit.

1.1.3.1 **For non-Sexual Assault Kit evidence**: Add 2 to 6 letters and/or numbers that describe the item, the item number, and the stain designation followed by a dash.

1.1.3.1.1 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 does not need the item or stain number; however, when a case has multiple samples or CODIS profiles, attempt to create specimen IDs that are easily distinguishable, e.g., REDCAP and BLUCAP rather than CAP1A and CAP1B.

1.1.3.2 **For Sexual Assault Kit (SAK) items and additional SAK evidence**: the abbreviated descriptions below should be used. For differential extractions, include the fraction abbreviated description.

SAK Item	Abbreviated Description
Dried secretion	DS
Oral swab	OS
Vaginal swab	VS
Vulvar swab	VU
Cervical swab	CS
Anal swab	AS
Vaginal/Cervical	VC
Perianal swab	PA
Perianal/anal swab (no indication if one or both)	PAA
Penile swab	PS
Underwear	UW

Differential Fraction	Abbreviated Description
F1 (formerly called “Epithelial Cell Fraction”)	F1 (formerly EC)
F2 (formerly called “Sperm Cell Fraction”)	F2 (formerly SF)
Substrate Remains Fraction	SR

1.1.4 OT/Grant Code: add the relevant special character followed by a dash. This segment should be omitted from the specimen ID if no grant was utilized. The first instance of grant assistance determines which symbol is used, it cannot be used more than once.

#	cases examined, written, or tech reviewed on weekend overtime grant money
$	cases worked with grant-funded supplies
+	cases examined, written, or tech reviewed on Post-Conviction casework

1.1.5 Case Type Identifier: the last notation is a pair of letters indicating the case type. Do not add segments after this segment. Use the primary charge listed on the 61 if possible. This allows management or CODIS staff to query by crime type in the database. The two-letter case type indicator should always be the last segment of the specimen ID.

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	used for any case type not covered above, including grand larceny

1.1.6 Considerations for Specimens Processed in BEAST LIMS:

1.1.6.1 Cases with evidence submitted from both the NYPD and the ME will be given separate BEAST LIMS case numbers. If database (DB) specimens are determined from both the NYPD and ME evidence, the case number associated with the primary NYPD evidence case should be used for the specimen ID. Ex. MDA was determined from a PM item for F25-07230 and MDB was determined from a NYPD-submitted swab for F25-07333 (the primary case). Both MDA and MDB specimen IDs should utilize F25-07333.

1.1.6.2 If a string of cases in BEAST LIMS is all to be reported under one primary case, use the primary case number for all specimen IDs, even if the DB profiles are developed from evidence under non-primary case numbers.

1.1.6.3 If additional work is done in BEAST LIMS for a case with CODIS specimens currently in CODIS from LV LIMS, the naming of the BEAST LIMS specimen should be based upon the LV LIMS case number. Ex., initial testing in LV LIMS resulted in a MDA profile for FB23-01234. Additional testing for the same/associated complaint numbers is done in BEAST LIMS for F25-05678 and results in a MDB profile. The specimen for MDB should use the LV LIMS case number, (23-01234) in its specimen ID.

1.1.6.4 If initial testing was done in LV LIMS but no deconvolutions/DB profiles were done, subsequent deconvolutions/DB profiles done in BEAST LIMS (CPW tested in LV, deconvoluted in BEAST) should use the BEAST LIMS case number. Ex. FB25-01234 is a CPW case with testing in LV LIMS but no deconvolutions; subsequent deconvolutions are done in BEAST LIMS under F25-02323. The specimen ID of resulting DB profiles should utilize F25-02323.

1.1.7 Examples

- <u>Example 1</u>: FB21-00022, voucher N123456, item #1: purple shirt, stain 1B; assault. Specimen ID will be: *21-00022-456-PSHT1B-AS*
- <u>Example 2</u>: FB00-1257, postmortem kit item PM 2F, vaginal swab, sperm cell fraction, homicide. Specimen ID will be: *00-1257-PM2F-VSSF-HO*
- <u>Example 3</u>: FB20-01034, voucher P124589, item #1B: glove scrapings, burglary, examined on a weekend. Specimen ID will be: *20-01034-589-GLSCR-#-BU*
- <u>Example 4</u>: FB11-05500, voucher 1000099832, item #1, auto theft case, cigar butt, sample amped using primers purchased on grant. Specimen ID will be: *11-05500-832-CB1-$-AU.*
- <u>Example 5</u>: Cellmark Diagnostics backlog case CD01-0001, voucher K321123, sexual assault kit underwear stain, sperm cell fraction, sexual assault, Male Donor A. Male Donor B and C also present on underwear stain. Specimen ID will be: *CD01-0001-123-UWSFA-SA*
- <u>Example 6</u>: F25-01234, voucher 13525273262, item #3, burglary, bottle. Specimen ID will be: *F25-01234-262-BOTTLE-BU.*
- <u>Example 7</u>: F26-03456, voucher 43273726525, item #1, robbery, hat. Specimen ID will be: *26-03456-525-HAT-RO.*
- <u>Example 8</u>*:* F26-03810, voucher, 43625382434, item #1.5.1, sexual assault, vaginal swab fraction 2. Specimen ID will be: *26-03810-434-VSF2-SA.*

1.2 LDIS Only Specimens

1.2.1 <u>For all LV LIMS cases and BEAST LIMS cases starting with F26- and beyond</u>, the standardized format for specimens eligible for the LDIS Only category is as follows:

LLL	–	**Case Number** Ex. 21-12345 (no "FB")	–	**Donor Abbreviation** (if multiple donors) FDA, MDA, DDA	–	**OT/Grant Code**

<u>For BEAST LIMS cases starting with F25-</u>, the standardized format for specimens eligible for

the LDIS Only category is as follows:

1.2.2 Donor abbreviations, such as –MDA or –FDA may be added to the end of the case number but before the grant code (if used) when there is more than one LDIS Only profile for a case to aid in distinguishing between the specimens.

1.2.3 The specimen category for LDIS Only profiles is “Forensic LDIS Only”. Ex. LLL-25-01234-MDA-#.

1.3 Suspect Specimens

1.3.1 Suspect specimen IDs will have the form XXX-YR-S#####, where “YR” will be the last two digits of the case year. Formatting will depend on the case year and LIMS system used for processing. Suspect profiles developed under BEAST LIMS case numbers starting with “F25” will have a F before the two-digit year.

Year	**Specimen ID**
2006 and earlier	XXX-##-S123
2007 – early 2018	XXX-##-S1234
2018 to 2025	XXX-##-S12345
2025 (processed in BEAST LIMS)	XXX-F25-S12345
2026 and on	XXX-##-S12345

1.3.1.1 If a suspect exemplar is tested in BEAST LIMS and will be modifying an existing suspect exemplar specimen from LV LIMS, the BEAST LIMS specimen ID should utilize the case number from the LV LIMS case. Ex., FBS23-02121 is a 20-locus profile from a pseudo tested in LV LIMS and is in LDIS as XXX-23-S02121. Subsequently, a true exemplar from the same individual is received and tested in BEAST LIMS under F25-05938. The specimen ID for the BEAST LIMS true exemplar should be XXX-23-S02121.

1.3.1.2 If a suspect specimen has been removed from CODIS and a new suspect sample is tested and eligible for LDIS, use the current case that the new suspect sample was tested under for the specimen ID.

1.3.1.3 If modifying a previous BEAST LIMS suspect profile with another BEAST LIMS suspect sample, the specimen ID of the new suspect profile should be the same as the exemplar profile currently in LDIS.

1.4 Lab Types Specimens

1.4.1 Profiles entered into Lab Types will have specimen IDs of the form ##### (ex. 12345)

1.5 Unidentified Human (Remains), Relatives of Missing Persons and Missing Persons Specimens

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

1.5.2 **Unidentified Human Remains:** utilize “PM” followed by a dash in place of voucher

- Example: case no: F26-01234, bone, PM1, unidentified human remains. Specimen ID number will be: *26-01234-PM-U-MP*

1.5.3 **Relatives of Missing Persons:** the abbreviated descriptions below will be used for samples from relatives. There is no need to add voucher number. If more than one sibling, other maternal relative or other paternal relative is submitted, designate each with a number after the abbreviated description:

M	Mother
F	Father
C	Child
S	Biological Sibling (full brother or full sister)
OM	Other Maternal Relative
OP	Other Paternal Relative
SP	Spouse (other parent of child(ren) in common)

- Example: F26-01234, brother and sister of Missing Person. Specimen ID numbers will be: *26-01234-S1-R-MP* and *26-01234-S2-R-MP*

- Example: F26-01234, paternal half-brother of Missing Person. Specimen ID number will be *26-01234-OP-R-MP*

1.5.4 **Missing Persons**: add 2-5 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.

- Example: F26-01234, toothbrush used by Missing Person. Specimen ID number will be *26-01234-TB-M-MP*

1.6 Pedigree Trees

1.6.1 Pedigree Trees will be created by the CODIS team for relatives of missing persons. The Pedigree Tree ID will use the following format: Case number followed by a dash; four numerals for month and day created, followed by a dash; and the letters “PT.”

- Example: For a pedigree tree for case F26-06802, created on January 23rd, the pedigree tree ID would be *26-06802-0123-PT.*

2 Guidelines for Entering STR Profiles into CODIS

2.1 General Guidelines

2.1.1 All STR profiles, Y STR profiles, and mtDNA sequences that are CODIS eligible must undergo a reporting analyst review followed by a technical review prior to entry into LDIS.

2.1.2 In order for a specimen to be eligible for CODIS, testing of all CODIS core STR loci must be attempted. Any additional technologies (as needed) must also be attempted on appropriate samples.

- Original 13 CODIS core loci – entered prior to 1/1/2017
- Expanded 20 CODIS core loci – entered after 1/1/2017

2.1.3 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 NDIS Procedures Manual.

2.1.4 Profiles must contain enough data to minimize the opportunity for fortuitous, non-matching candidate matches to be eligible for LDIS, SDIS, and NDIS. Refer to the sections below to determine profile eligibility.

2.1.5 Forensic profiles developed using Low Copy Number amplification techniques are not eligible for entry into NDIS.

2.1.6 All partial or mixed evidence profiles, as well as all partial suspect profiles with data at 10 or fewer loci, must satisfy a statistical threshold for match rarity. This is done by calculating the Moderate Match Estimate using the COSTaR MME Calculator (refer to the "MME Instructions" tab within the document for instructions). This calculation generates the number of expected matches a partial or mixed profile will generate if searched against a database of size N, composed of single-source, unrelated specimens

2.1.7 Composite Profiles: Specimens can be a composite of multiple amplifications (same or different kits) if the amplifications are from the same DNA extract. Unless there is a reasonable expectation of samples originating from a common source (ex. duplicate orifice swabs, known reference samples, bones), allelic data from separate extractions from different locations on a given item should not be combined into a composite database profile. Interpreting analysts must consult with the CODIS Manager if a composite profile is being considered from different extracts not included in the examples above.

2.1.7.1 The following guidelines should be used to create a composite database specimen from different amplification kits:

2.1.7.1.1 Composite database specimens may only be created for a DNA Donor if at least six fully assigned locations match exactly between the amplification kits.

2.1.7.1.2 All interpreted loci for the DNA Donor between amplification kits must be concordant. Examples below:

- 11, 12 is concordant with 11, Z or INC.
- 11, 12 is non-concordant with 11,13.

2.1.7.1.3 Composite database specimens from different amplification kits must be single source or fully assigned profiles if from a mixture. These composite database specimens can be interpreted from a single source sample or from a mixture, but there can be no mixed or partially assigned locations in a composite database profile created from different amplification kits.

2.1.7.1.4 If there are locations partially interpreted or inconclusive in one amplification kit solely due to drop out or amplification imbalance, the interpreting analyst can use fully assigned allelic data in the other kit to build the composite profile.

2.2 Profile Requirements for Entry and Upload

2.2.1 LDIS: A minimum of 6 fully assigned loci are necessary for search of and entry into LDIS. All partial or mixed evidence profiles and suspect profiles with data at 10 or fewer loci must have an MME greater than or equal to the current LDIS database size rounded up to the nearest ten thousand (see COSTaR MME Calculator). If the MME value is less than the LDIS MME threshold, the profile is not eligible for LDIS and should only be searched against Lab Types.

NOTE: Suspect profiles submitted in the “Suspect, Known” specimen category can only be entered into LDIS. Loci must be either “INC” or fully deconvoluted to be entered into CODIS.

2.2.2 SDIS: To be eligible for upload into SDIS, in addition to fulfilling all LDIS requirements, the profile must have data (i.e., fully deconvoluted, mixed, or partial loci) at a minimum of 6 of the original 13 CODIS core loci. All partial or mixed evidence profiles must have an MME greater than or equal to the current SDIS database size rounded up to the next hundred thousand to be eligible for SDIS.

2.2.2.1 For SDIS Gun Unknown, SDIS Gun Mixture, and SDIS Gun Partial, the profile must meet laboratory guidelines for a DNA Donor and have data (i.e., fully deconvoluted, mixed, or partial loci) at a minimum of 8 of the original 13 CODIS core loci. All partial or mixed evidence profiles must have an MME greater than or equal to the current SDIS database size rounded up to the next hundred thousand to be eligible for SDIS.

2.2.3 NDIS: To be eligible for upload into NDIS (including Forensic Targeted), in addition to fulfilling all SDIS requirements, the profile must have data (i.e., fully deduced, mixed, or partial loci) at a minimum of 8 of the original 13 CODIS core loci. All profiles intended for the Forensic Mixture and Forensic Partial indexes must have an MME greater than or equal to 10,000,000 (1×10^7) to be eligible for NDIS. All profiles intended for the Forensic Targeted index must have an Match Rareity Estimate (MRE) greater than or equal to 10,000,000 (1×10^7) to be eligible for NDIS.

2.2.4 For Missing Persons and Unidentified Human Remains cases, in order for upload to CODIS for routine identity searches, Amelogenin is required along with the following number of loci:

- Unidentified Human Remains:
  - LDIS: 6 fully assigned STR loci
  - SDIS/NDIS: 7 fully assigned original core STR loci (D2S441 and D19S433 accepted as core loci)
- Missing Persons and Deduced Missing Persons:
  - LDIS: 6 fully assigned original core STR loci
  - SDIS/NDIS: 7 fully assigned original core STR loci (D2S441 and D19S433 accepted as core loci)
- Relatives of Missing Persons:
  - LDIS: 13 fully assigned original core STR loci
  - SDIS/NDIS: 13 fully assigned original core STR loci

2.3 Profile Building

2.3.1 Only enter the complete genotype for Amelogenin. If the interpretation at Amelogenin is incomplete and a "DNA Donor" is being reported (i.e., not Male or Female Donor A), db entry is inconclusive (INC).

2.3.2 The DNA result for each locus will be entered in the LV LIMS DB profile as follows: p, q for heterozygotes (in ascending order) and p, p for homozygotes (for example: TH01 6, 7 or 6, 6). The DNA result for each locus will be entered in BEAST LIMS as p q or p,q for heterozygotes and p for homozygotes.

2.3.3 Off ladder alleles above or below the CODIS allelic ladder range are entered in the LIMS DB profile as < (lowest allowed allele at that locus) or > (highest allowed allele), respectively. The official standardized NDIS allelic ladder is listed in Appendix A at the end of this manual.

2.3.4 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 following specimen categories: Forensic Unknown, Forensic Partial, SDIS Gun Unknown, SDIS Gun Partial, Missing Persons/Deduced Missing Persons, Relatives of Missing Persons, Suspect, Known, Lab Types, and Unidentified Human Remains.

2.3.5 Single source database specimens can be entered into Forensic Unknown, Forensic Partial, Forensic Targeted, Forensic SDIS Only, SDIS Gun Unknown, SDIS Gun Partial, or Forensic LDIS Only specimen categories; however, considerations must be made regarding the rules/eligibility for each respective category. See CODIS Terms and Abbreviations, CODIS Specimen Category Eligibility Table, and table below.

2.3.6 Mixtures

2.3.6.1 A mixed CODIS specimen refers to database profiles that contain loci not fully assigned and the allelic data at those loci could be from more than one source.

2.3.6.2 No more than four alleles per locus may be used for DNA profiles in the following specimen categories: Forensic Mixture, Forensic Targeted, SDIS Gun Mixture, Forensic SDIS Only, and Forensic LDIS Only categories.

2.3.7 A locus may be designated inconclusive (“INC”) at the discretion of the interpreting analyst and the technical reviewer(s) if an ambiguity exists at that locus. This locus, however, can and should still be used in the confirmation process once a candidate match is made. See the STR Interpretation Manual for PowerPlex Fusion (3130xLs) and the Interpretation of PowerPlex® Fusion data run on 3500xL for further guidance.

2.3.8 When entering profiles from mixed samples, these profiles can be entered into Forensic Unknown, Forensic Mixture, Forensic Partial, Forensic Targeted, Forensic SDIS Only, SDIS Gun Unknown, SDIS Gun Partial, SDIS Gun Mixture or Forensic LDIS Only specimen categories; however, considerations must be made regarding the rules/eligibility for each respective category. See CODIS Terms and Abbreviations, CODIS Specimen Category Eligibility Table, and table below.

2.3.9 Obligate Alleles

2.3.9.1 In certain circumstances, a single obligate allele may be designated using a “+”; the allele would be entered in the DB profile as p+. Only one obligate allele may be designated per locus.

2.3.9.2 For DNA profiles entered into Forensic Partial or SDIS Gun Partial, a locus with a single obligate may not have any other alleles entered for that locus (e.g., 15+ not 15+, 16).

2.3.9.3 When a locus can only be partially deconvoluted, use of the obligate allele designator aids in moderate stringency searches by preventing some of the spurious moderate matches possible at mixed loci. Use of required alleles narrows the possible matches that are returned in a search. For example, a 13, 14, 15 would match 13,13; 14,14; 15,15; 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: 14,14; 13,14; or 14,15 would be returned. See table below.

2.3.9.3.1 NOTE REGARDING OBLIGATES: a 13,14+,15 will not match a 13+,15 at moderate stringency even though the 13 and 15 are in both profiles because the 14 does not appear in the other profile. If one non-matching locus is allowed in the search configuration, the above situation would not prevent a match from being returned, however two such instances in the same pair of samples would prevent the match from being detected.

2.3.9.4 Obligates may not be used for any known/exemplar samples entered into the CODIS database, whether they are LDIS categories, such as Suspect, Known or Lab Types, or samples uploaded to SDIS/NDIS, including Missing Persons, Relatives of Missing Persons, and Unidentified Human Remains samples. Forensic Unknown specimens should also not use this convention.

3 Eligibility Guidelines For Entering STR Profiles into LDIS

3.1 Profiles matching a victim or elimination sample (consensual sex partner, regular-legal-use-of-item individual, etc.), must not be entered into CODIS. For a profile to be attributed to the victim or elimination sample, an exemplar must be tested and compared to the profile in question.

3.1.1 A victim or elimination sample must be requested from the NYPD Forensic Investigations Division Liaison Unit or District Attorney’s office if it is possible a person documented (by name or otherwise) in the casefile could reasonably have deposited their DNA on the forensic sample the database specimen came from. Documentation on NYPD paperwork indicating the victim or witness refused to provide an elimination sample is not enough to satisfy this requirement. At least one request for a relevant elimination sample must be made by a member of Forensic Biology before a forensic specimen is entered into LDIS.

3.2 If the Interpreting Analyst believes the forensic specimen cannot be reasonably attributed to the perpetrator of the criminal act but cannot be certain because there is no matching victim or elimination sample to compare (see 3.1 above), the profile can be considered for LDIS Only specimen category. See Section 3.3 for guidance for specimens that are not eligible for CODIS (including LDIS). The Interpreting Analyst must enter a case narrative to document their reasoning that justifies their eligibility determination if case information and/or biological sex alone is used to support that the profile is likely not attributable to the putative perpetrator.

3.2.1 If the biological sex of the forensic profile is used to justify the profile is not from the putative perpetrator, AMEL, DYS391, and the male target quantitation results should support the same biological sex determination.

3.2.2 If the alleged perpetrator of a sexual assault is also documented as a consensual partner (engaging in consensual sexual activity within 120 hours prior to incident), and the biological location of the sample cannot be distinguished from the consensual act, LDIS Only should be evaluated. Specimen is not eligible for NDIS/SDIS in these instances.

3.2.3 For sexual assault cases, case details (for example: consciousness of the victim) can be considered when determining if there are possibly multiple or unknown putative perpetrators not stated by victim.

3.2.4 For eligibility guidance, discuss with the LDIS Administrator and document in case narrative.

3.3 Evidence profiles that are clearly unrelated to a case or crime will not be entered into CODIS. For example, a sperm cell fraction 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 CODIS Program Manager and CODIS Administrator. The determination can be aided using the CODIS *Guide to Determining What is Allowable for Entry into the Forensic Index at NDIS* (on network).

3.4 Criminal Possession of a Weapon Cases:

3.4.1 If the database profile: (1) is from an operable firearm taken off a listed individual; (2) Criminal Possession of a Weapon is a documented charge; and (3) meets data requirements, it is only eligible for SDIS Gun Unknown, SDIS Gun Partial, SDIS Gun Mixture, or LDIS Only.

3.4.2 Shortening of the Criminal Possession of a Weapon charge as “gun case” or “CPW” in a narrative/communication log is not sufficient documentation.

3.5 See table below for Eligibility Guidance:

CODIS Specimen Level Guidance Table

Step	**Question**	**Yes?**	**No?**
1	Does your profile match a victim or elimination sample?	Profile is not eligible for CODIS.	Go to Step 2.
2	Do you have 6 or more fully deconvoluted loci?	Go to step 3.	Profile is not eligible for CODIS – suitable for comparison only.
3	Is specimen from firearm, "Criminal Possession Weapon" documented as a charge and is there documentation that supports firearm was taken off suspect/arrestee's person+*?	Go to step 7.	Go to step 4.
4	Is the specimen from an item (not firearm) taken off suspect/arrestee's person+?	Profile is eligible for LDIS Only, pending MME calculation.	Go to step 5.
5	Do you have data at 6 or more original CODIS core loci?	Go to step 6.	Profile is eligible for LDIS Only, pending MME calculation.
6	Do you have data at 8 or more original CODIS core loci?	Profile is NDIS eligible, pending MME calculation. Consider MRE calculation if MME insufficient.	Profile is eligible for SDIS Only, pending MME calculation.
7	Do you have data at 8 or more original CODIS core loci?	Profile may be eligible for SDIS Gun Indexes (SDIS Gun Unknown, SDIS Gun Mixture, SDIS Gun Partial), pending MME calculation.	Profile is not eligible for SDIS Gun Indexes. Profile is eligible for LDIS only, pending MME calculation.

+includes suspect/arrestee's apartment/home, backpack, car, areas their DNA would reasonably be expected through actions separate from crime, or if such items are witnessed as being in possession by member of NYPD at time of arrest. This determination can sometimes be difficult. Contact LDIS Administrators to seek guidance if needed.

*Toy or prop firearms are not eligible for SDIS Gun Indexes

3.6 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. They will be entered into LDIS with the following exceptions:

3.6.1 A properly executed court order concerning a specific sample dictates otherwise. See the Attorney/Customer Requests manual.

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

3.6.3 The exemplar was submitted as a result of a familial search and does not match the case for which it was submitted.

3.7 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 the Suspect, Known category under the usual nomenclature and search conditions.

3.8 Non-victim DNA profiles derived from evidence that are not eligible for SDIS/NDIS entry will be entered into the LDIS Only specimen category (e.g., a profile obtained from the clothing of a suspect).

3.9 Lab types will be entered into LDIS and will be maintained by the QA team

3.10 See CODIS Specimen Category Requirements Table for more information.

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

3.11.1 Y STR data is occasionally entered for missing/unidentified persons cases, for casework samples involved in partial match resolution, and for cases involved in familial search requests. See Appendix A for Y-STR standardized CODIS allelic ladder range.

3.11.2 The rapidly mutating Y STRs (DYS449, DYS518, DYS570, DYS576, DYS627, and DYF387S1) will not be entered into CODIS and should be INC in DB profiles. These loci are known to have high mutation rates, which could impact comparisons.

3.12 If a 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 and/or CODIS Administrator.

3.13 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 Lab Types or one of the following CODIS categories: Forensic Unknown; Forensic Mixture; Forensic Partial; Forensic Targeted; Forensic SDIS Only; SDIS Gun Unknown; SDIS Gun Partial; SDIS Gun Mixture; Low Copy Number; Suspect, Known; Missing Persons; Relatives of Missing Persons; Unidentified Human (Remains). For procedural guidelines on how to enter a profile into LDIS, see the relevant module in the online FBI LMS.

4 Partial Loci Indicators

4.1 Specimens in BEAST LIMS will have obligate alleles and partial loci flagged by the interpreting analyst during DB profile creation.

4.2 Use the below table for guidance regarding the partial loci indicators.

Interp	DB	Obligate	Partial
A, B	A, B		
A	A, A		
INC	A, B		✓
INC	A, B, C		
INC	A, B, C, D		
A, Z	A+	✓	✓
A, Z	A+, B	A ✓ B	✓
A, Z	A+, B, C	A ✓ B C	
A, Z	A+, B, C, D	A ✓ B C D	

5 Searches

5.1 All CODIS eligible profiles will be searched against both LINKAGE and LDIS. Search results are documented as an activity within the LIMS DB Profile page.

5.2 Linkage:

5.2.1 Log into the Forensic Biology Data Management System, and click on “Linkage” on the left side menu.

5.2.2 Linkage searches your target entry exactly - it does not search at moderate or low stringency. Do not include obligates or locations with 3 or more alleles.

5.2.3 Only enter the alleles from your interpretation for the CODIS core loci into each cell. Do not use a comma. Only place a single space between heterozygous alleles. For homozygotes, enter the allele once.

5.2.4 Click Search.

5.2.5 In BEAST LIMS, the LINKAGE search will be documented with a “Specimen searched against” activity. LINKAGE “no matches” do not have to be documented with an activity. True LINKAGE matches will be documented with a “Found matching specimen in” activity.

5.3 Identity Searcher (LDIS search)

5.3.1 Open the CODIS Work Station. Click on “Searcher” on the bottom left-hand side.

5.3.2 Ensure your search settings are as follows:

5.3.2.1 Click the yellow wrench icon on top-left while in the Searcher Module to get to configuration menu:

- General: Check box for the following:
  Return all candidates
  Use metadata sex as match filter
- 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 Targeted
  Forensic SDIS Only
  Lab Types
  Pattern
  SDIS Gun Unknown
  SDIS Gun Mixture
  SDIS Gun Partial
  Subject
  Unidentified Human (Remains)
- Candidate View: [None]

5.3.2.2 Click OK to exit setup mode.

5.3.2.3 Set Locus Display Order to “Master”

5.3.2.4 Ensure the boxes for all Fusion loci (original CODIS core 13 plus the additional 9) are checked (they should automatically check as you enter alleles). Amelogenin, SE33, and DYS391 remain unchecked. After you enter values for Amelogenin, you must unclick it again.

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

5.3.2.6 Do “Save-as” for this Searcher configuration and name appropriately (e.g., “Local Forensic Search”).

5.3.2.7 Enter the alleles from your profile. Note: all three alleles from a tri-allelic locus may be entered.

5.3.2.8 Click “Search”

5.3.3 The person conducting the search will document the event/activity in the LIMS record. The Local Candidate Match Detail Report(s) from candidate matches generated from LDIS keyboard searches determined to be a match will be saved to the LIMs record. The reporting analyst (RA) will document their determination of “match” or “no match” in the LIMs record.

5.3.3.1 The LDIS search will be documented with the “Specimen searched against” activity.

5.3.3.2 True matches in LDIS will be documented with the “Found matching specimen in” activity.

5.3.3.3 A candidate match determined to be a “no match” will be documented with the “Specimen does not match in” activity.

5.3.3.4 Local match detail reports and associated DNA hit email notifications will be attached either in the DB profile page (LV LIMS) or via the Case node in each case (BEAST LIMS).

5.3.4 If the searched specimen (specimen A) matches to another specimen (specimen B) which matches to another specimen (specimen C), but CODIS did not produce a candidate match between specimen A and C, review each locus carefully between specimen A and C to see if more than one locus would fail to match at moderate stringency (and thus not generate a candidate match). CODIS is a tool used to help identify matches, but this does not mean a true match cannot be identified and confirmed outside of CODIS.

5.3.4.1 Determine if specimen A and specimen C are true matches by reviewing the eletropherograms and any STRmix reports. If determined to be a true match, determine if a DNA Hit is needed between specimen A and B or if the DNA Hit will be to specimen C (based on which of the specimens was entered into CODIS first). If a DNA Hit is needed directly between specimen A and C (match that did not generate in CODIS), enter DNA Hits match type as “Direct Match”.

5.4 Lab Types Only Searches:

5.4.1 This search is used when the sample only needs to be searched against Lab Types specimens (e.g., sample is under a protective order, QA/QC purposes)

5.4.2 Searcher settings for Lab Types Only searches

5.4.2.1 Click into the Searcher module, select your saved Local Forensic Search and then click yellow wrench icon to get to configuration menu.

- Click off all indexes EXCEPT Lab Types (ctrl + click to deselect an index)
- Click: OK
- Save and name appropriately (e.g., “Lab Types Only Search")

NOTE: add a note in the case communication log/narrative that the profile was checked against Lab Types

5.5 LDIS Auto Searches

5.5.1 LDIS Auto Searches 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 Auto Searches will be performed by the CODIS staff only.

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

5.5.3 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”).

5.5.4 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.

5.6 High/Moderate Match Stringency Examples

DB Profile Entry (target specimen)	Will Match (candidate specimen)	
	at High Stringency	at Moderate Stringency
9,9	9,9	9, Z
8,9	8,9	8, 8; 9, 9; 8, 9, Z
7,8,9+	n/a	7, 9; 8,9; 9,9; 7,8,9, Z
7,9+	7,9	9,9; 7,9, Z
9+	9,9	9, Z
7,8,9,10	n/a	7,7; 8,8; 9,9; 10,10; 7,8; 7,9; 7,10; 8,9; 8,10; 9,10

NOTE: When searching your target specimen at high stringency, candidate specimens will be returned only where all loci match at high stringency. When searching at moderate stringency, candidate specimens will be returned only where all loci match at either high or moderate stringency. The above table shows the combination of alleles, given your target specimen, that will return a high or moderate stringency loci match. For example, if searching at moderate stringency (the setting for searches done in Searcher), all above combinations (high and moderate) could result, with the respective match stringency denoted as "[H]" or "[M]" at each loci.

6 Modifying or Deleting an STR Profile from CODIS

6.1 Modification of data already entered in CODIS may result from:

- Completion of additional testing
- Discovery of an error regarding the profile data or eligibility of the profile
- Discovery of an administrative error, such as an error in the specimen ID

6.2 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 (either physical or electronic via BEAST activities or LV workflow events).

6.3 Please refer to the LIMS Database Profile Modification manual for instructions on how to submit the profile modification in LV LIMS. Refer to CODIS Profile Creation and Management for instructions on how to submit the profile modification in BEAST LIMS.

6.4 Profile modifications for paper-only files should be submitted on the traditional paper form (see CODIS Profile Modification Form). This includes all Backlog and Biotracks cases, Forensic Biology cases FB12-03799 and earlier, and Forensic Biology suspect cases FB12-S0949 and earlier. This applies only to cases with no database profile record in LIMS.

6.5 Profile modifications for LV LIMS-era files (FB12-03800 and later, and suspect files FBS12-00950 and later) must be submitted via the DB profile page in LIMS. The modified dataset should include data for all previous loci as well as those being updated. Profile modifications for BEAST LIMS-era files must be submitted via entering the appropriate activity in the DB profile.

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 one or more alleles present in the previous dataset(s), will NOT result in updating that locus to "INC". The technical reviewer who submits the modification MUST notify CODIS staff by email to ensure that the locus/loci in question are modified manually in CODIS. The email does NOT replace the need for the modification form.

6.6 Any profile modification will be documented in the appropriate profile modification log by a CODIS staff or designee. This includes profile modification documentation and specimen detail reports.

6.7 EXPUNGEMENTS SECTION

6.8 Removal (expungement) of data in CODIS may result when:

- A profile entered is later determined to be from a victim, witness, consensual partner, family member, etc.
- Documentation is provided for legal expungement request.
- 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.
- The identity of a missing or unidentified person has been confirmed.

6.9 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.

6.10 Please refer to the LIMS Database Profile Expungement manual for instructions on how to submit the profile expungement in LV LIMS. Refer to CODIS Profile Creation and Management for instructions on how to submit the profile expungement in BEAST LIMS.

6.11 Profile expungements for paper-only files should be submitted on the traditional paper form (see Profile Removal Expungement Form). This includes all Backlog and Biotracks cases, Forensic Biology cases FB12-03799 and earlier, and Forensic Biology suspect cases FB12-S0949 and earlier. This applies only to cases with no database profile in LIMS

6.12 Profile expungements for LIMS-era files (FB12-03800 and later, and suspect files FBS12-00950 and later) must be submitted via the DB profile page in LIMS.

6.13 Any profile expungement will be documented in the appropriate profile expungement log by a CODIS staff or designee. Documentation should include the profile expungement form and specimen delete report.

7 Activities/Events

7.1 In LV LIMS, events appear on the DNA Profile Evaluation form, Profile Modification Form (if the profile modified checkbox is checked for that event), and Expungement Form (if the profile expungement checkbox is checked for that event).

7.2 In BEAST LIMS, activities entered into the DB profile (BEAST) appear on the CODIS Report. Applicable activities that should be noted in BEAST LIMS can be found in the BEAST Database Profile Activities Appendix.

8 CODIS Group Email Notifications for Evidence Specimens Modified to Change CODIS Eligibility (CODIS Group Only):

8.1 If a CODIS specimen's eligibility in CODIS changes due to additional information subsequently obtained, a member of the CODIS group will send an email to FIDLU and the District Attorney Office to communicate the modification. Emails will also be distributed to NYPD via ECMS. Email will include FB#, CRT#, and complaint #.

8.1.1 If Profile is elevated in CODIS

8.1.1.1 The DNA profile below was submitted to the [choose all applicable - OCME local DNA databank/Local DNA Index System (LDIS)/State DNA Index System (SDIS)/National DNA Index System (NDIS)]. The DNA profile below is now eligible for [choose all applicable - Local DNA Index System (LDIS)/State DNA Index System (SDIS)/National DNA Index System (NDIS)].

8.1.2 If Profile is downgraded in CODIS

8.1.2.1 The DNA profile below was submitted to the [choose all applicable - OCME local DNA databank/Local DNA Index System (LDIS)/State DNA Index System (SDIS)/National DNA Index System (NDIS)]. The DNA profile below is now eligible only for [choose all applicable - Local DNA Index System (LDIS)/State DNA Index System (SDIS)/National DNA Index System (NDIS)].

8.1.3 If Profile is removed from CODIS (same as current CODIS expungement language)

8.1.3.1 The DNA profile below was submitted to the [choose all applicable - OCME local DNA databank/Local DNA Index System (LDIS)/State DNA Index System (SDIS)/National DNA Index System (NDIS)]. The DNA profile below is not eligible for the databanks because it [matched a victim/complainant/witness/consensual partner (choose one) OR no longer meets an eligibility requirement]. Therefore, it was removed from the [choose all applicable - OCME local DNA databank/Local DNA Index System (LDIS)/State DNA Index System (SDIS)/National DNA Index System (NDIS)]. Any further comparison to this DNA profile must be a direct comparison. Uploading Profiles to SDIS/NDIS and Search Policies

9 Uploading Profile to SDIS/NDIS and Search Policies

9.1 All LDIS profiles eligible for SDIS and/or NDIS will be uploaded to SDIS by the CODIS staff. Currently, New York State local DNA laboratories upload to SDIS five days a week, with the SDIS search performed shortly thereafter

9.2 Once uploaded to SDIS, all LDIS profiles eligible for NDIS are then uploaded to NDIS by the NY State Database Laboratory. See NYS CODIS Procedures Section 3.0 for upload schedule.

9.3 LDIS profiles for upload to SDIS/NDIS will NOT include profiles from the Suspect, Known or Lab Types specimen categories. Only forensic samples and missing persons/unidentified persons samples that meet the SDIS/NDIS criteria may be uploaded to SDIS/NDIS.

9.4 All putative perpetrator profiles in a Forensic Biology DNA pattern will be uploaded to SDIS. Previously, additional profiles developed in other cases in a pattern were placed into the Other (pattern) Index in LDIS and were not uploaded. This is no longer the case. Profiles previously placed into this index remain in this index.

10 Other Searches

10.1 Emergency Search and Upload Requests (EUSR)

10.1.1 The Emergency Search and Upload Requests (EUSR) functionality has replaced emergency manual keyboard search requests of SDIS and NDIS.

10.1.2 EUSR functionality allows NDIS participating laboratories to enroll/upload and immediately search a specific DNA specimen at SDIS and NDIS, without sending an incremental upload. This is not a replacement for incremental uploads.

10.1.3 EUSR should only be used for cases where timing is critical to the investigation, or high priority cases (e.g., public safety threat). The forensic specimen must be eligible for SDIS/NDIS pursuant to policies and procedures governing specimen eligibility (i.e., as if the specimen were regularly being uploaded during an incremental upload).

10.1.3.1 The following specimen categories are eligible for EUSR: Forensic Unknown, Forensic Partial, Forensic Mixture, Forensic Targeted, SDIS Gun Unknown, SDIS Gun Mixture, SDIS Gun Partial, and Unidentified Human Remains.

10.1.3.2 If EUSR is not available, a keyboard search request may still be submitted to quickly search a profile at SDIS. Profiles must meet CODIS eligibility requirements. Requests are submitted to the SDIS Administrator using a **Criminal Keyboard Search Request Form**.

10.1.4 FOR CASEWORK ANALYSTS

10.1.4.1 If you have a specimen that you believe to be EUSR eligible, confer with your supervisor, manager, and contact the CODIS group.

10.1.4.2 A local keyboard search of LDIS must be performed before a specimen is considered for EUSR eligibility, to ensure there are no matches to known specimens at the local level.

10.1.4.3 If the specimen ID contains the following characters an error message will be generated: #, <, $, +, %, >, !, `, &, *, ‘, |, {, ?, “, =, }, /, :, \, @, and blank spaces. If a specimen ID has already been generated for the specimen with one of these special characters, please contact the CODIS group.

10.1.5 FOR CODIS GROUP

10.1.5.1 Before uploading an EUSR specimen, the State CODIS administrator and DCJS should be notified. Communication should continue with both agencies throughout the process.

10.1.5.2 Only one forensic specimen can be sent in an EUSR; if there are multiple specimens to be sent, they must be sent one at a time.

10.1.5.3 The specimen enrolled in EUSR will be the Target Specimen, and a full auto search will occur at SDIS and NDIS, based upon the original 13 CODIS core loci, and subject to the specimen category eligibility (i.e., Forensic SDIS Only specimen will only be searched at the State level). If an auto search is currently running, the specimen will be placed in a queue to be searched next. The specimen will also be incorporated into the daily/weekly regular incremental auto search schedule – there is no need to “re-upload” the specimen following enrollment in EUSR.

10.1.5.4 The EUSR evidence specimen will be searched against Forensic Unknown, Convicted Offender, Arrestee, Detainee, and Legal specimen categories. Forensic Mixture and Forensic Partial categories will be searched in the next regularly scheduled auto search in order to prevent multiple, unintended reciprocal auto searches (e.g., all Forensic Mixture specimens searching against the enrolled specimen).

10.1.5.5 The EUSR unidentified human remains specimen will be searched against Convicted Offender, Arrestee, Detainee, Legal, Missing Person, and UHR categories.

10.1.5.6 To enroll a specimen in EUSR, select the specimen, right click, and select "Submit Emergency Upload and Search Request."

10.1.5.7 Two EUSR Reconciliation Reports will be generated in Message Center – one from SDIS and one from NDIS, if applicable.

10.1.5.8 If the specimen failed to be enrolled, a failure message will display in Message Center, and the reconciliation report will display the reason for rejection.

10.1.5.9 Any potential candidate matches that are returned will display via Match Messages in the Message Center. Matches should be evaluated and processed based on internal policies and procedures, but with an expedited time frame based on the immediacy/urgency of the case.

10.2 Laboratory to Laboratory Manual Keyboard Search Requests

10.2.1 NDIS participating laboratories may request a keyboard search of an NDIS eligible specimen from other LDIS laboratories. The request should be submitted to the SDIS laboratory and they may forward those requests to the LDIS laboratories.

10.2.2 These requests are fulfilled by completing a Laboratory-to-Laboratory DNA Search Request Form (found on the CODIS website). This form contains the profile, relevant case information, whether the profile is partial, the search stringency for each locus, and the reason for the search request. The form is submitted to the relevant State CODIS Administrator.

10.2.3 Search requests from external laboratories of our LDIS are directed to the Local CODIS Administrator, CODIS Manager, or laboratory director and are completed at their discretion. Search results are communicated directly with the requesting laboratory.

10.2.4 A manual keyboard search may only be requested once the profile is uploaded to NDIS.

10.2.5 Profiles that are requested to be searched must meet eligibility for CODIS entry, including having data at 7 original core loci and an MME threshold that meets 1 in 10 million. If a profile contains less than 6 original CODIS core loci with data, there should be justification in writing.

10.2.6 All requests from external laboratories will be documented and maintained, either in a binder or digitally on the network.

10.2.7 Requests from other labs to compare their forensic specimen to suspect specimens will not be approved and are not allowed. Only DNA profiles developed by the Department of Forensic

Biology may be compared to suspects in LDIS. Requests from other labs should only be searched against forensic LDIS specimens.

10.2.8 Keyboard search requests are only allowed for DNA profiles derived from evidence - DNA profiles from known individuals are not routinely allowed to be searched.

10.2.9 The Department of Forensic Biology does not routinely request keyboard searches of other NDIS laboratories. A request should only be made if there is a demonstrated and documented need to search another SDIS lab (e.g., public safety threat). If this is the case, analysts should contact their supervisor, manager, and the CODIS group with the request. The CODIS group will process all keyboard search requests.

10.3 International Searches

10.3.1 A forensic profile may be searched at a non-CODIS databank (e.g., Interpol). See the NDIS Procedures Manual for further information.

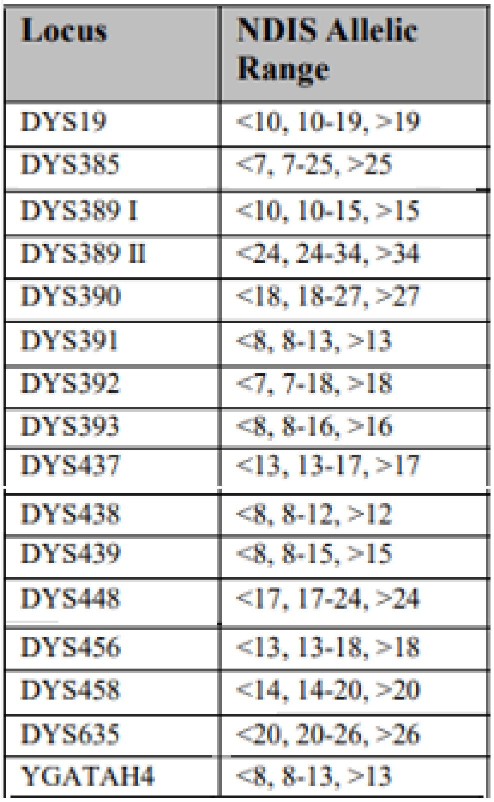
10.3.2 A non-U.S. forensic profile may be searched at NDIS upon request to the FBI and at their discretion. Such a profile may NOT be searched at LDIS**.**

APPENDIX A: CODIS Allelic Ladder Range

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 to be tested.

Amelogenin	X, Y		
*** D3S1358**	<12,	12-19,	>19
****D1S1656**	<9,	9-20.3,	>20.3
****D2S441**	<9,	9-16,	>16
****D10S1248**	<8,	8-18,	>18
*** D13S317**	<8,	8-15,	>15
Penta E	<6,	6-24,	>24
*** D16S539**	<5,	5-15,	>15
*** D18S51**	<9,	9-26,	>26
****D2S1338**	<15,	15-28,	>28
*** CSF1PO**	<6,	6-15,	>15
Penta D	<2.2,	2.2-17,	>17
*** TH01**	<5,	5-10,	>10
*** vWA**	<11,	11-21,	>21
*** D21S11**	<24.2,	24.2-38,	>38
*** D7S820**	<6,	6-14,	>14
*** D5S818**	<7,	7-16,	>16
*** TPOX**	<6,	6-13,	>13
*** D8S1179**	<8,	8-18,	>18
****D12S391**	<14,	14-27,	>27
****D19S433**	<9,	9-17.2,	>17.2
*** FGA**	<18,	18-30,	>30
****D22S1045**	<8,	8-19,	>19
D6S1043	<7,	7-25,	>25
SE33	<4.2,	4.2-37,	>37

The Y-STR standardized NDIS allelic ladder range:



Locus	NDIS Allelic Range
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
DYS437	<13, 13-17, >17
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