Case Management		
Status: Published		Document ID: 996
DATE EFFECTIVE 10/24/2022	APPROVED BY Quality Assurance Manager	PAGE 1 OF 10

Case Management

1 Guiding Principles and Scope

1.1 Case management is the process by which an analyst shepherds the evidence through the testing process. It is the responsibility of the analyst to ensure that evidence receives the necessary analysis, analytical results are evaluated promptly, any analytical problems resolved, the results interpreted, and the final report written within the time frame dictated by the target date.

2 Procedure

2.1 Most case management steps are done using the Laboratory Information Management System (LIMS); however, the "legacy" case management and documentation system in Forensic Biology, which utilizes various hard copy forms, is available for documenting the examination of evidence in exigent circumstances when the LIMS is unavailable for an extended period of time.

3 Production Team System

3.1 Many of the processes described in the following sections are handled by the Production Team staff and not necessarily the reporting analyst (RA). One goal of the Production Team system is to rapidly and efficiently extract, quantify, and amplify samples. Workflow and preparation of test batch samples is coordinated by the Production Teams.

3.2 Testing results are available to the RA through the LIMS interface.

3.3 It is the responsibility of the test batch reviewer to examine the samples and batch set-up information for completeness and accuracy of case numbers, sample identifiers, etc. Any discrepancies, inconsistencies, or omissions must be resolved before obtaining a witness and/or commencing testing.

3.4 It is the responsibility of the witness to examine the samples and batch set-up information for completeness and accuracy of case numbers, sample identifiers, etc. As above, resolve any issues prior to commencing testing.

4 Case Assignment

4.1 Case management begins as soon as evidence examination begins.

4.2 Cases are assigned based on priority and Evidence Received date. An initial priority level is assigned during the Sign-In process, but can be adjusted later.

4.2.1 High Priority – All parts of case that were promised (could just be semen Y/N, for example, or it could be a complete DNA report) are done ASAP, using overtime if necessary.

Designating a case as High Priority requires a phone call from an NYPD high-level manager to a Forensic Biology (FB) manager or the Forensic Biology Customer Liaison, or a phone call from a DAO Bureau Chief-level to an FB manager or the Forensic Biology Customer Liaison. A "regular" ADA cannot make such a request. The High Priority request is accompanied by a Priority Request Form which will specify the date of completion of testing requested by the customer. If the status goes away later, the priority can be downgraded.

4.2.2 Priority – Started next, but the rest of the case gets processed as usual; this is the same as "expedite". The Priority request is accompanied by a Priority Request Form which will specify the date of completion of testing requested by the customer. All stranger rapes are in this category. Remember that "stranger rape" is NOT the same as "no suspect". A "stranger rape" is a "stranger rape" whether there is a named/arrested suspect or not.

4.2.3 Routine – Average, everyday, sort of case (excluding stranger rapes).

4.2.4 Review the case information (see the Evidence Examination - general guidelines section of the Evidence Examination procedure) and ensure the subjects, complaint number, voucher number and other case details are entered correctly into the LIMS record.

4.2.5 The category of Victim will be used for Homicide reports, rather than Decedent. The category of Complainant will be used for all other reports.

4.3 If this is additional evidence or an exemplar on a previously reported case, evaluate the earlier work.

4.3.1 It may be necessary to submit earlier DNA extracts for additional testing.

4.3.2 If an exemplar is submitted, type it in all DNA systems necessary for comparison.

4.3.3 Suspect samples should be typed in the most current kit when:

4.3.3.1 The associated evidence has mixtures suitable for comparison only

4.3.3.2 The associated evidence only has partially deconvoluted profiles

4.3.3.3 The associated evidence is single source or a fully deconvoluted profile and matches a true suspect sample.

4.3.4 Suspects samples do not need to be re-typed if:

4.3.4.1 The associated evidence samples are insufficient and/or not suitable for comparison

4.3.4.2 The associated evidence is single source and suspect is excluded

4.3.4.3 The associated evidence is single source and matches a suspect abandonment sample

4.3.4.4 The associated evidence has a fully deconvoluted profile and matches a suspect abandonment sample, additional samples with the same DNA Donor can also be compared.

4.4 Obtain the evidence from the evidence storage area and complete the chain of custody.

5 Initial analyses

5.1 Examine the evidence (see Evidence Exam procedure).

5.2 Test samples for KM, PSA, Amylase, or male DNA through Zygem lysis and/or DNA extraction as needed. Ensure that true exemplar samples and abandonment samples are submitted on the appropriate exemplar extraction batches and that evidence samples are submitted on the appropriate non-exemplar extraction batches.

5.3 The RA managing the case should ensure that their name is listed in LIMS as the RA.

5.4 Evidence examination notes and any serology or Zygem lysis results are reviewed by the RA for completeness and accuracy. Discrepancies or omissions need to be corrected by the analyst who performed the test. Check especially for correct FB number, swab description or stain description.

5.4.1 If exam notes are not substantively wrong, then examining analysts should not be asked to make changes to their examination notes.

5.4.1.1 Substantive information is that which affects the meaning of what is written in notes (ie. can vs. can't, no vs. yes, wrong stain name written as proceeding to extraction, conflicting information in notes, complaint/voucher numbers listed differently than in paperwork, name of individuals listed incorrectly).

5.4.2 If something is substantively wrong with the exam notes, RAs can ask EAs to correct it.

5.4.3 The original EA's notes should not be changed by anyone but the EA as they are the person who performed the examination. If a situation arises where you need to confirm something (i.e., packaging markings, consumed or not, stain testing performed on, etc.), the EA, RA, or a designee can take out the evidence, perform confirmation and document the confirmation in the case notes. EAs should not make a correction from memory. Exceptions to this include mis-selections in the drop-down menu that are verifiable (such as a NY SAK being marked as made of "paper" instead of "cardboard").

5.5 Extraction and quantitation results are reviewed by the RA for completeness and accuracy; any discrepancies or omissions need to be corrected by the analyst who performed the test. Check

especially for correct FB number, swab description or stain description. The following information should be checked:

5.5.1 Does the extraction negative contain DNA?

5.5.2 If neat and dilution results were tested, do the results correlate with each other?

5.5.3 Is the DNA concentration too high?

5.5.4 Was there a problem with inhibition and/or background fluorescence preventing a determination of the DNA concentration? If so, the sample may need to be cleaned via microcon and re-quantified.

5.6 Re-quantitation needed due to any of the aforementioned reasons is generally taken care of in the Production Team System.

5.7 Microcon clean-up will be by the Production Team System.

6 DNA typing and case evaluation

6.1 Once acceptable quantitation results are available, the DNA samples requiring amplification will be processed.

6.1.1 In some instances, concordance of results may require additional amplification of samples. If this is the case, the sample(s) must be placed onto an amplification batch.

6.2 The RA reviews amplification and DNA typing results for completeness and accuracy; any discrepancies or omissions need to be corrected by the analyst who performed the test. Check especially for correct FB number, swab description or stain description. In addition, review all the electropherograms for your case.

6.2.1 Review the STR Control Review worksheet to ensure that the positive control, amplification negative, and extraction negative (if applicable) gave the expected results and to ensure that the STR batch review was completed. If the controls did not give the expected results, the samples may need to be re-amplified or even re-extracted.

6.2.2 Did your samples amplify? If not, it may be necessary to re-amplify with more DNA extract or less DNA extract (if PCR inhibitors are suspected), or perform a microcon procedure.

6.2.3 In some situations, it may be necessary to start the DNA analysis over at the DNA extraction step or consider organic extraction.

6.2.4 Was a partial DNA profile detected in your sample? If so, it may be necessary to perform further testing.

6.2.5 Alternatively, it may be necessary to re-amplify with more DNA extract or less DNA extract (if PCR inhibitors are suspected), or perform a microcon procedure.

6.2.6 Was your sample over-amplified? If so, submit the sample for amplification again with less DNA extract or run at a dilution.

6.2.7 Were your samples properly edited? Evaluate any editing that was done on your samples; examine the electropherograms for artifacts, over-amplification, or other problems. If the sample was not edited properly, the STR analysis analyst or the reporting analyst may re-edit and reprint the electropherograms; make sure the new editing is added to the editing worksheet in LIMS and update the allele table.

6.2.8 Is there a mixture of DNA in your sample? If so, it may require additional work in a DNA system (the same one or a different one) to achieve concordance. Mixtures may also be amplified with more template DNA for better results.

6.2.9 Are there other samples that may require additional work to meet concordance? If so, identify those samples and start the appropriate steps (i.e., re-extraction or re-amplification).

6.2.10 Do the DNA results make sense in the context of the case and/or sample? If not, there may have been a sample mix-up at the aliquot, amplification, or DNA typing steps. Discuss with your supervisor.

6.3 Review the DNA typing results as soon as possible so that ample time remains to deal with any analytical problems.

6.3.1 Refer to the appropriate Interpretation manual (in the Forensic Biology Protocols for Forensic STR Analysis manual) to interpret the results of DNA typing.

6.3.2 After reviewing results, if an elimination sample is needed but not yet requested, FIDLU should be contacted for cases with no listed suspect(s). If a listed suspect is present, the ADA handling the case should be contacted for an elimination sample. All efforts should be documented as a case contact. Refer to the Elimination Request template examples below.

6.3.3 For FIDLU requests (when there is no named suspect):

Good morning,

I am making a request for a reference sample for the following case in order to compare it to DNA results:

Complaint #:
Case Type:
FB #:

Complainant/Entity:
Comparison sample(s) needed:

If there is an arrest in this case, please notify us of the suspect's name, NYSID # and/or arrest #.

If you are unable to obtain a sample please let us know as soon as possible so the case can be completed.

Thank you,

6.3.4 For DAO requests (when there is an arrest or named suspect):

Good morning,

I am making a request for a reference sample for the following case in order to compare it to DNA results:

Complaint #:
Case Type:
FB #:
Complainant/Entity:
Suspect Information:
Comparison sample(s) needed:

The Forensic Biology analyst assigned to this case is:

If you are unable to obtain a sample please let us know as soon as possible (no later than two weeks from the date of this email) so the case can be completed.

Thank you,

6.4 Compare a single source or deconvoluted DNA profiles to the Lab Types Database within LDIS in order to detect possible exogenous DNA. Instructions for how to conduct searches of the database are found in the LAB TYPES DATABASE procedure in the Quality Assurance/Quality Control Manual.

6.4.1 If contamination is identified see the "Sample Contamination Policy" found in the GENERAL GUIDELINES FOR FORENSIC BIOLOGY AND DNA CASEWORK procedure (in the Forensic Biology Protocols for Forensic STR Analysis manual).

6.5 Compare DNA results to the LINKAGE database and LDIS for potential matches (exact or partial). In addition, it may be necessary to compare DNA profiles within a case to other profiles in the case, and to any suspects submitted for that case, to identify partial matches. This may

require you to determine the DNA profile(s) present in a mixture, and may require consultation with a supervisor.

6.5.1 Only single-source profiles (clean or deduced) with >10 CODIS core loci should be compared for the purposes of discovering partial matches. Only such profiles are eligible for evaluation of any partial matches found. Such profiles shall not contain INC or Z at any of the >10 CODIS core loci being used for partial match evaluation.

6.5.2 To compare a profile to LDIS, perform a keyboard search. Only profiles that meet the necessary number of loci and statistical threshold for entry into LDIS should be searched in LDIS.

6.5.3 Consider if a potential match may be due to law enforcement contamination. If contamination by law enforcement is suspected, see the Verifying and Reporting DNA Matches section of the CODIS Manual.

6.5.4 Before searching suspect exemplar profiles against Linkage and LDIS, ensure that there is not a Protective Order issued for that sample. Refer to the Protective Orders section of the ATTORNEY / CUSTOMER REQUESTS section of the Administrative Manual.

6.5.5 See the CODIS Manual for more detailed information regarding DNA matches.

6.5.6 Any potential case-to-case matches not identified in LINKAGE will be picked up by LDIS once the profile is entered there.

6.5.7 If a sample from your case matches a sample from a previous case, consult with your supervisor and follow the current local hit notification guidelines.

6.6 Not all samples require DNA analysis in all available DNA systems; in fact, the majority of samples require only STR DNA typing. Submission of samples for Y STR DNA typing is case dependent.

6.7 Follow the guidelines below to determine whether a case should be transferred when a comparison is needed between samples that were typed in different kits.

6.7.1 Comparisons that can be done by an analyst competent in Fusion only:

6.7.2 Suspect (Fusion) to Suspect (ID/Co/Pro)

6.7.3 Suspect (Fusion/ID/Co/Pro) to Evidence (Fusion)

6.7.4 Evidence (Fusion) to single source or fully deconvoluted profile in Evidence (ID), however the Fusion analyst can only testify to Fusion results.

6.7.5 Comparisons that must be done by an analyst competent in Identifiler:

6.7.6 Suspect (Fusion/ID) to Evidence (ID)

6.7.7 Evidence (Fusion) to Evidence mixture (ID)

6.7.8 For all other comparisons involving legacy kits consult the Technical leader.

6.8 The DNA system chosen for additional testing may depend on the nature of the case.

6.8.1 Were the only DNA alleles detected in a sample containing male DNA those of the victim? If so, amplification using Y-STRs may be needed.

6.8.2 Does it appear that there are multiple male donors? If so, amplification in Y-STRs may be needed.

6.8.3 Does the case involve a body identification of a male, and are there paternal relatives available for testing? If so, amplification using Y STRs may be needed.

6.8.4 Generally, Y-STR testing may be performed if a sufficient amount of male DNA is detected and the submitted paperwork lists the full name of a male person of interest.

6.8.5 For cases involving partial match where Y-STR testing may be used to confirm matches (i.e., between MDA and an elimination sample), a listed male person of interest may not be needed.

6.8.6 Ensure that the laboratory concordance policy is satisfied.

6.9 Prepare a profile generation report or table of results, if applicable,

6.10 Prepare a Statistics sheet, if necessary. Enter all alleles that meet the allele calling criteria.

6.10.1 If writing a suspect report and reporting a profile frequency statistic or Y haplotype statistic from the evidence (i.e., Male Donor A profile found on knife handle that now matches the suspect) refer to Population Frequencies for STR's section 2.4 to determine if a new statistic must be calculated. If not, and the statistic was already calculated and is present in the evidence file, a copy may be made of the relevant statistics sheet and placed in the suspect file.

6.11 Prepare a DNA Profile Evaluation form, if necessary. Follow the guidelines listed for eligible profiles to determine how many (if any) alleles to enter at each locus.

6.12 Review the case file to ensure that all the necessary paperwork is present and is organized in a logical format.

6.12.1 When reviewing left side paperwork, if a chain of custody deviation is needed from the EU, email the member of the EU and the Evidence supervisors to request the deviation be

entered in LIMS. Also, ask the EU for a copy of the deviation so that it can be added to the case file.

6.13 Finalize the draft case report, approve, and submit for the required technical and administrative reviews. Submitting the report for approval is captured in LIMS.

6.13.1 If a case has any pending Type I non-conforming work, the RA should not approve the report or casefile for tech review. This memo should be included so that the technical reviewer can evaluate the memo. The case should stay as Pending RA until the Type I non-conforming work documentation has been added to the LIMS case record.

6.13.2 If the case has any pending Type II or III non-conforming work, the RA may approve the report or casefile for tech review as long as a note is present in the case notes indicating the need for the non con. The non-conforming work memo can be added after the case report is approved and the case record can be recertified with the new information.

6.13.3 Before approving a negative SAK, the analyst should check with QA about SAK reanalysis if there is no indication it was previously reviewed. Candidates for SAK reanalysis must have underwear or small items, as well as samples that have not gone to EZ1 or differential extraction.

6.13.4 The results are considered reviewed and authorized once the Reporting Analyst has documented their review of the case file and submitted the report for technical and administrative review.

6.14 The Linked Cases tab should be evaluated within every case. The Sign-In team will link related cases that need to be compared to one another and, in some instances, checking this tab may be the only indication that two cases need to be compared. This could be for related incidents, pattern cases, or, most frequently, linked suspect and evidence files. Refer to the Reports manual to determine if a report needs to be written for a comparison of the linked cases.

6.14.1 If you suspect the case is part of a pattern, do not link cases in LIMS or update the record, consult the DNA Sign in team or the DNA Sign In Supervisor/Manager.

6.14.2 The complaint number may be searched in LIMS to see if any additional suspects are submitted for comparison to the evidence file. Additionally, if a suspect comes in with a different complaint number than the associated evidence case of comparison, that number may be searched as well to see if related evidence was also received.

7 Case Completion

7.1 A case is considered complete when the analytical work is done, the case report is written and passes technical and administrative reviews, and the case report is distributed to the requesting agency(s).

7.2 Evidence Return:

7.2.1 Within the LIMS, mark the individual vouchers of evidence for final return. The Evidence Unit will obtain the item(s) and prepare the item(s) for "pending release to the Property Clerk" using their normal procedures. With the exception of post-mortem items and exemplars, retained samples should no longer be indicated on the chain of custody.

8 Case Report Routing

8.1 Report distribution is usually done in conjunction with administrative review. For details see the Administrative Review procedure.

8.2 Most reports are distributed to the ECMS system of the NYPD. In addition to ECMS and the DA's offices, reports are distributed as follows:

8.2.1 Reports with a Medical Examiner Number: these reports are routed to the OCME Case Management System (CMS) and are sent to the DA's offices through LIMS. Therefore, any case designated as a Homicide should have CMS included in its distribution list.

8.2.2 Reports involving Special Narcotics, Arson, Family Court, Federal Court, or IAB cases: these reports should be sent to the Department's point of contact or office through LIMS. Contact the Forensic Biology Customer Liaison for current contact name.

8.2.2.1 Reports for Special Narcotics are typically sent to "SpecialNarcotics".

8.2.2.2 Reports for Arson cases are typically sent to "ArsonDistribution".

8.2.2.3 Reports for Family Court cases should not be distributed to the DA's offices unless case circumstances require such distribution or a special request is made. Reports should be sent to "FamilyCourt". .

8.2.2.4 Reports for Federal Court cases must be distributed to either the Eastern District "EasternDistrict" or Southern District "SouthernDistrict" offices , not the DA's offices unless case circumstances require such distribution or a special request is made.Reports for IAB cases must not be distributed to ECMS or the DA's offices.