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# ARKANSAS STATE CRIME LABORATORY CODIS SECTION QUALITY MANUAL

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## 1 SCOPE

This document consists of definitions, policies and procedures intended to satisfy the quality assurance measures and specific requirements placed on the CODIS Section of the Arkansas State Crime Laboratory by the Arkansas State Crime Laboratory Quality Manual, the FBI Director's Quality Assurance Standards, and the ANSI-ASQ National Accreditation Board (ANAB), which is based on the ISO/IEC 17025:2017 standards and the 2017 ANAB ISO/IEC 17025:2017 —Forensic Science Testing and Calibration Laboratories Accreditation Requirements (AR 3125).

DNA database testing is to be understood to begin at sample extraction or direct amplification; therefore, at a minimum all actions taken by ASCL personnel concerning DNA Testing will be subject to the guidelines contained in this CODIS Section Quality Manual (and the Forensic DNA Section Quality Manual, as appropriate) until the completion of DNA testing activities and the documented transfer of associated evidence or samples. Elements of the quality assurance program outlined in this manual may apply to steps which extend beyond the initiation or conclusion of DNA testing activities. Unless specifically noted, all DNA database activities will also be subject to the policies of the Arkansas State Crime Laboratory Quality Manual.

## 2 DEFINITIONS, AND REFERENCES

It is the intention of the CODIS Section to follow the standard definitions included in normative references listed as well as those found in the ASCL *QM*. For dated references, only the edition cited applies. For undated references, the latest edition of the referenced document (including any amendments) applies. Each document's location is referenced in brackets.

- A) ISO/IEC Guide 99, International vocabulary of metrology —Basic and general concepts and associated terms (VIM)[Qualtrax]
- B) ISO/IEC 17000, Conformity assessment —Vocabulary and general principles
- C) ISO/IEC 17025:2017, General requirements for the competence of testing and calibration laboratories
- D) ANAB ISO/IEC 17025:2017 –Forensic Science Testing and Calibration Laboratories Accreditation Requirements (AR 3125)
- E) Arkansas Code Annotated (A. C. A.) §§ 12-12-301 through 12-12-313 [Qualtrax]
- F) Quality Assurance Standards for Forensic DNA Testing Laboratories, 2020 [Qualtrax]
- G) Quality Assurance Standards for Forensic DNA Databasing Laboratories, 2020 [Qualtrax]
- H) NDIS Operational Procedures

Additional common acronyms used in this manual are listed

Arkansas State Crime Laboratory (ASCL)

Arkansas State Crime Laboratory Quality Manual (ASCL QM)

Forensic DNA Section Quality Manual (DNA QM)

FBI Director's Quality Assurance Standards (QAS)

ANSI-ASQ National Accreditation Board (ANAB)

Quality Assurance Program (QA)

Quality Assurance Concern Workflow (QAC)

DNA Technical Leader (DNA TL)

JusticeTrax LIMS-plus (JTx)

Qualtrax Compliance Management System (QTx)

ForensicBiology Shared Drive (FB Drive)[\\Davinci\Sections\ForensicBiology]

### 2.1 CODIS SECTION OVERVIEW

The Combined DNA Index System (CODIS) is a computerized program designed to house DNA profiles from convicted offender / arrestees, deceased individuals, missing persons and relatives of

missing persons, Arkansas State Crime Laboratory staff, forensic cases (both evidence samples and suspect's known reference samples). The purpose of CODIS is to create a national information repository where law enforcement agencies can share DNA information obtained from convicted offender / arrestees and forensic evidence. This system allows agencies to cross reference case evidence profiles with that of other agencies' case evidence profiles.

Currently, there are three levels of CODIS: National DNA Index System (NDIS), State DNA Index System (SDIS) and Local DNA Index System (LDIS). The Arkansas State Crime Laboratory participates as a State and Local system that has the capability to upload (movement of DNA profiles between systems at different levels) DNA profiles to the National level. The Arkansas State Crime Laboratory is responsible for not only analyzing all convicted offender / arrestee samples for the state, but also to enter and search crime scene samples obtained from forensic casework. The Federal Bureau of Investigation (FBI) maintains the National level.

As data is entered in the CODIS system it immediately becomes available to search at the State DNA Index System (SDIS).

The National DNA Index System (NDIS) is a centralized index of DNA profiles administered by the FBI. DNA profiles that are allowed by NDIS are contributed to NDIS by participating State CODIS laboratories. The profiles from all forensic cases nationally are searched at this level against the Offender and Arrestee Index and against all the profiles in the Forensic Index. NDIS requires a convicted offender / arrestee profile to contain results from all 20 CODIS core loci (CSF1PO, TPOX, TH01, vWA, D16S539, D18S51, D7S820, D13S317, D5S818, D3S1358, D8S1179, D21S11, FGA, D1S1656, D2S441, D2S1338, D10S1248, D12S391, D19S433, and D22S1045) and a forensic case profile to contain results from at least 8 of the 13 original core loci (in bold).

The CODIS software is designed by and provided to the Arkansas State Crime Laboratory by the FBI. Upgrades and modifications to the software are periodically provided to the lab by the FBI through the FBI's contractor. The use of the CODIS system in Arkansas is in accordance with the most current version of the CODIS User Guide, CODIS Training Reference Manuals, CODIS Installation support documents and CODIS Technical Notes provided to the lab by the FBI and the FBI's contractor. CODIS is a dynamic system and therefore undergoes frequent major and minor software upgrades, which may cause the actual operation of the software to not exactly reflect the policies and procedures in this document. Modifications to this manual will be made to accommodate the changes as necessary. Employees utilizing the CODIS database must receive proper training and clearance according to established NDIS guidelines.

## 3 QUALITY ASSURANCE PROGRAM

### 3.1 QUALITY MANUAL

The CODIS QM has been approved by the CODIS Administrator, DNA Technical Leader, Laboratory Quality Assurance Manager, Assistant Director, and Director and is accepted as routine operating policy of the CODIS Section within the *ASCL*.

- A) The FBI QAS serves as the basis for the ASCL CODIS QA program with supplementary guidance from the ASCL-QM.
- B) This QM is one component of the CODIS QA program; any elements not contained within this manual can be found in the QUALTRAX controlled document database.
- C) Any supplements and revisions to the FBI QAS guidelines will be reviewed for possible incorporation into the QA program.
- D) To discuss other possible revisions, meetings between the CODIS Supervisor and the CODIS staff will be held as needed.
- E) Any changes to this QA manual shall be approved by the same individuals as stated above, with affected manual pages and files updated. All CODIS employees shall be notified of the changes and shall be given any necessary training.
- F) Previous versions of revised documents are maintained in a separate Historical Archive.
- G) All Documents referenced within this manual shall be available or accessible on-site.

### 3.2 DOCUMENT RETENTION

The CODIS section shall retain the following documents and records of processes in accordance with ASCL QM policies. These documents and records are maintained in a variety of secure methods, including STACS-DB, JusticeTrax, Qualtrax, and the secure FB drive.

- A) proficiency tests and proficiency test plans [all]
- B) deviation requests and non-conformances [STACs and FB drive]
- C) QA Concerns, Preventative Action, and Corrective Actions [QTx]
- D) Audit Documents, ASCL Audit Responses, and NDIS Custodian Acceptance Letters [FB drive]
- E) training records [all]
- F) continuing education [QTx and FB drive]
- G) case files [STACS, JTx and FB drive]
- H) court testimony monitoring [QTx]
- I) QA documentation [STACS, QTx and FB drive]

### 3.3 ANNUAL REVIEW OF THE QUALITY SYSTEM

The CODIS section shall annually review the quality system under the direction of the DNA TL. This review shall be independent of any audit review with the purpose of ensuring that the

quality system remains in compliance with applicable standards and guidelines. The quality system review shall be documented and approved in a Qualtrax workflow by the DNA TL.

### 3.4 ANNUAL REVIEW OF PROCESSING

The CODIS section shall evaluate sample processing to ensure quality of product and adherence to the CODIS QM SOP. This review will be based on a semi-random selection by the DNA TL of at least one STACS batch from each plate type completed each month. The DNA TL shall endeavor to select batches from each analyst throughout each year, with preference given to sets containing Hit Confirmations and/or Rerun samples. This review will be separate from any technical review and shall be documented in memorandum or on the CODIS Database Review Form (CODIS-FORM-25). Reviewers will be restricted to the CODIS Administrator and DNA TL and will not be the analyst of record of the batch file in review. The DNA TL shall approve the results of the review and shall be consulted in determining any Nonconformance or Corrective Actions.

### 3.5 GOALS AND OBJECTIVES

IT IS THE MISSION OF THE CODIS SECTION TO BLEND FORENSIC SCIENCE AND COMPUTER TECHNOLOGY INTO AN EFFECTIVE TOOL FOR SOLVING CRIMES. WE ARE COMMITTED TO QUALITY AND INTEGRITY IN OUR WORK. WE PROFILE SAMPLES ALLOWED BY STATE AND FEDERAL LAWS TO SEARCH AGAINST CRIME SCENE PROFILES.

**Goals: It is the goal of the CODIS section of the Arkansas State Crime Laboratory to:**

- a) Provide the users of laboratory services access to a CODIS system for searching DNA profiles at a National level.
- b) Ensure the quality, integrity and accuracy of the DNA typing data and its presentation through the implementation of a detailed Quality Assurance/Quality Control program.
- c) Provide the criminal justice system with a functional DNA database (CODIS) to help law enforcement agencies solve criminal cases.
- d) To provide timely, accurate, high quality services to the state of Arkansas and all other states participating in the National DNA Index System.

**Objectives: It is the objective of the Quality Assurance (QA) program to:**

- A) Monitor on a routine basis the analytical testing procedure for DNA typing by means of Quality Control (QC) standards, proficiency test and audits.
- e) Verify that the entire DNA typing procedure is operating within the established performance criteria, as stated in the Analytical section of the Quality Manual and that the quality and validity of the analytical data are maintained.
- f) Ensure that problems are noted and that corrective action is taken and documented.
- g) Ensure the overall quality as outlined in the QAS and SWGDAM Guidelines.

## 4 ORGANIZATION & MANAGEMENT

### 4.1 MANAGEMENT

Under the guidance of the ASCL Administration, the operations of the CODIS section are directly managed by the DNA Technical Leader and the CODIS Administrator with the assistance of the section Quality Manager, Training Manager, and Safety officer.

#### 4.1.1 ASCL ADMINISTRATION

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The organization and authorizations of the ASCL Administrative positions can be located in the ASCL QM.

The ASCL Administration is responsible for ensuring facilities, funding, and policies for the efficient and quality standards-compliant operations of the CODIS DNA laboratory operations. The ASCL Administration is also responsible for providing the opportunity to comply with the requirement to stay abreast of developments within the field of DNA typing by making available current scientific or DNA applicable literature, and enabling attendance of seminars, courses or professional meetings through travel budget, membership dues and education expense reimbursement.

#### 4.1.2 TECHNICAL LEADER

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The DNA Technical Leader serves as Technical Leader of both the Forensic DNA and Databasing (CODIS) sections. The DNA Technical Leader is accountable for technical operations and quality assurance. The DNA Technical leader is a fully-qualified analyst and maintains proficiency in both Casework and Database DNA procedures.

#### 4.1.3 CODIS ADMINISTRATOR

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The CODIS Administrator is accountable for all CODIS operations as well as serving as the personnel manager for the CODIS Section and the DNA Technical Leader. The CODIS Administrator also serves as the Casework CODIS Administrator of the Forensic DNA section. The CODIS Administrator is a fully-qualified analyst and maintains proficiency in both Casework and Database DNA procedures.

#### 4.1.4 CODIS PERSONNEL

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The CODIS analysts and support staff are accountable for ensuring compliance of activities within the directives and guidelines of the section Quality manual. At no time is there fewer than two full-time, qualified CODIS Analysts employed by the ASCL.

### 4.1.5 ORGANIZATION

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The organization and personnel authorizations of the CODIS section are located in Qualtrax. The organizational chart can be found in Qualtrax as the *CODIS Organizational Chart* (ASCL-DOC-70-CODIS). Individual authorizations are documented in the Personnel tab of Qualtrax.

### 4.1.6 CONTINGENCIES

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In the event the technical leader position is vacated, the following contingency plan will be submitted to the FBI within 14 days for approval. Any work that is in progress may be completed during the 14 day period, but new casework shall not be started until the plan is approved by the FBI.

With the approval from the Director or his /her designee, the ASCL will conduct interviews within the laboratory among any qualified individuals to be appointed by the Director to temporarily fill the technical leader position. If there are no interested or qualified individuals the ASCL will contact the surrounding states to ask for the assistance of their technical leader until the technical leader position can be posted, interviewed and filled.

A newly appointed technical leader shall be responsible for the documented review of the validation studies currently used by the laboratory and educational and training records of currently qualified analysts.

In the event that the number of qualified CODIS analysts falls below two full-time employees, the following contingency plan will be submitted to the FBI within 14 days for approval. The CODIS Administrator and/or DNA Technical Leader shall singly or collectively assume CODIS analyst responsibilities and provide laboratory and analytical assistance to any remaining analyst in excess of a full-time qualified Forensic DNA analyst and work may be continued.

With the approval from the Director or his /her designee, the ASCL will conduct interviews within the laboratory among any other qualified individuals to be appointed by the Director to fill the CODIS analyst position. If there are no qualified individuals the ASCL will begin hiring new trainees. No DNA sample processing will begin within the ASCL until two fully-qualified DNA analysts are employed.

## 4.2 APPLICABLE STANDARDS

The CODIS section shall utilize the date of hire or appointment to a DNA position for determining applicable versions of standards for education, experience, and training requirements. Advancements subsequent to the initial employment of an Analyst (e.g. CODIS Analyst I to CODIS Analyst II, or CODIS Analyst II to CODIS Administrator) will not reset the date except those additional requirements that apply to the appointment of the Technical Leader, CODIS Administrator, or Alternate CODIS Administrator.



## 5 PERSONNEL

### 5.1 PERSONNEL QUALIFICATIONS AND JOB DESCRIPTIONS

The following establishes the job function, responsibility and qualifications for each position. This includes specification and description of lines of responsibility for developing, implementing, recording and updating the QA program. Job descriptions for personnel are established and located in each employee history binder. Each subordinate is accountable to one supervisor per function.

Records of qualifications, training, and experience will be maintained in training binders, as well as FB drive, JTx, and QTx as appropriate.

### 5.2 DNA TECHNICAL LEADER

#### 5.2.1 EDUCATION

The DNA TL shall meet the following minimum educational requirements: a Master's degree in a biology-, chemistry- or forensic science- related area and have successfully completed 12 semester or equivalent credit hours from a combination of undergraduate and graduate coursework covering the following subject areas: biochemistry, genetics, molecular biology, and statistics or population genetics.

- 5.2.1.1 The 12 semester or equivalent credit hours shall include at least one graduate level course registering three (3) or more semester or equivalent credit hours.
  - 5.2.1.2 The specific subject areas listed above shall constitute an integral component of any course work used to demonstrate compliance with this standard.
  - 5.2.1.3 Individuals who have completed course work with titles other than those listed above shall demonstrate compliance with this standard through a combination of pertinent materials such as a transcript, syllabus, letter from the instructor, or other document that supports the course content.
  - 5.2.1.4 If the degree requirements listed above were waived by the American Society of Crime Laboratory Directors (ASCLD) in accordance with criteria approved by the director of the Federal Bureau of Investigation (FBI), such a documented waiver is permanent and portable.
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## **5.2.2 EXPERIENCE**

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Any DNA TL appointed prior to July 1, 2009, shall have three years of forensic DNA laboratory experience obtained at a laboratory where forensic DNA testing was conducted for the identification and evaluation of biological evidence in criminal matters. Any DNA TL appointed on or after July 1, 2009, shall have a minimum of three years of human DNA (current or previous) experience as a qualified analyst on forensic samples.

## **5.2.3 NEW TL APPOINTMENTS**

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Any DNA TL appointed on or after July 1, 2020 shall be a currently or previously qualified analyst in each technology utilized in the laboratory, or have documented training in each technology utilized in the laboratory within one year of appointment.

Newly appointed technical leaders shall be responsible for the review of the following within one year of appointment:

- Validation studies and analytical procedures currently used by the laboratory; and
- Educational and training records of currently qualified analysts and technical reviewers.

## **5.2.4 AUDITOR TRAINING**

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The DNA TL shall have previously completed or will successfully complete the FBI's DNA auditor training course within one year of appointment.

## 5.2.5 RESPONSIBILITY

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The TL is ultimately responsible for technical operations and the QA program of the DNA sections and thus the management of the DNA analysis program including technical troubleshooting, validation and systems management. Therefore the DNA TL shall have the following authority and responsibility as required by the FBI QAS:

- Oversee the technical operations of the DNA Laboratory.
- The TL has the authority to initiate, suspend, and resume the DNA analytical operations for the laboratory or an individual.
- Monitor, evaluate, and approve the development, validation, and implementation of the DNA QA program, new methods and new technologies.
- Review the academic transcripts and training records for newly qualified analysts and approve their qualifications prior to independent casework analysis and document such review.
- Approve the technical specifications for outsourcing agreements.
- Review internal and external DNA audit documents and, if applicable, approve corrective action(s), and document such review.
- Review, on an annual basis, the procedures of the laboratory and the quality system, then approve and document such review.
- Review and approve training, quality assurance, and proficiency testing programs in the laboratory.
- Review and approve contract employees for employed by multiple NDIS participating and/or vendor laboratories for potential conflict of interests.

Additional responsibilities of the DNA TL include:

- Review validation and methodologies currently used by the laboratory and educational qualifications and training records of currently qualified analysts.
- Ensure compliance with FBI QAS and ANAB requirements.
- Establish professional liaisons with colleagues engaged in DNA testing and research.
- Monitor training and the proficiency testing programs for DNA Casework Section personnel.
- Analyzing samples, providing expert testimony, and performing other routine duties of a Casework Analyst.
- Stay abreast of developments within the field of DNA typing by reading current scientific or DNA applicable literature, attending seminars, courses or professional meetings.
- Review casework to ensure quality of product and adherence to the Forensic DNA QM SOP as part of the Annual Casework Review [DNA QM 3.4]

## 5.2.6 ACCESSIBILITY

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The technical leader shall be accessible to the laboratory to provide on-site, telephone, or electronic consultation as needed. Currently, the ASCL Forensic DNA testing is only available at the Main

Laboratory location. In the event that additional locations are offered, the DNA TL shall conduct and document a site visit to each laboratory at least semi-annually.

### **5.2.7 AUTHORIZATIONS**

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See ASCL QM section 6.2.6 for categories of Authorizations.

- Can initiate, suspend, and resume DNA analytical operations for the laboratory or an individual.
- Reviews DNA quality manager's actions in implementing the quality assurance program for the Forensic DNA section.
- Oversees the technical operations of the Forensic DNA laboratory.
- Approves method development, modification, verification, and/or validation.

## **5.3 CODIS ADMINISTRATOR**

The CODIS Administrator is responsible for the administration of the laboratory's local CODIS network. The CODIS Administrator is also responsible for the technical operations and provisions of the resources needed to ensure the required quality of the laboratory operations. The CODIS Administrator has the responsibility and authority to receive and take action on CODIS employee concerns.

### **5.3.1 EDUCATION**

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The CODIS Administrator shall meet the education requirements for an analyst as defined in DNA QM Section 5.5 (QAS Standard 5.4). A CODIS Administrator appointed prior to July 1, 2020 shall be deemed to have satisfied the minimum educational requirements; satisfaction of these minimum educational requirements shall be applicable to the specific laboratory by which the casework CODIS administrator is employed by prior July 1, 2020 and shall not be portable.

### **5.3.2 EXPERIENCE**

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A CODIS Administrator shall be a current or previously qualified analyst as defined in DNA QM Section 5.5 (QAS Standard 5.4) with documented mixture interpretation training. A CODIS Administrator appointed prior to July 1, 2009 who is not or has never been a qualified analyst (with documented training in mixture interpretation) shall be deemed to have satisfied the minimum experience requirements upon completion of FBI sponsored CODIS training; satisfaction of these minimum requirements shall be applicable to the specific laboratory the casework CODIS administrator is employed by prior to July 1, 2009 and shall not be portable.

### **5.3.3 CODIS TRAINING**

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The CODIS Administrator shall successfully complete the FBI-sponsored training in CODIS software within six months of assuming CODIS Administrator duties if the administrator had not previously completed such training. The CODIS Administrator shall successfully complete the FBI's DNA

auditor training course within one year of assuming his/her administrator duties if the administrator had not previously completed such training.

### **5.3.4 RESPONSIBILITY**

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The CODIS Administrator shall have the following minimum responsibilities as required by the QAS:

- Administer the laboratory's local CODIS network.
- Schedule and document the CODIS computer training of casework analysts.
- Ensure that the security of data stored in CODIS is in accordance with state and/or federal law and NDIS operational procedures.
- Ensure that the quality of data stored in CODIS is in accordance with state and/or federal law and NDIS operational procedures.
- Ensure that matches are dispositioned in accordance with NDIS operational procedures.

Additional responsibilities of the CODIS Administrator include:

- Ensure compliance with FBI QAS and ANAB requirements.
- Maintain a list of all employees with access to the CODIS database.
- Stay abreast of developments within the field of DNA typing by reading current scientific or DNA applicable literature, attending seminars, courses or professional meetings.
- Notify the NDIS Custodian, within five business days, of the following:
  - 1) If a CODIS User, CODIS IT User or CODIS WAN User in its laboratory has been arrested for, or convicted or, a criminal offense;
  - 2) If the laboratory loses its criminal justice agency status;
  - 3) If the laboratory loses its accreditations, has its accreditation suspended or has its accreditation revoked;
  - 4) if the laboratory loses the capability to perform DNA analysis at its facility;
  - 5) If the laboratory has fewer than two full-time employees who are qualified DNA analyst;
  - 6) If the laboratory has a vacancy in the laboratory's Technical Leader position when there is no one in the laboratory who meet the Quality Assurance Standards' qualifications and is available to serve in that positions; or
  - 7) If the laboratory is not in compliance with the external QAS audit requirements.

### **5.3.5 PARTICIPATION IN CODIS**

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The CODIS Administrator shall be authorized to terminate an analyst's or laboratory's participation in CODIS until the reliability and security of the computer data can be assured in the event an issue with the data is identified.

### **5.3.6 CONTINGENCY**

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In the event that the CODIS Administrator is unavailable such that they cannot administer the laboratory's CODIS network, the Alternate CODIS Administrator shall fulfill the role of CODIS Administrator. In the event that the role of CODIS Administrator is unoccupied, the ASCL shall not upload DNA profiles to NDIS.

## **5.4 ALTERNATE CODIS ADMINISTRATOR**

The Alternate CODIS Administrator is responsible for the administration of the laboratory's local CODIS network in the event that the CODIS Administrator is unavailable such that they cannot administer the laboratory's CODIS network.

### **5.4.1 EDUCATION**

---

The Alternate CODIS administrator shall meet the education requirements for an analyst as defined in DNA QM Section 5.5 (QAS Standard 5.4). An Alternate CODIS Administrator appointed prior to July 1, 2020 shall be deemed to have satisfied the minimum educational requirements; satisfaction of these minimum educational requirements shall be applicable to the specific laboratory by which the Alternate CODIS Administrator is employed by prior July 1, 2020 and shall not be portable.

### **5.4.2 EXPERIENCE**

---

An Alternate CODIS Administrator shall be a current or previously qualified analyst as defined in DNA QM Section 5.5 (QAS Standard 5.4) with documented mixture interpretation training. An Alternate CODIS Administrator appointed prior to July 1, 2009 who is not or has never been a qualified analyst (with documented training in mixture interpretation) shall be deemed to have satisfied the minimum experience requirements upon completion of FBI sponsored CODIS training; satisfaction of these minimum requirements shall be applicable to the specific laboratory the Alternate CODIS Administrator is employed by prior to July 1, 2009 and shall not be portable.

### **5.4.3 CODIS TRAINING**

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The Alternate CODIS Administrator shall successfully complete the FBI-sponsored training in CODIS software within six months of assuming CODIS casework administrator duties if the administrator had not previously completed such training. The Alternate CODIS Administrator shall successfully complete the FBI's DNA auditor training course within one year of assuming his/her administrator duties if the alternate administrator had not previously completed such training.

### **5.4.4 RESPONSIBILITY**

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In the event that the CODIS Administrator is unavailable such that they cannot administer the laboratory's CODIS network, the Alternate CODIS Administrator shall fulfill the role of CODIS Administrator.

## 5.5 CODIS ANALYST

The CODIS analyst is an employee or contract employee of the laboratory responsible for performing DNA analysis and specifically delegated QA responsibilities from the of CODIS Administrator. The analyst shall meet the following qualifications:

### 5.5.1 EDUCATION

The analyst shall have at a minimum a bachelor's (or its equivalent) or an advanced degree in a biology-, chemistry-, or forensic science-related area and shall have successfully completed coursework (graduate or undergraduate level) covering the following subject areas: biochemistry, genetics, and molecular biology.

- Any analyst hired/appointed/promoted prior to July 1, 2020, shall have coursework and/or training in statistics and/or population genetics as it applies to forensic DNA analysis.
- Any analyst hired/appointed/promoted on or after July 1, 2020, shall have successfully completed coursework covering statistics and/or population genetics.

#### 5.5.1.1 COURSEWORK

The specific subject areas listed in Section 5.5.1 shall be an integral component of any coursework for compliance with this standard. If coursework consists of the title listed (biochemistry, genetics, molecular biology, and statistics or population genetics), the coursework shall be considered to meet the integral component requirement. Coursework is generally assessed as the set number of credits on a transcript. Each course topic must be satisfied by a course in that subject or a course that is considered to meet the integral component requirement. Absent a course titled as listed, coursework used to fulfill the requirement should include the following components:

##### Biochemistry:

- Structure, function, and interaction of biological macromolecules such as proteins, carbohydrates, lipids and nucleic acids
- Enzymes and chemistry of enzyme-catalyzed reactions
- DNA, RNA, and protein synthesis
- Signal transduction
- Metabolism
- Cell membrane transport

##### Genetics:

- Laws and patterns of inheritance
- Basic structure and function of genes and chromosomes
- Mutation
- Mitosis/Meiosis
- Recombination
- Gene expression

#### Molecular Biology:

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- Prokaryotic and eukaryotic genome structure and function
- Interrelationship of DNA, RNA, and protein synthesis
- Transcription, translation, replication
- Gene expression and regulation
- Recombinant DNA techniques
- PCR
- DNA sequencing

#### Population Genetics:

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- Estimation and testing of measures of allelic association within and between loci (Hardy-Weinberg principle)
- Description and estimation of measures of relatedness at the individual and population level (population structure)
- Genetic drift, mutation, migration and selection
- Absent a course titled "Statistics," coursework used to fulfill the statistics requirement should include the following integral components:
  - Descriptive statistics
  - Sampling uncertainty and sampling distributions
  - Confidence limits and intervals
  - Discrete and continuous variables
  - Estimation and hypothesis testing, including the use of likelihoods
  - Laws of probability and independence
  - Bayes' Theorem

#### **5.5.1.2 APPOINTMENTS POST-JULY 1, 2009**

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Analysts appointed or hired on or after July 1, 2009 shall have a minimum of nine cumulative semester hours or equivalent that cover the required subject areas of biochemistry, genetics, and molecular biology.

#### **5.5.1.3 ALTERNATE COMPLIANCE**

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Analysts who have completed coursework with titles other than those listed in DNA QM 5.5.1 above shall demonstrate compliance with this standard through a combination of pertinent materials, such as a syllabus, letter from the instructor, or other document that supports the course content. The technical leader shall approve compliance with this standard.

#### **5.5.2 EXPERIENCE**

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The analyst shall have no less than six months of forensic human DNA laboratory experience. If prior forensic human DNA laboratory experience is accepted by a laboratory, the prior experience

shall be documented and augmented by additional training, as needed. The technical leader shall approve the extent of the prior experience.

Analyst training entails the analysis of a range of samples routinely encountered in forensic databasing prior to independent work using DNA technology. Additionally, the analyst shall successfully complete a competency test and proficiency test before beginning independent DNA analysis. A complete list of training requirements can be located in the Casework and CODIS Sections Analyst Training Manual. The analyst shall successfully complete the required training.

### 5.5.3 RESPONSIBILITY

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The CODIS analyst is responsible for any assigned tasks in the operations of the Forensic DNA Section.

- Implementing the QA program.
- Handling reagents.
- Establishing liaisons with colleagues in the field.
- Analyzing, interpreting and reporting casework.
- Providing expert testimony.
- Interacting with investigative personnel.
- Executing all duties of QA Manager, if so designated.
- Assisting in training new employees.
- Stay abreast of developments within the field of DNA typing by reading current scientific or DNA applicable literature, attending seminars, courses or professional meetings.
- All other duties as assigned.

### 5.5.4 AUTHORIZATIONS

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See [ASCL QM](#) section 6.2.6 for categories of Authorizations

- May recommend rejection of chemicals, reagents, supplies or materials that are found to be inadequate.
- May recommend termination of DNA testing if a technical problem is found.
- May Analyze and Report Results, Technically Review and Authorize Reports.

## 5.6 TECHNICAL REVIEWER

The technical reviewer shall be an employee or contract employee of the laboratory. The technical reviewer shall meet the education and experience requirements in CODIS QM section 5.5 (QAS Standard 5.4) and shall meet the following:

- A current or previously qualified analyst.
- Successful completion of documented training.

## 5.7 CODIS SUPPORT STAFF

The CODIS Support Staff are administrative personnel responsible for administratively processing CODIS-appropriate samples that are delivered to the laboratory.

### 5.7.1 EDUCATION

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The CODIS Support Staff shall have at a minimum, a high school diploma or equivalent.

### 5.7.2 EXPERIENCE

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The CODIS Support Staff shall complete the Support Staff training program established by the CODIS Administrator and CODIS Training Manager. This training entails the intake processing of a range of samples encountered in normal database operations. Additionally the CODIS Support Staff shall successfully complete a competency test before beginning independent DNA sample intake.

### 5.7.3 RESPONSIBILITY

---

The CODIS Support Staff are responsible for any assigned tasks in the operations of the CODIS Section.

- Implementing the QA program.
- Handling reagents.
- Establishing liaisons with colleagues in the field.
- Preparing database samples for analysis.
- Providing expert testimony.
- Interacting with investigative and corrections personnel.
- Assisting in training new employees.
- The CODIS Support Staff must stay abreast of developments within the field of DNA typing by reading current scientific or DNA applicable literature, attending seminars, courses or professional meetings.
- All other duties as assigned.

### 5.7.4 AUTHORIZATIONS

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See [ASCL QM](#) section 6.2.6 for categories of Authorizations

- Receives CODIS appropriate samples into the laboratory.
- Enters the CODIS appropriate samples into the State Convicted Offender / Arrestee Database System, STACS-DB, or JusticeTrax as applicable.
- Ships database collection kits to law enforcement personnel.
- Schedule training with law enforcement agencies.
- Facilitate communication between collection facilities.
- Prepares samples for DNA analysis.

- May recommend termination of DNA testing if a technical problem is found.

## 5.8 CODIS QUALITY MANAGER

The CODIS quality manager is responsible for implementing the quality assurance program for the CODIS section.

### 5.8.1 RESPONSIBILITY

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- Ensure proper maintenance is being performed according to the quality assurance manual.
- Ensure that the quality manual procedures are being followed.
- Maintain all logs documenting the quality check of new chemicals.

### 5.8.2 AUTHORIZATIONS

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See [ASCL QM](#) section 6.2.6 for categories of Authorizations

- Can reject any chemical, reagent, supply or material which fails to meet the specifications set forth in the CODIS QM. The rejection of any such item must be documented in the Reagent Preparation Manual.
- Can terminate DNA testing if a technical problem is identified and is not resolved by the Technical Leader. The CODIS Administrator and the rest of the CODIS Section must be notified and the specific problem(s) must be documented in the QA logs where the CODIS Administrator and/or Technical Leader will initial to signify approval.

## 5.9 CODIS SAFETY OFFICER

The CODIS safety officer is responsible for all aspects of the safety program for the CODIS section.

### 5.9.1 RESPONSIBILITY

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- Test safety equipment and complete required documentation.
- Maintain chemical inventory within the section as well as maintain MSDS binder.
- Responsible for the disposal of any chemical/biological waste.
- Complete safety survey on a semi-annual basis.
- Insures incident reports are completed and returned when an accident occurs.
- Maintain first aid kit.
- Provide safety orientation for new employees and manage the overall safety of the section.

## 6 TRAINING

### 6.1 TRAINING PROGRAM

Training will be guided by the appropriate DNA Training Manual. The six-month minimum training period for a database analyst will be dependent upon previous training and experience. Additionally, the analyst training period may consist of continuous training or it may consist of periods of training with time spent as an authorized technician in processing samples.

The Training Program shall:

- include all standard DNA procedures used in the laboratory. Training and authorization of advanced, or alternate, laboratory methodologies (e.g. bone/tooth extraction) will be addressed individually as with any new technology or methodology.
- include practical training exercises to include all routine casework and database processes.
- include instruction and supervised practical experience to learn the technical skills and knowledge required to perform DNA analysis as well as technical reviews.
- require successful completion of a moot court before performing independent casework.

See the Training Manuals for the complete training programs.

### 6.2 TRAINING MODIFICATIONS

The DNA Technical Leader, with the CODIS Administrator and Casework Supervisor, shall approve and document any modifications to or deviations from the training program including those based on prior experience.

### 6.3 COMPETENCY TESTING

At the completion of the training program, all employees will be required to successfully complete a competency test. For analysts, the test which shall include: a practical test (such as an expired external proficiency test), a written qualifying test, and an oral discussion of the written test. Processors will be required to successfully complete a practical competency test, at a minimum. Support Staff will be required to complete a written competency, at a minimum.

Competency testing for the following activities will be conducted and documented prior to these actions being performed on evidence:

- Database sample intake and entry
- Laboratory activities (testing and/or sampling)
- Analysis of results
- Review of results
- Authorization of results
- Verification of results
- Technical review
- Expressing an opinion or interpretation

## 6.4 NEW OR ADVANCED TESTING METHODOLOGY

As new methodologies are added to the DNA or CODIS Section or as an employee is to be qualified in an advanced method, each previously qualified analyst or processor shall receive training in the methodology and pass a competency in the method if they are to be qualified in the procedure. This competency test shall include a practical component at a minimum. A proficiency test in the technology must be completed within six (6) months of the qualifying exam.

## 6.5 NEW OR ALTERNATE ANALYSIS TECHNOLOGY

As new analytical technologies are added to the DNA or CODIS Section or as an analyst is to be qualified in an alternate technology, each previously qualified analyst shall receive training in the methodology and pass a competency in the technology if they are to be qualified in the procedure. This competency test shall include a practical component in addition to a knowledge assessment. A proficiency test in the technology must be completed within six (6) months of the qualifying exam.

## 6.6 TECHNICAL REVIEWS FOR NEW METHODS OR TECHNOLOGIES

All technical reviewers of new methods and technologies shall be fully qualified in the method or technology prior to the review.

## 6.7 LEGACY DATA FOR NEW ANALYSTS

New analysts are not qualified for previously retired methods and technologies without specific additional training. For an analyst to be qualified in reinterpretation of legacy data for which they were not previously qualified within the laboratory, the analyst shall receive training in the methods and technology required to interpret data, reach conclusions, and generate reports in the legacy technology, typing test kit, and/or platform.

### 6.7.1 LEGACY DATA COMPETENCY TESTING

The analyst shall successfully complete a competency test in the legacy technology, typing test kit, and/or platform to the extent of his/her participation in casework analyses. The competency testing shall include practical components of reinterpretation.

## 6.8 LEGACY DATA FOR PREVIOUSLY QUALIFIED ANALYSTS

An analyst previously qualified in a legacy method or technology may continue to reanalyze or perform technical review on the legacy data for one year from the date of completion of their last proficiency in the technology. Reanalysis of existing legacy data is permitted by an analyst within

two years of completion of the last proficiency in that data with expressed authorization by the Technical Leader.

For legacy data using analytical methods last proficiency tested more than two years prior, the analyst and DNA TL will review applicable historical documentation including the appropriate QM, SOP, and validation(s) for that technology, together.

### **6.8.1 LEGACY DATA REAUTHORIZATION**

The DNA TL shall evaluate the analyst's technical skills and knowledge of the technology and shall authorize the analyst to reinterpret the legacy data for a period of no more than two years.

## **6.9 TRAINING REVIEW**

The technical leader, with the Casework Supervisor and CODIS Administrator, shall review the training records for the analyst, technician, and/or technical reviewer and approve his/her qualifications prior to independent casework responsibilities.

## **6.10 AUTHORIZATIONS**

The analyst, technician, and/or technical reviewer shall be authorized to independently perform assigned job responsibilities and this authorization will be documented through QUALTRAX.

## **6.11 LABORATORY SUPPORT PERSONNEL**

Laboratory support personnel shall receive training specific to their job functions. This training will be documented and approved by their supervisor and reviewed by the DNA TL.

## **6.12 RETRAINING**

In the event that an analyst or processor is unable to maintain their proficiency testing cycle or is deemed by the DNA TL to have lost competency in a method or technology, the individual shall cease casework or reviews that involve the method or technology. The individual shall receive any necessary retraining as determined by the DNA TL and the DNA TL shall be responsible for assessing the effect of the retraining.

### **6.12.1 RETRAINING COMPETENCY TEST**

The individual shall successfully complete competency testing prior to his/her return to participation in casework analyses. This competency testing shall include a practical component.

## 6.13 TRAINING RECORDS

The laboratory shall maintain records on the training, including successful completion of competency testing, of the laboratory personnel through the use of Training Binders, JTx, QTx, and the FB drive.

## 7 FACILITIES

Note: The organization of this section does not strictly adhere to the numbering of the subsections of FBI QAS Standard 7.

### 7.1 OVERALL LABORATORY SECURITY

The ASCL system has security monitors that cover the external perimeter of the buildings and parking lots. Security cameras are also located on the first floor of the Main Crime Laboratory. Only authorized personnel are allowed access to the 2<sup>nd</sup> and 3<sup>rd</sup> floor unless accompanied by authorized personnel. Security fobs and keys are issued to authorized personnel in order to access the certain areas of the laboratory and must be approved by the Executive Director. The ASCL has a security fob access system controlled by a computer placed in the Administrative Section (access reports can be generated from the security fob access system software). Refer to the *ASCL QM* for comprehensive details regarding laboratory wide security.

The ASCL currently performs DNA laboratory activities at only one location:

- Main Laboratory: 3 Natural Resources Drive, Little Rock AR 72205

The Physical Evidence, CODIS and DNA Casework areas of the laboratory are limited in access to other laboratory personnel through the electronic security system. Each analyst is assigned a unique programmed fob that enables entry into the laboratory. If an area is not monitored by the electronic security system, then access to the area is controlled by physical lock-and-key, with only authorized personnel being issued the key to the area.

### 7.2 CODIS LABORATORY

The CODIS Laboratory spaces are designed to minimize contamination during the processing of samples. The sensitivity of PCR-based analysis, involving the amplification of minute quantities of DNA, makes it necessary to take certain precautions to avoid sample contamination. See Section 18.2 for a full discussion of contamination prevention guidelines. Records of critical environmental conditions will be stored in the *DNA QC Images* folder of the section shared drive.

#### 7.2.1 CODIS PRE-PCR LABORATORY

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The CODIS Pre-PCR area activities consist of sample handling, DNA extraction and isolation, and preparation of samples for amplification.

#### SPECIAL PRECAUTIONS:

- 1) Use disposable gloves at all times.

- 2) Sterilize the bench top before and after you use it with diluted bleach solution. Use disposable bench paper to prevent the accumulation of human DNA on permanent work surfaces. Bleach shall be used to decontaminate exposed work surfaces after each use.
- 3) Sample handling, extractions, and PCR setup shall be performed in separate spaces or separate times, always with a full decontamination of the bench before, after, and between
- 4) Sterilize those solutions which can be heated in an autoclave without affecting their performance. Steam sterilization under bacterial decontamination conditions degrades DNA to a very low molecular weight, rendering it un-amplifiable.
- 5) Always change pipette tips between handling each sample even when dispensing reagents. Never “blow out” the last bit of sample from a pipette. Blowing out may cause aerosols which may contaminate the sample.
- 6) Store reagents as small aliquots to minimize the number of times a given tube of reagent is opened. Record the lot numbers of reagents used in each set of samples so that if contamination occurs, it can be traced more readily. It is recommended that the small aliquots are retained until typing of the set of samples for which the aliquots were used is completed.
- 7) Centrifuge tubes before opening.
- 8) Include reagent blank controls with each set of DNA extractions to check for the presence of contaminating DNA in the reagents.
- 9) Wear a dedicated lab coat for pre-amplification sample handling when working in the pre-PCR DNA extraction work area. Lab coats should be washed on a monthly basis.
- 10) Face masks and/or face shields must be worn when working with evidence and setting up amplifications.
- 11) General housekeeping should be performed as needed (e.g. sweeping, mopping, dusting).
- 12) Doors will remain closed except for passage.

### **7.2.2 CODIS POST-PCR LABORATORY**

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The CODIS Post-PCR area consists of amplification and PCR product typing. It is important that there is a one-way flow from the Pre-PCR lab to the Post-PCR lab. This is to prevent possible contamination between areas. Amplified DNA must be handled carefully. Steps will be taken to avoid dispersing it around the room to reduce the potential for transfer of amplified DNA to other work areas.

#### **SPECIAL PRECAUTIONS:**

- 1) Always remove gloves and lab coat when leaving the Amplified DNA Work Area to avoid the transfer of amplified DNA into other work areas.
- 2) Sterilize the bench top before and after each use with diluted bleach solution.
- 3) Reduce the unnecessary dispersal of DNA around the work area by changing gloves whenever they may have become contaminated with amplified DNA.
- 4) Use disposable bench paper to cover the work area used to perform the typing steps to prevent the accumulation of amplified DNA on permanent work surfaces.
- 5) Plates of amplified DNA will be kept in the work area until all reviews are completed.
- 6) The doors are to remain closed except for passage.

### 7.2.3 DATABASE SECURITY

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To ensure the security of the DNA database, the CODIS Server must be contained within a locked server cabinet at all times unless in use by the CODIS Administrator or designee.

All Analysts that access the CODIS database must be DNA analysts and have an FBI background check as per the NDIS guidelines. Each computer is password protected with individual logons. Logons and passwords must not be shared. No analysts, except the CODIS Administrator, should be logged on to more than one CODIS computer concurrently.

## 7.3 CONVICTED OFFENDER / ARRESTEE SAMPLE CONTROL

See Arkansas State Crime Laboratory Quality Manual for lab wide policy regarding Evidence Control and Case Management

Convicted offender / arrestee samples are handled differently than casework evidence due to the fact that offender samples are not considered evidence at the Arkansas State Crime Laboratory. They are considered reference materials.

### 7.3.1 CONVICTED OFFENDER / ARRESTEE SAMPLE HANDLING PROCEDURES

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Convicted offender / arrestee samples enter the Arkansas State Crime Laboratory through the Evidence Receiving Section of the laboratory. Evidence Receiving will note the date the CODIS samples enter the lab. The samples are then sent to the CODIS section. The date the CODIS samples enter the lab will be documented by CODIS staff in the Kit Receipt module of STACS-DB. STACS-DB assigns a unique number to each convicted offender / arrestee sample in the Submission Check-In module. The chain of custody is documented by users in STACS-DB. The sample is stored in a secure area before and after analysis.

All samples are worked as they are received and processed through STACS-DB modules unless directed by the CODIS Administrator or designee. All CODIS hit confirmations will be expedited in the work flow process.

All samples are collected, received, handled, sampled and stored so as to preserve the identity, integrity, condition and security of the sample.

Before analysis begins, a second review is conducted by the CODIS Administrator and/or analyst to determine if there is anything more specific about the request and to determine if the laboratory has the capability and resources to perform the services requested (i.e. adequate standards, controls and approved test methods). Documentation is only noted if significant changes are observed. By starting analysis the analyst agrees to the request.

If the contract needs to be amended after work has begun, all affected personnel shall be notified.

### 7.3.2 CHAIN OF CUSTODY

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See the *ASCL Quality Assurance Manual* (ASCL-DOC-01) section 7.4.1.1.3 for Chain of Custody guidelines for evidence. As Convicted Offender / Arrestee Samples are not considered Evidence, the analogous chain of custody can be found for Database Samples in the STACS-DB sample submission history.

### 7.3.3 PACKAGING

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At times, evidence submitted for DNA testing is not adequately packaged. The analyst may document and correct the deficiency. If there is any concern that the packaging deficiency has affected the integrity or identity of the test item, the analyst's Section Chief and the customer agency shall be advised and consulted with for further instructions. If the analyst discovers an inconsistency between the stated and actual contents of a package, or if there is doubt about the suitability of an evidence item for testing, then the analyst shall attempt to contact the customer before proceeding. All contacts will be documented in the case record (e.g., using an *Agency Contact Form* (ASCL-FORM-06), by email). For minor inconsistencies, the analyst shall use their judgment on whether to contact the customer, but must make a note of the discrepancy in the case file. After analysis, the Analyst re-packages the evidence in a manner that will preserve the sample while in storage and awaiting trial.

### 7.3.4 TRANSFERRING

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STACS-DB documents the user (analyst and/or support staff) performing each process. This serves as documentation of possession of each sample.

### 7.3.5 RELEASE OF INFORMATION

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Refer to the Arkansas State Crime Laboratory Quality Manual for lab wide policy regarding confidentiality.

In addition, the Arkansas State Crime Laboratory, as an NDIS participant, is required to follow the NDIS Operational Procedures. The procedure is detailed verbatim below:

***NDIS Operational Procedures Manual: Version 9 (dated July 1, 2020)***

***3.2 Federal DNA Act Limits Access to DNA Records and DNA Samples***

*The Federal DNA Act provides that the National DNA Index System "shall include only information on DNA identification records and DNA analyses that are maintained by Federal, State, and local criminal justice agencies (or the Secretary of Defense in accordance with section 1565 of title 10, United States Code) pursuant to rules that allow disclosure of stored DNA samples and DNA analyses only--*

*(A) to criminal justice agencies for law enforcement identification purposes;*

*(B) in judicial proceedings, if otherwise admissible pursuant to applicable statutes or rules;*

*(C) for criminal defense purposes, to a defendant, who shall have access to samples and analyses performed in connection with the case in which such defendant is charged; or*

*(D) if personally identifiable information is removed, for a population statistics database, for identification research and protocol development purposes, or for quality control purposes.” [42 U.S.C. §14132(b)(3)]*

*The unauthorized disclosure of individually identifiable DNA information stored in the National Index is punishable by a fine not to exceed \$100,000 (42 U.S.C. §14133(c)(1)). Obtaining DNA samples or DNA information, without authorization, is punishable by a maximum fine of \$250,000 or imprisonment for not more than one year or both fine and imprisonment (42 U.S.C. §14133(c)(2)). A laboratory’s access to NDIS is subject to cancellation for noncompliance with these privacy requirements. The privacy requirements are applicable to NDIS participating laboratories by Federal law [42 U.S.C. §14132] and through the NDIS MOU.*

*The NDIS participating laboratory is responsible for compliance with the limited access and disclosure of DNA samples and DNA analyses required by the Federal DNA Act. While States may have DNA database laws that appear to permit more access to the DNA data, if that State is a participant in the National DNA Index System, the State agrees to abide by, and comply with, the more restrictive provisions contained in the Federal DNA Act by agreeing to the NDIS MOU.*

*As noted in the Introduction, recommendations from the Federal DNA Advisory Board have also shaped the administration of the National DNA Index System. In the House of Representatives Judiciary Committee Report on predecessor legislation, the DNA Identification Act of 1993, the Committee explained its expectations that the DNA Advisory Board “also advise the Director on other scientific and policy questions relating to forensic applications of DNA. In particular, it would be appropriate for the Board to address: (1) the statistical, and population genetics issues that have been raised; and (2) the privacy, law enforcement and technical issues associated with the FBI’s program to establish a databank of DNA profiles, known as CODIS.” Pursuant to this legislative direction and its charter, the DNA Advisory Board considered standards for acceptance of DNA profiles in CODIS which take account of relevant privacy, law enforcement and technical issues and endorsed the “current level of enforcement of such access and disclosure provisions by the Department of Justice and the FBI and encourages the continuation of such efforts.” The DNA Advisory Board also endorsed the interpretation of the Federal DNA Act to limit access of the anonymous DNA data to criminal justice agencies for a population statistics database, forensic identification, forensic research, forensic protocol development or quality control purposes.*

*NDIS participating laboratories are also responsible for complying with their applicable State law concerning access to the DNA data in their State DNA database, especially if those provisions are more restrictive than the Federal DNA Act.*

### *3.2.1 FBI Quality Assurance Standards Require Confidentiality*

*Standard 11 of the FBI’s QAS require confidentiality for reports, case files, DNA records and databases, unless otherwise provided by Federal or State law. The QAS require that “personally identifiable information only be released in accordance with applicable State and Federal law” and that laboratories have “procedures to ensure the confidentiality and privacy of the DNA samples, DNA records, case files, reports and databases;” see Forensic QAS Standards 11.3.1 and 11.3.3 and Databasing QAS Standards 11.2 and 11.2.2.*

### *3.2.2 Access by Participating Criminal Justice Agencies*

*In accordance with the Federal DNA Act, disclosure of DNA records at NDIS is authorized for law enforcement identification purposes to the Federal, State and Local criminal justice agencies who participate in NDIS.*

### **3.2.3 Access by Defendant to DNA Records at NDIS**

*In accordance with the Federal DNA Act, a defendant may have access to the DNA samples and analyses performed in connection with his/her case. A defendant may generally have access to the forensic evidence DNA records and his/her exemplars under this provision of the DNA Act.*

*This provision does not authorize a defendant to access all of the DNA records in the National DNA Index. Nor does this provision authorize access to candidate matches that are not confirmed as matches and for which no personally identifiable information is released. Thus, as currently worded, the Federal DNA Act entitles a defendant to access the defendant's DNA records at NDIS as well as the forensic evidence records for the case for which the defendant is arrested, charged and/or appealing. The FBI shall respond to requests for access to DNA records that were contributed to NDIS by a State and /or Local agency with a referral to the contributing State and/or Local agency. The FBI shall respond to a request for access to DNA records that were contributed to NDIS by the FBI, as authorized.*

### **3.2.4 Access by Persons Whose DNA Records are at NDIS**

*An individual may request access to his/her DNA record for the purpose of reviewing that record and/or challenging its accuracy or appropriateness for maintenance in NDIS. An individual making a request to review his/her DNA record to the FBI Freedom of Information Officer or CODIS Unit will be referred to the NDIS participating laboratory that contributed the DNA record to NDIS.*

*An NDIS participating laboratory is responsible for responding to requests for access to a DNA record it generated by the subject of that record once locally specified requirements are met. The FBI is responsible for responding to requests for access to FBI Laboratory-generated DNA records.*

## **7.3.6 DISPOSITION**

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All sample remaining after analysis will be retained by the CODIS section. The CODIS section will not store amplified products after sample has been uploaded to NDIS.

## **7.3.7 DESTRUCTION OF SAMPLES**

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The CODIS Section only destroys non-duplicate samples in accordance with section 4.7.5 and 4.7.6. The sample will be placed in a biohazard container and for expunged samples, witnessed on the CODIS sample destruction form. Documentation will be stored under the Submission Expungements module or submission history in STACS-DB.

## **7.3.8 SAMPLE HANDLING AND STORAGE**

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The following written policy ensures that samples will be handled, processed and preserved so as to protect against loss, contamination or deleterious change. Testing of CODIS samples is conducted to provide the maximum information with the least consumption of the sample. Whenever possible, a portion of the original sample is retained by the CODIS Section.

See the *ASCL Quality Assurance Manual* (ASCL-DOC-01) section 7.4.1.1.2 to find Test Item Packaging and Sealing requirements. Key points are listed below:

- DNA evidence will be sealed so that the contents cannot escape and that opening the container results in obvious damage or alteration.
- A proper seal includes the initial of the person sealing the evidence across the seal. As soon as is practicable once the examination is complete at least one layer of packaging will be properly sealed.
- DNA evidence will be protected from loss, cross-transfer, contamination, and deleterious change.
- If evidence must be stored or conditioned under special environmental conditions (e.g., refrigerated, frozen), then these conditions shall be maintained, monitored, and recorded.
- Whenever practical, the original seal will be left intact when opening a container.
- If the original packaging cannot be kept, complete documentation and a picture of original packaging must be retained in the case record.

### **7.3.9 SAMPLE LABELING**

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Each working sample must be labeled with a unique identifier. STACS-DB generates this unique identifier in the Submission Check-In module. For convicted offender and arrestee samples, this number is created in numerical order of submission check-in as YYYY-##### (STACS Bar Code). For staff samples, an external sample barcode is designated by YYYY-#### and a separate STACS barcode is created in numerical order of submission check-in. Other identifiers may be utilized if appropriate for the specific case. The numerical order of cases submitted will restart at the beginning of the year.

NOTE: All previous samples migrated to STACS-DB will follow the labeling according to previous manuals.

### **7.3.10 CONVICTED OFFENDER / ARRESTEE PROCESSING**

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The convicted offender / arrestee samples accepted for DNA are tracked during analysis and accounted for in STACS-DB modules.

- 1) Prepare the work area. The bench space must be clean and free of clutter.
- 2) A lab coat must be worn to protect ones clothing from contamination. Gloves must be worn to protect one from infectious diseases that could be present in biological material or for protection from toxic chemicals. Mask must be worn over nose and mouth to prevent contamination of evidence.
- 3) The CODIS Analyst documents appropriate information, sample numbers and lot numbers through the STACS-DB module workflow. Once samples are complete and imported into the CODIS system, information is stored in STACS-DB.

### **7.3.11 LONG TERM STORAGE**

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See the *ASCL Quality Assurance Manual* (ASCL-DOC-01) section 7.4.1.1 to find Test Item Storage requirements. For evidence storage purposes, DNA mag-locked areas meet the definition of “secure, limited-access area” and key-locked pre-amplification cleanroom areas meet the definition of “short-term storage location”.

Upon completion of the testing, the CODIS Analyst has the ultimate responsibility for long-term storage of the samples. All samples are returned to a CODIS Support Staff for long term storage. This is tracked by STACS-DB. All CODIS blood samples are stored in the Evidence Section of the Arkansas State Crime Laboratory indefinitely. All CODIS buccal samples are stored in the CODIS storage room located on the second floor of the Arkansas State Crime Laboratory indefinitely. Physical or digital copies of paperwork related to CODIS samples and hits will be securely retained for a minimum of 15 years.

The current location for the sample is found in STACS-DB. The history can be viewed through the History button in the offender/arrestee information screen and in the Sample History of the Reports module. Arrestee samples used for casework have an additional report for chain of custody in the Reports module.

### **7.3.12 REQUEST FOR BUCCAL COLLECTION KITS**

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All requests for database kits can be made in writing on the agency’s letterhead, by email, or other appropriate form of communication. All requests will be documented within the CODIS Section. All requested kits, if available, will be sent by the Arkansas State Crime Laboratory to the requesting agency.

### **7.3.13 RECEIPT OF SAMPLES INTO THE DATABASE**

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Upon receipt of samples into ASCL, the Evidence Receiving Section notes the date on the outer packaging. The sample will be transferred to the CODIS section and scanned into STACS-DB in the Kit Receipt module with the date received by the lab. The information supplied with the sample will be entered in the Submission Check-In module and Data Entry module then evaluated to make certain that sufficient information has been provided to ensure quality of the sample being submitted and to verify that the violation is a qualifying violation as per the statutes (Adults-Act 1740 of 2003 (AR 12-12-1101) & Act 543 of 2015 (AR 12-12-1006); Juveniles - Act 1265 of 2003 (AR 9-27-356)). If information is not completed, discrepant or other issues on the DNA Database Information Card, a ‘DNA Problem’ letter may be sent to the submitting agency. A copy of the letter will be stored in STACS-DB. If necessary a phone call or email can be made to the submitting agency to ensure quality of sample submission and documented in STACS-DB.

### **NON-QUALIFYING VIOLATIONS (ADULTS AND JUVENILES)**

Upon receipt of samples into the CODIS Section, the sample will be checked to ensure the violation meets the requirement of the law (Adults-Act 1740 of 2003 (AR 12-12-1101) & Act 543 of 2015 (AR

12-12-1006); Juveniles - Act 1265 of 2003 (AR 9-27-356)). If the violation is deemed to be a non-qualifying violation a 'DNA Problem' letter for a non-qualifying violation will be sent to the submitting agency. This will explain to the agency that the sample does not have a qualifying violation and will be retained for 30 days. After the elapsed time, if the CODIS section is not contacted or does not have notice of a qualifying violation the sample will be destroyed. A copy of the letter will be stored in STACS-DB. If necessary a phone call can be made to the submitting agency to ensure quality of sample submission and documented in STACS-DB.

### **7.3.14 EXPUNGEMENTS**

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It is recognized that occasionally a profile that was previously entered into CODIS will need to be expunged. The following process will allow for expungements:

#### **REMOVAL AND DESTRUCTION OF THE DNA RECORD AND DNA SAMPLE:**

Any person whose DNA record is included in the State DNA Database and whose DNA sample is stored in the State DNA Data Bank as authorized by Arkansas Law may apply to any circuit court for removal and destruction of the DNA record and DNA sample on the grounds that the adjudication of guilt that resulted in the inclusion of the person's DNA record in the database or the inclusion of the person's DNA sample in the databank has been reversed and the case dismissed.

Examples include:

- A) An acquittal;
- B) A dismissal;
- C) A nolle prosequi;
- D) A successful completion of a pre-prosecution diversion program or a conditional discharge;
- E) A conviction of a Class B misdemeanor or Class C misdemeanor; or has not resulted in a charge within one (1) year of the date of the arrest.

The State Crime Laboratory shall remove and destroy a person's DNA record and DNA sample by purging the DNA record and other identifiable information from the State DNA Data Base and the DNA sample stored in the State DNA Data Bank when the person provides the State Crime Laboratory with:

- 1) A written request for removal and destruction of the DNA record and DNA sample.
- 2) A court order for removal and destruction of the DNA record and DNA sample; and
- 3) Either of the following:
  - A) A certified copy of an order of acquittal;
  - B) An order of dismissal;
  - C) An order nolle prosequi;
  - D) Documentation reflecting a successful completion of a pre-prosecution diversion program or a conditional discharge;
  - E) A judgment of conviction of a Class B misdemeanor or Class C misdemeanor

- F) A court order that reverses the conviction that led to the inclusion of the DNA record and DNA sample; or
- G) A court order stating that a charge arising out of the person's arrest has not been filed within one (1) year of the date of the arrest.

The State Crime Laboratory shall not remove or destroy a person's DNA record or DNA sample if the person had a prior felony or Class A misdemeanor conviction or a pending charge for which collection of a DNA sample is authorized under Arkansas law.

An Expungement Request form should be completed with each Expungement process. When the State Crime Laboratory removes and destroys a person's DNA record, the State Crime Laboratory shall request that the person's DNA record be expunged from the National DNA Index System. The expungement documentation will be stored in STACS-DB in the Submission Expungement module.

## **EXPUNGEMENT RESPONSIBILITIES FROM NDIS**

Federal law requires that states participating in NDIS expunge the DNA records of persons whose qualifying convictions had been overturned.

The Federal DNA Identification Act of 2001 requires states that participate in NDIS promptly expunge DNA profiles if the state receives the following from the responsible agency or official:

- A certified copy of a final court order establishing that the specific qualifying offense has been overturned.
  - A court order is not considered “final” for these purposes if time remains for an appeal or application for discretionary review with respect to the order (Federal DNA Identification Act).

For states uploading the DNA data of arrestees, indicted persons or similar legal specimens, amendments made by the DNA Fingerprint Act of 2005 require expungements in the event of the charge is dismissed or results in an acquittal or no charge was filed within the applicable time period.

NDIS participating states are required to expunge from NDIS the DNA profile of a person included in NDIS by that State if:

- the person has not been convicted of an offense on the basis of which that analysis was or could have been included in the index and;
- the responsible agency or official of that State receives, for each charge against the person on the basis of which that analysis was or could have been included, a certified copy of a final court order establishing that such charge has been dismissed or has resulted in an acquittal or that no charge was filed within the applicable time period.

### **7.3.15 ADMINISTRATIVE REMOVALS**

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Administrative removal may be warranted in such occasions:

- 1) individual did not meet a qualifying offense,
- 2) the collection agency notifies the Arkansas State Crime Laboratory,
- 3) a procedural deficiency in the collection of the DNA sample cannot be resolved, or any other reason deemed necessary by the CODIS Administrator or Technical Leader.

To complete the Administrative Removal a 'Deleted/Amended Specimen Request' Form must be completed along with the supporting paperwork necessary and stored in STACS-DB in the Submission Expungement module. (Prior to STACS-DB, paperwork is stored on the S drive.)

In the event of a match confirmation for which the offender or arrestee is determined to have been collected under a non-qualifying offense (and there is not a qualifying offense in the criminal history), the match report will be issued to the investigating agency, notifying them that the sample was determined to be non-qualifying, and the sample will be administratively removed from the CODIS system

## 8 VALIDATION

### 8.1 REQUIREMENT OF VALIDATION

The laboratory shall only use validated methodologies for DNA analyses. These include any new methods and procedures for sampling, handling, transport, storage and preparation of items to be tested. There are two types of validation: developmental and internal. See the *ASCL QM* discussion for Validation procedures.

### 8.2 DEVELOPMENTAL VALIDATION

Developmental validation is required on any novel methodology for forensic DNA analysis. When method development is performed, a plan is approved by the DNA Technical leader and assigned to personnel approved to perform method validation. Adequate resources are made available and the underlying scientific principle(s) of the method must be published for peer-review.

During the method development, the process is reviewed to ensure that the original goals are still being fulfilled. If a modification to the plan is required, it will be approved and authorized by a revision of the plan document in Qualtrax.

The developmental validation shall include the following studies, where applicable:

- 1) Characterization of genetic markers.
- 2) Species specificity.
- 3) Sensitivity.
- 4) Stability.
- 5) Case-type samples.
- 6) Population.
- 7) Mixture.
- 8) Precision.
- 9) Accuracy.
- 10) PCR-based studies.
  - a) Reaction conditions.
  - b) Assessment of differential amplification.
  - c) Assessment of preferential amplification.
  - d) Effects of multiplexing.
  - e) Assessment of appropriate controls.
  - f) Product detection.

### 8.3 INTERNAL VALIDATION

Internal validation is required on any methodologies that are utilized for forensic DNA analysis in the laboratory. A developmentally validated methodology cannot be utilized in the laboratory until it has been internally validated, reviewed and approved by the technical leader. The internal validation procedure will be tested using known and non-probative evidence samples or database-type samples of a sufficient number and type to demonstrate the reliability and limits of the method. The validation shall contain the following studies where applicable:

- 1) Accuracy
- 2) Precision
- 3) Reproducibility
- 4) Sensitivity & Stability
- 5) Mixture.
- 6) Contamination assessment

Internal validation shall define quality assurance parameters and interpretation guidelines, including, as applicable, guidelines for mixture interpretation and the application of appropriate statistical calculations.

Mixture interpretation validation studies shall include samples with a range of the number of contributors, template amounts, and mixture ratios expected to be interpreted in casework.

Internal validation studies shall be conducted prior to implementing a change in platform instrument model or typing test kit.

Internal validation studies shall be documented and summarized. Internal validation shall be reviewed and approved by the DNA TL prior to implementing a procedure for forensic applications.

Before a processor can begin using an internally validated procedure for DNA casework, the processor must successfully complete training and a qualifying test. A proficiency test must be completed within (6) months of qualification of the new technology or methodology. See the *ASCL QM* for specific requirements of validation.

### 8.4 CERTIFIED REFERENCE MATERIAL

Newly validated DNA methods (from amplification through characterization), typing test kit, or platform instrument model shall be checked against an appropriate and available certified reference material (or sample made traceable to the certified reference material) prior to the implementation of the method for forensic analysis.

## 8.5 MATERIAL MODIFICATIONS

Material modifications made to validated procedures shall be evaluated and approved for use if the modifications are covered by the initial validation conditions by the DNA Technical Leader. An additional validation of the modification will be needed if determined by the technical leader.

The performance of a modified procedure shall be evaluated by comparison to the original procedure using similar DNA samples and the evaluation documented. The evaluation shall be reviewed and approved by the technical leader prior to the implementation of the modified procedure into casework applications.

## 8.6 MODIFIED RAPID VALIDATION

The ASCL does not perform Modified Rapid testing.

## 8.7 RAPID PERFORMANCE CHECK

The ASCL does not perform Rapid testing.

## 8.8 NEW SOFTWARE

New software or new modules of existing software and modifications to software shall be evaluated to assess the suitability of the software for its intended use in the laboratory and to determine the necessity of validation studies or software testing. This evaluation by the DNA TL shall include the determination of which studies will and will not be conducted and shall be documented.

### 8.8.1 DEVELOPMENTAL VALIDATION OF SOFTWARE

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New software or new modules of existing software that are used as a component of instrumentation, for the analysis and/or interpretation of DNA data, or for statistical calculations, shall be subject to developmental validation prior to implementation in forensic DNA analysis.

8.8.1.1 With the exception of legally protected information, the underlying scientific principle(s) utilized by software with an impact on the analytical process, interpretation, or statistical calculations shall be publicly available for review or published in a peer-reviewed scientific journal.

8.8.1.2 Developmental software validation studies for new software or new modules of existing software used as a component of instrumentation shall include at a minimum, functional testing and reliability testing.

8.8.1.3 Developmental software validation studies for new software or new modules of existing software for the analysis and/or interpretation of DNA data shall include at a minimum, functional testing, reliability testing, and as applicable, accuracy, precision, sensitivity, and specificity studies.

- 8.8.1.4 Developmental software validation studies for new software or new modules of existing software for statistical calculations shall include at a minimum, functional testing, reliability testing, and as applicable, accuracy, and precision studies.

## **8.8.2 INTERNAL VALIDATION OF SOFTWARE**

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New software or new modules of existing software that are used as a component of instrumentation, for the analysis and/or interpretation of DNA data, or for statistical calculations shall be subject to internal validation specific to the laboratory's intended use prior to implementation in forensic DNA analysis.

- 8.8.2.1 Internal software validation studies for new software or new modules of existing software used as a component of instrumentation shall include functional testing and reliability testing.
- 8.8.2.2 Internal software validation studies for new software or new modules of existing software for the analysis and/or interpretation of DNA data shall include functional testing, reliability testing, and, as applicable, precision and accuracy studies, sensitivity, and specificity studies.
- 8.8.2.3 Internal software validation studies for new software or new modules of existing software for statistical calculations shall include functional testing, reliability testing, and, as applicable, precision and accuracy studies.
- 8.8.2.4 Software that does not impact the analytical process, interpretation, or statistical calculations shall require at a minimum, a functional test.

## **8.8.3 MODIFICATION TO SOFTWARE**

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Modifications to software as described in Standards 8.8.1 and 8.8.2 shall be evaluated to determine if the modifications result in major or minor revisions to the software.

- 8.8.3.1 A major revision to software used as a component of instrumentation shall require validation prior to implementation. Software validation studies shall include functional testing, reliability testing, and regression testing.
- 8.8.3.2 A major revision to software used for the analysis and/or interpretation of DNA data shall require validation prior to implementation. Software validation studies shall include functional testing, reliability testing, regression testing, and, as applicable, precision and accuracy studies, sensitivity, and specificity studies.
- 8.8.3.3 A major revision to software used for statistical calculations shall require validation prior to implementation. Software validation studies shall include

functional testing, reliability testing, regression testing, and, as applicable, precision and accuracy studies.

8.8.3.4 A minor revision to software that does not impact the analytical process, interpretation, or statistical calculations shall require at a minimum, a functional test.

## **8.8.4 MULTIPLE LOCATIONS**

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The ASCL does not perform DNA processing at multiple locations.

## **8.8.5 RETENTION OF RECORDS**

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Software validation and testing shall be documented. Software validation and testing shall be reviewed and approved by the DNA TL prior to implementation.

## **8.9 RETENTION FOR REVIEW**

Developmental validation studies, internal validation studies, modified procedure evaluations, and software testing, including the approval of the DNA TL, shall be retained and available for review.

## 9 ANALYTICAL PROCEDURES (TEST METHODS)

### 9.1 APPROVED PROCEDURES

Following a review of submitted evidence by an Evidence Receiving technician or other approved ASCL personnel, a DNA request will be created in LIMS if appropriate. Requests for non-routine work must be reviewed by the Forensic DNA Section Chief or her designee. If approved, the Section Chief (or designee) must initial and date the *ASCL Evidence Submission Form* or LIMS-generated Submission sheet next to the request. Deviations from normal analytical procedures not covered under the ASCL Quality Manual (ASCL-DOC-01) standard 5.5.3 will be documented on the *Non-Conformance Form* (CODIS-FORM-17) to ensure technical justification and authorization.

The laboratory shall only use validated methodologies for DNA analyses (see Appendix A). Approved procedures are listed with instructions, appropriate controls and interpretation guidelines.

### 9.2 REAGENTS

#### 9.2.1 COMMERCIAL REAGENTS

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The following is a list of critical reagents used in the CODIS section:

**Commercial Kits:**

PowerPlex Fusion 6C	Promega
DNA Investigator Kits	Qiagen
Quantiplex Pro	Qiagen

**Miscellaneous Items:**

2800M	Promega
Buffer G2	Qiagen
Promega Punch Solution	Promega
PowerPlex Direct Amp Reagent	Promega

##### 9.2.1.1 SOURCES OF MATERIALS, REAGENTS, CHEMICALS AND SUPPLIES

A listing of commercial sources for all materials, reagents, chemicals, and supplies will be maintained in the Reagent Log. All commercial reagents will be labeled with the identity of the reagent, open date and the expiration date if applicable. Any commercial reagent used by the CODIS section will be labeled with a STACS generated bar code from the Receiving modules. All information relevant to material or services that must meet certain specifications for testing will be provided to the purchasing department. Only suitable externally-provided products will be used.

### 9.2.1.2 SUPPLY AND MATERIALS INVENTORY

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Upon receipt of all materials, reagents, chemicals and supplies, the packing slip will be checked for agreement with the items received when available. Reagents and supplies, which have passed their expiration date, will not be used on CODIS samples unless a performance check has been conducted and the technical leader has approved and documented the deviation to extend the expiration date.

### 9.2.1.3 SAFETY DATA SHEETS (SDS, PREVIOUSLY MSDS)

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The SDS received from the manufacturer for each chemical used in the laboratory can be found in the designated SDS book or electronically. These data sheets are readily available to all laboratory personnel. A master copy of all SDS sheets for the laboratory is kept by the Laboratory Health and Safety Manager.

## 9.2.2 LABORATORY PREPARED REAGENTS AND SOLUTIONS

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A log will be maintained for each laboratory prepared reagent and solution except dilutions of laboratory concentrates. Each reagent/solution prepared will have the following recorded in the log book:

- Identity
- Date of preparation
- Date of expiration
- Instructions on preparation of reagent
- Lot numbers of solvents and/or chemicals used in preparation of reagent
- A method to verify the reagent's reliability (if applicable)
- Initials of the person preparing reagent
- Initials of the person verifying reagent (if applicable)

### 9.2.2.1 LABELING REQUIREMENTS

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All laboratory prepared reagents and solutions including dilutions and aliquots will be clearly labeled. Labels will include at a minimum: identity of reagent; date of preparation or expiration; and identity of individual preparing reagent. Lot number, and storage requirements (as appropriate) may also be included. Labels may be placed on the individual reagent aliquots or on the specific container of the aliquots. A barcode may represent the lot number. Labels or records will also include identity of preparing analyst, components used, and expiration date.

### 9.2.2.2 STORAGE AND DISPOSAL

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All chemicals must be stored, used, and disposed of in a manner conforming to established safety requirements.

## 9.3 CRITICAL REAGENTS AND SUPPLIES

Critical consumables, supplies, and services which affect the quality of testing will be obtained from reliable suppliers. All critical reagents and supplies must be quality control tested for accurate, reliable performance prior to use in the CODIS Section. Quality control test results will be recorded in the Quality Control of Critical Reagents Log and information stored in the Receiving modules of STACS-DB.

### 9.3.1 DNA INVESTIGATOR KITS & COMPONENTS

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DNA investigator kits will be marked with the receive date and initials of the individual who receives the kit. A known blood sample will be processed through the extraction kit to check the quality of the reagents. The DNA extract will be amplified with a QC checked PowerPlex Fusion 6C kit, and analyzed to ensure the correct profile was produced. Once the lot has been verified the QC date will be placed on all received kits. If the kit does not produce the expected profile, the known blood samples will be re-extracted and re-analyzed. If the kit fails the QC a second time the Technical Leader, or designee will be informed. The Technical Leader, or designee, will examine the problem and contact the manufacturer if necessary.

### 9.3.2 QUANTITATION KITS

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The quantitation kits will be marked with the receive date and initials of the individual who receives the kit. A dilution of standards, as described in the SOP for each of the quantitation kits, will be run and analyzed to ensure the quality of the newly received kits. Using the guidelines in the appropriate SOP, a  $R^2$  of  $\geq 0.98$  will be considered passing. Once the lot has been verified the QC date will be placed on all received kits. If the standard curve does not have a  $R^2$  of  $\geq 0.98$ , the standard will be re-run and re-analyzed. If the standard fails the QC a second time the Technical Leader, or designee will be informed. The Technical Leader, or designee, will examine the problem and contact the manufacturer if necessary.

### 9.3.3 AMPLIFICATION KITS & COMPONENTS

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The genetic typing kits will be marked with the receive date and initials of the individual who receives the kit. The appropriate positive control as described in the corresponding SOP will be amplified in duplicate along with an AMP- sample. The samples will then be analyzed to ensure the appropriate DNA profile is obtained. Once the lot has been verified, the QC date will be placed on all received kits. Kit information for PowerPlex Fusion 6C will be entered in the Receiving modules of STACS-DB and appropriate bar codes will be generated for the kit and all kit components. If the kit does not produce the expected profile, the samples should be re-injected or re-amplified. If the positive or negative controls still do not produce the expected result, the Technical Leader, or designee will be informed. The Technical Leader, or designee, will examine the problem and contact the manufacturer if necessary. Critical Reagents purchased as a component of a kit may

only be used with a kit lot for which it has passed a Quality Check. Critical Reagents not purchased as a component of a kit are not restricted to use with only the lot used to perform the Quality Check.

## 9.4 CONTROLS AND STANDARDS

It is essential that proper control samples are included when samples are extracted, amplified and typed. The typing results obtained from these controls are important for the interpretation of the profiles obtained. All employees and supervisory personnel must be vigilant for any indication of nonconforming tests and work.

### 9.4.1 REAGENT BLANK (RB)

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The reagent blank consists of all reagents used in the test process, minus any sample, and is processed through all steps alongside the question or known samples. The reagent blank will be amplified at full strength. A reagent blank must be included with each extraction set unless the samples are processed with the direct amplification protocol.

\*During Direct Amplification, the RB and AMP- are equivalent, and in accordance with the SWGDAM clarification letter both do not need to be run.

The reagent blank is used to test for possible contamination of the sample preparation, reagents, and/or supplies by an external DNA source. If the reagent blank exhibits any typing results above the analytical threshold, the reagent blank can be re-amplified. If the typing results remain above threshold after re-amplification, then all DNA samples that were associated with the reagent blank should be considered inconclusive for analysis and re-extracted. If the DNA sample has been consumed and re-extraction is not possible, then the DNA technical leader, CODIS Administrator and/or Laboratory Director will be consulted to analyze the samples and reagent blank. If after analysis the source of the contaminating DNA does not appear to be in the samples, then the contamination will be noted in the report. If the extraneous DNA is present in both the reagent blank and associated sample the sample will be reported as inconclusive.

### 9.4.2 QUANTIFICATION STANDARDS

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The quantification standards (or standard curve), including a No Template Control (NTC), will be amplified and analyzed with each sample set. The standards quantify the instrument measurements to known amounts of DNA. Performance of the standard curve and NTC will be assessed to ensure appropriate set-up and functioning. Standards and kit components will be maintained by the Forensic DNA section and will be available for use by the CODIS section as needed.

A usable standard curve must consist of at least one replicate in 4 of the 5 dilutions.

## 9.4.3 AMPLIFICATION CONTROLS

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### 9.4.3.1 POSITIVE CONTROL

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The positive control contains DNA from a known source with a known DNA profile. The positive control will be amplified and analyzed concurrently in the same instrument with the same samples and same PCR kit.

The positive control tests to insure the proper performance of the amplification and typing procedure. The positive control provided with each amplification kit serves as the appropriate positive control. If the positive control does not exhibit the appropriate results, then samples associated with that positive control are considered inconclusive for analysis and must be re-amplified. Positive controls may be setup in duplicate to compensate for poor injections, spikes, or other artifacts. Only one of the positive controls is required to produce the expected results. If a positive control is lacking expected allele(s) at a locus, then the control can be used, but that locus will be marked as inconclusive in all samples associated with the positive control. If there are more than two loci that lack the expected allele(s) then all samples associated with the positive control must be re-injected or re-amplified.

NOTE: Internal Positive Control: A NIST traceable internal positive control may be run alongside the manufacturer's positive control. If the control genotypes are correct, the amplification is considered correct and the samples can be used.

### 9.4.3.2 NEGATIVE CONTROL (AMP-)

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The negative control (amplification blank) contains all the reagents for the amplification mix but no DNA. The negative control will be amplified and analyzed concurrently in the same instrument with the same samples and same PCR kit.

The negative control tests for contamination of samples during the setup of the amplification reactions. If the negative control exhibits unexplainable peaks above the analytical threshold that are not eliminated after re-injection, then all samples associated with the negative control are considered inconclusive for analysis and must be re-amplified.

## 9.4.4 INTERNAL SIZE MARKER AND ALLELIC LADDER

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Internal size marker is added to each sample and ladder prior to electrophoresis. The internal size marker allows the genetic analysis software to determine the size (in base pairs) of the peaks in the samples and ladders.

The allelic ladder is supplied with each of the amplification kits and is run with each set of samples. The allelic ladder allows Gene Mapper to assign an allele call to any peaks observed based on their size.

## 9.4.5 OTHER STANDARDS AND CONTROLS

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### 9.4.5.1 NIST STANDARD

DNA-typing procedures will be checked annually using the NIST PCR-based DNA Profiling Standard (SRM 2391 for autosomal STRs and Y-STRs or an internal NIST traceable sample). NIST SRM will remain suitable for use on annual retesting beyond manufacturer expiration provided that the materials continue to produce complete and correct profiles of comparable quality when compared to the original use of the material on the platform and with the technology and methodology. New or modifications to existing methodologies, new technologies or new platforms require NIST SRM within manufacturer expiration limits.

#### 9.4.5.1.1 INTERNAL NIST STANDARDS

Internal NIST Traceable Standards are created by running NIST Standard Reference Material alongside the internal standard. The internal standard will be viable until a new lot is taken or until an internal expiration date (if applicable). If expired, remaining stock of the internal standard expiration date may be renewed by rerunning along with a NIST SRM. All internal NIST traceable standards will be labeled with a lot designator and will be maintained as labeled.

#### 9.4.5.1.2 NIST STANDARDS HANDLING, STORAGE, & PREVENTION OF DETERIORATION

NIST SRM samples will be maintained as the manufacturer recommends. All NIST samples will be transported, handled, and used as all casework samples to prevent contamination and deterioration and to protect the integrity of the sample.

#### 9.4.5.1.3 NIST QUANTITATION STANDARDS

NIST Human DNA Quantitation Standard (SRM 2372) samples will be maintained as the manufacturer recommends. The NIST quantitation standard may be used to adjust analysis settings for the sequence detection software v.1.2.3 and the expected IPC and Y-intercept value ranges in use for casework quantitation. An annual check of DNA quantitation procedures is not required.

## 9.5 INTERPRETATION GUIDELINES

Note: The organization of this section does not strictly adhere to the numbering of the subsections of FBI QAS Standard 9.5. See Appendix A for Standard Operating Procedures.

### 9.5.1 QUANTITATION INTERPRETATION

The QIAGEN Investigator Quantiplex Pro (Quant Pro) system is used for the quantification of amplifiable total human and human male DNA in a sample. The DNA quantitation assay combines a

target-specific human DNA assay, target-specific human male DNA assay, and an internal PCR control (IPC) assay. Quant Pro also includes a human DNA degradation assay.

When these methods are used, the Forensic DNA QM will be followed (See DNA-DOC-01 19.5). The quantitation process is not tracked through STACS-DB modules. Paperwork is stored on the ForensicBiology shared drive.

## 9.5.2 DNA TYPING INTERPRETATIONS

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Upon collection of any DNA Typing data, the standards and controls shall be interpreted first to ensure suitability of the sample results for interpretation.

### 9.5.2.1 GENERAL TYPING CONTROLS

#### SIZING STANDARDS

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The Data Collection software for the 3500xl Analyzers has a quality-check function which automatically detects marginal or failing sizing quality. In this event, an analyst, or processor in consultation with an analyst, may immediately reinject the injection set and analyze only the new data. A note about the reinjection will be included in the casefile(s) associated and the raw data will be securely retained.

If the raw data is analyzed in a GeneMapper ID-X project, the analyst shall:

- examine the sizing quality flag (SQ) for each control in the Project Window
- open the Raw Data View for any flagged controls to confirm the injection did not fail
- verify that the analysis range is between 60bp and 600bp and the correct Analysis Method and Sizing Standard are selected
- In the Size Match Editor Size Matches window, confirm the peaks are correctly labeled on the failing controls. Include a passing sample to allow simple comparison.

Analysts do not routinely correct incorrect sizing labels. In the event a high quality injection experiences an issue such as a Spike which disrupts the size-calling, the DNA TL may be asked to examine, and if deemed appropriate, correct the peak designation. Due to the nature of direct amplification, detection of sizing standards in punched samples may be difficult and a lower AT of 75 rfu may be needed for the sizing standard. If necessary, the DNA TL will assess each sample and adjust the AT to restore automatic sizing. Any controls with passing flags may be examined in the Samples Plot view. Failing controls shall be reinjected if a second like control is not passing.

#### ALLELIC LADDERS

After confirming the Sizing quality, the analyst shall examine the Allelic Ladders to confirm that the injections are satisfactory. Occasionally, an injection will result in a rising baseline which appears in the analyzed data as shortening and broadening of the larger fragment peaks. The analyst shall confirm that the peaks are correctly called and if necessary, shall re-designate the ladder as a "Sample" and reanalyze the project. A minimum of one passing ladder per project is necessary.

## ANALYTICAL CONTROLS

After confirming the Sizing quality, the analyst shall examine the Analytical Controls to confirm that the injections are satisfactory. The analyst shall confirm that the peaks are correctly called for the positive control(s) and that the locus specific quality flags are passing or the issue is addressed. A minimum of one passing positive control is required per project (also see 9.5.3.1). The negative control and reagent blanks shall be examined for any peaks above analytical threshold, or any patterns of below threshold peaks which indicate possible allelic origin (also see 9.5.3.2). Failing controls can be reinjected, and failing reagent blanks may be reamplified to attempt passing results, but failing amplification controls will require the entire project to be reamplified. See also section 9.5.

### 9.5.2.2 STR INTERPRETATION GUIDELINES

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The purpose of these guidelines is to establish a general framework and outline minimum standards to ensure that:

- Conclusions for CODIS samples are scientifically supported by the analytical data, including that obtained from appropriate standards and controls.
- Interpretations are made as objectively as possible, consistently from analyst to analyst, and within established limits.
- The goal of the evaluation and interpretation is to analyze amplified STR data and determine the DNA profiles for NDIS.
- A peak is defined as a distinct, triangular section of an electropherogram.
- Genotypes are determined from the diagnostic peaks of the appropriate color and size range for a particular locus.

NOTE: Reinterpretation and comparison of DNA records generated by legacy amplification kits (kits previously used by the laboratory but no longer in use) with DNA records generated with amplification kits currently in use by the laboratory shall be performed in accordance with the *SWGDM Clarification on the Reinterpretation of Data Typed with Legacy Amplification Test Kits*. For purposes of these procedures, assessing/evaluating allele calls, genotype calls (to include potential allelic drop-out), a change in the assumptions used, or removing alleles (or entire loci) from statistical estimates from legacy amplification test kit data, are all considered reinterpretation.

See DNA-DOC-01 19.2 for additional Y-STR Interpretation Guidelines.

#### 9.5.2.2.1 ANALYTICAL THRESHOLD

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The minimum peak height threshold will be set at 175 (Relative Fluorescent Unit) RFU for PowerPlex 16 HS, Fusion 6C, and Y23 and at 100 RFU for Yfiler Plus. The interpretation threshold is set at 175 RFU for PowerPlex 16 HS, Fusion 6C and Y23 and 100 RFU for Yfiler Plus. Optimal peak

height values range between 1000-4000 RFU, although acceptable and typeable signals may occur outside of this range.

- **INCONCLUSIVE ALLELE CALLS**

In those cases where peaks are not present or are below the minimum 175 RFU for Fusion 6C, allele calls for that sample at that locus may be designated as inconclusive “INC”. If any of the CODIS core loci have alleles that are not present or are below the RFU threshold, the sample must be re-amplified to gain a complete profile at the 20 core loci. (All previous samples follow the 13 original core loci requirements).

#### **9.5.2.2.2 STOCHASTIC THRESHOLD**

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The stochastic threshold is the value that denotes both peaks for a heterozygous locus will be detected and it is set at 600 RFU for PowerPlex Fusion 6C. For PowerPlex 16HS reanalysis, the stochastic threshold is set at 500 RFU.

#### **9.5.2.2.3 PEAK HEIGHT RATIO**

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Peak height ratios of heterozygote alleles are defined as the ratio of the lower peak’s height to the higher peak’s height, expressed as a percentage. Peak height ratios lower than 50% may indicate a mixture. Occasionally a non-mixed sample will be outside of this range. Depending upon the sample source, the loci in question, the number of loci affected and the percent disparity between alleles, the sample may need to be re-amplified and typed.

Homozygote allele peak heights are approximately twice that of heterozygotes as a result of a doubling of the signal from two alleles of the same size.

#### **9.5.2.2.4 OFF LADDER VARIANTS**

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Off ladder (OL) calls are first converted to size in base pairs (bp), and then compared to the size of the appropriate ladder alleles and the allelic designation determined. If the OL is not a “perfect” repeat, but rather varies by 1, 2 or 3 bp from a ladder allele, then it will be designated as an integer of that variation. For example, if a green OL peak size is 238.39 bp, and the 36 allele of the **D21S11** ladder is 236.32 bp, then the peak will be designated a **D21S11 36.2**. If an allele falls above the largest or below the smallest peak of the sizing ladder, the allele will not need to be re-injected or re-amplified and will be designated as either greater than (>) or less than (<) the respective ladder allele.

The analyst will re-amplify or re-inject, then type any sample containing a peak not properly interpreted as an allele by the software, especially if it is not appropriately balanced with an associated allele or at a height expected for a homozygote.

An off ladder variant which has been seen and confirmed at least two times in the population sampled at the Arkansas State Crime Laboratory is no longer considered a rare variant. These peaks can be confidently and accurately called without confirmation.

#### **9.5.2.2.5 TRI-ALLELE**

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A tri-allelic system is one which contains three distinct alleles, rather than the normal one or two. In order to insure that the sample is a true tri-allelic specimen, the sample should be re-amplified and run a second time. However, if observed in overlapping systems or in multiple samples from the case, tri-allelic loci may be considered confirmed. If there is not enough extract left for re-amplification, the sample may be re-loaded. However, if the tri-allelic sample cannot be confirmed, the locus may be reported as inconclusive or a technical note may be recorded in the case file (the CODIS Administrator or Technical Leader may need to be notified to determine how to report the locus).

#### **9.5.2.2.6 ARTIFACTS**

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Artifacts can occur and need to be recognized. These may include, but are not limited to, the following: spikes, pull-up, stutter, and non-template nucleotide addition.

##### **9.5.2.2.6.1 SPIKES**

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Spikes are artifactual peaks usually observed in at least two colors. Spikes can be caused by urea crystals in the capillary, power surges, or other instrument related issues. A spike will not exhibit the same morphology as a peak, but will be sharper or “spike” shaped. Spikes are unique to fragments analyzed using capillary electrophoresis. Spikes will have fragment sizes which vary only slightly in the 3500xl data. Above threshold spikes should be noted and may be re-injected.

##### **9.5.2.2.6.2 STUTTER (ST)**

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In addition to an allele’s primary peak, artifactual minor “stutter” peaks can occur at 2-, 3-, 4-, or 5-base intervals. The most common stutter peaks observed in all loci are four bases smaller than the primary peak (“n-4”). It is also possible to see additional “n+4” peaks (four bases larger), especially when excessive amounts of DNA are amplified.

Stutter peaks are evaluated by examining the ratio of the stutter peak height to the height of the appropriate adjacent allele, expressed as a percentage. The height of stutter peaks can vary by locus, and longer alleles within a locus generally have a higher percentage of stutter. In general, the maximum expected percentage of stutter is less than 30% for any locus. Peaks in the stutter positions greater than this value may indicate the presence of a mixture. Therefore, CODIS samples will be evaluated with a global stutter ratio of 30%.

Analyzed peak heights above the optimal range may be “off-scale” in the raw data, meaning that the CCD camera may be saturated. While the Gene Mapper ID-X software will alert the analyst to any off-scale raw data peaks, the analyzed peak may be assigned a lower value due to smoothing and base-lining functions. Therefore, the observed percent stutter will be inaccurately high. If the stutter peak is greater than the maximum allowed and the primary peak is above 10,000 RFU and/or has been labeled off-scale, the analyst should interpret the results with caution. The sample may be re-amplified with less input DNA or re-injected.

Approved STR Stutter Ratios can be seen in table form in Appendix E.

#### **9.5.2.2.6.3 NON-TEMPLATE NUCLEOTIDE ADDITION (-A)**

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Amplification conditions have been set to maximize the non-template addition of a 3' terminal nucleotide by DNA polymerase. Failure to attain complete terminal nucleotide addition results in “band splitting”, visualized as two peaks one base apart. This is most often seen when an excessive amount of DNA is amplified or amplification is performed under sub-optimal PCR conditions.

#### **9.5.2.2.6.4 PULL-UP**

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Small artifactual peaks can appear in other colors under true peaks. This phenomenon is termed “pull-up”. Pull-up is a result of spectral overlap between the dyes, which is normally corrected for by the spectral calibration. If a pull-up peak is above the minimum peak height detection threshold, it will be sized at approximately the same size as the true peak. Pull-up can occur as a result of the following:

Application of a sub-optimal spectral can cause pull-up. If necessary, spectral standards can be injected on the same capillary after the analytical run and a new spectral can be made and applied.

Amplification using excess input DNA can lead to off-scale peaks. The matrix may not perform properly with off-scale data.

#### **9.5.2.2.6.5 OTHER**

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In addition to amplification artifacts described above the following anomalies can arise during electrophoresis and analysis:

Significant room temperature fluctuation may result in size variation between injections such that allelic ladder peaks differ by more than 0.5 bp from allelic peaks in other injections. This will disrupt sample analysis using the Gene Mapper ID-X program. Analyzing samples with an injection of allelic ladder nearest the questioned samples may alleviate this problem. If desired, the sample(s) and an allelic ladder may be re-injected to confirm the typing.

Artifactual peaks of a single color will not display the typical spectral overlap characteristic of the five fluorescent dyes in the raw data. Peak width may not be similar to the peaks resulting from dye-labeled DNA. These peaks can be shown to be artifactual by re-injection of the sample.

See DNA-DOC-01 19.7 for additional information on Y-STR artifacts.

### **9.5.2.3 RE-RUNS (RE-WORK IN STACS-DB)**

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All samples that have been labeled as re-work will be reprocessed. The sample will be marked and verified for re-work. Recently entered samples into SDIS will be compared to all samples in the DNA Database during the weekly offender to offender search. It is noted, that problematic samples (both CODIS and Medical Examiner samples) can be extracted, quantitated and amplified using the sample methods employed in the Casework Section. When these methods are used, the Casework SOP will be followed. This process is tracked in the Manual Worklist and Tracked Manual Processing modules in STACS-DB. Paperwork is stored on the S drive.

### **9.5.2.4 Y-STR INTERPRETATION GUIDELINES**

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Some CODIS samples, such as for Missing Persons, Unidentified Remains, or for Familial Searching may need to have Y-chromosomal STR typing analysis. When Y-STR methods are used, the Forensic DNA QM will be followed (See DNA-DOC-01 19). The process is not tracked through STACS-DB modules. Paperwork is stored on the ForensicBiology shared drive.

## **9.6 MODIFIED RAPID DNA INTERPRETATION GUIDELINES**

No methods for Modified Rapid DNA Analysis have been validated for use by the ASCL Forensic DNA or CODIS sections.

## **9.7 RAPID DNA INTERPRETATION GUIDELINES**

No methods for Rapid DNA Analysis have been validated for use by the ASCL Forensic DNA or CODIS sections.

## **9.8 DETECTION AND CONTROL OF CONTAMINATION**

The Arkansas State Crime Laboratory employs several safeguards to detect any contamination that might occur. The reagent blank and/or the amplification blank detects contamination during extraction and during the setup of amplification. In order to reduce the possibility of contamination the Arkansas State Crime Laboratory has devised procedures listed in the section on sample handling and processing.

Additional information on instrument cleaning can be found in Section 10 and other general contamination control information can be found in Section 18.

If contamination has been discovered, the laboratory will try to discover the source of the contamination. The incident will be documented on a Non-Conformance Report, stored in the Non-Conformance Report module under the Utilities section in STACS-DB. If a CODIS analyst is found to be the source of the contamination, the CODIS Administrator will be notified and take the necessary corrective actions. If the contamination is from outside the CODIS section, the appropriate supervisor will be notified to address the contamination source. If the contamination is a systemic issue, the lab wide Quality Manager will be notified and a Corrective Action Request (CAR) may be necessary.

## 10 EQUIPMENT

### 10.1 BACKGROUND

Only suitable and properly operating equipment will be employed and only authorized personnel should operate the equipment. The purpose of the procedures in this section is to ensure that the parameters of the testing process are routinely monitored in the manner necessary to maintain the success and reliability of the testing procedures. The ASCL CODIS section does not use equipment outside of ASCL permanent control.

In order to safeguard irreplaceable and/or limited samples, quality control (QC) procedures will focus as much as possible on preventing problems before they occur rather than dealing with them after they happen. As such, it is the responsibility of all DNA personnel to report quality issues to the CODIS Quality Manager, CODIS Administrator, and/or DNA Technical Leader. In the event a quality issue is found which may affect analyzed samples, it is preferable that effected samples be reprocessed. However, where the samples are irreplaceable and/or limited in amount, reprocessing may not be a viable option. In such a case, it is possible to verify “after the fact” that the equipment, materials and reagents used in an analysis have not significantly affected the reliability of the results.

*For example, controls utilized during each phase of the testing procedure are designed to signal potential problems in the analysis. If acceptable results are obtained on these controls, it is reasonable to assume that the results from other samples analyzed simultaneously are also reliable.*

If the controls indicate a problem with the analysis, it may be possible to determine the source of the problem and make corrections. Depending on the nature of the problem, re-analysis of the samples may be required.

### 10.2 INSTRUMENT AND EQUIPMENT

New employees shall be trained on the appropriate equipment during their training program and be authorized to operate the equipment. This authorization will be documented on Analyst & Technician Competency Authorization, ASCL-FORM-62, and shall be maintained in Qualtrax. Validation of new equipment, procedures, and software shall require training of personnel before authorization. Only individuals trained in the proper use of the equipment shall be authorized to operate it independently. Instructions on the use and maintenance of equipment shall be available for use.

#### 10.2.1 CRITICAL INSTRUMENTS

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The following Category 1 equipment is considered to be critical for the forensic CODIS section:

Pipettes	Thermocyclers	EZ-1
3500xl	7500	
Heat Blocks	NIST-Thermometer	Drift-Con

### 10.2.2 INVENTORY

An inventory log will be maintained on the ForensicBiology drive for each instrument or piece of equipment considered to be essential for DNA analysis. This log may include the manufacturer, model number, serial number, purchase date, replacement date, and if present, asset number and all additional requirements of the *ASCL QM*.

### 10.2.3 OPERATING MANUALS

Warranty information and operating manuals will be filed in the laboratory and readily available to all operators of instruments and equipment in either paper or electronic form.

## 10.3 PERFORMANCE CHECKS

Any new critical instruments or equipment that has been serviced requires a performance check to ensure it is operating properly before being used for casework analysis. The performance check will be documented and approved by the DNA technical leader.

- a) 7500: Following the maintenance, repair, or moving of a 7500, a performance check will be performed. The performance check requires a set of standards be run (that have already been QC checked) and have a passing R2 value of .98 or above and the top standard be within 2 standard deviations of the validation values.
- b) 3500xL: Following the maintenance, repair, or moving of a 3500xl, a performance check will be performed. The performance check requires a ladder to be injected using the standard protocol. The run will then be analyzed in GeneMapper ID-X to ensure that the ladder passes the requirements setup in GeneMapper ID-X.
- c) Thermocycler: Following maintenance, repair, or moving, a performance check will be performed. The performance check requires a set (minimum of 2) of positive controls (2800M, CG, etc) and an AMP\_Neg to be amplified according to the current Autosomal STR amplification protocol. The samples will then be run on the 3500xl and analyzed in GeneMapper ID-X to ensure the samples amplified properly. All samples are required to amplify properly to pass the performance check. The DNA Technical Leader can override this requirement if there are documented reasons for the failure.
- d) Qiagen EZ1: Following maintenance, repair, or moving, a performance check will be performed. The performance check requires a set (minimum of 2) of blood with known profiles on FTA to be extracted, quantified, amplified, and run on a 3500xl. The set will then be analyzed with GeneMapper ID-X to ensure the extraction occurred properly. A passing performance check is when the amount of DNA extracted is at least 0.05 ng/ $\mu$ L and the sample produces the expected DNA profile.

- e) NIST-Traceable Thermometer (new), Drift-Con, and Pipettes: performance checks will be performed by calibrating vendor and documented in the associated vendor records as the “As Left” value.
- f) Heat Blocks/Incubators used in analytical procedures: performance checks will be performed on new instruments or annually with a NIST-Traceable Thermometer to ensure that each is operating within specification. As all thermometers are NIST-Traceable, the daily temperature logs shall be sufficient to verify the continued performance of each heat block.

## 10.4 MAINTENANCE SCHEDULES AND RECORDS

DNA testing methods do not result in reports of metrological data. The DNA sections are not required to establish an Uncertainty based on measurements. However, it is desirable that equipment which can influence laboratory activities be treated as critical to the overall findings.

Each instrument/piece of equipment considered essential for DNA typing will be maintained and calibrated or verified on an appropriate schedule. A schedule for maintenance is found in the *DNA-FORM-12 DNA Equipment Care Schedule*. A maintenance log entry is maintained on any instrument or piece of equipment in which the following has occurred: damage, malfunction or modification or repair to equipment. After expiration of any initial warranty period, the BSD600, AB7500, AB3500xl, EZ1xl advanced, Qiacube, and Qiagility will have Annual Maintenance contracts with the manufacturers which will include an annual Preventative Maintenance visit. At a minimum, each instrument will pass a performance check annually. Any calibrated equipment with a defined period of validity will be labeled to indicate the calibration status. The date all equipment is removed from service is recorded and maintained on the DNA drive for a minimum of one full accreditation cycle.

### 10.4.1 ANNUALLY (OR AS NEEDED)

- Spatial for 3500xls (whenever array window door is opened a spatial must be performed according to the manufacturer)
- Spectral for 3500xls must be performed in the following instances:
  - Use of a dye set that does not have a valid calibration on the instrument
  - Change the capillary array
  - Maintenance involves an optical service procedure (realignment of optics, replacement of laser or CCD camera)
  - An increase in pull-up peaks is seen in DNA profiles
- Pipettes – performance-check and calibration for traceability, no MOU estimation needed.
  - Repairs, calibration and performance check to be performed by an outside vendor meeting ASCL-DOC-01 6.5.1.1 specifications.
  - The acceptability criteria for ‘as found’ calibration is 8% or less for single channel micropipettes. The criteria will be doubled for multichannel pipettes.

- NIST Traceable Thermometer – A NIST-traceable thermometer will be purchased annually to ensure continuous traceability for all DNA thermometers. No performance check needed.
- Thermometer – performance check and verification for traceability.
  - Verification to be performed by laboratory personnel.
  - Annually or prior to being placed into service (unless currently NIST-traceable)
  - Traceability criteria: detailed on DNA-Form-19
- Drift-con – (Thermocycler calibration system) performance-check and calibration for traceability.
  - Calibration to be performed by an outside vendor meeting ASCL-DOC-01 6.5.1.1 specifications.
  - Traceability criteria:  $t_{90-t} \leq 0.25^{\circ}\text{C}$  @ 30 °C, 60 °C, 90 °C, and 95 °C
- Thermocyclers and Quantitative PCR Thermocyclers – Drift-con temperature verification
  - Verification to be performed by laboratory personnel
  - Traceability criteria:
    - Accuracy: +/- 1°C @ 30 °C, 50 °C, 60 °C, 70 °C, 90 °C, & 95 °C @ 15, 30, & 90 seconds
    - Spread: +/- 1°C @ 30 °C, 50 °C, 60 °C, 70 °C, 90 °C, & 95 °C @ 15, 30, & 90 seconds
  - If test fails, an outside company is called for service and unit is taken out of service.
- Balances – performance check and verification
  - Verification to be performed by laboratory personnel
  - NIST-traceable weights are calibrated or replaced every 10 years
  - Traceability criteria: detailed on DNA-FORM-06
    - Accuracy (BAL-2): +/- 1% @ 1g, 2g, 3g, 5g, 10g, 20g, 30g, 50g, and 100g
    - Accuracy (BAL-1): +/- 5% @ 1g, 2g, 3g, 5g, 10g, 20g, 30g, 50g, 100g, and 500g

#### 10.4.2 QUARTERLY

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- Biological safety hoods – serviced and calibrated by outside company, if needed. Monitoring and Management is performed on a lab-wide basis beyond the scope of this manual.

#### 10.4.3 MONTHLY

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- Back-up the CODIS drive.
- STACS-DB server to back-up tapes

#### 10.4.4 BI-WEEKLY (BY LABORATORY PERSONNEL AS NEEDED)

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- The 3500xl and computers shall be restarted.
- Wet the seals on the 3500xl.
- Polymer is changed on the 3500xl.
- Conditioning wash is performed on the 3500xl.
- Change buffer containers, septa, and reagents on the 3500xl.

#### 10.4.5 WEEKLY (BY LABORATORY PERSONNEL, AS NEEDED)

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- Grease O-rings on the EZ1 robots, if used.

#### 10.4.6 EACH DAY OF USE (BY LABORATORY PERSONNEL AS NEEDED)

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- Autoclave – check water levels before use.
- Check temperature of refrigerators and freezers in pre-amp and post-amp rooms (DNA-FORM-17) if lab space is used.
- Heat Blocks – temperature checked prior to use (DNA-FORM-17).
- Bench tops – CODIS & DNA (pre-Amp): After each use, the bench tops must be cleaned with a 10% bleach solution and documented on DNA-FORM-11.
- BSD 600 – Before each use, wipe down the punching unit with ethanol.
- EZ1 - End of day (after last protocol), if used:
  - Clean Piercing unit:
    - Close Door
    - Press “2” MAN (Manual Function), then press “3” Clean
    - Press “Start”, then open door.
    - Clean piercing units with a soft wipe and alcohol. **\*\*Piercing unit is sharp!\*\***
    - Wipe piercing unit with deionized water.
    - Close Door and Press “ENT”, then press “ESC
  - Check that the tray and racks are clean, if needed, clean with ethanol and then deionized water.
  - Run UV decontamination cycle for 20 minutes.
  - Document decontamination on DNA-FORM-41

#### 10.4.7 CODIS SERVER BACK-UP AND SOFTWARE MAINTENANCE PROCEDURES

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- Using Backup Exec 16, a daily backup of the CODIS Server is captured to tape storage. Tapes are replaced weekly and stored in a fire resistant safe away from the server room. Additionally, one tape is securely stored off-site each month.
- Using McAfee ENS on the CODIS server and CODIS workstations, antivirus updates are applied automatically on a weekly basis.
- Audit records of user and system activities within the CODIS server and CODIS workstations are captured by saving event logs into a file for consolidation and review. Log files are retained for at least a period of 6 months.
- The ASCL is subscribed to the automated software update services (WSUS) provided by the FBI and updates are applied within 30 calendar days to the CODIS server and CODIS workstations.

## 10.4.8 INSTRUMENT OR EQUIPMENT CLEANING PROCEDURES

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### CENTRIFUGES

Wipe out the inside of the centrifuge with 10% bleach solution as needed, or appropriate cleaner as recommended by manufacturer.

### BIOLOGICAL SAFETY HOOD

After each use, wipe down inside of hood with 10% bleach.

## 10.4.9 TRANSPORT/STORAGE OF EQUIPMENT

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In the event the equipment needs to be stored or transported the following precautions will be taken to ensure proper functioning and to prevent contamination and deterioration.

### STORAGE

Equipment will be decontaminated and processed for storage according to manufacturer recommendations.

### TRANSPORT

Equipment will be prepared for movement if necessary according to manufacturer's recommendations. Non-portable equipment sensitive to movement (eg. 3500xl) will be, at a minimum, performance checked according to Section 7.6.

## 10.4.10 SERVICE RECORDS

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Anytime an instrument or piece of equipment requires calibration, service or maintenance, that information will be documented and maintained on the ForensicBiology drive.

In the event that any piece of equipment fails or does not pass its specific requirements, the equipment must be taken out of service until it can be maintained properly.

- a) All equipment failing must be documented on the ForensicBiology drive
- b) A sign must be placed on the equipment as "Out of Service"
- c) No equipment will be placed back into service until proper performance is demonstrated.
- d) The CODIS Quality Manager must inform the Technical Leader and/or CODIS Administrator of all equipment failure.
- e) A Quality Assurance Concern (QAC) workflow will be initiated if needed as noted in *ASCL QM*.
- f) If an adjustment/repair is performed because a calibration does not meet specifications, then pre- and post-adjustment/repair data will be retained

## 11 DOCUMENTATION

### 11.1 PROCEDURES

The laboratory shall have and follow procedures for maintaining documentation for database, known or casework reference samples. The laboratory shall maintain all analytical documentation generated by technicians and/or analysts related to database analyses. The laboratory shall retain, in written, printed, or electronic format, sufficient documentation for each technical analysis to support the profile data such that another qualified individual can evaluate what was done and interpret the data.

### 11.2 MATCH VERIFICATION AND REPORTING

The laboratory shall have and follow a documented procedure for the resolution, verification and reporting/notification of database matches.

### 11.3 CONFIDENTIALITY

Except as otherwise provided by state or federal law, the information in DNA records and DNA databases shall be confidential.

#### 11.3.1 RECORDS RELEASE POLICY

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The laboratory shall have and follow policies and/or procedures for the release of DNA records and databases, in accordance with applicable state or federal law.

#### 11.3.2 PII RELEASE POLICY

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The laboratory shall have and follow policies and/or procedures for the release of personally identifiable information in accordance with applicable state and federal law.

##### 11.3.2.1 PII IN MATCH REPORTS

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The laboratory shall have and follow a procedure for the release of personally identifiable information in connection with a database hit.

## 12 REVIEWS

The testing period is defined in the examination notes as the date punched to the date analyzed.

Any examination records prepared by an individual other than the analyst who interprets the findings and/or authors the record will have the preparing staff member's name or initials included on the worksheet or electronic audit record .

Prior to the import of data into SDIS, all CODIS samples are subject to technical reviews. All CODIS hit documents are subject to an administrative review.

### 12.1 REVIEWS

The CODIS section complies with all *ASCL Quality Assurance Manual* (ASCL-DOC-01) section 7.7.1.2 lab wide review requirements.

All convicted offender samples must have a 100% review of the electronic data before entered into the CODIS system. The Technical Review Checklist in the Analysis module of STACS-DB must be completed and all discrepancies must be alleviated before any sample can be entered into CODIS.

After processing all Convicted Offender / Arrestee Samples, files are kept in STACS-DB under the appropriate modules. STACS-DB documents all aspects of the lab process, including the individual performing each step. Sample information can be found in the 'Sample History Report'. Plate information can be found in the 'View Plates' module and 'Plate History'.

For any documentation not recorded in STACS-DB, handwritten notes and observations must be in ink. Nothing in the handwritten information will be obliterated or erased. Any corrections will be made by a single line strikeout (so that what is stricken can still be read) and initials. Correction fluid or correction tape may not be used. Files will be stored on the S drive.

The unique CODIS plate number, examiner's initials or name, and date must be on each page of the examination documentation or stored in STACS-DB in the case record. Observations, data and calculations shall be recorded at the time they are made and shall be identifiable to the specific task.

#### 12.1.1 THE TECHNICAL REVIEWER

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The technical reviewer shall be or have been an analyst qualified in the methodology being reviewed and not the author of the current record The technical reviewer will review all documentation in the record to ensure that there is sufficient basis for the scientific conclusion(s) in the record and then complete and sign the technical review sheet, if used, indicating that a technical review has been completed. The technical reviewer will electronically initial that the technical review was completed in Analysis module of STACS-DB. If a discrepancy is found and an agreement is not reached between the DNA analyst and the reviewer(s), the CODIS Administrator

will be consulted. The Technical Leader will be notified of all technical issues and consulted for a final decision if there is still a discrepancy.

## 12.2 TECHNICAL REVIEW

The laboratory will conduct a technical/peer 100% review of all case files and reports. This review can be conducted using a validated Expert System.

All CODIS samples will be technically reviewed. An examiner qualified under the QAS guidelines will execute the review. The technical reviewer must be:

- Previously qualified analyst in the methodologies being reviewed.
- Successful completion of a competency test administered by the NDIS participating laboratory prior to participating in the technical review for DNA data
- Participation in an external proficiency testing program at an NDIS participating laboratory on the same technology, platform and typing amplification test kit used to generate the DNA data being reviewed.

The Technical Leader or CODIS Administrator should resolve discrepancies and concerns that are detected by the technical or administrative review. The Technical Leader or CODIS Administrator will ensure that appropriate action has been taken before permitting any sample to be entered into the CODIS system.

Steps performed by the Technical Reviewer if an Expert System is not used for review of data:

- Technical reviewer must examine all areas described on the Technical Review Checklist.
- During the review process, the reviewer must do the following in addition to those items listed on the review form.
- All allele calls must be checked for accuracy and the absence of mixtures.
- All profiles are acceptable for upload to NDIS
- If discrepancies occur or clarification is needed during the technical review process, the reviewer must notify the CODIS analyst or the CODIS Administrator. The Technical Leader is responsible for any unresolved discrepancies between the analysts and reviewer.
- A review of all notes, all STACS data, and the electronic data (or electropherograms) supporting the results.
- A review to ensure all non-electronic examination documents are marked with the plate number and handwritten initials.
- A review of all DNA types to verify that they are supported by the raw or analyzed data (electropherograms).
- A review of all controls, internal lane standards and allelic ladders with expected results
- A review to confirm that reworked samples have appropriate controls
- A review of the accuracy of specimen categories

## 12.3 ADMINISTRATIVE REVIEWS

CODIS hit letters must have an administrative review of the official correspondence. The reviewer must document that he/she reviewed the hit on the 'CODIS Hit Verification' form located in the Hit Tracking entry in the Hit Tracking module. The clerical errors must be documented in the comments of the Hit Tracking Entry. The review cannot be performed by the author of the report.

The review consists of the following:

- A review of individual's biographical data, qualifying offense, and DNA profile
- A review of accuracy of information
- A review of clerical errors

Note: A review of known or casework reference samples processed as evidence will be performed to the standards in the *Forensic DNA QM*.

A list of all Convicted Offenders/Arrestees can be printed and compared to the database to determine which samples have not had a profile entered into SDIS. This process ensures that all samples are entered into the database.

## 12.4 DISCREPENCIES

Corrective actions will be performed according to the Arkansas State Crime Laboratory quality manual.

### 12.4.1 NONCONFORMING WORK

Nonconforming testing is testing in which Forensic DNA procedures are not followed or the agreed-upon requirements of the customer (e.g., testing of standards and controls, test precision and accuracy, the care and handling of evidence, instrument performance) are not met. All CODIS staff, including analysts and supervisory personnel, must be vigilant for any indication of nonconforming testing.

For CODIS, there are two key levels of non-conforming work, each of which requires a different response:

- Simple corrections in which an isolated incident can be resolved immediately and documented in the sample processing record, when appropriate, or requiring *Non-Conformance Form* (CODIS-FORM-17) to ensure technical justification, supervisor acknowledgement, and authorization for performing or reporting the deviation.
- Level 1 & 2 Nonconformities which require a *Quality Assurance Concern* (QAC) workflow be initiated. See the *ASCL Quality Assurance Manual* (ASCL-DOC-01) for more information

## 12.4.2 AUTHORITY AND ACCOUNTABILITY

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The CODIS Administrator will be responsible to assure that discrepancies are acknowledged, the effect of the discrepancy is documented, and corrective actions are documented according to the Arkansas State Crime Laboratory Quality Manual. Corrective actions shall not be implemented without the documented approval of the technical leader. Any deviation from the CODIS Quality Manual (CODIS-DOC-01) will be approved by the CODIS Administrator and DNA Technical Leader. A log will be kept of each deviation from the CODIS Quality Manual.

## 12.5 CODIS ENTRY REVIEW

Any samples processed through STACS-DB are automatically assigned to the correct specimen categories, based on sample type. This includes Medical Examiner samples, Offenders, and Arrestees. All other samples for CODIS entry are reviewed on DNA-FORM-31 or DNA-FORM-32 prior to CODIS entry. The entry is then verified by the technical reviewer on the casefile review sheet.

## 13 PROFICIENCY

Proficiency testing is used periodically to demonstrate the quality performance of the DNA laboratory and serves as a mechanism for critical self-evaluation. This is accomplished by the analysis and reporting of results from appropriate biological specimens, submitted to the laboratory as open and/or blind case evidence.

All specimens submitted as part of a proficiency test must be analyzed and interpreted according to the DNA analysis protocol approved by the laboratory at the time of the proficiency test.

Since the proficiency-testing program is a critical element of a successful QA program, it is an essential requirement. When possible, the Arkansas State Crime Laboratory utilizes proficiency testing offered from approved ISO/IEC 17043 providers.

Open proficiency test specimens are presented to the laboratory and its staff as proficiency specimens and are used to demonstrate the reliability of the laboratory's analytical methods as well as the interpretive capability of the DNA Analyst. Participation in the open proficiency test program is the primary means by which the quality performance of this DNA laboratory is judged and is an essential requirement since this laboratory performs analysis.

### 13.1 PERSONNEL AND FREQUENCY

Proficiency testing pertains to those DNA personnel actively engaged in DNA testing. Each proficiency test may consist of dried specimens of blood and/or other physiological fluids, either singly or as a mixture. Each sample to be tested should contain an amount sufficient so that a conclusion can be drawn from the results of the analysis.

External, (or Inter-Laboratory) Proficiency tests are performed semi-annually for each DNA Analyst, (once in the first six months of the year and a second in the second six months of the year). There must be at least four months between each test, and not more than eight months between tests. Tests are taken quarterly with individual analysts alternating between test-taker and reviewer roles to ensure separation between test answers and test takers.

Newly qualified personnel will complete an external proficiency test within 6 months of their qualification.

In the event that an external Proficiency test is missed (such as due to medical leave or military service) an internal (or Intra-Laboratory) Proficiency will be taken before resuming casework or reviews. An expired external Proficiency test may be used as an internal test. The individual will resume external Proficiency testing as soon as is practicable.

#### 13.1.1 PER TECHNOLOGY

All analysts and technical reviewers shall be external proficiency tested at least once per year in each of the DNA technologies which they perform analysis or review.

Current Technologies: STR, (see *Forensic DNA QM* for Y-STR)

### **13.1.2 PER TEST KIT**

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All analysts and technical reviewers shall be external proficiency tested at least once per year in each of the test kits for DNA typing in which they perform analysis or reviews.

Current Kits: PowerPlex Fusion 6C (see *Forensic DNA QM* for Quantiplex Pro and Yfiler Plus)

### **13.1.3 PER METHODOLOGY**

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All analysts, technical reviewers, and processors shall be external proficiency tested at least once per year in at least one method of each methodology for which they perform analytical procedures.

Current Methods: EZ1 extraction, Blood card (direct amp), Bode Buccal collector (direct amp)

### **13.1.4 ASSIGNMENT**

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DNA personnel shall conduct all portions of a test up to the limit of their qualification, alone and without selecting or accepting any assistance from other persons. Additional personnel may be assigned to complete aspects of the test for which the original individual is not qualified.

Violation may result in disciplinary action for those receiving and those rendering assistance. If the personnel have any questions or require assistance, they will contact the DNA TL. In order to avoid unfair advantages to other personnel at different stages of analyzing the same proficiency test samples, they may not consult one another with regard to their samples, procedures, analysis or interpretations. To do so defeats the purpose of proficiency testing for the individual and the laboratory.

## **13.2 PROFICIENCY PROVIDER**

The laboratory shall use an external proficiency test provider that is accredited to the current applicable standard of the International Organization for Standardization and the applicable test is included on the proficiency test provider's scope of accreditation. External proficiency testing shall be an open proficiency testing program and shall be submitted to the proficiency testing provider in order to be included in the provider's published external summary report.

Current Provider: BODE IQAS

## **13.3 DATE OF PERFORMANCE**

Beginning January 1, 2017, the date of proficiency submission to the proficiency provider has been designated as the date of test performance or completion for external proficiencies. For internal proficiencies, the date of proficiency submission for Proficiency Review to the DNA TL has been designated as the date of test completion.

## 13.4 DOCUMENTATION OF PROFICIENCY TEST RESULTS

See the *ASCL Quality Manual* (ASCL-DOC-01) for additional information.

When the proficiency test is complete, all results (proficiency paper test case file) will be given to the Technical Leader or designee. The official case file is stored in JusticeTrax. The official electronic version must include all administration, examination documentation, how samples were obtained or created (if internal test), results from provider, and any corrective action reports.

The Technical Leader or designee will provide a yearly summary of who was tested and status of their performance. This information will be documented in a separate secure filing system.

\*It is noted that all proficiency tests must be processed consistent with the normal processing of casework, including all associated documentation (technical and administrative review.)

### DATA DOCUMENTATION

Upon the completion of a proficiency test, at a minimum, the following proficiency test data and information will be collected and submitted to the Technical Leader. The Technical Leader (or their appointed person) will be responsible for providing to the external test source the required data for evaluation:

- 1) Proficiency Test Set Identifier
- 2) Identity of DNA Analyst
- 3) Dates of Analysis and Completion
- 4) Copies of all Work Sheets/Notes and supporting conclusions
- 5) GeneMapper ID-X worksheets
- 6) Any discrepancies noted
- 7) Corrective actions taken (if applicable)
- 8) Test Results

### REPORT FORMAT FOR DNA ANALYST'S TEST FINDINGS

Some conclusion is required as to whether the unknown and known specimens could have a common origin or whether an exclusion can be demonstrated. Adequate and correct discrimination must be demonstrated in order to pass the proficiency test.

### REVIEW AND REPORTING OF PROFICIENCY TEST RESULTS

The Technical Leader and either the CODIS Administrator or Casework Supervisor (depending on proficiency cycle) reviews all test materials and compares results to the information from the test manufacturer and informs the DNA Analysts of the tests results and documents their performance. The Scientific Operations Director will review the results of the Technical Leader and CODIS Administrator and document it on the proficiency log. This review should be conducted in a timely manner. The electronic copy of the proficiency test is the official copy

## 13.5 EVALUATION OF PROFICIENCY TEST

### PROFICIENCY TEST REVIEW GUIDELINES

- 1) No analyst performing/assigned to a proficiency test will be involved in the proficiency review process. Except for the technical leader see #2.
- 2) The technical leader must review and initial on *DNA-FORM-36* (DNA Proficiency Review Form) that any inconclusive result complies with the laboratory's guidelines.
- 3) All final reports are graded as satisfactory or unsatisfactory.
  - a) A satisfactory grade is attained when there are no analytical errors for the DNA profile typing data. Administrative errors shall be documented and action taken to minimize the error in the future.
    - i. All reported major and minor alleles are correct according to ASCL DNA interpretation guidelines.
    - ii. All reported inclusions and exclusions are correct.
    - iii. All reported genotypes and/or phenotypes are correct according to consensus genotypes/phenotypes or within established empirically determined ranges.
    - iv. All reports reported as inclusive or un-interpretable are consistent with written laboratory guidelines. The basis for inconclusive interpretations in proficiency tests must be documented.
    - v. Minor allele calls: If there is a discrepancy between the provider results versus the analyst's results, the test can be graded satisfactory if the minor alleles meet interpretational guidelines (refer to Section 6.2.2.2).
  - b) An unsatisfactory grade is attained when any of the above satisfactory criteria are not met. The CODIS Administrator must initiate a Quality Assurance Concern (QAC) in Qualtrax.
- 4) Proficiency tests are documented in Qualtrax in the Proficiency Testing Workflow. The date that the PT results are submitted to the proficiency provider is considered the Date of Completion. The date under Results Review indicates the date the results from the proficiency provider are reviewed.
- 5) If there is a discrepancy between the expected results and the experimental results, the CODIS Administrator and/or DNA Technical Leader must notify the labwide QA Manager. Minor discrepancies may be deemed satisfactory based on the following factors with approval of the labwide QA Manager: Discipline interpretation guidelines or Consensus results.
- 6) All discrepancies/errors and subsequent corrective actions must be documented.
- 7) All proficiency test participants shall be informed of the final test results.

### PROFICIENCY TEST REVIEW PROCEDURE

- 1) All proficiency tests will be reviewed the same as casework. See section 9 for technical and administrative review procedures.
- 2) Since reports do not include the locus and alleles, the proficiency test documentation to be sent to the proficiency provider must be technically reviewed to eliminate transcription errors. As a further measure to additionally eliminate any transcription errors, the Administrative Reviewer

must also examine the locus and alleles that are being transcribed onto the proficiency provider's worksheets.

- 3) **Submission Review** - In addition to the normal technical and administrative casefile reviews, a specific review of the proficiency results paperwork will be performed and documented on DNA-FORM-36 (DNA Proficiency Review Form) by the TL, Casework Supervisor, or CODIS Administrator, whichever is not assigned a test in the set. This review will ensure that the correct electronic paperwork will be submitted to the proficiency provider.
- 4) **Consensus Assessment** - When the results are available from the proficiency provider, the submitted results will be compared to the consensus results by the TL and another non-tested analyst, typically the Casework Supervisor or the CODIS Administrator to ensure a complete and thorough review. This review will be documented on DNA-FORM-36 (DNA Proficiency Review Form). Any discrepancies will be noted and any explanations or Corrective Actions will be documented.

## 13.6 NOTIFICATION

Upon completion of the Proficiency Test Review and evaluation of results, the final reviewer shall notify the test participant(s), the DNA TL, and if unsatisfactory, the CODIS Administrator.

The results of evaluation of the proficiency tests and corresponding identifiers are kept in the Qualtrax Proficiency Testing Workflow. Any corrective action needed due to one of the following discrepancies must be documented in Qualtrax.

## 13.7 CORRECTIVE ACTION FOR PROFICIENCY TEST ERRORS

The following clearly defines the specific policies, procedures and criteria for any corrective action taken as a result of a discrepancy in a proficiency test. These terms as used in this section are limited to proficiency testing in the Forensic DNA and CODIS sections.

### 13.7.1 AUTHORITY AND ACCOUNTABILITY

It is the responsibility of the CODIS Administrator and Technical Leader to assure that discrepancies are acknowledged and that any corrective action is documented.

### 13.7.2 TYPES OF ERRORS

#### 13.7.2.1 ADMINISTRATIVE ERROR (LEVEL 2 NONCONFORMITY)

Any significant discrepancy in a proficiency test determined to be the result of administrative error (clerical, sample mix-up, improper storage, documentation, etc.) may be corrected as follows:

- 1) A second sample set may be submitted to an individual within one week if the CODIS Administrator believes discrepancies occurred in the first test sample set. The second sample

or test material will be different than the first sample but will apply to the same subject matter under testing. The individual will immediately examine the second sample upon receipt.

- 2) If an error of this type is not detected until the Analyst has concluded their analysis, and therefore negates their work, they must be issued an additional proficiency test set. The duplication of analysis due to administrative error in no way reflects negatively on the analyst. However, the cause of the error should be found and eliminated from future proficiency tests.
- 3) If an error is due to any clerical or administrative error (typographical or otherwise – not including analyst sample mix-up or improper storage), the internal review processing steps must be evaluated to eliminate or reduce errors.

#### **13.7.2.2 SYSTEMIC ERROR (LEVEL 1 NONCONFORMITY)**

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Any significant discrepancy in a proficiency test determined to be the result of a systematic error (equipment, materials, environment) may require a review of all relevant case work since the DNA unit's last successfully completed proficiency test. Once the cause of the discrepancy has been identified and corrective action taken, all DNA Analysts should be made aware of the appropriate corrective action in order to minimize the recurrence of the discrepancy.

#### **13.7.2.3 ANALYTICAL / INTERPRETATIVE ERROR**

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- 1) Any significant discrepancy in a proficiency test result determined to be the consequence of an analytical /interpretative discrepancy must prohibit the individuals involved in producing the discrepant result from further examination of case evidence until the cause of the problem is identified and corrected. The Technical Leader determines the need to audit prior cases based upon the type of error and its cause.
- 2) Before resuming analysis or interpretation of casework, an additional set of open proficiency samples must be successfully completed by the individual responsible for the discrepancy.

### **13.7.3 DOCUMENTATION**

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The results of the proficiency tests and corresponding identifiers are kept in the Qualtrax Proficiency Testing Workflow. Any corrective action needed due to one of the above discrepancies must be documented in Qualtrax.

## **13.8 STORAGE**

Once the proficiency has been completed it will be transferred to proficiency storage, and may serve as training samples.

## 14 CORRECTIVE ACTIONS

Corrective actions will be performed according to the *ASCL QM*. See section 13.7 for policies regarding Proficiency Test Corrective Actions.

### 14.1 NONCONFORMING WORK

Nonconforming testing is testing in which CODIS procedures are not followed or the agreed-upon requirements of the customer (e.g., testing of standards and controls, test precision and accuracy, the care and handling of evidence, instrument performance) are not met. All Forensic DNA staff, including analysts and supervisory personnel, must be vigilant for any indication of nonconforming testing.

For CODIS, there are three key levels of non-conforming work, each of which requires a different response:

- Simple corrections in which an isolated incident can be resolved immediately and documented in the casefile or record, when appropriate.
- Simple nonconformities requiring *Non-Conformance Form (CODIS-FORM-17)* or STACS-DB Nonconformance audit trail to ensure technical justification, supervisor acknowledgement, and authorization for performing or reporting the deviation.
- Level 1 & 2 Nonconformities which require a *QAC* workflow to be initiated. See the *ASCL QM* for more information

### 14.2 CORRECTIVE ACTION

The Nonconformance Form or QAC shall include:

- A description of the non-conformance,
- the identification (when possible) of the cause(s) of the nonconformity,
- corrective actions taken with time frames (where applicable),
- Preventive measures taken (where applicable) to minimize its reoccurrence.
- Corrective action plans shall be approved by the technical leader prior to implementation.
- The CODIS administrator shall be notified when the nonconformity impacts DNA records entered into CODIS.

#### 14.2.1 AUTHORITY & ACCOUNTABILITY

The CODIS Administrator will be responsible to assure that discrepancies are acknowledged and corrective actions are documented according to the *ASCL QM*. Corrective actions shall not be implemented without the documented approval of the technical leader. Any deviation from the *CODIS QM* shall be approved by the CODIS Administrator and DNA TL. A log will be kept of each deviation from the *CODIS QM*. The CODIS Administrator will be notified of any corrective action.

## 15 AUDITS

Audits are an important aspect of the QA program. They are an independent review conducted to compare various aspect of the DNA laboratory's performance with a standard for that performance. The audits are not punitive in nature, but are intended to provide management with an evaluation of the laboratory's performance in meeting its quality policies and objectives.

### 15.1 OVERALL REQUIREMENTS

The DNA laboratory shall be audited annually in accordance with these standards. The annual audits shall occur every calendar year and shall be at least six months and no more than 18 months apart.

### 15.2 EXTERNAL AUDIT REQUIREMENTS

At least once every two years, an external audit shall be conducted by one or more auditor(s) from a second agency(ies). At least one auditor shall be or have been an analyst previously qualified in the laboratory's current DNA technologies and platforms.

#### 15.2.1 PERSONNEL REVIEW

Each analyst, technical reviewer, casework CODIS administrator, and technical leader shall have his/her education, experience, and training qualifications evaluated and approved during two successive, separate external audits. Approval of an individual's education, experience, and training qualifications shall be documented in the Audit Document.

An analyst or technical reviewer that receives additional qualification in an additional technology(ies), typing test kit(s), or platform(s) shall have the additional training qualifications evaluated and approved during one external audit. Approval of additional training qualifications shall be documented in the Audit Document.

#### 15.2.2 VALIDATION EVALUATION

Each validation study shall be evaluated and approved during one external audit. Approved validation studies shall be documented in the Audit Document.

### 15.3 INTERNAL AUDIT REQUIREMENTS

Internal audits shall be conducted by an audit team that includes at least one auditor. At least one audit team member shall be or have been an analyst previously qualified in the DNA laboratory's current DNA technologies and platforms.

## 15.4 QAS REQUIREMENT

Internal and external audits shall be conducted utilizing the FBI DNA QAS Audit Document in effect at the time of the audit.

## 15.5 DNA TL REVIEW

Internal and external audit documentation and, if applicable, corrective action(s) shall be reviewed by the technical leader to ensure that findings, if any, were appropriately addressed and this review shall be documented.

### 15.5.1 CODIS ADMINISTRATOR NOTIFICATION

Internal and external audit documentation, and if applicable, corrective action(s) shall be provided to the CODIS administrator.

### 15.5.2 NDIS CUSTODIAN NOTIFICATION

For NDIS participating laboratories, all external audit documentation and laboratory responses shall be provided to the FBI within 30 days of laboratory receipt of the Audit Document or report.

## 15.6 DOCUMENT RETENTION

Internal and external audit documentation shall be retained and available for inspection during subsequent audits.

## 16 PROFESSIONAL DEVELOPMENT

### CONTINUING EDUCATION AND DOCUMENTATION

The technical leader, CODIS administrator, analyst(s), and technical reviewers shall stay abreast of topics relevant to the field of forensic DNA analysis and Human Identification Databasing by attending seminars, courses, professional meetings, or other documented lectures or classes in relevant subject areas for a minimum of eight cumulative hours each calendar year.

The continuing education hours shall be documented through the *DNA/CODIS TL Continuing Education Approval* workflow in Qualtrax. Attendance at a regional, national, or international conference with content including topics relevant to the field of forensic DNA analysis and Human Identification Databasing shall be deemed to provide a minimum of eight hours of continuing education. Documentation of attendance such as certificates, attendance lists, or travel documentation shall be maintained in the QTx Personnel tab and are the responsibility of the individual.

With the exception of approved conferences, the laboratory shall maintain documentation of content through a mechanism such as agenda/syllabus, record of presentation content, or the curriculum vitae of the presenter. These records shall be maintained in the QTx Personnel tab and are the responsibility of the individual.

CEUs based on electronic delivery shall be subject to the approval of the DNA TL. Approved content can be found in the *CEU List.xlsm* file on the FB Drive. These completed forms shall be uploaded to the workflow along with any certificate or other documentation to demonstrate completion of the training. Approval for CEUs without prior approval can be requested through the same Qualtrax workflow. Any internal continuing education must be documented, including title, CV of presenter, attendance, dates, and notes or records of the presentation. Records of training should also be maintained in the QTx Personnel tab and are the responsibility of the individual. The TL will ensure that each analyst has a planned activity for meeting the 8 hour minimum requirement by mid-year. The TL will be responsible for an annual review of all DNA personnel training to ensure quality and completeness of continuing education.

### REVIEW OF SCIENTIFIC LITERATURE

The laboratory has requirement for the periodic review of scientific literature that documents the analysts' ongoing reading of scientific literature on a quarterly basis. An excel sheet located on the shared drive will be filled out to document the article read. Beginning Q1 of 2024, performance for each individual may be recorded via Qualtrax Training workflow initiated by the TL.

Access to current FSI:Genetics is available in the Literature folder of the FB Drive. Requests for other journal articles can be directed to the Assistant Director or DNA TL via the section supervisor. Articles of particular interest can be shared via the literature folder within the DNA/CODIS discipline on Qualtrax. The DNA sections are also in possession of several common DNA Typing texts.

## TESTIMONY REVIEW

The CODIS section shall follow the ASCL QM policy 7.7.1.2.3 regarding testimony review. The testimony review shall be documented on a *Testimony Evaluation Form* (ASCL-FORM-04) and be provided to the testifying individual. Any deficiency and subsequent corrective actions, as applicable, shall be documented per ASCL policy.

All qualified analysts shall have their testimony technically reviewed by a technically competent and authorized reviewer at least once per ANAB audit cycle, as practicable. This review may be via direct observation or review of transcripts, or other method as approved by the supervisor. Technically competent reviewers include: DNA or CODIS supervisors, DNA Technical Leader, or other fully authorized DNA analysts.

For years in which a technical review of testimony is not performed for an analyst, a review by direct observation by court or other personnel will be performed, as practicable. This review shall also be documented on the *Testimony Evaluation Form*.

## 17 OUTSOURCING

### 17.1 QAS COMPLIANCE

The ASCL will only outsource to a vendor laboratory that complies with Quality Assurance Standards and accreditation requirements of federal law and can provide documentation of the compliance. The accreditation documentation will be stored in Qualtrax. All vendor laboratories must also comply with standards set forth in the *ASCL QM*. Prior to any outsourcing of data generation, the DNA Technical Leader will document the approval of the technical specifications.

### 17.2 PRIOR APPROVAL

The DNA TL shall approve the technical specifications of the outsourcing agreement between the ASCL and any vendor laboratory before it is awarded. If a vendor laboratory is performing forensic DNA analysis on behalf of a law enforcement agency or other entity for the purposes of ownership by the ASCL, the vendor laboratory shall not initiate analysis until approval has been obtained from the DNA TL.

For instances, such as court ordered testing, where the ASCL is requested to take ownership and no outsourcing agreement exists, the DNA TL shall document the following prior to acceptance of ownership of product(s) of forensic DNA analyses from the vendor laboratory:

- Approval of the CODIS administrator and written permission from the NDIS Custodian for any scenario that involves CODIS entry or searching;
- Approval of the technical specifications of testing;

- Conduct or review the documentation of an on-site visit of the vendor laboratory from within 18 months in accordance with DNA QM 17.4.2.

### 17.3 OWNERSHIP REVIEW

The data generated from samples that are outsourced by the ASCL may be technically and administratively reviewed by the vendor laboratory, or may be re-analyzed by a qualified, proficient DNA analyst in the methodology used by the vendor laboratory, depending on the approved technical specifications and specific scenario of the case. The re-analysis and/or CODIS eligibility review will give ownership of the data to the analyst performing the task and shall verify specimen eligibility and the correct specimen category prior to entry into CODIS. The ownership review shall be documented on [DNA-FORM-43](#) and shall include the following elements:

- A review of all DNA types that the ASCL will take ownership of to verify that they are supported by the raw and/or analyzed data (electropherograms or images).
- A review of all associated analytical controls, internal size standards and allelic ladders to verify that the expected results were obtained.
- A review of the final report (if provided) to verify that the results/conclusions are supported by the data.
- If samples are to be entered into CODIS, verification of the DNA types, eligibility, and the correct specimen category by a current CODIS user.

If re-analyzed, a new report will be generated by the ASCL analyst, and the data must be technically reviewed prior to being searched in the CODIS system. If no reanalysis is performed, the vendor laboratory report will be forwarded to the requesting agency and any associated CODIS entry will be reported by the ASCL in a new DNA request. After CODIS entry, the casefile will then get an administrative review before the report can be released.

### 17.4 ON-SITE VISIT

The DNA Technical Leader or his/her designee will conduct an initial on-site visit to the vendor laboratory to assess analytical performance. If the contract extends beyond one year, an annual on-site visit will be required between 6- and 18-months. The laboratory may accept the findings of an on-site visit conducted by another NDIS participating laboratory in lieu of conducting an on-site visit in person. See [DNA-FORM-34](#) for the on-site visit documentation.

### 17.5 INTERLABORATORY EVIDENCE TRANSFER

If the ASCL finds it necessary to transfer evidence to an outside laboratory (e.g. FBI, UNT), an *Inter-Laboratory Evidence Transfer Form* (see [ASCL-FORM-07](#)) must be completed and entered into the case file. The Inter-Laboratory Evidence Form may be waived for items funded out of a grant and/or items under a contract. Any cost incurred by the laboratory must be approved by the Fiscal Officer. If there will be a cost incurred to the customer, the customer must be notified and approve

of the arrangement. This must be documented and placed in the case file. The Quality Assurance Manager maintains a register of all subcontractors used for testing and/or calibrations and maintains documentation of their competency and compliance.

The Arkansas State Crime Laboratory can enter into CODIS outsourced data for other agencies. Data may only be entered into CODIS if the following criteria are met:

- All requirements of Standard 17 from the QAS Document are fulfilled
- A letter from the laboratory the case originated stating:
  - NDIS eligibility
  - All potential court cost will be covered by the originating laboratory
  - ASCL has permission to enter the case into the CODIS system
  - A brief synopsis of the case
- Contact between the ASCL and the originating state's CODIS Administrator should be made and documented.

A casefile in JusticeTrax may then be set up to electronically maintain the data. A review of all documents must occur prior to entering any data into CODIS. Once the data has been uploaded to CODIS a letter to the appropriate State CODIS Administrator (or applicable individual) should be mailed. All potential CODIS hit letters should be delivered to the appropriate CODIS State Administrator or applicable individual.

## 18 MISCELLANEOUS

### 18.1 SAFETY

All safety protocol and information is contained in the Arkansas State Crime Laboratory Health and Safety Manual (ASCL-DOC-08). The safety manual covers general laboratory safety. The Arkansas State Crime Laboratory tries to maintain a safe working environment. It is the responsibility of the DNA/CODIS staff to familiarize themselves with all exit doors, safety showers and fire extinguishers. The crime lab provides training in chemical hygiene, blood borne pathogens, CPR, and first aid to all of the employees.

### 18.2 DNA LABORATORY CONTAMINATION PREVENTION

The Arkansas State Crime Laboratory Forensic DNA and CODIS Databasing sections may share several laboratory spaces for analytical processes. In an effort to ensure that all Databasing and Forensic DNA staff consistently employ work habits that minimize the risk of DNA contamination — either sample to sample or laboratory staff to sample— the following list of basic preventive measures will be employed as necessary by analysts when performing DNA analysis. Some of the measures listed below may not be practicable or relevant at all times, but the principles of contamination prevention will apply. Shared analytical spaces include:

Cleanrooms:	301 (SAK Room), 309 (Window Room), 311 (Windowless Room), 317 (Bone Room), and 272 (CODIS Clean)
Post-PCR rooms:	312 (DNA Post), 272 (CODIS Post)
Other rooms:	313 (Reagent Room), 272 (CODIS Prep)

#### 18.2.1 PERSONAL PROTECTIVE EQUIPMENT:

Lab coats with cuffs that can be covered with disposable gloves will be worn in Cleanrooms.

Lab coats will be changed and laundered on a regular basis. If the risk of contamination is heightened based upon the activities that have occurred while wearing a lab coat, it should be replaced with a newly laundered one. Examples of when to change a lab coat include but are not limited to: after the processing of a case consisting of several items of bloody clothing or after an analyst knows that the exterior surfaces of a lab coat may have become contaminated with DNA, such as after a sneeze.

Lab coats will be worn when collecting biohazardous waste for disposal. They will be decontaminated properly when the activity is complete.

Face masks will be used for all analytical activities in the Cleanroom spaces. Face masks will be worn such that the nose and mouth will be completely covered. Facemasks and other personal effects such as glasses should not be handled directly during the course of evidence examination and special care should be taken to avoid the use of gloved hands to manipulate such items.

Personnel should avoid talking over evidence during evidence screening and/or sampling.

Personnel should only touch items of evidence with fresh, clean gloves.

Prior to use, personnel should visually inspect gloves for defects; if any damage is observed before or during examination of evidence, new gloves should be used.

Gloves should be changed with high frequency. Generally, if an analyst cannot recall when they last put on fresh gloves, the gloves should be changed.

Personnel should not use gloves that have come in contact with evidence to also touch computer keyboards, iPads, pens, pencils, etc., unless those items are specifically designated for use during the analytical process.

### **18.2.2 TOOLS AND REAGENTS**

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Computers in the laboratory spaces will be decontaminated regularly by wiping mice and keyboards (or keyboard covers) with a bleach-saturated towel. A “gloves-off” policy for all shared computers in laboratory spaces will be implemented.

For electronic equipment shared between administrative and analytical workspaces, special care should be taken to avoid cross contamination. At a minimum, a washable cover of sufficient size to cover input controls, such as touchscreen or keys and mouse pad, should be used.

“Analytical-use only” pens, pencils, markers, rulers, etc. will be used during evidence examination. When not in use, they should be stored in a location that is less susceptible to contamination. These items should be decontaminated on a regular basis.

Water dropper bottles used during analysis should only be handled with gloves and should be stored in a location that is less susceptible to contamination. The bottles should be regularly decontaminated and refreshed with clean, autoclaved deionized water. Water dropper bottles shall not leave the Cleanroom spaces except for sterilization. In addition, the analyst should avoid touching the swab with the dropper bottles.

Clean gloves shall be used when handling swab packaging when the swabs will be used for DNA sample collection. Swab heads should not touch anything other than the item being swabbed.

### **18.2.3 DECONTAMINATION**

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A dilute bleach solution (or product containing bleach) will be used to clean workspaces and tools prior to evidence processing. Alcohol (ethanol and isopropanol are both acceptable) or clean deionized water should be used to rinse residual bleach from those items that will come in direct contact with the evidence. Commercial disinfectant products (such as Clorox wipes) will not be used for the purposes of decontamination unless they contain bleach or are designed specifically for laboratory surface decontamination.

Analysts will adopt a “bleach-in-bleach-out” approach. Prior to initiating evidence screening and/or sampling at the beginning of a given work day, work surface(s) and tools will be decontaminated. Additional decontamination will continue as appropriate throughout the day. A final decontamination should occur at the close of the work-session.

A regular workspace decontamination schedule will be established. This will include benches, cabinets, drawer pulls, computer keyboards, mice, exteriors of reagent bottles, cameras, etc.

#### **18.2.4 GENERAL EVIDENCE HANDLING:**

An enclosed biohood must be available in every Cleanroom. Analysts should use these hoods for the processing of liquid blood or other biohazardous samples.

Clean paper or other bench covering shall be used under items of evidence. Paper or other covering material will be changed between items. Bench covering material should not be stored uncovered outside of the Cleanroom workspaces.

Evidence should not be placed directly on top of external packaging and or in a location that will come into direct contact with external packaging. Evidence packaging is often handled without gloves and cross-contamination from the packaging to the evidence may occur.

### **18.3 COMPLAINTS**

See the *ASCL QM* section 7.9 for the lab wide policy for addressing Complaints

### **18.4 MANUALS AND DOCUMENTS**

All controlled documents and manuals are maintained on Qualtrax. These are the official copies and are approved by the appropriate personnel.

The CODIS Quality Manual must be reviewed and approved by the CODIS Administrator, DNA Casework Supervisor, DNA Technical Leader, QA Manager, Assistant Director and Executive Director. Internally generated documents should be prepared by personnel with adequate expertise in the subject. Individuals may print hardcopies of internal documents as needed for personal use; however, these copies are unofficial.

External documents, software, or any other document in which a particular revision/version is required, will be referenced in the appropriate internally generated controlled document (i.e. Quality Manuals, Training Manuals, etc.) or as an attachment to the appropriate document. The reference must identify the current revision/version and location of the document. These documents will be available at each location where related work is conducted.

Documents shall be available at all locations where operations essential to the effective functioning of the laboratory are performed (i.e. annex building, illicit lab scenes, etc.).

Employees will destroy outdated documents upon receiving updated documents. It is the employee's responsibility to verify that they are using the current revision of any document.

Internally generated documents should be prepared by personnel with adequate expertise in the subject. Individuals may print hardcopies of internal documents as needed for personal use; however, these copies are unofficial.

The Preparer of the document is responsible for:

- Preparing the document in the proper format.
- Addressing or resolving comments from reviewers.
- Submitting the document in Qualtrax.

The CODIS Administrator and Technical Leader are responsible for:

- Ensuring that all CODIS documents have been reviewed annually (refer the *ASCL Quality Manual*)  
Reviewing and approving all discipline specific controlled documents.
- Ensuring that the documents are scientifically suitable for issue.
- Ensuring that the documents contain the required quality assurance elements (i.e., QC, measurement of uncertainty, traceability)

Revised documents are subject to the same review, approval, documentation and issuance requirements of the original document.

Case-related discussions with the customer documented on an *Agency Contact Form* (ASCL-FORM-06), e-mail, or equivalent document.

## 18.5 CODIS HIT COUNTING

The effectiveness of CODIS can be measured in the number of crimes the Hits solve. Thus an accurate measure of hit counting is important. There is a two track metrics involved in hit counting. The primary metric is the number of investigations aided by CODIS. The second metric is the number of hits made by CODIS. Counting the number of Hits gives laboratories credit for their investment in CODIS and indirectly shows the value CODIS adds to fighting crime. The best measurement of CODIS' value to society is the number of criminal investigations it assists.

### MATCH

A match occurs when CODIS makes an association between two or more DNA profiles and a confirmation process is started by designated laboratory personnel from each affected laboratory.

### HIT

A hit occurs when a confirmed or verified match aids in an investigation and one or more of the case(s) involved in the match is unsolved.

### HIT COUNTING RULES

**Rule #1:** The level in the CODIS hierarchy (LDIS, SDIS, NDIS) at which hit occurs get credit for the hit. The following metrics reflects the investment in and activity of the different levels of CODIS.

**Rule #2:** An offender hit disposition takes precedence over a forensic hit disposition when the hits occur during the same search. In the event where an unsolved case profile matches a solved case previously identified as an offender hit, the hit disposition will be "Offender Hit" for that hit and all

subsequent hits. Previous forensic hits will not be reclassified when they match an offender. Since offender hit dispositions take precedence, new forensic to forensic matches shall be dispositioned as “Investigative Information”.

**Rule #3:** A hit is counted for each unique set of matching profiles where at least one of the matching profiles is from an unsolved case. Since it takes two samples for a hit to occur, the total number of hits equals the total number of samples minus one (N-1)

**Rule #4:** An investigation may be aided only once. Count the number of actual investigations CODIS has aided and not the number of times CODIS has assisted a particular investigation or investigations. This reflects a direct one-to-one relationship between the metric and cases involved. As a point of clarification, an investigation with profiles from more than one source may be aided only once. Laboratories may only count their own investigations as having been aided.

**Rule #5:** A single hit may aid more than one investigation. A single hit may associate several separate cases. Laboratories may claim credit for all of the cases aided within their jurisdiction.

**Rule #6:** An investigation aided must be associated with a hit. An investigation is aided if CODIS provides value to the investigation.

**Rule #7:** Only investigation of unsolved cases may be aided.

## MISSING PERSONS

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### MATCHES

For searches involving missing persons or unidentified human (remains), some of the results can be defined as matches, while others are considered to be associations. When a search result involves profiles that may have originated from the sample individual, the term match may be used. In most instances for missing person ‘hits’, the appropriate disposition is ID pending, and the metric reported to NDIS by the laboratory responsible for the unidentified human (remain) or missing person is a Putative Identification. The laboratory responsible for the other samples may count one Identification Aided. If unidentified human (remains) match to a forensic unknown, the laboratory responsible for hit forensic sample may report the Identification Aided. The remains subsequently match to an offender that may result in a Putative Identification but no further Identifications Aided shall be counted.

It is important to note that the disposition and metric do not conclusively state that an Identification has been made. Only the competent legal authority in each jurisdiction can issue a death certificate confirming the identity of the unidentified human (remains). It is the responsibility of the Arkansas State Crime Laboratory Medical Examiner’s Office to notify the CODIS Administrator that this has occurred. The disposition can then be updated to ID Confirmed and the metric updated to a Confirmed Identification. The changes do not need to be reported to NDIS, as Putative and Confirmed Identification will be grouped together.

### ASSOCIATIONS

When a search in CODIS involves the Relatives of Missing Person or Pedigree Tree Indexes, the result is not considered to be a match. In these cases, the target and candidate profiles are not believed to have originated from a common source. Instead, the search indicated that the unidentified human (remains) may be those of the missing person sought by the relatives(s). For this reason, the term “association” is used. Associations are produced by using an Identity Search for single family references. These results will appear in match manager. Pedigree Tree Searches produce a ranked list of associations of unidentified remains to each Pedigree. A confirmed association may still be considered a ‘hit’ and shall be dispositioned as ID Pending. The rules for counting and reporting these hits are the same as matches.

### MISSING PERSON HIT COUNTING RULES

The following rules applied only to hits, not matches or associations:

**Rule #1:** The level in the CODIS hierarchy (LDIS, SDIS, NDIS) at which hit occurs get credit for the hit. The following metrics reflects the investment in and activity of the different levels of CODIS.

**Rule #2:** A hit involving a direct match takes precedence over a hit arising from an association when the hit occurs during the same search. If more than one hit involving a direct match occurs during the same search, when an unidentified human (remains) hit is to an offender profile, it takes precedence over an unidentified human (remains) hit to a forensic profile. Any subsequent hits shall be dispositioned as Investigative Information.

**Rule #3:** A hit is counted for each unique set of unidentified human (remains) entered into CODIS. If a single investigation involves two sets of remains, then there may be up to two Putative Identifications and two Identifications Aided. Note that this is different that Rule #4 for Forensic Hits.

**Rule #4:** An Identification may be aided only once. Count the number of actual identifications CODIS has aided not the number of times CODIS has assisted a particular identification or identifications. This reflects a direct one-to-one relationship between the metric and cases involved.

**Rule #5:** A single hit may aid more than one Identification. A single hit may associate several separate cases. Laboratories may claim credit for all of the cases aided within their jurisdiction.

**Rule #6:** An identification aided must be associated with a hit. An investigation is aided if CODIS provided value to the investigation.

### REPORT CODIS HIT STATISTICS

Hit statistics should be reported to NDIS before the 10<sup>th</sup> of every month. NDIS shall total the number of national hits and shall not calculate interstate (NDIS) forensic hits by state. At the state and local level, states may continue to track the number of NDIS hits they participated in as AH<sub>N</sub>, DH<sub>N</sub>, FH<sub>N</sub> LH<sub>N</sub> and OH<sub>N</sub> as described below.

The following methods will be used to minimize the duplicate counting of national hits:

- For offender hits, the Casework Laboratory will report the number of investigations aided and the Offender Laboratory will report the number of offender hits
- For forensic hits where one case is solved, the Laboratory with the unsolved case will report the number of investigations aided and the Laboratory with the solved case will report the forensic hit
- For forensic hits where neither case is solved, each Laboratory will report the number of investigations aided and Laboratories will agree on who reports the hit to NDIS.

The following methods should be used to report hits:

- AH<sub>S</sub>: Arrestee hits within the state (match detected by SDIS)
- AH<sub>N</sub>: Arrestee hits at national (match detected by NDIS)
- DH<sub>S</sub>: Detainee hits within the state (match detected by SDIS)
- DH<sub>N</sub>: Detainee hits at national (match detected by NDIS)
- FH<sub>S</sub>: Forensic hits with in the state (sum of FH found by SDIS)
- FH<sub>N</sub>: Forensic hits at national (match detected by NDIS)
- IA: Investigations aided
- IC<sub>S</sub>: Confirmed Identifications within the state (sum of Identifications found by SDIS)
- IC<sub>N</sub>: Confirmed Identifications within the state (sum of Identifications found by NDIS)
- ID: Identifications Aided
- LH<sub>S</sub>: Legal Index hits within the state (match detected by SDIS)
- LH<sub>N</sub>: Legal Index hits within the state (match detected by NDIS)
- OH<sub>S</sub>: Convicted Offender hits within the state (match detected by SDIS)
- OH<sub>N</sub>: Convicted Offender hits at national (match detected by NDIS)
- PI<sub>S</sub>: Putative Identifications within the state (sum of Identifications found by SDIS)
- PI<sub>N</sub>: Putative Identifications at NDIS (Identification detected by NDIS)

**Note: All relevant NDIS Procedures are followed at the Arkansas State Crime Laboratory.**

## 19 APPENDIX A – STANDARD OPERATING PROCEDURES

*Note: Due to the high variety of DNA samples submitted, the sampling plan for each extraction type is at best a recommendation based on typical amounts of DNA obtained from each sample type in a typical scenario under optimal conditions. DNA samples are not homogenous and the sampling method will be considered non-statistical. Therefore, Forensic DNA findings may only be applied to the portion of the sample consumed.*

In some circumstances, deviation in methods and procedures may be necessary. At such times the *Deviations/Non-Conformance Form* (CODIS-FORM-17) must be completed and signed by the CODIS Administrator and/or the DNA Technical Leader to ensure the proposed deviation is within validated guidelines.

### 19.1 DIRECT REFERENCE STANDARD SAMPLES

Direct reference standards (DRS) are those that are collected directly from the person for whom a profile is desired in the Database. As Convicted Offender and Arrestee Samples are processed in the CODIS Section, the staff must check to ensure that the sample quality is adequate, that there is accurate and sufficient offender/arrestee biographical information provided and that a qualifying violation is met. A new sample may be requested if the sample quality is not adequate. The sample will not be processed if a qualifying violation is not met.

#### 19.1.1 INTAKE OF CONVICTED OFFENDER / ARRESTEE SAMPLES (BLOOD SAMPLES)

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- a) Database envelopes are released from Evidence Receiving to the CODIS Section.
- b) Envelopes are opened in a clean area. Gloves will be worn during the processing of any biological sample. A kit bar code is assigned to the sample (\*Blood kits do not have a kit bar code available with the kit so a supply of kit bar codes is available to assign to any kit received without a kit bar code on the kit to allow the sample to be processed through the STACS-DB workflow). The kit bar code is scanned in the Kit Receipt module with the date the kit was received at the lab.
- c) The kit is moved to the Reagent Room and the kit bar code is scanned in the Submission Check-In module to assign the collection type, specimen nature, and ensure the name and signature match on the card (\*If not, the sample is marked "Pending Reject" and reason noted). A STACS bar code is generated and five labels are printed. Each blood sample is halved. One half of the blood stain card is placed in a coin envelope to be analyzed and the other half is to be retained for confirmation purposes. The STACS bar code labels are placed on the outside of the coin envelope, the inside of the coin envelope (loose), the database card/upper left corner on fingerprint side, the database card/inside on "Place Barcode Here", and on the cut sample.

- d) The coin envelope is stored in the Reagent Room CODIS locker in numerical order of the STACS bar code. The database card is taken to CODIS support staff for data entry.
- e) In the Data Entry Worklist module, the STACS bar code on the card will be scanned, opening the Data Entry screen for the associated submission. All convicted offender / arrestee data on the database card is carefully entered into the Data Entry screen. \*If the entered data is a duplicate, a notification will appear to verify information and link the duplicate to the original submission. (Any missing offender / arrestee information will be marked as “Pending Reject” and reason noted. The sample will go to the Pending Rejects module and information can be obtained through phone call, email, or searched using ACIC (see ACIC Access 6.2.1.4), eOMIS or any other available software.)
- f) Once all data is entered, the sample will be listed in the Submission Scanning module for the card image to be scanned and attached to the Submission Files.
- g) The database cards (the half with the offender’s information) are boxed numerically for storage.
- h) After punching, the coin envelopes are removed from the Reagent Room CODIS locker and filed with the original database cards.

NOTE: If inadequate sample amount or inadequate information is given on the database card, a phone call can be made to the submitting officer or his/her supervisor and documented in the Pending Rejects module.

### **19.1.2 INTAKE OF CONVICTED OFFENDER / ARRESTEE SAMPLES (BUCCAL SAMPLES)**

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- a) Database envelopes are released from Evidence Receiving to the CODIS Section.
- b) Database envelopes are opened in the CODIS office. The kit bar code on the information card is scanned in the Kit Receipt module with the date the kit was received at the lab. Both bar codes (on the information card and transport pouch) are checked to ensure they match.
- c) The information card and transport pouch are kept together and moved to the Reagent Room. The transport pouch is opened for the kit bar code on the stick to be compared to the information card and transport pouch kit bar codes by scanning all 3 bar codes in the BodeBarcodeChecker.v.1.0.xlsm (located on \\davinci\Section\ForensicBiology\CODIS\CODIS Images\Barcode\_Check) and ensuring names match. If the 3 kit bar codes do not match or there is a name mismatch, the sample is brought to the CODIS Administrator before scanning through STACS-DB.
- d) If all kit bar codes and names match, the kit bar code is scanned in STACS-DB in the Submission Check-In module to assign the collection type and specimen nature (\*If names, signatures, or kit bar codes do not match, the sample is marked “Pending Reject” and reason noted). A STACS bar code is generated and five labels are printed. The STACS bar code labels are placed on the

front and back of the information card, the outside of the transport pouch, and on the sample collector (The additional bar code can be discarded).

- e) The transport pouch is stored in the Reagent Room CODIS locker in numerical order of the STACS bar code. The information card is taken to CODIS support staff for data entry.
- f) In the Data Entry Worklist module, the STACS bar code on the card will be scanned, opening the Data Entry screen for the associated submission. All convicted offender / arrestee data on the database card is carefully entered into the Data Entry screen. \*If the entered data is a duplicate, a notification will appear to verify information and link the duplicate to the original submission. (Any missing offender / arrestee information will be marked as "Pending Reject" and reason noted. The sample will go to the Pending Rejects module and information can be obtained through phone call, email, or searched using ACIC (see ACIC Access 6.2.1.4), eOMIS or any other available software.)

NOTE: If inadequate sample amount or inadequate information is given on the database card, a phone call can be made to the submitting officer or his/her supervisor and documented in the Pending Rejects module.

- g) Once all data is entered, the sample will be listed in the Submission Scanning module for the card image to be scanned and attached to the Submission Files.

NOTE: If sample is from the Remote Collection module by Law Enforcement Agencies, the sample will not appear on the Data Entry Worklist module after Submission Check-In. It will appear on the Submission Scanning module.

- h) DNA Collectors are punched and placed in Long Term Storage.

### **19.1.3 INTAKE OF ARRESTEE SAMPLES WITH SUBMITTED CASES**

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- a) If arrestee samples are submitted to the CODIS Section with case numbers referencing specific cases in which the arrest was made, the sample can be processed for both the database and for the DNA Casework Section. The sample can also be processed if documentation from the submitting agency or the prosecutor requesting the Arrestee sample be referenced to the specific case the individual was arrested. In order for the sample to be used for both sections the qualifying violation the individual was sampled for must also be the case submitted to the DNA Section.
- b) Prior to use in Casework an 'Arrestee Confirmation Sheet' (CODIS-Form-43) must be completed. Once the 'Arrestee Confirmation Sheet' is completed it should be scanned in JusticeTrax along with biographical information.
- c) An 'Arrestee' Request in JusticeTrax must be created and canceled to inform an analyst that a sample related to his/her case is in the CODIS Section.

- d) A duplicate sample is not re-run in the CODIS Section. DNA Casework can work the sample if necessary and retain it with the appropriate evidence. It is noted that this can be changed on a case-by-case basis upon approval of the CODIS Administrator and/or the Casework Supervisor. If the duplicate sample is transferred to the casework analyst, the Chain of Custody for Arrestees Report can be printed from the Reports module in STACS.
- e) If an arrestee sample that is referenced to an ASCL case number is given to the CODIS Section, and it is deemed to have a non-qualifying violation, the sample can be stored for the DNA Casework Section.
- f) All completed 'Arrestee Confirmation Sheets' are stored in Submission Files in STACS-DB. Any additional hits from the arrestee sample will need to have the DNA profile confirmed.
- g) All arrestee profiles (autosomal and Y-STR) should be developed and entered into Specimen Manager by a CODIS Analyst for the Casework Analyst to obtain. It is noted that this can be changed on a case-by-case basis upon approval of the CODIS Administrator and/or Casework Supervisor.

#### **19.1.4 INTAKE OF MEDICAL EXAMINER'S BLOOD SAMPLES**

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The CODIS Section processes most blood samples from the Medical Examiner's (ME) Office. The samples are entered in the Data Entry module to assign and generate a STACS bar code for processing through STACS modules. The lab protocol for these samples is the same as the protocol for offender blood samples. It is not recommended that ME samples are processed on the same direct amplification plate as convicted offender and arrestee samples.

#### **19.1.5 ACIC ACCESS**

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Prior to obtaining access to the Arkansas Criminal Information Center (ACIC), an individual must attend a training class and be issued a unique CSN (Central System Number) and certification. The training gives options to access different data depending on the "known" information available.

#### **19.1.6 TO ACCESS CRIMINAL HISTORY OF AN OFFENDER:**

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- a) LOGON
- b) After confirmation of "Connection Successful" and "LOGON Accepted" information can be obtained
- c) F4: Query Name; can be accessed when only the name is known
- d) F5: The agency information will be automatically filled in. Under "PERSON DATA" enter all available information for the offender
- e) F6: REQUESTING OFFICER (OFC) is the name of the individual requesting the data (last name, first initial). Fill in the "OPERATOR DATA" (OPR) the same as OFC data.
- f) Use the "+" key to enter data (not "enter" key)

- g) F7: Queries with only the SID (State ID) number
  - h) F2: LOGOFF
- NOTE: Most information is listed under the F5 option

## 19.2 MISSING PERSON'S SAMPLES/UNIDENTIFIED REMAINS

### 19.2.1 DNA SOURCES

The best reference sample for a missing person is a Direct Reference Sample (DRS). These should be obtained whenever possible. There are many different sources for DNA testing all of which could be appropriate for identifying a missing person. Medical specimens, such as bone marrow donor sample, blood sample, PKU cards taken at birth or biopsy taken from medical tests or procedures are the most useful types of specimens. A good DNA sample can also be taken from the victim's personal items such as a toothbrush or hairbrush, but it is important that the items were used only by the victim. Prior to upload to CODIS, the validity of a DRS should be established by comparison to other known references (ie-parents, children).

If a DRS is not possible, DNA from close relatives (biological parent, offspring, and sibling) can be collected. Other relatives such as half-sibling, cousin, aunts and uncles can also be collected. Ideally, samples from first order relatives are most suitable. If a DRS is not available, a minimum of two family references should be obtained when possible. These family reference samples should be documented in the creation of a Pedigree Tree. Obtaining as much metadata as possible regarding the missing person and/or unidentified remains is also important for CODIS.

### 19.2.2 DNA TESTING ON MISSING PERSON/UNIDENTIFIED CASES

Any missing person case that will be entered into CODIS at the Arkansas State Crime Laboratory should be analyzed using autosomal and Y-STRs as appropriate. All samples should be followed according to established guidelines set forth in the quality manuals. Any DRS should be uploaded into CODIS as a Missing Person or a Deduced Missing Person as appropriate. Remains should be uploaded as Unidentified Human Remains.

Family reference samples will be typed using at a minimum autosomal testing. If appropriate, Y-STRs should be performed at the Arkansas State Crime Laboratory. These samples should be uploaded into the appropriate specimen category and a Pedigree Tree created. The lack of a second technology does not prevent the inclusion of samples in CODIS. However, a second (and third, where applicable) technology will ensure the most robust search possible.

All family reference samples must have a consent form prior to entry in CODIS. This ensures that the relative is aware his/her sample is going to be placed in the database for searching purposes. Accordingly, the DNA profile of a relative of a missing person shall be removed from CODIS under the following circumstances: (1) if the missing person corresponding to this reference sample has been identified; (2) if it is determined that the individual voluntarily providing the reference

sample is not related to the missing person; (3) at the request of the individual who voluntarily provided the reference sample. If the missing person is identified to a set of partial remains, the relative samples may remain in CODIS at the discretion of the laboratory to facilitate identification of other remains.

If additional technologies are needed that are not available at the Arkansas State Crime Laboratory, a CMF file can be exported with all technologies that have been performed and sent to an NDIS participating laboratory that has the ability to complete the desired testing. The second laboratory will conduct additional testing as needed on the samples and append the results to the samples stored in CODIS.

Unidentified remains and family reference samples will be submitted to the DNA casework section and if additional technologies are needed, the CODIS administrator will follow the instructions of the second laboratory for the submission of the samples. The second laboratory will conduct additional testing as needed on the family reference samples and/or unidentified remains and append the results to the samples stored in CODIS. Any reports received from the second laboratory will be stored in the case file in JusticeTrax.

### **19.2.3 MISSING PERSON NCIC AND NAMUS INFORMATION**

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DNA profiles entered into CODIS' "Missing Person," "Relatives of Missing Person" or "Unidentified Remains" Indexes should reference the record in the NCIC Missing Person File and the DNA related fields in NamUs, whenever possible. The CODIS section should work in conjunction with the ME office and submitting agency to ensure that the information regarding DNA testing is kept current.

### **19.2.4 SEARCHING PARAMETERS**

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Missing Persons, Relatives of Missing Persons, and Unidentified Human Remains Indexes are auto-searched weekly at SDIS and monthly at NDIS. For a complete list of search parameters, please see the AutoSearcher program.

## **19.3 SAMPLE PROCESSING PROTOCOLS**

### **19.3.1 BSD PUNCH**

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NOTE: The humidity level can be low at the Arkansas State Crime Laboratory especially in the winter season. A low humidity level can make punching using the BSD punch difficult. If this occurs the humidifier can be used to increase the humidity in the DNA pre-amplification room. It is recommended to use the humidifier if the humidity falls below 25% prior to using the BSD punch. The humidity levels will be logged on CODIS-Form-19 and stored in the DNA QC Images folder of the section shared drive.

a) Making Plates: Plate Create module in STACS-DB

- 1) Select the plate type.
- 2) Auto Select samples to add to the plate.
- 3) Scan envelope bar codes for samples selected. Print plate bar code label
- 4) Scan plate bar code

b) Filling Plates: Punch module in STACS-DB

NOTE: Buccal plates are processed in the Plate Preparation module prior to this step (See 6.2.2)

- 1) Scan BSD instrument bar code and scan plate bar code and create input file.
- 2) BSD software will open.
- 3) Click 'Continue' when button appears.
- 4) Click 'Continue' at next screen.
- 5) Select appropriate plate in left hand list. Only the plate you want should be check marked.
- 6) Click 'Continue'.
- 7) Click 'Continue'
- 8) Click cursor in bar code area and scan plate bar code and click 'Accept'
- 9) For cleaning plate, click 'Continue'
- 10) Start scanning the sample bar codes and punching the appropriate samples.
- 11) If a bar code is entered manually, click 'Continue with manually entered bar code'.
- 12) After last spot is punched, close out of BSD software program. Click 'All Spots Present' on pop up screen.
- 13) Back in STACS, click 'Yes" to create BSD output file.

### 19.3.2 MANUAL SAMPLING

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Samples being processed for Autosomal STR testing can be extracted, quantitated and amplified using the sample methods employed in the Casework Section. When these methods are used, the Casework SOP will be followed. This process is tracked in the Manual Worklist and Tracked Manual Processing modules in STACS-DB. Paperwork is stored on the ForensicBiology shared drive.

### 19.3.3 SAMPLING AND TECHNICAL RECORDS

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See the *ASCL Quality Assurance Manual* (ASCL-DOC-01) section 7.3.3 & 7.5.1 to find required Sampling and Examination Records. Due to Information Restrictions in the NDIS Operational Guidelines, the CODIS section does not store sampling or technical records in JusticeTrax. All sampling records are retained in STACS-DB and technical records may be stored in STACS-DB or on the ForensicBiology shared drive.

- a) Punched Bode Buccal and FTA Blood Powerplex Fusion 6C sampling records, technical records, and review records are maintained in STACS-DB

- b) Manually processed Powerplex Fusion 6C sampling records, technical records, and review records are maintained in STACS-DB with additional data stored on the ForensicBiology shared drive.
- c) Manually processed YfilerPlus sampling records, technical records, and review records are stored on the ForensicBiology shared drive.

## 19.4 QUANTITATION PROTOCOLS

The QIAGEN Investigator Quantiplex Pro (Quant Pro) system is used for the quantification of amplifiable total human and human male DNA in a sample. The DNA quantitation assay combines a target-specific human DNA assay, target-specific human male DNA assay, and an internal PCR control (IPC) assay. Quant Pro also includes a human DNA degradation assay.

When these methods are used, the Casework SOP will be followed (See DNA-DOC-01 19.5). The quantitation process is not tracked through STACS-DB modules. Paperwork is stored on the ForensicBiology shared drive.

## 19.5 AMPLIFICATION PROTOCOL

### 19.5.1 BACKGROUND

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#### 19.5.1.1 PREVIOUSLY USED POWERPLEX 16 HS

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The PowerPlex 16 HS System allows co-amplification and three-color detection of sixteen loci (15 STR loci and Amelogenin), including Penta E, D18S51, D21S11, TH01, D3S1358, FGA, TPOX, D8S1179, vWA, Amelogenin, Penta D, CSF1PO, D16S539, D7S820, D13S317 and D5S818. One primer for each of the Penta E, D18S51, D21S11, TH01 and D3S1358 loci is labeled with fluorescein (FL); one primer for each of the FGA, TPOX, D8S1179, vWA and Amelogenin loci is labeled with carboxytetramethylrhodamine (TMR); and one primer for each of the Penta D, CSF1PO, D16S539, D7S820, D13S317 and D5S818 loci is labeled with 6-carboxy-4',5'-dichloro-2',7'-dimethoxy-fluorescein (JOE). All sixteen loci are amplified simultaneously in a single tube and analyzed in a single injection or gel lane. It is noted that PowerPlex 16 HS is no longer in active use by the ASCL for Autosomal STR amplification or new sample HID analysis. See the Forensic DNA Section Quality Manual for more information about the PowerPlex 16 HS amplification system.

## 19.5.1.2 POWERPLEX FUSION 6C

The PowerPlex Fusion 6C System (a–h) is a 27-locus multiplex for human identification applications including forensic analysis, relationship testing and research use. This six-color system allows co-amplification and fluorescent detection of the 18 autosomal loci in the expanded CODIS core loci (CSF1PO, FGA, TH01, vWA, D1S1656, D2S1338, D2S441, D3S1358, D5S818, D7S820, D8S1179, D10S1248, D12S391, D13S317, D16S539, D18S51, D19S433 and D21S11) as well as Amelogenin and DYS391 for gender determination. The Penta D, Penta E, D22S1045, TPOX, SE33, DYS570 and DYS576 loci are included to increase discrimination. This extended panel of STR markers satisfies CODIS and ESS recommendations. (Table 2)

**Table 1.** The PowerPlex® Fusion 6C PCR Amplification System

STR Locus	Label	Chromosomal Location	Alleles in PowerPlex Fusion6C Allelic Ladder	Control 2800M
Amelogenin	FL-6C	Xp22.1-22.3 and Y	X, Y	X, Y
D3S1358	FL-6C	3p21.31 (45.557Mb)	9-20	17, 18
D1S1656	FL-6C	1q42 (228.972Mb)	9-14, 14.3, 15, 15.3, 16, 16.3, 17, 17.3, 18, 18.3, 19, 19.3, 20.3	12, 13
D2S441	FL-6C	2p14 (68.214Mb)	8-11, 11.3, 12-17	10, 14
D10S1248	FL-6C	10q26.3 (130.567Mb)	8-19	13, 15
D13S317	FL-6C	13q31.1 (81.62Mb)	5-17	9, 11
Penta E	FL-6C	15q26.2 (95.175Mb)	5-25	7, 14
D16S539	JOE-6C	16q24.1 (84.944Mb)	4-16	9, 13
D18S51	JOE-6C	18q21.33 (59.1Mb)	7-10, 10.2, 11-13, 13.2, 14-27	16, 18
D2S1338	JOE-6C	2q35 (218.705Mb)	10, 12, 14-28	22, 25
CSF1PO	JOE-6C	5q33.1 (149.436Mb)	5-16	12, 12
Penta D	JOE-6C	21q22.3 (43.88Mb)	2.2, 3.2, 5-17	12, 13
TH01	TMR-6C	11p15.5 (2.149Mb)	3-9, 9.3, 10-11, 13.3	6, 9.3
vWA	TMR-6C	12p13.31 (5.963Mb)	10-24	16, 19
D21S11	TMR-6C	21q21.1 (19.476Mb)	24, 24.2, 25, 25.2, 26-28, 28.2, 29, 29.2, 30, 30.2, 31, 31.2, 32, 32.2, 33, 33.2, 34, 34.2, 35, 35.2, 36-38	29, 31.2
D7S820	TMR-6C	7q21.11 (83.433Mb)	5-16	8, 11
D5S818	TMR-6C	5q23.2 (123.139Mb)	6-18	12, 12
TPOX	TMR-6C	2p25.3 (1.472Mb)	4-16	11, 11
D8S1179	CXR-6C	8q24.13 (125.976Mb)	7-19	14, 15
D12S391	CXR-6C	12p12 (12.341Mb)	14-17, 17.3, 18, 18.3, 19-27	18, 23
D19S433	CXR-6C	19q12 (35.109Mb)	5.2, 6.2, 8-12, 12.2, 13, 13.2, 14, 14.2, 15, 15.2, 16, 16.2, 17, 17.2, 18, 18.2	13, 14
SE33	CXR-6C	6q14 (89.043Mb)	4.2, 6.3, 8-20, 20.2, 21, 21.2, 22, 22.2, 23.2, 24.2, 25.2, 26.2, 27.2, 28.2, 29.2, 30.2, 31.2, 32.2, 33.2, 34.2, 35-37, 39	15, 16
D22S1045	CXR-6C	22q12.3 (35.779Mb)	7-20	16, 16
DYS391	TOM-6C	Y	5-16	10
FGA	TOM-6C	4q28 (155.866Mb)	14-18, 18.2, 19, 19.2, 20, 20.2, 21, 21.2, 22, 22.2, 23, 23.2, 24, 24.2, 25, 25.2, 26-30, 31.2, 32.2, 33.2, 42.2, 43.2, 44.2, 45.2, 46.2, 48.2, 50.2	20, 23
DYS576	TOM-6C	Y	11-23	18
DYS570	TOM-6C	Y	10-25	17

### 19.5.1.3 POWERPLEX Y23

The PowerPlex® Y23 PCR Amplification Kit is a short tandem repeat (STR) multiplex assay that amplifies 23 Y-STR loci in a single PCR reaction. The following table shows the loci amplified by the Y23 kit and the corresponding dyes used. The Y23 Kit Allelic Ladder is used to genotype the analyzed samples. The alleles contained in the allelic ladder and the genotype of the Control DNA 2800M are listed in the table. (Table 2)

**Table 2.** The PowerPlex® Y23 PCR Amplification System

<b>STR Locus</b>	<b>Label</b>	<b>Alleles Included in Y23 Allelic Ladder</b>	<b>Control 2800M</b>
DYS576	Fluorescein	11-23	18
DYS389I	Fluorescein	9-17	14
DYS448	Fluorescein	14-24	19
DYS389II	Fluorescein	24-35	31
DYS19	Fluorescein	9-19	14
DYS391	JOE	5-16	10
DYS481	JOE	17-32	22
DYS549	JOE	7-17	13
DYS533	JOE	7-17	12
DYS438	JOE	6-16	9
DYS437	JOE	11-18	14
DYS570	TMR-ET	10-25	17
DYS635	TMR-ET	15-28	21
DYS390	TMR-ET	17-29	24
DYS439	TMR-ET	6-17	12
DYS392	TMR-ET	4-20	13
DYS643	TMR-ET	6-17	10
DYS393	CXR-ET	7-18	13
DYS458	CXR-ET	10-24	17
DYS385 a/b	CXR-ET	7-28	13, 16
DYS456	CXR-ET	11-23	17
Y GATA H4	CXR-ET	8-18	11

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### 19.5.1.4 YFILER PLUS

The Yfiler Plus PCR Amplification Kit is a 6-dye, short tandem repeat (STR) multiplex assay that amplifies 27 Y-STR loci in a single PCR reaction, see Table 3. The Yfiler Plus Kit Allelic Ladder is used to genotype the analyzed samples when using GeneScan™ 600 LIZ™ Size Standard v2.0. The genotype of the Control DNA 007 and the alleles contained in the allelic ladder are listed in the table (Table 3).

**Table 3.** The Yfiler Plus PCR Amplification System

<b>Locus designation</b>	<b>Dye label</b>	<b>Alleles included in Allelic Ladder</b>	<b>DNA Control 007</b>
<b>DYS576</b>	<b>6-FAM™</b>	10-25	19
<b>DYS389I</b>		9-17	13
<b>DYS635</b>		15-30	24
<b>DYS389II</b>		24-35	29
<b>DYS627</b>		11-27	21
<b>DYS460</b>	<b>VIC™</b>	7-14	11
<b>DYS458</b>		11-24	17
<b>DYS19</b>		9-19	15
<b>YGATAH4</b>		8-15	13
<b>DYS448</b>		14-24	19
<b>DYS391</b>		5-16	11
<b>DYS456</b>	<b>NED™</b>	10-24	15
<b>DYS390</b>		17-29	24
<b>DYS438</b>		6-16	12
<b>DYS392</b>		4- 20	13
<b>DYS518</b>		32-49	37
<b>DYS570</b>	<b>TAZ™</b>	10-26	17
<b>DYS437</b>		10-18	15
<b>DYS385 a/b</b>		6-28	11,14
<b>DYS449</b>		22-40	30
<b>DYS393</b>	<b>SID™</b>	7-18	13
<b>DYS439</b>		6-17	12
<b>DYS481</b>		17-32	22
<b>DYS387S1</b>		30-44	35,37
<b>DYS533</b>		7-17	13

## 19.5.2 AMPLIFICATION SETUP

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### 19.5.2.1 POWERPLEX FUSION 6C

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#### 19.5.2.1.1 MANUAL AMPLIFICATION PROCESSING

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Samples being manually processed can be extracted, quantitated and amplified using the sample methods employed in the Casework Section. When these methods are used, the Casework SOP will be followed (See DNA-DOC-01 19.6.1). Paperwork is stored on the FB drive.

#### 19.5.2.1.2 BLOOD ON FTA CARDS

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1. In Master Mix Addition module, scan plate bar code and click 'Get Scenario' to scan reagent bar codes. In 'Plate Comments', list volumes of reagents and document bench space used. Create a master mix of PCR reagents by combining the reagents following ratios:

	Half Rxn.	Full Rxn
PowerPlex Fusion 6C PCR Reaction Mix	2.5 µL	5.0 ul
PowerPlex Fusion 6C Primer Set	2.5 µL	5.0 ul
Promega Direct Amp Solution	7.5 µL	15.0 ul
Total Volume	12.5 µL	25 ul

2. Place appropriate volume of Master Mix into each required well on a 96-well plate.
3. Add 2 µL of the positive control to the appropriate well.
4. Punch a 1.2 mm pill into the appropriate well. (See Punch module instructions in 6.2.1.5).
5. Cover the plate with PCR septa.
6. Briefly spin the plate in the centrifuge, and turn on the power to the thermocycler.
7. In Amplification module, scan plate bar code and scan thermocycler bar code. Click 'Start Process' and place into the thermocycler
8. Press Run
9. Scroll to the appropriate program
10. Press Start
11. Ensure the proper volume is entered
12. Press Start again

The following is the thermocycler parameters that are used during amplification of PowerPlex Fusion 6C:

96°C	1min	
96°C	5sec	27cycles

60°C      1min 27cycles  
 60°C      10min  
 4°C        forever

### 19.5.2.1.3 BUCCAL ON BODE DNA COLLECTORS

1. In the Plate Preparation module, scan plate bar code and click 'Get Scenario'. Scan reagent bar code for Promega Punch Solution. Place 2 ul Promega Punch Solution into the appropriate wells.
2. Punch a 1.2 mm pill into the appropriate wells. (See Punch module instructions in 6.2.1.5).
3. In Master Mix Addition module, scan plate bar code and click 'Get Scenario' to scan reagent bar codes. In 'Plate Comments', list volumes of reagents and document bench space used. Create a master mix of PCR reagents by combining the reagents following ratios:

	Half Rxn.	Full Rxn
PowerPlex Fusion 6C PCR Reaction Mix	2.5 µL	5.0 ul
PowerPlex Fusion 6C Primer Set	2.5 µL	5.0 ul
<u>Promega Direct Amp Solution</u>	<u>7.5 µL</u>	<u>15.0 ul</u>
Total Volume	12.5 µL	25 ul

4. Place appropriate volume of Master Mix into each required well on a 96-well plate.
5. Add 1 µL of the positive control to the appropriate well.
6. Cover the plate with PCR septa.
7. Briefly spin the plate in the centrifuge, and turn on the power to the thermocycler.
8. In Amplification module, scan plate bar code and scan thermocycler bar code. Click 'Start Process' and place into the thermocycler.
9. Press Run
10. Scroll to the appropriate program
11. Press Start
12. Ensure the proper volume is entered
13. Press Start again

The following is the thermocycler parameters that are used during amplification of PowerPlex Fusion 6C:

96°C      1min  
 96°C      5sec 28cycles  
 60°C      1min 28cycles  
 60°C      10min  
 4°C        forever

### 19.5.2.2 YFILER PLUS

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Samples being processed for Y-STR testing can be extracted, quantitated and amplified using the sample methods employed in the Casework Section. When these methods are used, the Casework SOP will be followed (See DNA-DOC-0119.6). The Y-STR process is not tracked through STACS-DB modules. Paperwork is stored on the ForensicBiology shared drive.

### 19.5.2.3 SAMPLE SETUP FOR THE 3500XL INSTRUMENT

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#### 19.5.2.3.1 POWERPLEX 16 HS

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PowerPlex 16HS is no longer used by the Arkansas State Crime Laboratory for Autosomal STR amplification or new sample HID analysis.

#### 19.5.2.3.2 POWERPLEX FUSION 6C

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After amplification is complete, samples are set up for the 3500xl. A 96 opti-well plate is used. In the Electrophoresis Plate Preparation module in STACS-DB, click 'Create Plate' to create and print 'Daughter' plate bar code. Click 'Get Scenario' to scan reagent bar codes. In 'Plate Comments', list volumes of reagents. Create a master mix solution in the following ratios:

0.5  $\mu\text{L}$  of Internal Lane Standard (WEN ILS-500)

9.5  $\mu\text{L}$  of HiDi Formamide

- 1) \*BLOOD ONLY\* (optional) Pipette 10 $\mu\text{l}$  of HiDi Formamide into each sample well on the amplification plate to dilute the sample before making the 3500xl plate.
- 2) Pipette 10 $\mu\text{l}$  of mix into each well used.
- 3) Ensure that all the wells of an injection contain master mix. The 3500xl should never inject sample from a dry well.
- 4) Add 1  $\mu\text{l}$  of sample to each well (a multi-channel pipette is beneficial).
- 5) Add 1  $\mu\text{l}$  of ladder to each ladder sample. At minimum, 1 ladder per plate must be present.
- 6) Briefly spin the plate in the centrifuge.
- 7) In Electrophoresis Plate Denaturation module, scan the heat block bar code and the 'Daughter' plate bar code. Heat the plate for approximately 3 minutes. Chill the plate for approximately 3 minutes.

#### 19.5.2.3.3 YFILER PLUS

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After amplification is complete, samples are set up for the 3500xl. The Casework SOP will be followed (See DNA-DOC-01 19.6). The Y-STR process is not tracked through STACS-DB modules. Paperwork is stored on the ForensicBiology shared drive.

## 19.5.2.4 3500XL INSTRUMENT SETUP

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### 19.5.2.4.1 POWERPLEX FUSION 6C

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In STACS-DB, in the Post PCR module, scan the 3500xl instrument bar code and scan the 'Daughter' plate bar code. Click 'Create Sample Sheet' to send txt file to 3500xl computer. Place the plate into the 3500XL instrument.

- 1) On the 3500 computer, go to the Data Collection software,
- 2) Go to Library, then click on Import
- 3) Select the STACS-DB txt file to import
- 4) Edit as needed. The typical plate setup from STACS-DB is for a single 12- or 24-second injection at 1.2 kV for each sample depending on sample type. Number of injections and duration may be adjusted manually, but a note must be added to STACS-DB. Edit settings as necessary in the AB Data Collection and click Okay.
- 5) Click 'OK'
- 6) It is best to start the oven approximately 15 minutes before the run starts.
- 7) Go to the Dashboard
- 8) Press the Pre-Heat Button
- 9) Link the appropriate plate to the plate map under the 'Load Plates for Run'.
- 10) To start the run Click on the Start Run Button

### 19.5.2.4.2 YFILER PLUS

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- 1) Go to Library
- 2) Click on Import
- 3) Select the txt file to import
- 4) Click 'OK'
- 5) It is best to start the oven approximately 15 minutes before the run starts.
- 6) Go to the Dashboard
- 7) Press the Pre-Heat Button
- 8) Link the appropriate plate to the plate map under the 'Load Plates for Run'.
- 9) To start the run Click on the Start Run Button

## 19.5.2.5 ANALYSIS OF RAW DATA / GENEMAPPER ID-X

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### 19.5.2.5.1 POWERPLEX 16 HS – PREVIOUS

### 19.5.2.5.2 POWERPLEX FUSION 6C

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GeneMapper ID-X analysis software is used to analyze the raw data collected by the 3500xl Genetic Analyzer.

- A matrix file is applied to the raw data to create a single baseline as well as to correct for spectral overlap and produce peaks of the five individual colors.
  - A size curve is created using co-injected DNA fragments of known size and the unknown peaks are assigned a size by interpolation.
- 1) Open the GeneMapper ID-X program with a blank project window or from the GeneMapper ID-X program select **File>Add Samples to Project**.
  - 2) Select the appropriate run folder saved on the DNA drive and click **Add to List**. Once all samples have been added to the list, click **Add** to import the files.
  - 3) In the Sample Type column, assign the correct sample type to each sample (i.e. sample, ladder, control)
  - 4) Select Analysis Method.
  - 5) Select **PowerPlex\_Fusion\_6C\_Panels\_IDX\_v1.1** as the Panel.
  - 6) Select **WEN\_ILS\_500\_CS** as the Size Standard.
  - 7) Click the green arrow to analyze the project.
  - 8) View the raw data to examine the ILS. Verify that the analysis range is between 60bp and 600bp and the peaks are correctly labeled.
  - 9) Review controls:
    - Display each control (including positive and negative amplification controls, and blank controls).
    - If peaks above 175 RFU are observed in the negative controls, the sample can be re-injected.
    - Examine the Positive control and verify the correct calls of the alleles.
  - 10) Examine the allelic ladders.
    - Verify that the allelic ladder is called correctly for each marker.
  - 11) Analyzed samples can be viewed as a group or individually by highlighting the samples to view. After selecting the sample click the **Display Plots** button. There are several options available to view the electropherogram.
  - 12) Edit any labels as appropriate e.g. spike, background, -A
  - 13) Review the remaining sample files. Evaluate the following parameters:

- Peak shape and height (optimal values between 1000-6000 RFU, although acceptable and typeable signals may occur outside of this range).
- Matrix quality (baselines should be relatively flat and there should not be a pattern of pronounced peaks or dips below true DNA peaks in the other four colors).
- Peak profile (examine for artifactual peaks e.g. spikes).

14) In “Table Settings”, change to ‘STACS’. Select the ‘Genotypes’ tab. Select ‘File’ and export table to S drive in ‘Working’ directory.

15) In the Analysis module of STACS-DB, select plate from ‘Analysis’ list and click ‘Analyze/Review’.

### 19.5.2.5.3 YFILER PLUS

GeneMapper ID-X analysis software is used to analyze the raw data collected by the 3500xl Genetic Analyzer.

- A matrix file is applied to the raw data to create a single baseline as well as to correct for spectral overlap and produce peaks of the five individual colors.
- A size curve is created using co-injected DNA fragments of known size and the unknown peaks are assigned a size by interpolation.

1) Open the GeneMapper ID-X program with a blank project window or from the GeneMapper ID-X program select **File>Add Samples to Project**.

2) Select the appropriate run folder saved on the DNA drive and click **Add to List**. Once all samples have been added to the list, click **Add** to import the files.

3) In the Sample Type column, assign the correct sample type to each sample (i.e. sample, ladder, control)

4) Select Analysis Method, **ASCL\_Yfiler+\_v1.0**

5) Select **Yfiler\_Plus\_Panel\_v4\_ASCL** as the Panel.

6) Select **GS600\_LIZ\_(60-460)** as the Size Standard.

7) Click the green arrow to analyze the project.

8) View the raw data to examine the ILS. Verify that the analysis range is between 60bp and 600bp and the peaks are correctly labeled.

9) Review controls:

- Display each control (including positive and negative amplification controls, and blank controls).
- If peaks above analytical threshold are observed in the negative controls, the sample can be re-injected.
- Examine the Positive control and verify the correct calls of the alleles.

10) Examine the allelic ladders.

- Verify that the allelic ladder is called correctly for each marker.

11) Analyzed samples can be viewed as a group or individually by highlighting the samples to view. After selecting the sample click the **Display Plots** button. There are several options available to view the electropherogram.

12) Edit any labels as appropriate e.g. spike, background, -A

13) Review the remaining sample files. Evaluate the following parameters:

- Peak shape and height (optimal values between 1000-6000 RFU, although acceptable and type able signals may occur outside of this range).
- Matrix quality (baselines should be relatively flat and there should not be a pattern of pronounced peaks or dips below true DNA peaks in the other four colors).

### 19.5.2.6 INTERPRETATION GUIDELINES

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The purpose of these guidelines is to establish a general framework and outline minimum standards to ensure that:

- Conclusions for CODIS samples are scientifically supported by the analytical data, including that obtained from appropriate standards and controls.
- Interpretations are made as objectively as possible, consistently from analyst to analyst, and within established limits.
- The goal of the evaluation and interpretation is to analyze amplified STR data and determine the DNA profiles for NDIS.
- A peak is defined as a distinct, triangular section of an electropherogram.
- Genotypes are determined from the diagnostic peaks of the appropriate color and size range for a particular locus.

NOTE: Reinterpretation and comparison of DNA records generated by legacy amplification kits (kits previously used by the laboratory but no longer in use) with DNA records generated with amplification kits currently in use by the laboratory shall be performed in accordance with the *SWGDM Clarification on the Reinterpretation of Data Typed with Legacy Amplification Test Kits*. For purposes of these procedures, assessing/evaluating allele calls, genotype calls (to include potential allelic drop-out), a change in the assumptions used, or removing alleles (or entire loci) from statistical estimates from legacy amplification test kit data, are all considered reinterpretation.

See DNA-DOC-01 19.7 for additional Y-STR Interpretation Guidelines.

#### 19.5.2.6.1 THRESHOLD

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The minimum peak height threshold will be set at 175 (Relative Fluorescent Unit) RFU for PowerPlex 16 HS, Fusion 6C, and Y23 and at 100 RFU for Yfiler Plus. The interpretation threshold is set at 175 RFU for PowerPlex 16 HS, Fusion 6C and Y23 and 100 RFU for Yfiler Plus. Optimal peak height values range between 1000-4000 RFU, although acceptable and typeable signals may occur outside of this range.

#### 19.5.2.6.2 PEAK HEIGHT RATIO

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Peak height ratios of heterozygote alleles are defined as the ratio of the lower peak's height to the higher peak's height, expressed as a percentage. Peak height ratios lower than 50% may indicate a mixture. Occasionally a non-mixed sample will be outside of this range. Depending upon the sample source, the loci in question, the number of loci affected and the percent disparity between alleles, the sample may need to be re-amplified and typed.

Homozygote allele peak heights are approximately twice that of heterozygotes as a result of a doubling of the signal from two alleles of the same size.

#### 19.5.2.6.3 OFF LADDER VARIANTS

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Off ladder (OL) calls are first converted to size in base pairs (bp), and then compared to the size of the appropriate ladder alleles and the allelic designation determined. If the OL is not a "perfect" repeat, but rather varies by 1, 2 or 3 bp from a ladder allele, then it will be designated as an integer of that variation. For example, if a green OL peak size is 238.39 bp, and the 36 allele of the **D21S11** ladder is 236.32 bp, then the peak will be designated a **D21S11** 36.2. If an allele falls above the largest or below the smallest peak of the sizing ladder, the allele will not need to be re-injected or re-amplified and will be designated as either greater than (>) or less than (<) the respective ladder allele.

The analyst will re-amplify or re-inject, then type any sample containing a peak not properly interpreted as an allele by the software, especially if it is not appropriately balanced with an associated allele or at a height expected for a homozygote.

An off ladder variant which has been seen and confirmed at least two times in the population sampled at the Arkansas State Crime Laboratory is no longer considered a rare variant. These peaks can be confidently and accurately called without confirmation.

#### 19.5.2.6.4 TRI-ALLELE

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A tri-allelic system is one which contains three distinct alleles, rather than the normal one or two. In order to insure that the sample is a true tri-allelic specimen, the sample should be re-amplified and run a second time. However, if observed in overlapping systems or in multiple samples from the case, tri-allelic loci may be considered confirmed. If there is not enough extract left for re-amplification, the sample may be re-loaded. However, if the tri-allelic sample cannot be confirmed, the locus may be reported as inconclusive or a technical note may be recorded in the case file (the CODIS Administrator or Technical Leader may need to be notified to determine how to report the locus).

#### 19.5.2.6.5 ARTIFACTS

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Artifacts can occur and need to be recognized. These may include, but are not limited to, the following: spikes, pull-up, stutter, and non-template nucleotide addition.

## SPIKES

Spikes are artifactual peaks usually observed in at least two colors. Spikes can be caused by urea crystals in the capillary, power surges, or other instrument related issues. A spike will not exhibit the same morphology as a peak, but will be sharper or “spike” shaped. Spikes are unique to fragments analyzed using capillary electrophoresis. Spikes will have fragment sizes which vary only slightly in the 3500xl data. Above threshold spikes should be noted and may be re-injected.

## STUTTER (ST)

In addition to an allele’s primary peak, artifactual minor “stutter” peaks can occur at four-base intervals. The most common stutter peaks observed in all loci are four bases smaller than the primary peak (“n-4”). It is also possible to see additional “n+4” peaks (four bases larger), especially when excessive amounts of DNA are amplified.

- STUTTER IN POWERPLEX FUSION 6C

Stutter peaks are evaluated by examining the ratio of the stutter peak height to the height of the appropriate adjacent allele, expressed as a percentage. The height of stutter peaks can vary by locus, and longer alleles within a locus generally have a higher percentage of stutter. In general, the maximum expected percentage of stutter is less than 30% for any locus. Peaks in the stutter positions greater than this value may indicate the presence of a mixture. Therefore, CODIS samples will be evaluated with a global stutter ratio of 30%.

Analyzed peak heights above the optimal range may be “off-scale” in the raw data, meaning that the CCD camera may be saturated. While the Gene Mapper ID-X software will alert the analyst to any off-scale raw data peaks, the analyzed peak may be assigned a lower value due to smoothing and base-lining functions. Therefore, the observed percent stutter will be inaccurately high. If the stutter peak is greater than the maximum allowed and the primary peak is above 10,000 RFU and/or has been labeled off-scale, the analyst should interpret the results with caution. The sample may be re-amplified with less input DNA or re-injected

See DNA-DOC-01 6.2.8.4.3.4 for additional information on Y-STR stutter

## NON-TEMPLATE NUCLEOTIDE ADDITION (-A)

Amplification conditions have been set to maximize the non-template addition of a 3’ terminal nucleotide by DNA polymerase. Failure to attain complete terminal nucleotide addition results in “band splitting”, visualized as two peaks one base apart. This is most often seen when an excessive amount of DNA is amplified or amplification is performed under sub-optimal PCR conditions.

## PULL-UP

Small artifactual peaks can appear in other colors under true peaks. This phenomenon is termed “pull-up”. Pull-up is a result of spectral overlap between the dyes, which is normally corrected for by the spectral calibration. If a pull-up peak is above the minimum peak height detection

threshold, it will be sized at approximately the same size as the true peak. Pull-up can occur as a result of the following:

Application of a sub-optimal spectral can cause pull-up. If necessary, spectral standards can be injected on the same capillary after the analytical run and a new spectral can be made and applied.

Amplification using excess input DNA can lead to off-scale peaks. The matrix may not perform properly with off-scale data.

#### OTHER

In addition to amplification artifacts described above the following anomalies can arise during electrophoresis and analysis:

Significant room temperature fluctuation may result in size variation between injections such that allelic ladder peaks differ by more than 0.5 bp from allelic peaks in other injections. This will disrupt sample analysis using the Gene Mapper ID-X program. Analyzing samples with an injection of allelic ladder nearest the questioned samples may alleviate this problem. If desired, the sample(s) and an allelic ladder may be re-injected to confirm the typing.

Artifactual peaks of a single color will not display the typical spectral overlap characteristic of the five fluorescent dyes in the raw data. Peak width may not be similar to the peaks resulting from dye-labeled DNA. These peaks can be shown to be artifactual by re-injection of the sample.

See DNA-DOC-01 6.2.8.4.3 for additional information on Y-STR artifacts.

### 19.5.2.7 STR PROFILE INTERPRETATION GUIDELINES

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Amplified products from convicted offender / arrestee samples will be interpreted based on peak quality, peak morphology and RFU values. It is a requirement of the analyst, based on experience, to determine which sample peaks meet the criteria for allele designation. All peaks called in the CODIS section must meet a minimum RFU threshold of 175 for Fusion 6C.

In general, a single source profile at each locus will appear as a single peak or a double peak. On rare occasions, a tri-allelic pattern may be detected. The observation of tri-allelic patterns does not preclude that locus from interpretation. However, a tri-allelic pattern must be confirmed by, at minimum, re-injecting the sample.

- INCONCLUSIVE ALLELE CALLS

In those cases where peaks are not present or are below the minimum 175 RFU for Fusion 6C, allele calls for that sample at that locus may be designated as inconclusive "INC". If any of the CODIS core loci have alleles that are not present or are below the RFU threshold, the sample must be re-amplified to gain a complete profile at the 20 core loci. (All previous samples follow the 13 original core loci requirements).

### **19.5.2.8 RE-RUNS (RE-WORK IN STACS-DB)**

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All samples that have been labeled as re-work will be reprocessed. The sample will be marked and verified for re-work. Recently entered samples into SDIS will be compared to all samples in the DNA Database during the weekly offender to offender search. It is noted, that problematic samples (both CODIS and Medical Examiner samples) can be extracted, quantitated and amplified using the sample methods employed in the Casework Section. When these methods are used, the Casework SOP will be followed. This process is tracked in the Manual Worklist and Tracked Manual Processing modules in STACS-DB. Paperwork is stored on the S drive.

## **19.5.3 CODIS DATA IMPORT AND SEARCHING**

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### **19.5.3.1 IMPORT STR DATA**

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All STR data created by the Arkansas State Crime Laboratory or a contract company which is NDIS acceptable (see NDIS Acceptance Form) will be entered and searched in CODIS.

Profiles can be manually entered or entered using the import program into the system. Any profiles entered into CODIS by the import program must be in the Common Message Format (CMF). Each CMF file must have a unique file name to ensure that the correct file is entered into CODIS. The Arkansas State Crime Laboratory maintains several indexes of data in CODIS.

#### **19.5.3.1.1 CREATING A CMF FILE**

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- 1) After technical review in the Analysis module is completed, the samples will go to the CODIS Upload module to create a CMF import file.
- 2) Save the file on desktop or a thumb drive

#### **19.5.3.1.2 IMPORTING A CMF FILE**

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- 1) Open specimen manager
- 2) Click "Import"
- 3) Locate and highlight files ready for import
- 4) Click "Open"
- 5) Assign Read, when prompted and Click "OK"
- 6) Ensure that correct number of files are imported
- 7) Open Message Center
- 8) Under the "Import Files" tab, click on each file imported to either verify or execute the file
- 9) Under "Import Reports" tab, click each file to create a reconciliation report.
- 10) Ensure all loci/samples have successfully been imported.
- 11) In the CODIS Confirmation module of STACS-DB, select the file and highlight samples that were imported and click 'Confirm All'.

## 19.5.3.2 SEARCHING THE CODIS INDEXES

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### 19.5.3.2.1 KEYBOARD SEARCHES

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Upon entering a new forensic sample into CODIS, the analyst may perform a search of the appropriate sample indices for potential matches between the new sample and samples already in the database. Manual searching is not required since Autosearches are scheduled to run nightly.

Typically, forensic profiles can be searched with the default configuration. The default search configuration requires that a forensic profile have 8 of the 13 original core loci to be searched. Matches will be returned for samples with at least eight loci that match at moderate stringency. When searched with these search parameters, some forensic profiles (such as mixture profiles, partial profiles, and profiles that are homozygous at several loci) may result in a large number of ambiguous candidate matches. The search stringency may be customized to high at some loci to allow for a more efficient search. If a sample has less than 8 loci, the analyst will need to modify the configuration to require less than 8 loci to report a match. Customization of the search stringency must be done with careful consideration. The main goal is to not erroneously eliminate the actual perpetrator from the pool of candidates by improper stringency customization when the search is conducted. Analysts may seek the assistance of a CODIS Administrator or another qualified analyst for non-routine searches.

If no matches are returned, other than to the sample itself, the analyst can close Searcher without saving the matches. If possible matches are returned, the analyst should save the results to Match Manager. The analyst will then assess each possible match by a locus to locus comparison and disposition matches in the disposition window. Matches may also be dispositioned by a CODIS Administrator. Candidate matches, at less than high stringency, between an offender and an unknown forensic specimen or between two forensic specimens (at least one in which the source is unknown) require assessment by two qualified analysts. A list of possible dispositions is provided in Section 6.2.3.3. If there is a forensic or offender hit (e.g., identifying the source of a sample that was previously unknown) the CODIS section should be notified to start the Hit Verification.

**NOTE:** No profile will be searched in the CODIS system until a technical review is performed on the sample in question.

### 19.5.3.2.2 AUTOSEARCHES

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- 1) Autosearches are performed daily (Monday through Friday). Many indexes are searched against each other. For a complete list of indexes searched, please see the Autosearcher program.
- 2) All relevant convicted offender / arrestee sample matches must be confirmed.
- 3) All hits must be investigated to determine the disposition of the match

### 19.5.3.2.3 NDIS SEARCHES

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- 1) Monday through Friday, a daily search is performed at the NDIS level. The matches are routinely checked.
- 2) Convicted offender / arrestees are verified and confirmations are sent once requested by the agency with the hit. The confirmations are sent to other NDIS hits on “CODIS DNA Match Data Response” forms.
- 3) Matches with ASCL cases and other NDIS agencies convicted offender / arrestees are requested for verification by using “CODIS Match Data Requested”. Once the confirmation is received, a CODIS hit letter is sent to the investigating agency.

### 19.5.3.2.4 CODIS HITS

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Every convicted offender / arrestee match must be confirmed before a “CODIS Hit Letter” is sent to the agency. The CODIS Administrator or designee will send the letter to the agency.

- 1) Inform the CODIS Administrator or CODIS Analyst of any hit that should be confirmed. Hits will also be determined by routine Autosearches.
- 2) Matches will be reviewed in CODIS and the ‘Match Report’ will be imported to the Hit Tracking module of STACS-DB.
- 3) A “CODIS Hit Verification” form should be completed in the Hit Tracking module.
- 4) The violation and biographical information is verified.
- 5) The Database Card or DNA Collector is taken from secure storage
- 6) The sample is processed (See Section 6)\*
- 7) The fingerprint is confirmed in the Latent Print Section\*
- 8) After confirmation and review that is tracked through the Hit Tracking module by ‘Match ID’, a “CODIS Hit Letter” is sent to the investigating agency or a “CODIS DNA Match Data Response” is sent to the CODIS Administrator of the other matching laboratory.

NOTE: A minimum of 8 core loci have to be obtained for a CODIS confirmation.

\*If a Rush priority is requested on a Hit confirmation, the CODIS Administrator or designee may release the identifying information of the offender/arrestee involved in the match following the biographical information verification. The request must be documented and stored with the offender/arrestee information in STACS-DB.

#### 19.5.3.2.4.1 CODIS HIT VERIFICATIONS REQUIREMENTS

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It is a requirement for best effort to resolve all candidate matches within 30 business days. Any candidate match verifications exceeding the 30 day window will require additional documentation explaining the delay and the CODIS Administrator must be notified.

The CODIS Hit Verification is considered a technical record and will therefore contain an electronic signature stored under each ‘Match ID’ in the Hit Tracking module and Submission

Files in STACS-DB. Every CODIS Hit Verification is unique and may need different items to ensure the complete verification. However, there are a few items that are needed in each Hit Tracking verification file. These items include: the CODIS Hit Verification electronic form and the Match Detail Report. Other items that may be in the Hit Tracking file include, but are not limited to the following: submission sheet(s), offender/arrestee detail report, copy of offender/arrestee information card, electropherograms, fingerprint card, conversation sheet/email, ACIC report, or out-of-state hit report.

NOTE: Additional documentation may be needed if verification if the profile or offender/arrestee biographical data is in question.

#### **19.5.3.2.4.2 CODIS HIT REVIEW**

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All reviews of CODIS hits are documented on the Hit Tracking module by 'Match ID'.

##### **1) TECHNICAL REVIEW**

Each CODIS hit must be reviewed for accuracy. The Technical Reviewer must check for the following information:

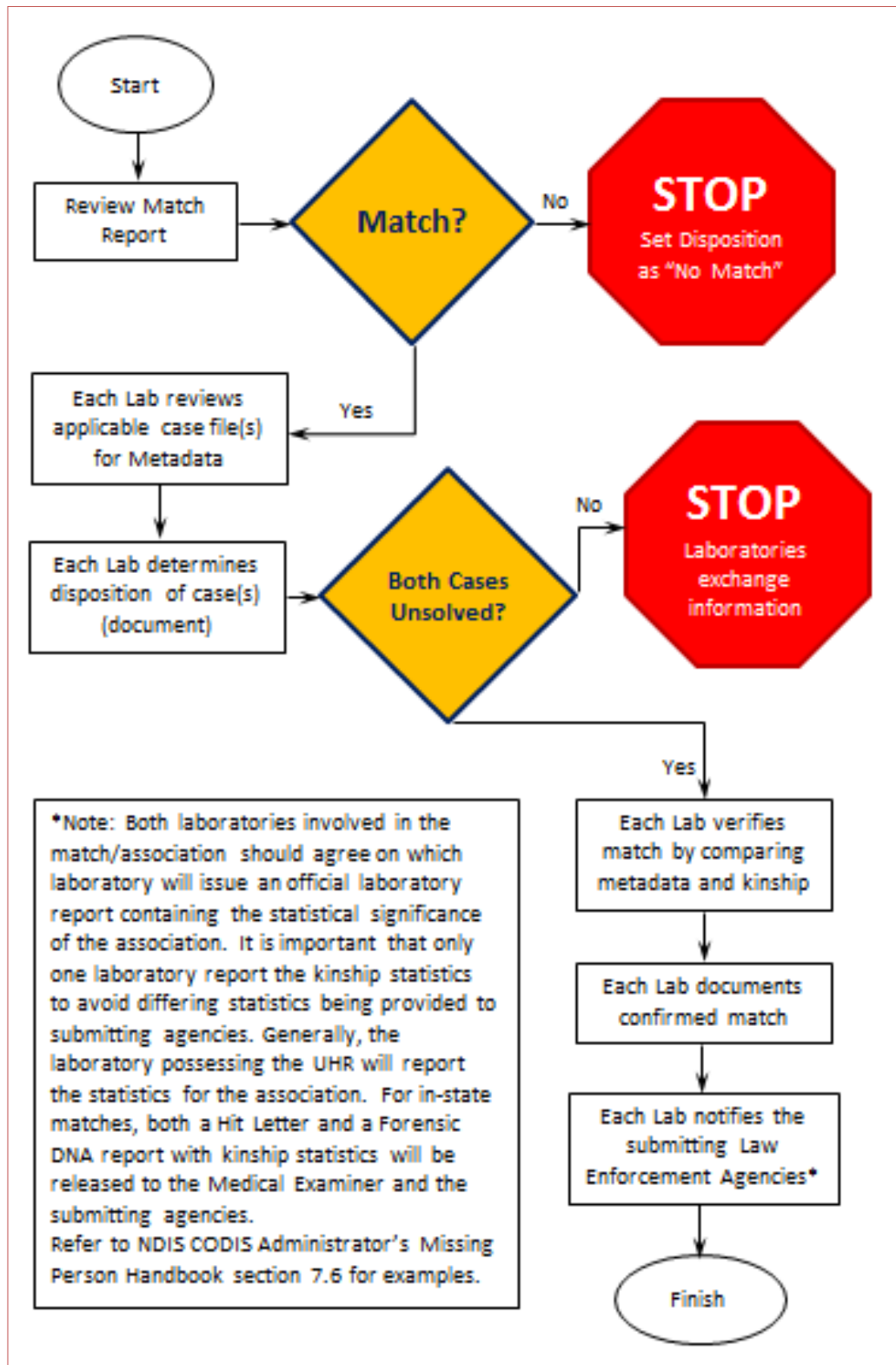
- The profiles match
- The offender number matches what is confirmed
- The case number matches what is confirmed
- The offense is a qualifying offense
- DNA profile that was confirmed is correct and matches the profile in CODIS
- The biographical data of the offender is correct

##### **2) ADMINISTRATOR REVIEWER**

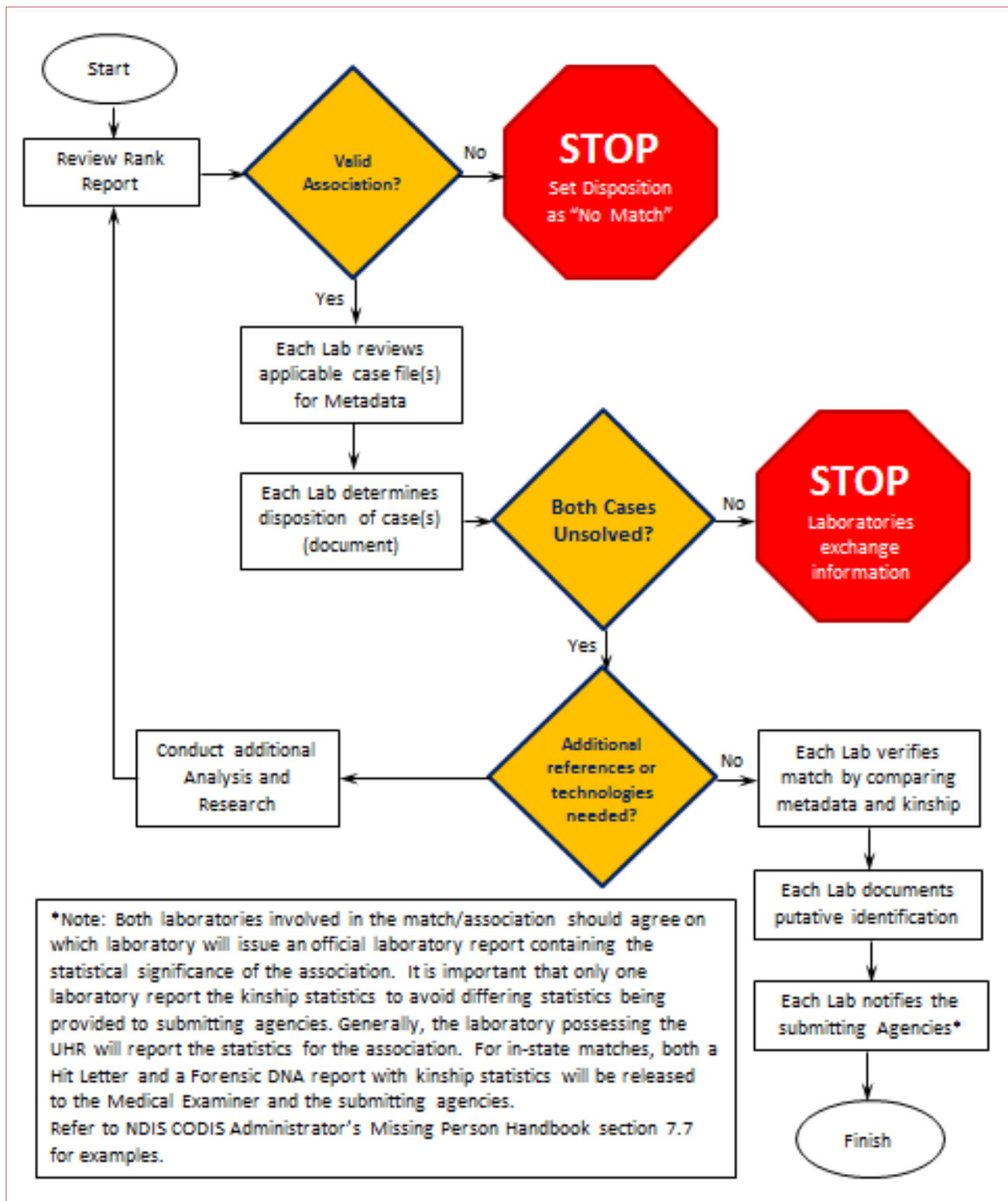
Each CODIS hit must be administratively reviewed for accuracy. The Administrative Reviewer must check for the following information:

- The profiles match
- The offender number matches what is confirmed
- The case number matches what is confirmed
- The offense is a qualifying offense
- DNA profile that was confirmed is correct and matches the profile in CODIS
- The biographical data of the offender is correct
- The hit letter is correct

### 19.5.3.2.4.3 CODIS MISSING PERSON/UNIDENTIFIED REMAINS CONFIRMATIONS



*CODIS Missing Person Match Confirmation Process*



*CODIS Missing Person Association Confirmation Process*

#### 19.5.3.2.5 FAMILIAL SEARCHING/PARTIAL MATCHES

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The Arkansas State Crime Laboratory routinely enters DNA profiles into state and national databases for the purpose of matching unknown forensic profiles to known contributors through routine database searches. These routine searches may yield a partial match to a close biological relative. This relationship may be explored with additional DNA testing by the ASCL and further verified by the investigating agency.

Familial Searching is an additional search of a DNA database conducted after a routine search has been completed and no profile matches are identified during the process. Unlike a routine database search which may spontaneously yield partial match profiles, familial searching is a deliberate search of a DNA database for the intended purpose of potentially identifying close biological relatives to the unknown forensic profile obtained from crime scene evidence. Familial Searching is based on the concept that first-order relatives, such as siblings or parent/child relationships, will have more genetic data in common than unrelated individuals. See Appendix C for the ASCL Familial Searching Policy.

In order to perform a familial search, a specific search configuration is utilized in the CODIS software using the pedigree index called “Familial Search”. The unsolved forensic profile will be added to the associated Familial Search pedigree category as the target profile and searched against Arkansas State Database (SDIS) profiles of Convicted Offenders, Arrestees, Suspect Knowns, and Deceased Individuals. A search will be conducted for Node 1 (sibling) and Node 2 (parent/offspring). For additional information on the search configuration, see CODIS Searcher. Candidates are returned by the search in a rank list that is sorted using the Joint Pedigree Likelihood Ratio (JPLR) from highest to lowest. The candidate lists will then be combined and the top candidates will be further investigated.

#### 19.5.3.2.6 SPECIMEN CATEGORIES

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##### **ARRESTEE:**

The known sample from a person who has been arrested in accordance with the law of the applicable jurisdiction is required to provide a DNA sample for analysis and entry into a state DNA database. The term ‘arrestee’ includes persons who have been charged in a formal criminal instrument, such as an indictment or information. The DNA profile for this specimen category is stored in an Arrestee Index.

##### **BIOLOGICAL CHILD:**

The known reference sample voluntarily provided by an adult child or provided with the parental/guardian consent for a minor child of a reported missing person. The DNA record for this specimen category is stored in the Relatives of Missing Person Index.

##### **BIOLOGICAL FATHER:**

The known reference sample voluntarily provided by the biological father of a reported missing person. The DNA record for this specimen category is stored in the Relatives of Missing Person Index.

**BIOLOGICAL MOTHER:**

The known reference sample voluntarily provided by the biological mother of a reported missing person. The DNA record for this specimen category is stored in the Relatives of Missing Person Index.

**BIOLOGICAL SIBLING:**

The known reference sample voluntarily provided by the full or half biological adult sibling or provided with the parental/guardian consent for a by the full or half biological minor sibling of a reported missing person. The DNA record for this specimen category is stored in the Relatives of Missing Person Index.

**CONVICTED OFFENDER:**

The known sample from a person who has been convicted of a state qualifying offense in a jurisdiction that requires that persons convicted of enumerated crimes or qualifying offenses provide a DNA sample for analysis and entry into a state DNA database. The DNA profile for this specimen category is stored in a Convicted Offender Index.

**DEDUCED MISSING PERSON:**

The DNA record of a reported missing person that has been generated by examining intimate items purported to belong to the missing person, (such as a toothbrush or glasses), and compared to close biological relatives, if possible. Considered a reference sample, this DNA record is stored in the Missing Person Index.

**DETAINEE:**

The known sample from a non-United States (U.S.) person detained under the authority of the U.S. and required by law to provide a DNA sample for analysis and entry into a state/national DNA database.

**ELIMINATION SAMPLE:**

A biological sample from a known individual, other than the alleged perpetrator or victim, which is analyzed for purposes of identifying those portions of a forensic DNA profile attributable to the alleged perpetrator. The DNA profile for this specimen category may be stored at the state and/or local levels.

**FORENSIC MIXTURE:**

A specimen category in the CODIS software that is stored in the Forensic Index and originates from a forensic sample (biological sample found at the scene of a crime) that contains DNA contributed from more than one source.

**FORENSIC UNKNOWN:**

A specimen category in the CODIS software that is stored in the Forensic Index and originates from a single source (or a fully deduced profile originating from a mixture) forensic sample attributable to the putative perpetrator having all 13 Original CODIS core loci and shall not have more than 3 alleles at one locus while the remaining loci can have up to 2 alleles.

**FORENSIC PARTIAL:**

A specimen category in the CODIS software that is stored in the Forensic Partial Index and originates from a single source (or a fully deduced profile originating from a mixture). forensic sample attributable to the putative perpetrator with either locus or allelic dropout at any of the 13 Original CODIS core loci and shall not have more than 3 alleles at one locus while the remaining loci can have up to 2 alleles.

**FORENSIC TARGETED:**

A specimen category in the CODIS software that is stored in the Forensic Targeted Index. A forensic targeted specimen originates from a forensic partial or a forensic mixture that does not meet the NDIS moderate match estimate threshold of 1 in 10 million, but does meet the match rarity estimate of 1 in 10 million if searched at a specified stringency by locus (high or moderate) and has 8 of the Original CODIS core loci.

**INCOMPLETE FORENSIC UNKNOWN:**

A specimen category in the CODIS software that is stored in the Forensic Index and originates from a single source (or a fully deduced profile originating from a mixture). This category contains profiles from crime scene evidence deemed appropriate for entry into CODIS that contain less than 8 Original CODIS core loci. The DNA record for this specimen category is stored in the Incomplete Forensic Profile Index and is only searched at the state level.

**INCOMPLETE FORENSIC MIXTURE:**

A specimen category in the CODIS software that is stored in the Forensic Index and originates from a forensic sample (biological sample found at the scene of a crime) that contains DNA contributed from more than one source. This category contains profiles from crime scene evidence deemed appropriate for entry into CODIS that contain less than 8 Original CODIS core loci. The DNA record for this specimen category is stored in the Incomplete Forensic Profile Index and is only searched at the state level.

**MATERNAL RELATIVE:**

The known reference sample voluntarily provided by a maternal biological relative who is not a mother, child or sibling of a reported missing person. The DNA record for this specimen category is stored in the Relatives of Missing Person Index.

**MISSING PERSON:**

The known reference sample from an individual that is missing. The source of the DNA has been verified as originating from the missing person and is stored in the Missing Person Index.

**PATERNAL RELATIVE:**

The known reference sample voluntarily provided by a paternal biological relative who is not a father, child or sibling of a reported missing person. The DNA record for this specimen category is stored in the Relatives of Missing Person Index.

**PEDIGREE TREE:**

A Pedigree tree contains genetic information from two or more biological relatives of a missing person (may include spouses, where applicable).

A Single Typed Node Pedigree contains the genetic information from only one biological relative of a missing person.

**PROFICIENCY:**

The samples from all proficiency test. The DNA record for this specimen category is stored at SDIS and does not search other specimens in the proficiency category.

**SUSPECT KNOWN:**

A biological sample from a known individual submitted with a DNA case. The DNA profile for this specimen category may be stored and searched at the state level.

**UNIDENTIFIED PERSON:**

A specimen category in the CODIS software that is stored in the Unidentified Human (Remains) Index. It originates from the recovered deceased (including body parts and tissue) or an individual who is unidentified (e.g., children who can't and others who can't or refuse to identify themselves).

**Y-STR ONLY:**

A specimen category in the CODIS software that originates from a forensic sample or suspect sample that has a Y-STR profile but does not have an autosomal profile entered in CODIS. The DNA record for this specimen category is stored and searched only at the state level. It is not intended for samples for the Missing Person Index.

### 19.5.3.3 MATCH DISPOSITIONS

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#### **CANDIDATE MATCH**

Candidate Match is defined as a possible match between two or more DNA profiles reported by CODIS software after a search. This is an interim disposition and laboratories must assess each candidate match to disposition appropriately.

#### **WAITING FOR MORE DATA**

Waiting for More Data is an intermediate missing person disposition, indicating that additional genetic analyses and/or metadata evaluation is being conducted to confirm or refute a match or rank

#### **PENDING**

Pending is an intermediate disposition, indicating that the Candidate Match is in the process of being confirmed or refuted.

#### **OFFENDER HIT**

A match between a convicted offender's DNA profile and the DNA profile from a forensic unknown or forensic mixture profile in an unsolved forensic case where it aids the investigation.

#### **FORENSIC HIT**

A match between a forensic unknown or forensic mixture profile in an unsolved case and a forensic unknown, known or forensic mixture profile from another solved or unsolved case. The match is considered a forensic hit if the match aids the investigation in some way.

When a SDIS match occurs between a forensic unknown and a suspect known the DNA casework section will be notified about the match.

#### **CONVICTION MATCH**

A Conviction Match occurs when CODIS matches a forensic unknown or forensic mixture DNA profile to a DNA profile from an offender (Convicted Offender Index, Arrestee Index, Detainee Indexes, Legal Index), but the crime from which the evidence was collected has already been solved or the match does not aid the investigation in any way. The forensic lab must determine in some manner that the identity of the matching offender is the same as the identified subject in their solved case.

#### **BENCH WORK MATCH**

Benchwork Matches occur when forensic profiles linked externally to CODIS are also matched by CODIS. When CODIS makes the association no new information or assistance is provided to the investigation.

#### **OFFENDER DUPLICATE**

A match made between two offender (Convicted Offender Index, Arrestee Index, Detainee Index, or Legal Index) profiles that does not provide probative information.

### **INVESTIGATIVE INFORMATION**

This disposition is used as a generic category for matches that do not provide probative information and/or does not readily fit the other disposition categories.

### **NO MATCH**

During the confirmation process a qualified DNA analyst determines that a match is dispositioned as Candidate, Pending or Waiting for More Loci is not a confirmed DNA match.

### **TWINS**

This disposition is used when it is believed that a match involves two individuals that share the same profile and are believed to be the result of the same pregnancy.

### **USER DEFINED #1**

Used Defined #1 disposition is used when the sample matches itself, or another sample(s) within the case. This is also a disposition for all miscellaneous matches that are not considered true or valuable matches.

### **USER DEFINED #2**

User Defined #2 is reserved for all matches that occur because of contamination reasons.

### **USER DEFINED #3**

User Defined #3 is used when a sample from the deceased victim's index matches a convicted offender.

### **ARRESTEE HIT**

A match between an arrestee's DNA profile and the DNA profile from a forensic unknown or forensic mixture profile in an **unsolved** forensic case where it aids the investigation.

### **DETAINEE HIT**

A match between a detainee's DNA profile and the DNA profile from a forensic unknown or forensic mixture profile in an **unsolved** forensic case where it aids the investigation.

### **DUPLICATE**

A match made between any two profiles that does not provide probative information.

### **DUPLICATE MATCH**

The same match is already in the database (same Candidate and Target DNA profiles).

### **ID CONFIRMED**

A match or association between an unidentified human (remains) profile and a pedigree, reference profile or another profile of known origin where the identification has been confirmed by the appropriate authorities (such as a coroner or medical examiner).

### **ID PENDING**

A match or association between an unidentified human (remains) profile and a pedigree, reference profile or another profile of known origin where the identification has **not** been confirmed by the appropriate authorities (such as a coroner or medical examiner).

### **INSUFFICIENT DATA**

This missing person disposition is used following a match or rank when the combination of metadata and genetic information is lacking in either quantity or quality to either confirm or refute kinship or issue a report to law enforcement.

### **LEGAL INDEX HIT**

A match between a legal index DNA profile and the DNA profile from a forensic unknown or forensic mixture profile in an **unsolved** forensic case where it aids the investigation.

### **MATERNAL RELATIVES**

This disposition is used following a match or rank and indicates that although the association does not represent the specific relationship being sought, the two profiles likely originate from individuals of the same maternal lineage.

### **NO PROFILE**

Indicates that the search had no data for the selected technology (STR or mtDNA).

### **OFFENDER DUPLICATE**

A match made between two offender (Convicted Offender Index, Arrestee Index, Detainee Index, or Legal Index) profiles that does not provide probative information.

### **PATERNAL RELATIVES**

This disposition is used following a match or rank and indicates that although the association does not represent the specific relationship being sought, the two profiles likely originate from individuals of the same paternal lineage.

### **REQUESTING MORE REFERENCES**

This missing person disposition is used when the laboratory requests more reference samples to confirm or refute the validity of an association.

## **SIBLINGS**

This disposition is used when it is believed that a match involves two individuals in the database that share at least one biological parent.

### **19.5.3.4 INDEXES**

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#### **CONVICTED OFFENDER INDEX**

This index contains profiles from individuals convicted of felonies, misdemeanor sex offenses and violent offenders as according to Arkansas Law (Act 1470 of 2003). It also contains qualifying juvenile offenses according to Arkansas Law (Act 1780 of 2001). This index is uploaded to NDIS. For specimens that contain out-of-bin microvariants or tri-allelic patterns, the remaining loci may be entered into CODIS pending confirmation.

#### **ARRESTEE INDEX**

This index contains profiles from individuals arrested of felony offenses according to Arkansas Law (Act 543 of 2015). This index is uploaded to NDIS. For specimens that contain out-of-bin microvariants or tri-allelic patterns, the remaining loci may be entered into CODIS pending confirmation.

#### **DETAINEE INDEX**

A Detainee Index consists of DNA records from non-United States (U.S.) persons detained under the authority of the U.S. and required by law to provide a DNA sample.

#### **FORENSIC UNKNOWN INDEX**

This index contains profiles from crime scene evidence deemed appropriate for entry into CODIS. This index is uploaded to NDIS. The primary purpose of entering a forensic casework profile into the database is to identify the possible perpetrator of that particular crime for which the DNA analysis was conducted. This should be kept in mind when considering whether a profile is probative and should be entered into CODIS. Forensic 'Unknown' samples for which there is no suspect or the suspect has been eliminated should be entered in as the case number, the item number followed by a question mark (ex. YYYY-000000Q1?). 'Unknown' samples which include a submitted suspect should be entered in as the case number, the item number, followed by a CFM (Case File Match) (ex. YYYY-000000Q1CFM) CODIS entries should be documented on the "CODIS Entry Sheet". The source ID on case work samples should be marked as either "Yes" or "No" depending if the source has been identified through DNA testing. If a Forensic Unknown profile is incomplete, it can only be entered into the system if it contains all 13 Original CODIS core loci.

## **FORENSIC MIXTURE INDEX**

This index contains a profile from crime scene evidence which has multiple contributors. Mixtures are only deemed appropriate for CODIS if Moderate Match Estimator (MME) is  $\geq 1.00E+007$  and the number of original CODIS core loci is  $\geq 8$ . If numerous matches are made it is the discretion of the CODIS Administrator, or designee, to remove the sample. Analyst discretion will be used to determine what alleles will be entered into CODIS. The victim's profile will be subtracted from the mixture, leaving the profile that is determined to be the Most Likely Profile (MLP) to have come from the suspect. The profile will be entered into CODIS as the case number, the item number followed by MLP (ex. YYYY-000000Q1MLP). The MLP is determined by placing the victim's and evidence profile on the "CODIS Entry Sheet". Another qualified analyst must review the mixture and the MLP determination prior to entering the sample into CODIS.

When three alleles are present and the victim is heterozygous at that locus, the analyst must determine the obligate allele. The following is an example:

Victim = 12, 17 Evidence = 12, 17, 18

The analyst would search and enter this locus as 12, 17, 18+ (+) indicated the obligate allele.

## **FORENSIC PARTIAL INDEX**

A Forensic Partial Index consists of DNA profiles from single source forensic samples that do not contain results for all 13 core CODIS loci and/or that may indicate a possibility of allelic dropout. Forensic Partials are only deemed appropriate for CODIS if Moderate Match Estimator (MME) is  $\geq 1.00E+007$  and the number of Original CODIS core loci is  $\geq 8$ .

## **LEGAL INDEX**

A Legal Index consists of DNA records of persons whose DNA samples are collected under applicable legal authorities.

## **PEDIGREE TREE INDEX**

A Pedigree Tree Index consists of DNA records of biological relatives and spouses of missing persons that are associated with a Pedigree Tree.

## **RELATIVES OF MISSING PERSON INDEX**

A Relatives of Missing Person Index consists of DNA records from biological relatives of individuals reported missing.

## **SPOUSE INDEX**

A Spouse Index consists of the DNA records of a presumptive parent of a common child of a missing person.

## **DECEASED INDIVIDUALS INDEX**

This index contains samples from all deceased individuals which are submitted to the DNA Section by the Medical Examiner's Section. This index is not uploaded to NDIS. The profile will be entered into CODIS as the case number, K#, and V or ME####-## (ex. 2006-li-12345K1V). The source identified field should be marked as "Yes".

## **UNIDENTIFIED HUMAN REMAINS INDEX**

This index contains profiles from living persons of unknown identity and profiles from recovered dead persons whose identities are not known. This index is uploaded to NDIS.

## **MISSING PERSONS INDEX**

This index contains profiles of Known samples of missing persons and profiles obtained by examining intimate items purported to belong to a reported missing person, such as a tooth brush.

## **STAFF INDEX**

This index contains profiles of all Arkansas State Crime Laboratory staff members hired since July 18, 2005 and all staff members who worked at the lab prior to that date who volunteered their samples. Each member of the staff is given a unique number that is only known to the CODIS Administrator.

## **SUSPECT KNOWN INDEX**

This index contains profiles of suspects submitted in DNA cases. The suspect "Knowns" do not need to be entered on Case File Matches (CFM), only the evidence sample profile should be entered. The profile will be entered into CODIS as the case number and K# (ex. 2013-123456K1).

## **INCOMPLETE FORENSIC PROFILES INDEX**

This index contains profiles from crime scene evidence deemed appropriate for entry into CODIS that contain less than 8 loci. This index is not uploaded to NDIS. This index contains both specimen categories of Incomplete Forensic Unknowns and Incomplete Forensic Mixtures.

Incomplete Forensic Mixture is the SDIS version of NDIS Forensic Mixture category for samples not meeting NDIS threshold requirements. Mixtures are only deemed appropriate for Incomplete Forensic Mixture category if Moderate Match Estimator (MME) is  $\geq 4.000E+004$  and the number of Original CODIS core loci is  $\geq 6$ .

Incomplete Forensic Unknown is the SDIS version of NDIS Forensic Partial category for samples not meeting NDIS threshold requirements. Partial are only deemed appropriate for Incomplete Forensic Partial category if Moderate Match Estimator (MME) is  $\geq 4.000E+004$  and the number of Original CODIS core loci is  $\geq 6$ .

## **FORENSIC TARGETED INDEX**

This index contains profiles from forensic partials and forensic mixtures that do not meet the NDIS moderate match estimate threshold of 1 in 10 million, but do meet the match rarity estimate of 1 in 10 million if searched at a specified stringency by locus (high or moderate) and have 8 of the Original CODIS core loci.

NOTE: The CODIS Administrator will resolve all discrepancies on match dispositions, CODIS index and STR entries.

#### **19.5.4 GENEMAPPER ID-X AS AN EXPERT SYSTEM:**

GeneMapper ID-X v1.4 is not validated as an expert system. If an expert system is validated for use, a requirement for quarterly performance checks will be included in the equipment schedule.

### **19.6 REPORTS**

No reports are required for the CODIS Section per the *ASCL Quality Assurance Manual* (ASCL-DOC-01) section 7.8.1.2. A CODIS hit letter informs the agency about a hit. The letter is produced by the CODIS Administrator or her Designee. All CODIS hit documentation is stored in the CODIS section. A copy of official hit letter is also stored in JusticeTrax in the case file(s). Amendments to hit letters will generally follow the guidelines set by the *ASCL Quality Assurance Manual* (ASCL-DOC-01) section 7.8.8.

## 20 APPENDIX B

State Acts relating to CODIS samples can be accessed on Qualtrax System under CODIS discipline section.

## Familial Search Policy at Arkansas State Crime Lab

### Definition and Background

The Arkansas State Crime Laboratory routinely enters DNA profiles into state and national databases for the purpose of matching unknown forensic profiles to known contributors through routine database searches. These routine searches may yield a partial match to a close biological relative. This relationship may be explored with additional DNA testing by the ASCL and further verified by the investigating agency.

Familial Searching is an additional search of a DNA database conducted after a routine search has been completed and no profile matches are identified during the process. Unlike a routine database search which may spontaneously yield partial match profiles, familial searching is a deliberate search of a DNA database for the intended purpose of potentially identifying close biological relatives to the unknown forensic profile obtained from crime scene evidence. Familial Searching is based on the concept that first-order relatives, such as siblings or parent/child relationships, will have more genetic data in common than unrelated individuals.

### Authority:

The Executive Director of the Arkansas State Crime authorizes the use of familial searches on cases that meet the acceptance requirements established under this policy.

### Case Submission and Acceptance

1. The case is under authority / jurisdiction of an Arkansas law enforcement agency.
2. The case is an unsolved homicide or sexual assault and the case is active and under investigation.
3. All investigative leads have been exhausted.
4. A commitment by the law enforcement agency and the respective Prosecuting Attorney's Office to further investigate a positive association developed by the familial searching process.
5. A CODIS eligible STR and Y-STR DNA profile has been developed from the forensic unknown sample. The profile should be single source (allows for deduced and clearly discernable major or minor) and contain at a minimum the 13 original CODIS core loci.

A proposal meeting shall take place and the following laboratory personnel shall be in attendance:

CODIS Administrator, Physical Evidence and DNA Supervisor, Executive and/or Assistant Director

If the case meets the criteria for review, familial search meeting(s) will be scheduled with the law enforcement agency and the Prosecuting Attorney's Office to review and discuss all law

enforcement case files as well as ASCL case files to ensure all relevant evidence has been submitted.

If it is determined that the case is a good candidate for familial searching, the proper paperwork will be submitted, to include:

Official letter requesting familial searching from the law enforcement agency

MOU with all respective agencies:

Law enforcement agency

Prosecuting Attorney's Office

## Searching

The forensic unknown STR profile, having been searched at the State and National level, will be searched in the Familial Search program.

The results will be compiled and a male only candidate list will be formed. Female candidates will not be included at this time.

The candidate list will be released to the appropriate personnel included in the familial search meeting.

The law enforcement agency will investigate metadata associated with the candidate list. Metadata includes information on any known relatives of the candidate, such as age, residency or location at time of crime, criminal history, etc.

Once the law enforcement agency reviews and examines the list of candidates using appropriate metadata, the candidate matches will be examined by the ASCL for possible inclusion.

Candidates will be analyzed using Y-STR techniques.

## Results

Upon completion and review by the ASCL, the law enforcement agency and Prosecuting Attorney's Office will be notified of the familial search results in either of the following manners.

1. A matching candidate Y-STR profile to the Y-STR profile of the forensic unknown is a positive association. It is considered an investigative lead only.

A candidate sample that is a positive association will undergo a verification process to the extent possible, which may include:

- Re-analysis of the candidate sample.

- Fingerprint comparison and verification of the sample information card, or submission sheet.

A letter will be generated that lists the candidate's information and will be provided to the law enforcement agency and Prosecuting Attorney's Office during the closing familial search meeting.

2. No candidate Y-STR profile matching to the Y-STR profile of the forensic unknown is a negative association.

A letter will be generated indicating that the results of the familial search did not produce any matches

Cases can be re-submitted for familial search processing after six months. This timeframe will allow an increase in the size of the candidate database.

### **Data and Records**

Administrative documents will be retained in the original case file. This documentation may include the following:

- Familial Search Request Letter
- MOU
- Results Letter

All analytical paperwork and results will be retained electronically in a file separate from the original case file

A familial search summation report will be entered into the Familial Search Request in JusticeTrax. The wording will be similar to the following:

“A familial search was performed on sample ####-#####Q# on (date). See case file for correspondence.”