CODIS
Interface Specification (CMF 3.2)
Revision 9

CODIS Operations and Maintenance Support Services
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Prepared for:

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Revision History

Rev#	Date	Initials	Description
03	07/29/03	KME	First deployed version of CMF 3.2.
04	02/11/04	KME	DTI 2155 – Increased length of CODISLabType fields from 9 characters to 10 characters.
05	07/18/04	KME	DTI 2650 – Corrected the import.xsd in Appendix B to show that SeqAllele can occur a maximum of 1. A locus may have 8 alleles. An allele may have only one allele value.
06	03/08/05	CAE	Changed CODIS Help Desk Phone Number
07	04/11/05	KME	Changed the cover page
08	02/24/06	KME	DTIs: 3649, 3650, 3651 – Removed "Indicted Person" specimen category. Added "Spouse" and "Legal" specimen categories.
09	8/18/06	CJL	Updated cover page, incorporated comments from DTI 3597, i.e. no leading space in the comments field.

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1 Overview

This specification describes the interface between CODIS and external systems. This specification consists of the following sections:

- **Common Message Format –** summarizes the components of the CODIS Interface Specification Common Message Format (CMF).
- **Implementation –** describes the CODIS Interface Specification implementation for STR-based DNA typing.
- **Appendix A-Example Import CMF 3.2 file.**
- **Appendix B-Import XML XSD file –** defines the valid XML structure for a CMF file using an XML schema definition file.
- **Appendix C – Locus Information** – lists the currently delivered CODIS loci.
- **Appendix D –Specimen Category Information** – lists the currently delivered CODIS specimen categories.
- **Appendix E –PCR Kit Information** – lists the PCR Kits that are currently delivered by CODIS.
- **Appendix F – Import CMF 1.0 Message Format** – defines the current Import CMF 1.0 file using only the necessary PCR elements.

Questions regarding this document and requests for an electronic copy of this document and all schemas, etc. should be referred to the CODIS Help Desk at 1-877-CODISHD (263-4743) or email at CODISHelp@saic.com.

2   Common Message Format

The CODIS Interface Specification uses a Common Message Format (CMF) to enable the exchange of data between CODIS and external systems. The CMF defines the packaging of information for import into CODIS and is based on the Extensible Markup Language (XML) industry standard.

A CMF message has the following general format:

CMF Header
Specimen1
Specimen2
•
•
•

2.1   CMF Header

The CMF Header contains the following information:

- CMF Header Version
- CMF Message Type
- Destination Laboratory ORI
- Source Laboratory Name
- Submitting User ID
- Submit Date/Time
- Batch ID
- Kit

2.2   Specimen

Specimens have the following characteristics:

- Specimen ID
- Source ID
- Case ID
- Specimen Category
- Partial Profile Indicator
- Specimen Comment
- Loci

2.3   CMF Data Types and Formats

CMF files are described using consistent data types and formats.

2.3.1   Data Types

XML is a specification created by the W3C (the World Wide Web Consortium, http://www.w3c.org/) in 1998 in an effort to standardize text markup. Data types referred to in this document are defined by the W3C. All of the XML defined data types are mapped to SQL Server 2000 defined data types via the XML mapping schema. For more information, see the W3C XML Schema Part 2: Datatypes Recommendation at http://www.w3.org/TR/2001/REC-xmlschema-2-20010502:

- decimal – Represents arbitrary precision numbers. None of the values defined as decimal in the XML document are stored in the SQL Server database.

- string -- Represents character strings. Character data consists of any combination of letters, symbols, and numeric characters. Avoid using the pipe symbol (|) and semi-colon (;). These characters will cause problems when creating reports in CODIS.

  Certain characters in XML have a specific meaning to parsers, such as < and >. If any data in the CODIS import CMF file uses these special characters, a character reference string must be used for the parser to correctly interpret the character. The following table lists character reference strings:

Character Reference String	Resultant Character
&	&
>	>
<	<
'	'
"	"

- datetime – Represents a specific instance of time in a subset of the ISO 8601 format. The pattern for **dateTime** is CCYY-MM-DDThh:mm:ss where CC represents the century, YY the year, MM the month, and DD the day, preceded by an optional leading negative (-) character to indicate a negative number. If the negative character is omitted, positive (+) is assumed. The T is the date/time separator and hh, mm, and ss represent hour, minute, and second respectively. Additional digits can be used to increase the precision of fractional seconds if desired. For example, the format ss.ss... with any number of digits after the decimal point is supported. The fractional seconds part is optional.

  In SQL Server 2000, the dates in the XML document are stored as a datetime or smalldatetime data type.

  Note: The date format specified for CMF 1.0 import files is **not** valid for CMF 3.2 import files.

- Boolean – Represents Boolean values, which are either **true** or **false**.

3   Implementation

3.1   File Format

The CMF file, coded in XML, contains information about the specimens to be imported into CODIS.   This file consists of a CMF Header and one or more specimens structured in the format listed below. For readability in this document, the format shown below does not include the actual XML syntax. Tabs, carriage returns, and blanks may be inserted at the beginning or end of any line to improve readability. A carriage return and line feed character are at the end of each line in the Import CMF 3.2 file to allow easy viewing in text editors such as Microsoft Notepad. Microsoft Internet Explorer can also be used to view import files.   Comments may be included in the file following the XML comment syntax. No leading spaces are allowed in the comments field. See *Appendix A* for an example Import CMF 3.2 file. *Appendix B* includes the XML Schema Definition (XSD) document used in interpreting and validating the XML file.

CMF Header:

CMF Header Version (3.2 decimal)
CMF Message Type (Import, 6 characters)
CODIS Laboratory (destination) ORI (10 characters)
Source Laboratory Name (10 characters)
Submit By User ID (20 characters)
Submit Date/Time of this file (datetime, CCYY-MM-DDThh:mm:ss)
Batch Identifier (32 characters, optional)
Kit (32 characters, optional)

Specimen:

FOR each SPECIMEN
       CODIS Specimen Identifier (24 characters)
       CODIS Specimen Category (21 characters)
       Source ID (10 characters, optional)
       Case Identifier (32 characters, optional)
       Partial Profile Indicator (boolean, optional)
       Specimen Comment (255 characters with no leading spaces, optional)
       FOR each Locus
              CODIS Locus Name (10 characters)
              Reading By (20 characters, User ID of CODIS user)
              Reading Date/Time (datetime, CCYY-MM-DDThh:mm:ss)
              Batch Identifier (32 characters, optional)
              Kit (32 characters, optional)
              FOR each allele
                     Allele Value (10 characters)
                     Allele Required (boolean, optional)
              ENDFOR
       ENDFOR
ENDFOR

3.1.1 Import Header Values

The following table lists details for fields in the Import CMF header:

Field	Values/Formats	Validate[1]	XML Tag	Comments
CMF Header Version	3.2 Decimal 1 to Max	Schema	HEADERVERSION	Used to specify the version of the CMF header used. As requirements change, newer versions/formats of the CMF Header will be used.
CMF Message Type	Import Up to 6 characters.	Schema	MESSAGETYPE	The only valid message type is Import.
Destination ORI	Up to 10 characters.	CODIS	DESTINATIONORI	CODIS ORI for the destination CODIS laboratory that will import the CMF file.
Source Laboratory Name	Up to 10 characters.	CODIS	SOURCELAB	The name of the source laboratory producing the CMF file. This could contain the name of the contract laboratory or be the same as the destination ORI.
Submit By User ID	Up to 20 characters.	CODIS	SUBMITBYUSERID	The user id of the person submitting the import file.
Submit Date/Time	Datetime, CCYY-MM-DDThh:mm:ss	CODIS	SUBMITDATETIME	The date/time for when the CMF file was created.
Batch Identifier	Up to 32 characters.	CODIS	BATCHID	An identifier for the batch to which the specimen belongs. Some labs refer to this field as gel or plate identifier. A specimen may have loci from multiple batches. This field is optional. If the field is not specified, loci will be inserted without a batch identifier. It is not necessary to specify a batch identifier for each locus if all of the loci in this import file were produced using the same batch.
PCR Kit	Up to 32 characters.	Schema	KIT	The PCR kit that was used to produce the readings for the specimens in the CMF file. See Appendix E for

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[1] The validate column indicates if CODIS Import module is responsible for validating the content of the field or if the Import XML schema will validate the content of the field.

				valid PCR kits.
				This field is optional. If the field is not specified, loci will be inserted without a kit. It is not necessary to specify a kit for each locus if all of the loci in this import file were produced using the same kit.

3.1.2 Import Specimen Values

The table below describes the fields defining a specimen. No limit exists for the number of specimens that can be within an import file.

<u>Field</u>	<u>Values/Formats</u>	<u>Validate</u>	<u>XML Tag</u>	<u>Comments</u>
CODIS Specimen Identifier	Up to 24 characters. Symbols allowed include the pound sign (#), single quote ('), double quote ("), slash (/) and hyphen (-).	Schema	SPECIMENID	An identifier for the specimen within the import file. Specimen identifiers must be unique within each CMF import file.
CODIS Specimen Category	Up to 21 characters.	Schema	SPECIMENCATEGORY	See Appendix D for valid specimen categories. Schema validation is case sensitive for specimen categories.
Source Identified	Up to 10 characters.	Schema	SOURCEID	This field is an indicator if the identity of the specimen contributor is known. This field is optional. If the field is not specified, specimens will be inserted using a default value that is configured in CODIS per specimen category.
Case Identifier	Up to 32 characters.	Schema	CASEID	An identifier for the case to which the specimen belongs. This field is optional. If the field is not specified, specimens will be inserted without a case identifier.
CODIS Partial Profile Indicator	Boolean value of either true or false.	Schema	PARTIAL	This field is an indicator if the specimen may have additional information. Possible allele drop-out could be a condition for indicating that the profile is partial. This field is optional. If the field is not specified, specimens are inserted into the database as not Partial.
Specimen Comment	Up to 255 characters.	Schema	SPECIMENCOMMENT	Any comment that provides information regarding the specimen. No leading spaces.

Field	Values/Formats	Validate	XML Tag	Comments
				This field is optional. If the field is not specified, specimens are inserted into the database without a comment.

The following table describes the format for each locus belonging to a specimen. Specimens are limited to 32 loci per specimen.

Field	Values/Formats	Validate	XML Tag	Comments
CODIS Locus name	Up to 10 characters.	Schema	LOCUSNAME	See Appendix C for valid Locus names. Locus names must be unique within each specimen. If more than one kit is used to process the specimen, then the duplicate overlapping loci should be removed before importing into CODIS. Each kit can also be imported as separate CMF import files. Schema validation is case sensitive for locus names.
Reading By	Up to 20 characters.	CODIS	READINGBY	A valid CODIS User ID of the person performing the reading.
Reading Date/Time	Datetime, CCYY-MM-DDThh:mm:ss	CODIS	READINGDATETIME	Date/time the reading was performed.
Batch Identifier	Up to 32 characters.	CODIS	BATCHID	An identifier for the batch to which the locus belongs. Some labs refer to this field as gel or plate identifier. A specimen may have loci from multiple batches. This field is optional. If the field is not specified, loci will be inserted without a batch identifier unless a batch identifier was specified for the entire import file. Do not specify a batch identifier for the locus if the batch identifier is the same as the batch identifier specified for the entire file. If a batch identifier is specified for entire file and a different batch identifier is specified for the locus, then the batch identifier for the locus will be inserted. A specimen may have loci from

Field	Values/Formats	Validate	XML Tag	Comments
				multiple batches.
PCR Kit	Up to 32 characters.	Schema	KIT	The PCR kit that was used to produce this reading for this locus in the CMF file.

This field is optional. If the field is not specified, the locus will be inserted without a kit unless a kit was specified for the entire import file. Do not specify a kit for the locus if the kit is the same as the kit specified for the entire file. If a kit is specified for entire file and a different kit is specified for the locus, then the kit for the locus will be inserted. A specimen may have loci from multiple kits. |

The following table describes the format for each allele belonging to a locus. Loci are limited to 8 alleles per locus.

Field	Values/Formats	Validate	XML Tag	Comments
Locus Allele Value	Up to 10 characters.	CODIS	ALLELEVALUE	Contact the CODIS Administrator for a list of valid alleles values for each locus.
Locus Allele Required	Boolean value of either true or false.	Schema	ALLELEREQUIRED	This field is an indicator if the allele is required to be present for a match to be reported when searching. This field is optional. If the field is not specified, alleles are inserted into the database as not required. Only one allele may be required for each locus within a specimen.

When providing allele values in the import CMF file, the following suggestions can improve performance of processing import files:

1. Allele values should avoid the necessity of off-ladder allele conversion by using only allele values defined within CODIS.
2. Duplicated homozygous alleles should be replaced by a single allele (*e.g.* A) instead of two identical allele values (e.g. AA).
3. Allele values for a STR genotype should be sorted according to the nomenclature defined by the Software Working Group on DNA Analysis (SWGDAM). For example, <9, 9, 9.1, 9.2, 9.3, 10, >10.

Note: Symbols such as < and > must by replaced by character reference strings before importing into CODIS. See String Data Types, section 2.3.1, for more information.

4 Validation

The Import application validates both the format of the CMF 3.2 file and the data contained within the file. Contractors using an XML Validator can also validate the format of the CMF 3.2 file without having to install CODIS. Please contact the CODIS Help Desk at 1-877-CODISHD (263-4743) or email at CODISHelp@saic.com to request this utility.

Appendix A. Example CMF 3.2 File

An example of an Import CMF 3.2 file results follows:

```xml
<?xml version="1.0" encoding="UTF-8"?>
<CODISImportFile xmlns="urn:CODISImportFile-schema">
 <HEADERVERSION>3.2</HEADERVERSION>
 <MESSAGETYPE>Import</MESSAGETYPE>
 <DESTINATIONORI>IADCI0000</DESTINATIONORI>
 <SOURCELAB>IADCI0000</SOURCELAB>
 <SUBMITBYUSERID>KEllis</SUBMITBYUSERID>
 <SUBMITDATETIME>2002-02-14T21:51:44</SUBMITDATETIME>
 <BATCHID>GEL2004_10_04_101</BATCHID >
 <KIT>PowerPlex 16</KIT>
 <SPECIMEN SOURCEID="Yes" CASEID="FL2004_10_04_ABC" PARTIAL="true">
  <SPECIMENID>IMP_0001A</SPECIMENID>
  <SPECIMENCATEGORY>Forensic, Unknown</SPECIMENCATEGORY>
  <SPECIMENCOMMENT>Off-ladder allele value observed for FGA.</SPECIMENCOMMENT>
  <LOCUS BATCHID="GEL2004_10_04_100">
   <LOCUSNAME>CSF1PO</LOCUSNAME>
   <READINGBY>KELLIS</READINGBY>
   <READINGDATETIME>2002-02-13T21:50:42</READINGDATETIME>
   <ALLELE ALLELEREQUIRED="true">
    <ALLELEVALUE>10</ALLELEVALUE>
   </ALLELE>
   <ALLELE>
    <ALLELEVALUE>11</ALLELEVALUE>
   </ALLELE>
  </LOCUS>
  <LOCUS BATCHID="GEL2004_10_05_67" KIT="PowerPlex 1.2">
   <LOCUSNAME>D13S317</LOCUSNAME>
   <READINGBY>KELLIS</READINGBY>
   <READINGDATETIME>2002-02-13T21:50:42</READINGDATETIME>
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   </ALLELE>
   <ALLELE ALLELEREQUIRED="true">
    <ALLELEVALUE>9</ALLELEVALUE>
   </ALLELE>
  </LOCUS>
  <LOCUS>
   <LOCUSNAME>D16S539</LOCUSNAME>
   <READINGBY>KELLIS</READINGBY>
   <READINGDATETIME>2002-02-13T21:50:42</READINGDATETIME>
   <ALLELE>
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   </ALLELE>
   <ALLELE>
    <ALLELEVALUE>7</ALLELEVALUE>
   </ALLELE>
  </LOCUS>
  <LOCUS>
   <LOCUSNAME>D18S51</LOCUSNAME>
   <READINGBY>KELLIS</READINGBY>
```

```xml
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  </ALLELE>
  <ALLELE>
   <ALLELEVALUE>12</ALLELEVALUE>
  </ALLELE>
 </LOCUS>
 <LOCUS>
  <LOCUSNAME>D21S11</LOCUSNAME>
  <READINGBY>KELLIS</READINGBY>
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  </ALLELE>
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```

```
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  </LOCUS>
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  <SPECIMENCATEGORY>Forensic, Unknown</SPECIMENCATEGORY>
```

```
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minumum peak threshold.</SPECIMENCOMMENT>
    <LOCUS BATCHID="GEL2004_10_05_68" KIT="PowerPlex 1.1">
     <LOCUSNAME>CSF1PO</LOCUSNAME>
     <READINGBY>KELLIS</READINGBY>
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```

```
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        <LOCUSNAME>vWA</LOCUSNAME>
        <READINGBY>KELLIS</READINGBY>
        <READINGDATETIME>2002-02-13T21:50:47</READINGDATETIME>
        <ALLELE>
          <ALLELEVALUE>15</ALLELEVALUE>
        </ALLELE>
        <ALLELE>
          <ALLELEVALUE>16</ALLELEVALUE>
        </ALLELE>
      </LOCUS>
      <LOCUS>
        <LOCUSNAME>Amelogenin</LOCUSNAME>
        <READINGBY>KELLIS</READINGBY>
        <READINGDATETIME>2002-02-13T21:50:47</READINGDATETIME>
        <ALLELE>
          <ALLELEVALUE>X</ALLELEVALUE>
        </ALLELE>
        <ALLELE>
          <ALLELEVALUE>Y</ALLELEVALUE>
        </ALLELE>
      </LOCUS>
      <LOCUS>
        <LOCUSNAME>Penta D</LOCUSNAME>
        <READINGBY>KELLIS</READINGBY>
        <READINGDATETIME>2002-02-13T09:51:48</READINGDATETIME>
        <ALLELE>
```

```
      <ALLELEVALUE>7.3</ALLELEVALUE>
    </ALLELE>
    <ALLELE>
      <ALLELEVALUE>&gt;17</ALLELEVALUE>
    </ALLELE>
  </LOCUS>
  <LOCUS>
    <LOCUSNAME>Penta E</LOCUSNAME>
    <READINGBY>KELLIS</READINGBY>
    <READINGDATETIME>2002-02-13T00:00:00</READINGDATETIME>
    <ALLELE>
      <ALLELEVALUE>15</ALLELEVALUE>
    </ALLELE>
    <ALLELE>
      <ALLELEVALUE>16</ALLELEVALUE>
    </ALLELE>
  </LOCUS>
 </SPECIMEN>
</CODISImportFile>
```

Appendix B. Import XML XSD File

The Import XML XSD file used for validation follows:

```
<xsd:schema xmlns:xsd="http://www.w3.org/2001/XMLSchema" xmlns="urn:CODISImportFile-schema"
   xmlns:sql="urn:schemas-microsoft-com:mapping-schema" elementFormDefault="qualified"
targetNamespace="urn:CODISImportFile-schema"
   xmlns:r="urn:CODISImportFile-schema">
   <xsd:element name="CODISImportFile" sql:is-constant="true">
     <xsd:complexType>
       <xsd:sequence maxOccurs="1" id="SeqImportFile" minOccurs="1">
         <xsd:element name="HEADERVERSION" type="CODISHeaderVersionType" minOccurs="1"
maxOccurs="1" sql:mapped="false" />
         <xsd:element name="MESSAGETYPE" type="CODISMessageType" minOccurs="1"
maxOccurs="1" sql:mapped="false" />
         <xsd:element name="DESTINATIONORI" type="CODISLabType" minOccurs="1"
maxOccurs="1" sql:mapped="false" />
         <xsd:element name="SOURCELAB" type="CODISLabType" minOccurs="1" maxOccurs="1"
sql:mapped="false" />
         <xsd:element name="SUBMITBYUSERID" type="CODISUserType" minOccurs="1"
maxOccurs="1" sql:mapped="false" />
         <xsd:element name="SUBMITDATETIME" type="CODISImportDate" minOccurs="1"
maxOccurs="1" sql:mapped="false" />
         <xsd:element name="BATCHID" type="BatchIDType" maxOccurs="1" minOccurs="0"
sql:mapped="false" />
         <xsd:element name="KIT" type="KitType" maxOccurs="1" minOccurs="0" sql:mapped="false" />
         <xsd:element name="SPECIMEN" type="SpecimenType" minOccurs="1"
maxOccurs="unbounded" sql:relation="Import_Specimen"
         sql:key-fields="SPEC_ID">
         <xsd:unique name="UNIQUE_LOCI">
           <xsd:selector xpath="r:LOCUS" />
           <xsd:field xpath="r:LOCUSNAME" />
         </xsd:unique>
       </xsd:element>
     </xsd:sequence>
   </xsd:complexType>
   <xsd:unique name="UNIQUE_SPEC">
     <xsd:selector xpath="r:SPECIMEN" />
     <xsd:field xpath="r:SPECIMENID" />
   </xsd:unique>
 </xsd:element>
 <xsd:simpleType name="CODISHeaderVersionType">
   <xsd:restriction base="xsd:decimal">
     <xsd:totalDigits value="2" />
     <xsd:fractionDigits value="1" />
   </xsd:restriction>
 </xsd:simpleType>
 <xsd:simpleType name="CODISMessageType">
   <xsd:restriction base="xsd:string">
     <xsd:length value="6" />
     <xsd:enumeration value="Import" />
   </xsd:restriction>
 </xsd:simpleType>
 <xsd:simpleType name="CODISLabType">
```

```xml
    <xsd:restriction base="xsd:string">
      <xsd:maxLength value="10" />
      <xsd:minLength value="1" />
    </xsd:restriction>
  </xsd:simpleType>
  <xsd:simpleType name="CODISUserType">
    <xsd:restriction base="xsd:string">
      <xsd:maxLength value="20" />
      <xsd:minLength value="1" />
    </xsd:restriction>
  </xsd:simpleType>
  <xsd:simpleType name="CODISImportDate">
    <xsd:restriction base="xsd:dateTime">
      <xsd:minExclusive value="1900-01-01T00:00:00" />
      <xsd:maxExclusive value="2079-06-06T00:00:00" />
    </xsd:restriction>
  </xsd:simpleType>
  <xsd:simpleType name="SpecimenIDType">
    <xsd:restriction base="xsd:string">
      <xsd:maxLength value="24" />
      <xsd:minLength value="1" />
    </xsd:restriction>
  </xsd:simpleType>
  <xsd:simpleType name="SpecimenCategoryType">
    <xsd:restriction base="xsd:string">
      <xsd:maxLength value="21" />
      <xsd:minLength value="1" />
      <xsd:enumeration value="Convicted Offender" />
      <xsd:enumeration value="Forensic, Unknown" />
      <xsd:enumeration value="Population" />
      <xsd:enumeration value="Suspect, Known" />
      <xsd:enumeration value="Unidentified Person" />
      <xsd:enumeration value="Victim, Known" />
      <xsd:enumeration value="Elimination, Known" />
      <xsd:enumeration value="Biological Mother" />
      <xsd:enumeration value="Biological Father" />
      <xsd:enumeration value="Biological Sibling" />
      <xsd:enumeration value="Alleged Mother" />
      <xsd:enumeration value="Alleged Father" />
      <xsd:enumeration value="Biological Child" />
      <xsd:enumeration value="Proficiency" />
      <xsd:enumeration value="Other" />
      <xsd:enumeration value="Missing Person" />
      <xsd:enumeration value="Forensic Mixture" />
      <xsd:enumeration value="Maternal Relative" />
      <xsd:enumeration value="Paternal Relative" />
      <xsd:enumeration value="Deduced Victim Known" />
      <xsd:enumeration value="Arrestee" />
      <xsd:enumeration value="Deceased" />
      <xsd:enumeration value="Deduced Suspect" />
      <xsd:enumeration value="Staff" />
      <xsd:enumeration value="Juvenile" />
      <xsd:enumeration value="CO Duplicate" />
      <xsd:enumeration value="Volunteer" />
      <xsd:enumeration value="Spouse" />
      <xsd:enumeration value="Legal" />
```

```xml
        </xsd:restriction>
      </xsd:simpleType>
      <xsd:simpleType name="SpecimenCommentType">
        <xsd:restriction base="xsd:string">
          <xsd:maxLength value="255" />
          <xsd:minLength value="0" />
        </xsd:restriction>
      </xsd:simpleType>
      <xsd:simpleType name="SourceIDType">
        <xsd:restriction base="xsd:string">
          <xsd:maxLength value="10" />
          <xsd:minLength value="0" />
          <xsd:enumeration value="Yes" />
          <xsd:enumeration value="No" />
          <xsd:enumeration value="N/A" />
        </xsd:restriction>
      </xsd:simpleType>
      <xsd:simpleType name="CaseIDType">
        <xsd:restriction base="xsd:string">
          <xsd:maxLength value="32" />
          <xsd:minLength value="0" />
        </xsd:restriction>
      </xsd:simpleType>
      <xsd:simpleType name="LocusNameType">
        <xsd:restriction base="xsd:string">
          <xsd:maxLength value="10" />
          <xsd:minLength value="1" />
          <xsd:enumeration value="AMEL" />
          <xsd:enumeration value="Amelogenin" />
          <xsd:enumeration value="CSF1PO" />
          <xsd:enumeration value="D13S317" />
          <xsd:enumeration value="D16S539" />
          <xsd:enumeration value="D18S51" />
          <xsd:enumeration value="D19S433" />
          <xsd:enumeration value="D21S11" />
          <xsd:enumeration value="D2S1338" />
          <xsd:enumeration value="D3S1358" />
          <xsd:enumeration value="D5S818" />
          <xsd:enumeration value="D7S820" />
          <xsd:enumeration value="D8S1179" />
          <xsd:enumeration value="FGA" />
          <xsd:enumeration value="Penta D" />
          <xsd:enumeration value="Penta E" />
          <xsd:enumeration value="TH01" />
          <xsd:enumeration value="THO1" />
          <xsd:enumeration value="TP0X" />
          <xsd:enumeration value="TPOX" />
          <xsd:enumeration value="vWA" />
        </xsd:restriction>
      </xsd:simpleType>
      <xsd:simpleType name="BatchIDType">
        <xsd:restriction base="xsd:string">
          <xsd:maxLength value="32" />
          <xsd:minLength value="0" />
        </xsd:restriction>
      </xsd:simpleType>
```

```xml
<xsd:simpleType name="KitType">
  <xsd:restriction base="xsd:string">
    <xsd:maxLength value="32" />
    <xsd:minLength value="0" />
    <xsd:enumeration value="COfiler" />
    <xsd:enumeration value="Identifiler" />
    <xsd:enumeration value="Profiler Plus" />
    <xsd:enumeration value="PowerPlex 1.1" />
    <xsd:enumeration value="PowerPlex 1.2" />
    <xsd:enumeration value="PowerPlex 2.1" />
    <xsd:enumeration value="PowerPlex 16" />
    <xsd:enumeration value="Monoplex D5S818" />
    <xsd:enumeration value="Monoplex D7S820" />
    <xsd:enumeration value="Monoplex D13S317" />
    <xsd:enumeration value="Monoplex D16S539" />
    <xsd:enumeration value="Monoplex TH01" />
    <xsd:enumeration value="Monoplex TPOX" />
    <xsd:enumeration value="Monoplex CSF1PO" />
    <xsd:enumeration value="Monoplex vWA" />
    <xsd:enumeration value="SGM Plus" />
  </xsd:restriction>
</xsd:simpleType>
<xsd:simpleType name="AlleleValueType">
  <xsd:restriction base="xsd:string">
    <xsd:maxLength value="10" />
    <xsd:minLength value="1" />
  </xsd:restriction>
</xsd:simpleType>
<xsd:complexType name="SpecimenType">
  <xsd:sequence id="SeqSpecimen" minOccurs="1">
    <xsd:element name="SPECIMENID" type="SpecimenIDType" minOccurs="1" maxOccurs="1"
sql:field="SPEC_ID" />
    <xsd:element name="SPECIMENCATEGORY" type="SpecimenCategoryType" minOccurs="1"
maxOccurs="1"
      sql:field="SPEC_CATEGORY" />
    <xsd:element name="SPECIMENCOMMENT" type="SpecimenCommentType" maxOccurs="1"
minOccurs="0" sql:field="COMMENT" />
    <xsd:element name="LOCUS" minOccurs="1" maxOccurs="32" sql:relation="Import_Locus"
sql:relationship="SpecimenLocus"
      sql:key-fields="SPEC_ID LOCUS_NAME">
      <xsd:complexType>
        <xsd:sequence id="SeqLocus" minOccurs="1" maxOccurs="32">
          <xsd:element name="LOCUSNAME" type="LocusNameType" minOccurs="1"
maxOccurs="1" sql:field="LOCUS_NAME" />
          <xsd:element name="READINGBY" type="CODISUserType" minOccurs="1" maxOccurs="1"
sql:field="READING_BY" />
          <xsd:element name="READINGDATETIME" type="CODISImportDate" minOccurs="1"
maxOccurs="1" sql:field="READING_DT"
            sql:datatype="datetime" />
          <xsd:element name="ALLELE" type="AlleleType" minOccurs="1" maxOccurs="8"
sql:relation="Import_Allele"
            sql:relationship="LocusAllele" sql:key-fields="SPEC_ID LOCUS_NAME PCR_VALUE" />
        </xsd:sequence>
        <xsd:attribute name="BATCHID" type="BatchIDType" sql:field="BATCH_ID" />
        <xsd:attribute name="KIT" type="KitType" sql:field="KIT_NAME" />
      </xsd:complexType>
```

```
      </xsd:element>
    </xsd:sequence>
    <xsd:attribute name="SOURCEID" type="SourceIDType" sql:field="SOURCE_ID" />
    <xsd:attribute name="CASEID" type="CaseIDType" sql:field="CASE_ID" />
    <xsd:attribute name="PARTIAL" type="xsd:boolean" sql:field="PARTIAL" />
  </xsd:complexType>
  <xsd:complexType name="AlleleType">
    <xsd:sequence id="SeqAllele" minOccurs="1" maxOccurs="1">
      <xsd:element name="ALLELEVALUE" type="AlleleValueType" minOccurs="1" maxOccurs="1"
sql:field="PCR_VALUE" />
    </xsd:sequence>
    <xsd:attribute name="ALLELEREQUIRED" type="xsd:boolean" sql:field="ALLELE_REQUIRED"
default="false" />
  </xsd:complexType>
  <xsd:annotation>
    <xsd:appinfo>
      <sql:relationship name="SpecimenLocus" parent="Import_Specimen" parent-key="SPEC_ID"
child="Import_Locus"
        child-key="SPEC_ID" />
      <sql:relationship name="LocusAllele" parent="Import_Locus" parent-key="SPEC_ID
LOCUS_NAME" child="Import_Allele"
        child-key="SPEC_ID LOCUS_NAME" />
    </xsd:appinfo>
  </xsd:annotation>
</xsd:schema>
```

Appendix C. Valid STR Loci

The table below shows the currently delivered CODIS STR loci. CODIS laboratories have the ability to add other loci.

STR Locus Name
Amelogenin
CSF1PO
D13S317
D16S539
D18S51
D19S433
D21S11
D2S1338
D3S1358
D5S818
D7S820
D8S1179
FGA
Penta D
Penta E
TH01
TPOX
vWA

Appendix D. Valid Specimen Categories

The table below shows the currently delivered CODIS specimen categories. CODIS laboratories have the ability to add other specimen categories.

Specimen Category
Alleged Father
Alleged Mother
Arrestee
Biological Child
Biological Father
Biological Mother
Biological Sibling
CO Duplicate
Convicted Offender
Deceased
Deduced Suspect
Deduced Victim Known
Elimination, Known
Forensic Mixture
Forensic, Unknown
Juvenile
Legal
Maternal Relative
Missing Person
Other
Paternal Relative
Population
Proficiency
Spouse
Staff
Suspect, Known
Unidentified Person
Victim, Known
Volunteer

Appendix E. Valid PCR Kits

The table below shows the PCR kits currently delivered by CODIS. CODIS laboratories have the ability to add other kits:

CODIS Kit Name	Manufacturer	Kit Description
Profiler Plus	Applied Biosystems	AmpFLSTR® Profiler Plus™ (Part Number 4303326)
COfiler	Applied Biosystems	AmpFLSTR® COfiler™ (Part Number 4305246)
	Applied Biosystems	AmpFLSTR® Profiler Plus™ and AmpFLSTR® COfiler™ (Part Number 4305979)
Profiler Plus	Applied Biosystems	AmpFLSTR® Profiler Plus™ ID (Part Number 4330284)
	Applied Biosystems	AmpFLSTR® Profiler Plus™ ID and AmpFLSTR® COfiler™ (Part Number 4330621)
Identifiler	Applied Biosystems	AmpFLSTR® Identifiler™ (Part Number 4322288)
SGM Plus	Applied Biosystems	AmpFLSTR® SGM Plus® (Part Number 4307133)
PowerPlex 1.1	Promega	PowerPlex® 1.1(Catalog numbers DC6091/6090)
PowerPlex 1.2	Promega	PowerPlex® 1.2 (Catalog numbers DC 6101/6100)
PowerPlex 2.1	Promega	PowerPlex® 2.1 (Catalog numbers DC 6471/6470)
PowerPlex 16	Promega	PowerPlex® 16 (Catalog numbers DC 6531/6530)
PowerPlex 16	Promega	PowerPlex® 16 BIO (Catalog numbers DC 6541/6540)
Monoplex D5S818	Promega Monoplex*	Monoplex D5S818 (Catalog number DC6161)
Monoplex D7S820	Promega Monoplex*	Monoplex D7S820 (Catalog number DC6141)
Monoplex D13S317	Promega Monoplex*	Monoplex D13S317 (Catalog number DC6151)
Monoplex D16S539	Promega Monoplex*	Monoplex D16S539 (Catalog number DC6131)
Monoplex TH01	Promega Monoplex*	Monoplex TH01 (Catalog number DC5081)
Monoplex TPOX	Promega Monoplex*	Monoplex TPOX (Catalog number DC5111)
Monoplex CSF1PO	Promega Monoplex*	Monoplex CSF1PO (Catalog number DC5091)
Monoplex vWA	Promega Monoplex*	Monoplex vWA (Catalog number DC5141)

* Monoplexes are all fluorescene-labeled and have same chemistry as when in multiplex kits.

Appendix F. Import CMF 1.0 Message Format

The Import CMF 1.0 information expected from the external imaging system consists of an ASCII file containing analysis information for those specimens processed by the external imaging system.[2] The file is a CMF message consisting of the following information. (Each line represents a single line of text in the CMF file.)

CMF Header:

CMF Header Version (1.0)
CMF Message ID (Integer) *
CMF Message Type (IMPORT)
Imaging system (source) ORI (9 characters)
CODIS Laboratory (destination) ORI (9 characters)
Creation Date/Time of this file (DD-MMM-YYYY HH:MM:SS)
Imaging system organization/company (up to 64 characters) *
Imaging system utilized (up to 64 characters) *
Number of packets in this file (Integer)

CMF Packets: The IMPORT message contains the specified number of the following types of CMF packets.

FOR each CMF packet
        CMF Packet Type (DNA Analysis Result)
        CMF Packet Version (1.0)
        CODIS Technology used for analysis (PCR)
        CODIS Specimen Number (24 characters)
        CODIS Sample ID (0)
        CODIS Specimen Category (21 characters)
        CODIS Tissue Type (Unknown)*
        CODIS Tissue Form (Unknown) *
        CODIS Population Group (Unknown) *
        Number of markers (Must be >=1 and <=32)
        FOR each marker
                CODIS Marker Name
                Number of readings (1)
                Reading By (8 characters, User ID of CODIS user)
                Reading Date (DD-MMM-YYYY)
                Reading Time (HH:MM:SS)
                Number of alleles (Must be >=1 and <=8)
                FOR each allele
                        PCR Value
                ENDFOR
        ENDFOR
ENDFOR

---

[2] This document is based on the *CODIS Imaging Application Program Interface, 2/3/1997.*

* These fields are ignored by the CODIS Import utility, but must be present as lines within the CMF Import file.

An example of a CMF 1.0 import file looks like the following (this is the same file as in the CMF 3.2 example in Appendix A). Source ID, Case ID, Kit, Batch ID, Partial Profile Indicator, Specimen Comments and Required Alleles are not supported in the CMF 1.0 format.

```
1.0
1
IMPORT
IADCI0000
IADCI0000
14-FEB-2002 21:51:44
IMP_0001.dat
GenoTyper
2
DNA Analysis Result
1.0
PCR
IMP_0001A
0
FORENSIC, UNKNOWN
UNKNOWN
UNKNOWN
UNKNOWN
13
CSF1PO
1
KELLIS
13-FEB-2002
21:50:42
2
10
11
D13S317
1
KELLIS
13-FEB-2002
21:50:42
2
8
9
D16S539
1
KELLIS
13-FEB-2002
21:50:42
2
6
7
D18S51
1
KELLIS
13-FEB-2002
21:50:42
2
11
12
D21S11
```

1
KELLIS
13-FEB-2002
21:50:47
2
28
29
D3S1358
1
KELLIS
13-FEB-2002
21:50:47
2
14
15
D5S818
1
KELLIS
13-FEB-2002
21:50:47
2
9
10
D7S820
1
KELLIS
13-FEB-2002
21:50:47
2
8
9
D8S1179
1
KELLIS
13-FEB-2002
21:50:47
2
11
12
FGA
1
KELLIS
13-FEB-2002
21:50:47
2
24
25
TH01
1
KELLIS
13-FEB-2002
21:50:47
2
8
9
TPOX

1
KELLIS
13-FEB-2002
21:50:47
2
10
11
vWA
1
KELLIS
13-FEB-2002
21:50:47
2
15
16
DNA Analysis Result
1.0
PCR
IMP_0001B
0
FORENSIC, UNKNOWN
UNKNOWN
UNKNOWN
UNKNOWN
16
CSF1PO
1
KELLIS
13-FEB-2002
21:50:42
2
<6
8.2
D13S317
1
BKNOLL
2-MAR-2001
11:50:42
2
13
>15
D16S539
1
CLEE
1-JAN-2001
02:50:42
4
6
7
13.1
14.2
D18S51
1
KELLIS
13-FEB-2002
21:50:42

1
11
D21S11
1
KELLIS
13-FEB-2002
21:50:47
3
<25
28
29
D3S1358
1
KELLIS
13-FEB-2002
21:50:47
2
14
15
D5S818
1
KELLIS
13-FEB-2002
21:50:47
2
9
10
D7S820
1
KELLIS
13-FEB-2002
21:50:47
2
8
9
D8S1179
1
KELLIS
13-FEB-2002
21:50:47
2
11
12
FGA
1
KELLIS
13-FEB-2002
21:50:47
2
24
25
TH01
1
KELLIS
13-FEB-2002
21:50:47

2
8
9
TPOX
1
KELLIS
13-FEB-2002
21:50:47
2
10
11
vWA
1
KELLIS
13-FEB-2002
21:50:47
2
15
16
Amelogenin
1
KELLIS
13-FEB-2002
21:50:47
2
X
Y
Penta D
1
KELLIS
13-FEB-2002
09:51:48
2
7.3
>17
Penta E
1
KELLIS
13-FEB-2002
00:00:00
2
15
16