

**DNA SOP-6 Report Templates,Statistic Templates, Stutter
and Criticals**

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Approved by Director: Dr. Guy Vallaro

Section 1 Responsibility:

DNA Section Personnel.

Section 2 DNA Report Templates:

Note: The DNA Report Template is located in the controlled Report Template folder on the S drive. Electronic versions of final reports are located on the U drive in the “CASEREPORTS” folder.

Nuclear DNA Reports

Formerly, there were multiple types of DNA Reports. Going forward, all DNA Reports will be called DNA Reports.

Mitochondrial DNA Reports

Formerly, Mitochondrial DNA Reports were separate from the Nuclear DNA Reports. The mtDNA report statements have been incorporated into the DNA Report Template. See mtDNA SOP-10 for guidelines on mtDNA report writing.

Supplemental Report Numbering

Supplemental reports for each report heading are numbered independently of each other. For example:

DNA Report

Supplemental DNA Report

Supplemental DNA Report II

Amended DNA Report

Statistics Templates

Note: See DNA SOP-5 for single source and mixture profile interpretations and statistic details.

Statistics are calculated and documented for case files using DNA QR-40 (single source), QR-41 (mixture), QR-42 (paternity) and QR-43 (Y-STR). The Excel workbooks containing these listed quality records are found on the S:Drive.

Frequency data to calculate the statistical weight of DNA matches may be derived from the following databases:

CODIS Popstats Database

National Y-STR Database (<https://usysrtdatabase.org/>)

State of CT Autosomal Database

Per specific requests, other peer reviewed Databases may be used.

Identifiler Plus:

1. Identifiler Plus report statement for single-source profiles:
 - a. The results are consistent with NAME being the source of the DNA profile from item #. The expected frequency of individuals who could be the source of the DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations.
 - b. NAME cannot be eliminated as the source of the DNA profile from item #. The expected frequency of individuals who cannot be eliminated as the source of the DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations.
2. Identifiler Plus report statement for mixture profiles:

Note: If a mixture is not fully confirmed, use the following statement: The results are consistent with item # being a mixture. (if only one three+ allele locus is present)

- a. The results demonstrate that item # is a mixture. NAME is included as a potential contributor to the DNA profile from item #. The expected frequency of individuals who could be a contributor to the DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or is approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.
- b. The results demonstrate that item # is a mixture. NAME cannot be eliminated as a potential contributor to the DNA profile from item #. The expected frequency of individuals who cannot be eliminated as a contributor to the DNA profile from item # (at loci.../ at all loci tested except...) is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or is approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.

c. Assumed 2-person mixture (major): The results demonstrate that item # is a mixture. Assuming two contributors to the mixture, a major profile was deduced at loci x,y, and z. The results are consistent with NAME being the source of the major profile deduced from item #. The expected frequency of individuals who could be the source of the major DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or is approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.

d. Assumed 2-person mixture(minor): The results demonstrate that item # is a mixture. Assuming two contributors to the mixture, a minor profile was deduced at loci x,y, and z. The results are consistent with NAME being the source of the minor profile deduced from item #. The expected frequency of individuals who could be the source of the minor DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or is approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.

e. 3+ person mixture with deduced major: The results demonstrate that item # is a mixture. A major profile was deduced at loci x,y, and z. The results are consistent with NAME being the source of the major DNA profile from item #. The expected frequency of individuals who could be the source of the major DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or is approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.

4. Identifier Plus report statement for mixture profiles when using the restricted CPI calculation:

a. The results demonstrate that item # is a mixture. A major DNA mixture profile was detected at loci x,y and z. NAME is included as a potential contributor to the major DNA mixture profile from item #. The expected frequency of individuals who could be a contributor to the major DNA mixture profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or is approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.

Yfiler:

1. Y-STR report statement for single-source profiles:

- a. The results are consistent with NAME (or another member of the same paternal lineage) being the source of the Y-STR DNA profile from item #. The expected frequency of individuals who could be the source of the Yfiler STR profile from item # is approximately 1 in xx in the African American male population, approximately 1 in xx in the Caucasian male population, and approximately 1 in xx in the Hispanic male population (use figure with 95% confidence interval already applied).
- b. For partial profile situation: NAME (or another member of the same paternal lineage) cannot be eliminated as the source of the Y-STR DNA profile from item #. The expected frequency of individuals who cannot be eliminated as the source of the Yfiler STR profile from item # is approximately 1 in xx in the African American male population, approximately 1 in xx in the Caucasian male population, and approximately 1 in xx in the Hispanic male population (use figure with 95% confidence interval already applied).

2. Y-STR report statement for mixtures profiles:

Note: If a mixture is not fully confirmed, use the following statement: The results are consistent with item # being a mixture.

Note: For mixtures, you may use the CT Y-STR population database if there are too many haplotype combinations to use the National Y Database. Report conclusions.

- a. The results demonstrate that item # is a mixture. NAME (or another member of the same paternal lineage) is included as a potential contributor to the Y-STR DNA profile from item #. The expected frequency of individuals who could be a contributor to the Y-STR DNA profile item # is approximately 1 in xx in the African American male population, approximately 1 in xx in the Caucasian male population, and approximately 1 in xx in the Hispanic male population.
- b. For partial profile situation: NAME (or another member of the same paternal lineage) cannot be eliminated as a potential contributor to the Y-STR DNA profile from item #. The expected frequency of individuals who cannot be eliminated as a contributor to the DNA profile from item # (at loci.../ at all loci tested except...) is approximately 1 in xx in the African American male population, approximately 1 in xx in the Caucasian male population, and approximately 1 in xx in the Hispanic male population.

3. If Y and autosomal STR results are present, combine into one report statement:
 - a. The Identifiler Plus results demonstrate that item # is a mixture. Name cannot be eliminated as a **potential** contributor to the Identifiler Plus DNA profile from item #xx. The results are consistent with NAME (or another member of the same paternal lineage) being the source of the Y-STR DNA profile from item #. The expected frequency of individuals who cannot be eliminated as a contributor to the Identifiler Plus DNA profile from item # and who could be the source of the Y-STR DNA profile from item # less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or is approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.

Note: There may be other variations of the combinations between the Identifiler Plus and Y-STR profiles. In addition, Minifiler profiles may also be added to form statistical statements. Please follow the logic of above to combine statements.

Minifiler and Minifiler with Identifiler Plus:

1. Minifiler (MF) report template for single-source profiles (when only MF amplified):
 - a. The results are consistent with NAME being the source of the Minifiler DNA profile from item #. The expected frequency of individuals who could be the source of the Minifiler DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.
 - b. NAME cannot be eliminated as the source of the Minifiler DNA profile from item #. The expected frequency of individuals who cannot be eliminated as the source of the Minifiler DNA profile from item is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.
2. Minifiler and Identifiler Plus (IDP) report template for single-source autosomal STR profiles – statement for composite autosomal results:

a. The results are consistent with NAME being the source of the Identifiler Plus and Minifiler DNA profile from item #. The expected frequency of individuals who could be the source of the Identifiler Plus and Minifiler DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population. *(make 1 statistic sheet, using all alleles at all included loci from both IDP and MF – for overlapping loci, must be fully included in at least one system)*

b. NAME cannot be eliminated as the source of the Identifiler Plus and Minifiler DNA profile from item #. The expected frequency of individuals who cannot be eliminated as the source of the Identifiler Plus and Minifiler DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population. *(make 1 statistic sheet, using all alleles at all included loci from both IDP and MF – for overlapping loci, must be fully included in at least one system)*

Note: There may be other variations of the combinations between the Identifiler Plus and Minifiler profiles. In addition, Y-STRs statements may also be added to form statistical statements. Please follow the logic of above to combine statements.

3. Minifiler report statement for mixture profiles (when only MF amplified):

Note: If a mixture is not fully confirmed, use the following statement: The results are consistent with item # being a mixture.

a. The Minifiler results demonstrate that item # is a mixture. NAME is included as a potential contributor to the Minifiler DNA profile from item #. The expected frequency of individuals who could be a contributor to the Minifiler DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.

b. The Minifiler results demonstrate that item # is a mixture. NAME cannot be eliminated as a potential contributor to the Minifiler DNA profile from item #. The expected frequency of individuals who cannot be eliminated as a contributor to the Minifiler DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.

4. Minifiler and Identifiler Plus: composite report statement for autosomal mixtures:

a. Mixture statements:

1. The Identifiler Plus and Minifiler results demonstrate that item # is a mixture. *(If either IDP or Minifiler results are a mixture, or The composite Identifiler (Plus)/Minifiler profile has 3 called alleles at more than 1 locus, or 4 + alleles at 1 locus.)*
2. The Identifiler Plus and Minifiler results are consistent with item # being a mixture. *(if only one three+ allele locus is present in either the IDP or Minifiler results, or if 3 different alleles are noted for the composite Minifiler/IDP results at 1 locus (e.g. called 28 in IDP, and called 29,30 in Minifiler)*

b. NAME is included as a potential contributor to the Identifiler Plus and Minifiler DNA profile from item #. The expected frequency of individuals who could be a contributor to the Identifiler Plus and Minifiler DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population. *(make 1 statistic sheet, using all alleles at all included loci from both IDP and MF)*

c. NAME cannot be eliminated as a potential contributor to the Identifiler Plus and Minifiler DNA profile from item #. The expected frequency of individuals who cannot be eliminated as a contributor to the Identifiler Plus and Minifiler DNA profile from item # is less than 1 in 7 billion in the African American, Caucasian, and Hispanic populations, or approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population. *(make 1 statistic sheet, using all alleles at all included loci from both IDP and MF – for overlapping loci, must be fully included in at least one system)*

d. NAME is eliminated as a potential contributor to the Identifiler Plus and MF DNA profile from item #.

Note: There may be other report statements for specific IDP/MF result scenarios with TL approval. In addition, Y-STRs statements may also be added to form additional report statements. Please follow the logic of above to combine statements.

Statistics statement for paternity (RMNE):

1. The expected frequency of males who could be the father of NAME is approximately 1 in xx in the African American population, approximately 1 in xx in the Caucasian population, and approximately 1 in xx in the Hispanic population.

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Amended report letter (sample):

Date

Asst. State's Attorney
Hartford State's Attorney's Office
101 Lafayette St.
Hartford, CT 06106

RE: Connecticut DESPP, Division of Scientific Services, Case ID, Police Department
Case #.

Dear Ms. Attorney:

During a review of the supplemental DNA report dated 11-30-09 for the above case a
typographical error was noted.

In section 3 the second to last sentence should read:
Item #1 was returned to the appropriate submitting agency.

Enclosed is an amended copy of the report. Please forward this information to the
appropriate individual(s).

Thank you for your attention in this matter.

Sincerely,

Analyst
Forensic Science Examiner

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Section 3: STR Stutter Data.

Minifiler Stutter Values:

<u>LOCUS</u>		<u>ALLELE</u>		<u>THRESHOLD%</u>
D13S317		to 13.3		10
		14-14.3		12
		15 +		14
D7S820		to 13.3		10
		14		11
D2S1338		to 18.3		10
		19-21.3		13
		22 +		15
D21S11		to 29.3		10
		30-35.3		14
		36 +		17
D16S539		to 11.3		10
		12-13.3		11
		14 +		13
D18S51		to 13.3		10
		14-18.3		13
		19-21.3		15
		22 +		18
CSF1PO		to 14.3		10
		15 +		12
FGA		to 19.3		10
		20-43.3		13
		44 +		18

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Identifiler Plus Stutter Values:

N – 1 Repeat				N + 1 Repeat		
Locus	Parent Allele	Threshold %		Parent allele	Threshold %	
D8S1179	to 9.3	8		all	2.0	
	10 – 12.3	10				
	13 - 16	12				
	16.1+	14				
D21S11	to 27.3	10		all	2.0	
	28 – 32.3	12				
	33 – 35.3	13				
	36	14				
D7S820	to 9.3	8		all	2.0	
	10 – 13.3	10				
	14+	12				
CSF1PO	to 9.3	8		all	2.0	
	10 – 12.3	10				
	13+	12				
D3S1358	to 14.3	10		all	3.5	
	15 – 17.3	12				
	18+	14				
TH01	to 7.3	5		all	2.0	
	8+	7				
D13S317	to 9.3	7		all	3.0	
	10 – 11.3	10				
	12+	12				
D16S539	to 9.3	8		all	2.0	
	10 – 11.3	10				
	12 – 12.3	12				
	13+	14				

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D2S1338	to 16.3	10	all	2.0
	17 – 23.3	12		
	24+	15		
D19S433	to 13	10	all	2.0
D19S433	13.1 – 14.3	12		
	15+	15		
vWA	to 14.3	10	all	2.0
	15 – 17.3	12		
	18+	15		
TPOX	to 10.3	8	all	2.0
	11+	10		
D18S51	to 10.3	8	all	3.0
	11 - 13	10		
	13.1 - 15	12		
	15.1 - 18	15		
	18.1+	18		
D5S818	to 9.3	10	all	3.0
	10 – 13.3	12		
	14	14		
FGA	to 18.3	10	all	2.0
	19 – 23.3	12		
	24 – 32.2	15		
	32.3+	18		

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Yfiler Stutter Values:

<u>LOCUS</u>	<u>ALLELE</u>	<u>THRESHOLD%</u>
<u>DYS456</u>	<u>to 14</u>	<u>10</u>
	<u>14.1 - 17</u>	<u>13</u>
	<u>17.1 +</u>	<u>14</u>
<u>DYS389I</u>	<u>to 13.3</u>	<u>10</u>
	<u>14+</u>	<u>12</u>
<u>DYS390</u>	<u>to 23</u>	<u>10</u>
	<u>23.1 +</u>	<u>12</u>
<u>DYS389II</u>	<u>to 26.3</u>	<u>12</u>
	<u>27 - 29</u>	<u>14</u>
	<u>29.1 +</u>	<u>16</u>
<u>DYS458</u>	<u>to 15.3</u>	<u>10</u>
	<u>16 - 18</u>	<u>12</u>
	<u>18.1 +</u>	<u>14</u>
<u>DYS19</u>	<u>to 15.3</u>	<u>10</u>
	<u>16 - 18</u>	<u>12</u>
	<u>18.1 +</u>	<u>14</u>
<u>n-2 bases</u>	<u>all</u>	<u>14</u>
<u>n+2 bases</u>	<u>all</u>	<u>2.5</u>
<u>DYS385</u>	<u>to 13</u>	<u>10</u>
	<u>13.1 - 15</u>	<u>12</u>
	<u>15.1 - 19</u>	<u>15</u>
	<u>19.1 +</u>	<u>18</u>
<u>DYS393</u>	<u>to 10</u>	<u>10</u>
	<u>10.1 - 13</u>	<u>12</u>
	<u>13.1 - 15</u>	<u>14</u>
	<u>15.1 +</u>	<u>15</u>
<u>DYS391</u>	<u>to 11</u>	<u>10</u>
	<u>11.1 +</u>	<u>12</u>

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<u>DYS439</u>	<u>to 10.3</u>	<u>10</u>	
	<u>11 +</u>	<u>12</u>	
<u>DYS635</u>	<u>to 20</u>	<u>10</u>	
	<u>20.1 +</u>	<u>12</u>	
<u>DYS392</u>	<u>to 12</u>	<u>12</u>	
	<u>12.1 - 13</u>	<u>14</u>	
	<u>13.1 +</u>	<u>18</u>	
<u>n+3 bases</u>	<u>all</u>	<u>10</u>	
<u>GATA_H4</u>	<u>to 11</u>	<u>10</u>	
	<u>11.1 - 12</u>	<u>12</u>	
	<u>12.1 +</u>	<u>14</u>	
<u>DYS437</u>	<u>to 14.3</u>	<u>9</u>	
	<u>15 +</u>	<u>11</u>	
<u>DYS438</u>	<u>to 12</u>	<u>5</u>	
	<u>12.1 +</u>	<u>6</u>	
<u>DYS448</u>	<u>all</u>	<u>7</u>	

Section 4: List of Critical Reagents and Equipment.

All critical reagents will be appropriately tested to ensure proper performance prior to their use in casework samples. See SOP-8 for QC testing.

6-4.1 **Critical reagent chemicals and solutions:**

dH₂O (used for sample prep through amplification)

Extraction Buffer

Dithiothreitol (DTT)

Formamide

CE Buffer

6-4.2 **Critical Enzymes/Biologicals/Kits:**

Proteinase K

DNA IQ Kit

Quantifiler Trio Kit

Amplitaq Gold Polymerase (if not as part of an assembled kit)

Primer Sets (if not as part of an assembled kit)

Allelic Ladders (if not as part of an assembled kit)

Identifiler Plus Kit

EZ1 Extraction Kits

Minifiler Kit

Yfiler Kit

GeneScan-500LIZ

Pop-4

6-4.3 Evaluation and testing of critical reagents and solutions Refer to **DNA SOP-8.**

6-5 **Critical Instruments:** are those requiring an annual performance check prior to use. Below is a list of what is included as a critical instrument.

6-5.1 Thermometers that are traceable to national or international standard(s)

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6-5.2 Balance/Scales

6-5.3 Thermal cyclers

6-5.4 Thermal cycler temperature-verification system (NOTE: this instrument is not currently in use due to an outside vendor conducting performance checks of thermal cyclers (see SOP-9))

6-5.5 Real-Time PCR Instruments

6-5.6 Electrophoresis Detection Systems (Agilent Bioanalyzers-mtDNA)

6-5.7 Robotic Systems (Biomek, EZ1, etc.)

6-5.8 Genetic Analyzers

6-5.9 Pipettes

6-5.1 Refer to DNA SOP-9 for performance check information on the above listed equipment. Refer to mtDNA SOP-12 for Agilent Bioanalyzer.
Refer to mtDNA SOP-1 for mtDNA Critical Reagents.

Section 5: General Chemical Inventory.

Dry Chemicals:

1. Dithiothreitol (DTT)
2. Dryrite
3. (EDTA) Ethylenediaminetetraacetic acid disodium, dihydrate
4. Potassium Chloride
5. Sodium Chloride
6. Sodium Dodecyl Sulfate (lauryl sulfate)
7. Sodium Hydroxide
8. TRIS, ULtraPure Grade
9. TRIS Hydrochloride
10. TRIS-base (hydroxymethyl amino methane)

Liquid Chemicals:

1. Ethanol, Reagent
2. Hydrogen Peroxide
3. pH Buffer
 - a. 4.00
 - b. 7.00

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c. 10.00

4. Proprietary Solvent, anhydrous
5. Sodium Hypochlorite (bleach)
6. CE 10X Buffer (stock)

Enzymes/Biologicals:

1. ABI 3130 Matrix Standards
2. AmpliTaq Gold
3. Proteinase K

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