USACIL’S DNA_DataAnalysis v2.1.3 Protocol
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**Background**

Prior to using DNA_DataAnalysis software, it requires the processing and analysis of allele calls in GeneMapper ID software (GMID) (Applied Biosystems, Foster City, CA). Once data analysis is complete in GMID, the resulting peak height, base pair size, and allele calls must be exported into tables recognized by DNA_DataAnalysis software. The data table generated using GMID must be formatted such that it is recognizable to DNA_DataAnalysis.

**Procedure**

**Setup in GeneMapperID**

The table to be imported into DNA_DataAnalysis must be set up in a specific fashion.

1.) To create this table, in GeneMapper ID, go to Tools → GeneMapper Manager.

2.) On the Table Settings Tab, select the New button to create a new table setting for import of data into DNA_DataAnalysis.

3.) On the General Tab, enter the name of the table in the top box and any more information in the bottom box.

4.) On the Samples Tab, the settings can be left as the default settings unless the user wishes to change these.

5.) On the Genotypes Tab, select to show only the Sample File (1), Sample Name (2), Marker (6), Allele (8), Size (9), Height (10), Allele Display Overflow (16), and User Defined Custom 1 (36). Also, under the Allele Settings, enter “35” as the Number of Alleles and check the box to keep Allele, Size, Height, Area, Data Point, Mutation, and Comment together.

See Figure 1
### Figure 1

![Table Setting Editor](image.png)

The image shows a Table Setting Editor window with various columns and settings. Each column has options to show or hide specific data fields, such as "Sample Name," "Sample ID," "Run Name," "P/lost," etc. The window includes options for font settings and a section for allele settings.

**Columns Settings:**
- Show or hide various data fields.
  - Example File
  - Sample Name
  - Sample ID
  - Run Name
  - P/lost
  - Marker
  - Dye
  - allele
  - Size
  - Height
  - Peak Area
  - Data Point
  - Mutation
  - All Comment
  - Integration Comments
  - Allele Displays (Overlap)
  - Allele Edit
  - Genetab Clustering (SNP)
  - Off-Tab
  - Sharp Peak (M)
  - Wide Repair Allele (M)
  - Single Peak Artifact (M)
  - Split Peak (M)
  - Out of Bin Allele
  - Peak Height Value
  - Low Peak Height
  - Spectral Pulp
  - allele Number
  - Broad Peak
  - Double Peak (SH)
  - Remaining Bin (SH)
  - Cross Over Concordance
  - Cross Over (MO)
  - Cross Talk
  - Genotyp Quality
  - User Defined Column 1
  - User Defined Column 2
  - User Defined Column 3

**Allele Settings:**
- Number of Alleles: 35
- Keep Allele, Size, Height, Area, Data Point, Mutation and Comment together

---

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6.) Select OK, and then Done. This Table Setting is now available for use.

NOTE: DNA_DataAnalysis looks for allelic ladders to be identified with the “Ladder” in the sample name (case sensitive). This ensures that the width of the data cells will ignore the large number of alleles found in the ladder loci. Alternatively, the data table can be opened in most any text editing program and fixed using the fine and replace functions.

Exporting Data from GeneMapper ID for Import into DNA_DataAnalysis

Once the data has been fully analyzed in GeneMapper ID it is ready to be exported for analysis in DNA_DataAnalysis.

1.) To export the table from GeneMapper ID, while in the Genotypes Tab, select the DNA_DataAnalysis Table from the Table Setting Drop-Down Menu. This will arrange the data in the order required for import into DNA_DataAnalysis.

See Figure 2
2.) In GeneMapper ID, go to File → Export Table.
3.) Navigate to the user chosen location for DNA_DataAnalysis import files. Enter the File Name.

See Figure 3
4.) Select Export Table. The table is now available for import into DNA_DataAnalysis.
Start DNA_DataAnalysis and Set the Kit for the Correct Loci

1.) Double click on the DNA_DataAnalysis file in the DNA_DataAnalysis folder.
2.) Right click on the top white row or top most grey row on the Analyst_Data (default) page to open the Print / Select pages to view / Select user name box.
4.) Left click the bottom right button (default is “Set Identifiler”) until the correct kit is displayed. Then click “OK” at the top right.
5.) The user name to be printed on all pages can be set at the bottom left.

See Figure 4

![Print / Select pages to view / Select user name window](image-url)
Importing Data into DNA_DataAnalysis

1.) To import data into DNA_DataAnalysis right click in the gray area below the listed loci and to the right of the Sample ID column.

See Figure 5

Figure 5
This will bring up the Get data/ Compare/ Check/ Fit/ Misc window.

See Figure 6

Figure 6
Under the ‘Get Analyst table’ select GMID I, and click OK.

See Figure 7

Figure 7
2.) Select the file created by the first analyst and click open.

See Figure 8
3.) The data will appear on the ‘Analyst_Data’ tab.

See Figure 9

NOTE: Additional tables can be brought in by going through the same steps. The samples can be re-sorted by clicking on ‘Sort by Sample ID’ on the form used to start the import process.
4.) Right click on any of the allele calls within the ‘Analyst_Data’ to open the **Get data/Compare/Check/Fit/Misc** box. In the ‘Select view’ box select ‘Samples’.

See Figure 10

![Figure 10](image-url)
5.) This will list only the samples in the project.

See Figure 11

<table>
<thead>
<tr>
<th>Sample ID</th>
<th>C121116</th>
<th>C121119</th>
<th>C121120</th>
<th>C121121</th>
<th>C121122</th>
<th>C121123</th>
<th>C121124</th>
<th>C121125</th>
<th>C121126</th>
<th>C121127</th>
<th>C121128</th>
<th>C121129</th>
<th>C121130</th>
<th>C121131</th>
<th>C121132</th>
<th>C121133</th>
<th>C121134</th>
<th>C121135</th>
<th>C121136</th>
<th>C121137</th>
<th>C121138</th>
</tr>
</thead>
<tbody>
<tr>
<td>000133</td>
<td>000132</td>
<td>000131</td>
<td>000130</td>
<td>000129</td>
<td>000128</td>
<td>000127</td>
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<td>000125</td>
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<td>000121</td>
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<td>000118</td>
<td>000117</td>
<td>000116</td>
<td>000115</td>
<td>000114</td>
<td>000113</td>
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</tr>
<tr>
<td>000136</td>
<td>000135</td>
<td>000134</td>
<td>000133</td>
<td>000132</td>
<td>000131</td>
<td>000130</td>
<td>000129</td>
<td>000128</td>
<td>000127</td>
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<td>000125</td>
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<td>000126</td>
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<td>000119</td>
<td>000118</td>
</tr>
<tr>
<td>000142</td>
<td>000141</td>
<td>000140</td>
<td>000139</td>
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<td>000137</td>
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<td>000129</td>
<td>000128</td>
<td>000127</td>
<td>000126</td>
<td>000125</td>
<td>000124</td>
</tr>
</tbody>
</table>

**Figure 11**
6.) Right click on any of the allele calls within the ‘Analyst_Data’ to open the **Get data/Compare/Check/Fit/Misc** box. In the ‘Select view’ box select ‘Controls’.

See Figure 12

![Figure 12](image-url)

**Figure 12**
7.) This will list only the controls in the project.

See Figure 13

Figure 13
8.) Right click on any of the allele calls within the ‘Analyst Data’ to open the Get data/Compare/Check/Fit/Misc box. In the ‘Select view’ box select ‘All’.

See Figure 14

Figure 14
9.) This will list all of the samples and controls in the project. This is also the default view.

See Figure 15

Figure 15
10.) Right click on any of the allele calls within the ‘Analyst_Data’ to open the **Get data/Compare/Check/Fit/Misc** box. In the ‘Select view’ box select the ‘Alleles’ button. This will show the allele calls for each peak. This is the default setting when initially viewing the ‘Analyst_Data’ tab.

See Figure 16

**Figure 16**
11.) Select ‘RFU’s’ to view the relative fluorescent units for each peak on the ‘Analyst_Data’ page.

See Figure 17
12.) Select ‘Base Pairs’ to view the base pair size for each peak on the ‘Compare Data’ page.

See Figure 18
13.) Right click on any of the allele calls within the ‘Analyst_Data’ to open the Get data/Compare/Check/Fit/Misc box. In the ‘Do checks’ box, select the ‘Controls GMID’ button.

See Figure 19

![Figure 19](image)
14.) This will perform the checks on the ladders, positive controls, negative controls, and quality assurance samples for proper allele calls. Any samples that do not meet laboratory specifications will be highlighted in pink while samples that pass will be highlighted in green.

See Figure 20

![Figure 20](attachment:Figure_20.png)
15.) Right click on any of the allele calls within the ‘Analyst_Data’ to open the Get data/Compare/Check/Fit/Misc box. In the ‘Do checks’ box, click on the ‘Clear checks’ button after each check.

See Figure 21

Figure 21
16.) Right click on any of the allele calls within the ‘Analyst_Data’ to open the **Get data/Compare/Check/Fit/Misc** box. In the ‘Do checks’ box, select the ‘Stutter’ button.

See Figure 22

**Figure 22**
17.) This will perform the check for potential stutter. Any samples that do not meet laboratory specifications will be highlighted in pink.

See Figure 23

<table>
<thead>
<tr>
<th>Sample ID</th>
<th>Check</th>
<th>Potential Stutter</th>
<th>Lab Report</th>
<th>Result</th>
<th>Note</th>
</tr>
</thead>
<tbody>
<tr>
<td>12345</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>56789</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td>1234</td>
<td>Yes</td>
<td>No</td>
<td>Yes</td>
<td>No</td>
<td></td>
</tr>
</tbody>
</table>

Figure 23

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Page 27
18.) To check that all of the allele calls within the samples are able to be uploaded into the CODIS database right click on any of the allele calls within the ‘Compare_Data’ tab. The Get Data/Compare/Check/Fit/Misc box will appear.

19.) Within the ‘Do Checks’ box select the ‘CODIS alleles’ button.

See Figure 24
20.) Any data containing off-ladder alleles, an Amelogenin locus with only a Y, or any other text will be highlighted in pink. All data that is ready to be uploaded into the CODIS database will remain unhighlighted.

See Figure 25

![Figure 25](image)

21.) To check the data set for peaks that do not meet laboratory thresholds right click on any of the allele calls within the ‘Compare_Data’ tab. The Get Data/Compare/Check/Fit/Misc box will appear.
22.) Left click once on the ‘RFUs high’ button to highlight loci which contain one or more alleles with heights above the user-defined threshold. Any areas of interest will be highlighted in pink.

See Figure 26
23.) Left click twice on the ‘RFUs high’ button to change the button to ‘RFUs low’.

See Figure 27
24.) This will highlight loci which contain one or more alleles with heights that fall below the user-defined threshold. Any areas of interest will be highlighted in pink.

See Figure 28
25.) Left click three times on the ‘RFUs high’ button to change the button to ‘RFUs ratio’.

See Figure 29
26.) This will check the data for heterozygote ratios below the user-defined threshold. Any areas of interest will be highlighted in pink.

See Figure 30
27.) To import a second review of the data, right click on the gray area below the listed loci and to the right of the Sample ID column.

See Figure 31
28.) This will bring up the **Get data/ Compare/ Check/ Fit/ Misc** window again. Select the GMID I tab under the ‘Get Review Table’ and click OK.

See Figure 32

![Figure 32](image-url)
29.) Select the file created by the second analyst and click open.

See Figure 33

![Open File Dialog Box](image)
30.) A second tab will appear at the bottom labeled ‘Review_Data’.

See Figure 34

31.) Repeat steps 15-28 for the ‘Review_Data’ page as done for the ‘Analyst_Data’ page.

32.) Once all checks are complete, in the Review_Data page, right click within any of the listed allele calls to open the Get_data/Compare/Check/Fit/Misc widow.
33.) Under the ‘compare tables’ box select the ‘Analyst to Review’ tab.

See Figure 35

![Figure 35](image-url)
34.) The ‘Compare_Data’ tab will open. This will compare the analyst’s data to the reviewer’s data. Data between the analyst and reviewer which matches will be highlighted in teal, while any discrepancies within the data will be highlighted in pink.

See Figure 36

To Match References within a set of Samples:

37.) On the Analyst_Data tab, under the ‘Sample ID’ column right click on the name of the sample you would like to designate as a reference. This will bring up the Match/Send for a reference/Send profile/Other box. To compare your

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analyst data or review data to a single reference, navigate to the ‘Select a Reference(s) and do matches’ area, select the ‘Match to a Reference’ button.

See Figure 37

Figure 37
38.) This will highlight the sample being used as a reference in orange.

See Figure 38
39.) To conduct a two part match, select a sample from the list as described above to bring up the **Matching/Send for reference/Send profile/Other** box. In the ‘Select a Reference(s) and do matches’ area select ‘Match to reference 1 of 2’ to designate the selected sample as reference 1. To designate a different sample as reference 2 follow the same procedure as above and select the ‘Match to reference 2 of 2’ box.

See Figure 39

![Figure 39](image-url)
40.) In the pane in the back, samples that are an exact match to Source 1 will be highlighted in pink, to Source 2 will be highlighted in blue, and any samples that match both (contain all alleles of both sources) will be highlighted in yellow.

See Figure 40

Figure 40
41.) If the sample you would like to use as a reference is found in a tab other than analyst data or review tab, you may send that sample to a different tab by right clicking on the sample name listed under the ‘Sample ID’ column. This will bring up the Matching/Send for reference/Send profile/Other box. Select the tab you would like that profile to be sent to (Analyst Data, Review Data, Temp Data, Staff Profile, QA Profiles or NIST Profiles).

See Figure 41
42.) The sample name and profile will now appear at the top of the selected page above the listed loci. The sample name will be highlighted in orange.

See Figure 42
43.) Once a specified reference has been moved to its designated page right click on any sample ID name for the Matching/Send for reference/Send profile/Other box to appear. Options will now appear under the ‘With an existing match (a Ref is at page top)” box.

See Figure 43

![Figure 43](image)

44.) There are now four options that can be selected:
   a.) Find where Ref is included: Highlights sample profiles which include the reference profile
   b.) Find where Ref includes Foreign: highlights sample profile which contain alleles foreign to the reference profile
   c.) Find inclusive in the Reference: Compares the sample profiles to the reference, highlighting the same alleles.
   d.) Find foreign to the reference: Compares the sample profiles to the reference, highlight the alleles which are found in the samples, but not in the reference.
NOTE: Once selected, see bottom of tab for color coded descriptions of what information is being highlighted.

**Frequency Statistics:**

Single Source:

45.) To perform frequency calculations on a sample from a single source right click on the sample ID name to bring up the **Matching/Send for reference/Send profile/Other** box. Under the ‘Send selection for statistics to’ box select the ‘Freq_SS’ button.

See Figure 44
46.) This will bring up a new ‘Freq_SS’ tab at the bottom of the screen. Left click on this tab to view the frequency calculation page.

See Figure 45

![Figure 45]

<table>
<thead>
<tr>
<th>Locus</th>
<th>Profile</th>
<th>Allele1</th>
<th>Allele2</th>
<th>Frequency: Unrelated</th>
<th>Frequency: Full siblings</th>
<th>Frequency: Parents and Childspring</th>
<th>Frequency: Half siblings/Uncles/Nieces</th>
<th>Frequency: First Cousins</th>
<th>Database Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>D81179</td>
<td>12, 13</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D21511</td>
<td>28, 29, 30</td>
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<td>D73020</td>
<td>9, 10</td>
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<td>CSF1PO</td>
<td>10, 11, 12</td>
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<tr>
<td>TH01</td>
<td>6, 9, 3</td>
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<td>D18S37</td>
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</tr>
<tr>
<td>D18S59</td>
<td>9, 12, 13</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Figure 45
47.) Once in the ‘Freq_SS’ tab right click on the red triangle located in the upper right hand corner of the ‘Locus Profile’ box to import the profile and apply the frequency calculations.

See Figure 46

![Figure 46](image-url)
48.) Once the calculations have been run the frequency of each of the allele calls at a specific locus are given for the Caucasian, African-American, and Hispanic populations, respectively.

See Figure 47

![Figure 47](image)

49.) To the right of these frequencies, relatedness calculations are shown, also separated into Caucasian, African-American, and Hispanic populations.

(see Figure 46, green box)
50.) At the bottom of the Freq_SS tab the frequency calculations are presented in both general form as well as major ethnicity for the entire profile. The calculations are currently performed using the statistics of the FBI Database. The statistics are shown in both exponential and alphanumerical form.

See Figure 48

<table>
<thead>
<tr>
<th>Locus Profile</th>
<th>Allele1</th>
<th>Allele2</th>
<th>Frequency: Unrelated</th>
<th>Frequency: Full siblings</th>
<th>Frequency: Parents and Cousins</th>
<th>Frequency: Half Sibs, Uncles, Nephews</th>
<th>Frequency: First Cousins</th>
<th>Database Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>FGA 22, 25</td>
<td>22.2</td>
<td>25</td>
<td>0.0126</td>
<td>0.001764</td>
<td>0.270866</td>
<td>0.040080</td>
<td>0.021807</td>
<td>0.011835</td>
</tr>
<tr>
<td></td>
<td>0.0129</td>
<td>0.1000</td>
<td>0.002780</td>
<td>0.279170</td>
<td>0.056380</td>
<td>0.029808</td>
<td>0.018422</td>
<td>0.018423</td>
</tr>
<tr>
<td></td>
<td>0.0128</td>
<td>0.1379</td>
<td>0.003392</td>
<td>0.288336</td>
<td>0.075100</td>
<td>0.059246</td>
<td>0.023819</td>
<td>0.023819</td>
</tr>
</tbody>
</table>

51.) To change theta (\(\Theta\)) left click on the box to the right of \(\Theta\) and type in the theta value you would like to use.

NOTE: Only theta values of 0.01 or 0.03 are acceptable within DNA_DataAnalysis. The default value for theta is 0.01

52.) Right click on the right triangle in the top right corner of the ‘locus profile’ box to run the frequency calculations again using the new value. (see Figure 45)

Two person mixture (especially for calculating minor contributor):

53.) When performing frequency calculations on a sample containing a two person mixture, it is optional to first apply references to later easily determine any obligate allele. This stat page is designed for profiles where one person can be assumed and the other contributor is probative, or when the minor contributor is probative, but there is concern about masking by the major contributor or allelic drop out.
54.) To apply references, navigate back to the ‘Analyst_data’ tab and double left click on any of the allele calls of the profile you would like to designate as a reference. This will bring up the **2 or 3 contributor Mixture Interpretation** box, select the reference number you would like to set the profile to (ie: Ref 1 or Ref 2) by clicking the appropriate button under the ‘Set’ column.

See Figure 49

**Figure 49**
55.) The sample ID will now be highlighted in the designated color for that reference number.

See Figure 50

<table>
<thead>
<tr>
<th>Sample ID</th>
<th>Sample Name</th>
<th>Sample Type</th>
<th>Condition</th>
<th>Comment</th>
</tr>
</thead>
<tbody>
<tr>
<td>12345678</td>
<td>Sample A</td>
<td>Control</td>
<td>Healthy</td>
<td>Good</td>
</tr>
<tr>
<td>87654321</td>
<td>Sample B</td>
<td>Test</td>
<td>Diseased</td>
<td>Poor</td>
</tr>
</tbody>
</table>

**Figure 50**
56.) Double left click on any of the alleles from the same profile to view the **2 or 3 contributor Mixture Interpretation** box again. Select ‘apply’ to apply that profile to the calculations that will be performed.

See Figure 51

![Figure 51](image)

**Figure 51**

NOTE: It is possible to set up to six references, but the mixture interpretation tool only helps to deconvolute 2 and 3 person mixtures.
57.) Right click on the sample ID name of the profile you would like to calculate frequency statistics on, to bring up the Matching/Send for reference/Send profile /Other box. Under the ‘Send selection for statistics to’ box select the ‘Freq_Mix’ button.

See Figure 52

Figure 52
58.) This will bring up a new ‘Freq_Mix’ tab at the bottom of the screen. Left click on this tab to view the frequency calculation page.

See Figure 53

**Figure 53**
59.) Double left click on the red triangle located in the upper right hand corner of the ‘Locus Profile’ box to import the profile.

See Figure 54
60.) Double left-click on the alleles listed at a particular locus under the ‘Locus Profile’ column to bring up the **2 or 3 Contributor Mixture** box.

NOTE: This step is not necessary to use the Freq_Mix page; however, this is an easy way to be reminded of any obligate alleles.)

See Figure 55

![Figure 55](image-url)
61.) Within the mixture interpretation window, apply the reference(s) of choice. In the bottom pane all of the combinations that are possible and their corresponding probabilities will be displayed. This data can be utilized to find all remaining required alleles. Subtracting out the alleles of the known will leave only the required allele(s) needed for the next step.

See Figure 56

![Figure 56](image-url)
62.) Exit out of the 2 or 3 Contributor Mixture box, and locate the locus of choice on the Freq_Mix tab. All designated alleles (up to 4 alleles) will be listed under the corresponding column (ie: Allele 1, Allele 2, etc.). Select the allele or alleles needed (i.e., any obligate allele of the minor contributor) to include only the allele combinations possible by double left clicking on the allele call. This will bring the allele call and its possible combinations over to the ‘Type’ columns.

See Figure 57

NOTE: The ‘required’ alleles are the possibilities shown in the 2 or 3 Contributor Mixture box after applying the reference and subtracting out the known profile(s).
NOTE: It may not be necessary to consider all combinations in the stat. Double left clicking on an allele in an unnecessary combination will remove that combination from the calculation. Type 5 allows for possible drop-out. To remove this possible combination from the calculation double left click on the genotype.

63.) Continue this process for each locus listed. Once all alleles have been selected and all required combinations are listed under the ‘Type’ columns double left click on the red triangle located in the top right corner of the “Sum of” column. The calculations will be performed on selected loci and appear under the ‘Sum of” column.

See Figure 58
64.) At the bottom of the Freq_Mix tab the frequency calculations are presented in both general form as well as major ethnicity. The calculations are currently performed using the statistics of the FBI Database. The statistics are shown in both exponential and alphanumeric form.

See Figure 59
Probability of Inclusion

65.) To look at the probability of the inclusion of a particular sample within the population navigate back to the Analyst_Data tab. Right click on the desired sample to bring up the Matching/Send for a reference/Send profile/Other box. Under the ‘Send selection for statistics to’ area select the ‘Freq_PI’ button.

See Figure 60

![Figure 60](image-url)
66.) A new ‘Freq.PI’ tab will appear at the bottom of the screen. Navigate to this tab and double click on the red triangle in the upper right hand corner of the ‘Locus Profile’ box.

See Figure 61

<table>
<thead>
<tr>
<th>Locus</th>
<th>Probability of Inclusion</th>
<th>Allele 1</th>
<th>Allele 2</th>
<th>Allele 3</th>
<th>Allele 4</th>
<th>Allele 5</th>
<th>Allele 6</th>
<th>Allele 7</th>
<th>Allele 8</th>
<th>PE</th>
<th>PI</th>
</tr>
</thead>
<tbody>
<tr>
<td>D6S1179</td>
<td>12, 13</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D21S11</td>
<td>129.30</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D7S820</td>
<td>10</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C8H10</td>
<td>10, 10</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D8S1168</td>
<td>15, 16</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TH01</td>
<td>6.93</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D3S137</td>
<td>6.12</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D16S539</td>
<td>12, 13</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Figure 61
67.) This will import the profile and perform the calculations for probability of inclusion (PI) and probability of exclusion (PE). The frequency calculations, separated by Caucasian, African-American, and Hispanic respectively, will be listed under each allele. The probability of exclusion and probability of inclusion will be listed to the right of the screen, also separated by ethnic group.

See Figure 62
68.) To remove a particular loci from the calculation right click on the PI calculation. This will bring up the **Frequency Calculations** pane.

See Figure 63

![Frequency Calculations](image)

**Figure 63**

**NOTE:** It is possible to use this procedure on all stat pages to remove a locus from the calculation.
69.) All of the loci will be listed on this pane. Select the locus or loci you wish to remove from the calculation and click ‘Clear locus’ under the far right ‘show’ column. This will remove the selected locus/loci from further calculations within this pane.

See Figure 64

Figure 64
70.) At the bottom of the Freq_PI tab the frequency calculations are presented in both general form as well as major ethnicity. The calculations are currently performed using the statistics of the FBI Database. The statistics are shown in both exponential and alphanumerical form.

See Figure 65

<table>
<thead>
<tr>
<th>Allele</th>
<th>X</th>
<th>D5S818</th>
<th>12</th>
<th>0.3639</th>
<th>0.3566</th>
<th>0.2906</th>
<th>0.8746</th>
<th>0.8736</th>
<th>0.8156</th>
<th>0.8733</th>
<th>0.8933</th>
<th>0.8819</th>
<th>0.9863</th>
<th>0.9983</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>22, 24</td>
<td>22</td>
<td>24</td>
<td>0.1888</td>
<td>0.1379</td>
<td>0.2250</td>
<td>0.1861</td>
<td>0.1773</td>
<td>0.1256</td>
<td>0.8933</td>
<td>0.8933</td>
<td>0.8933</td>
<td>0.8933</td>
<td>0.8933</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>1 in ...</th>
<th>5.101E+11</th>
<th>4.612E+13</th>
<th>4.281E+12</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1 in ...</td>
<td>5.10 billion</td>
<td>4.612 trillion</td>
<td>4.28 trillion</td>
</tr>
</tbody>
</table>

**Figure 65**
Likelihood Ratios:

71.) To import a sample into the L_Ratio tab, navigate back to the ‘Analyst_data’ tab and right click on the Sample ID of the single-source reference sample you would like to perform the calculation on. This will bring up the Matching/Send for reference/Send profile/Other pane. Under the ‘Send selection for statistics to’ box select the ‘L Ratio’ button.

See Figure 66
72.) A new ‘L Ratio’ tab will appear at the bottom of the screen. Navigate to the ‘L Ratio’ tab and double left click on the red triangle located in the top right corner of the locus profile box.

See Figure 67

<table>
<thead>
<tr>
<th>Locus</th>
<th>Locus Profile</th>
</tr>
</thead>
<tbody>
<tr>
<td>D9S179</td>
<td>12, 13</td>
</tr>
<tr>
<td>D21S11</td>
<td>28, 30</td>
</tr>
<tr>
<td>D2S1309</td>
<td>9, 10</td>
</tr>
<tr>
<td>CSF1PO</td>
<td>19, 11, 12</td>
</tr>
<tr>
<td>D5S1388</td>
<td>15, 16</td>
</tr>
<tr>
<td>THO1</td>
<td>6, 9, 13</td>
</tr>
<tr>
<td>D13A18</td>
<td>6, 13, 12</td>
</tr>
<tr>
<td>D16S539</td>
<td>7, 12, 13</td>
</tr>
</tbody>
</table>

Figure 67
73.) The allele frequencies at each locus will be imported and displayed in the columns labeled ‘a’, ‘b’, ‘c’, etc.

See Figure 68

<table>
<thead>
<tr>
<th>Locus Profile</th>
<th>x</th>
<th>y</th>
<th>z</th>
<th>a</th>
<th>b</th>
<th>c</th>
<th>1Ps</th>
<th>2Ps</th>
<th>1</th>
<th>C1</th>
<th>C2</th>
</tr>
</thead>
<tbody>
<tr>
<td>DYS1994</td>
<td>12,13</td>
<td>0.1464</td>
<td>0.3395</td>
<td>0.0307</td>
<td>0.3051</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D21611</td>
<td>12,13,30</td>
<td>0.1568</td>
<td>0.3071</td>
<td>0.2392</td>
<td>0.1999</td>
<td>0.1388</td>
<td>0.9210</td>
<td>0.2064</td>
<td>0.3002</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DF566B9</td>
<td>9,10</td>
<td>0</td>
<td>0.1470</td>
<td>0.2566</td>
<td>0.0471</td>
<td>0.3363</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CSFPO</td>
<td>15,16,22</td>
<td>0.2037</td>
<td>0.2039</td>
<td>0.2039</td>
<td>0.2039</td>
<td>0.2039</td>
<td>0.2039</td>
<td>0.2039</td>
<td>0.2039</td>
<td></td>
<td></td>
</tr>
<tr>
<td>D351308</td>
<td>13,16</td>
<td>0.2003</td>
<td>0.2325</td>
<td>0.2325</td>
<td>0.2325</td>
<td>0.2325</td>
<td>0.2325</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T3891</td>
<td>6,9,3</td>
<td>0.2166</td>
<td>0.2054</td>
<td>0.0795</td>
<td>0.1046</td>
<td>0.2011</td>
<td>0.2410</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D18S2117</td>
<td>12,11,12</td>
<td>0.0695</td>
<td>0.3309</td>
<td>0.3007</td>
<td>0.3007</td>
<td>0.3007</td>
<td>0.3007</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D7S539</td>
<td>9,12,15</td>
<td>0.1743</td>
<td>0.2031</td>
<td>0.1594</td>
<td>0.1386</td>
<td>0.1386</td>
<td>0.1386</td>
<td>0.1386</td>
<td>0.1386</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Double left click on a specific locus to perform the calculation on that particular locus. The allele calls will appear in 2 different boxes, both boxes will be highlighted in pink. The top box, adjacent to the ‘Locus Profile’ box is for designating C1, or the prosecution. The bottom box is for designating C2, or the defense. Both boxes should be highlighted in pink. Pink highlighting indicates an allele that is “known” according to the particular hypothesis.

See Figure 69
75.) Double left click any allele that is from an unknown contributor for the two competing hypotheses. The selected allele is now highlighted in green, which indicates it is from an unknown contributor. In a typical scenario the prosecution hypothesis may be that there are no unknown alleles, while the defense hypothesis may be that any allele not found in the profile of the Victim is from an unknown individual.

See Figure 70.

![Figure 70]

**Figure 70**

NOTE: In Figure 70, the 12 and 13 alleles are “known” in the prosecution’s hypothesis, while in the defense’s the 12 is “unknown” and the 13 is “known.”

NOTE: You can use the 2 or 3 Contributor Mixture Interpretation tool to determine which alleles are known and unknown for the L_Ratio page the same way described above for the Freq_Mix page.
75.) For each locus there are four boxes grouped together under the ‘1 Px/ blank/ 2 Px/ 1’ column. Right click on the cell in the row that contains the alleles to set up the conditions of the two competing hypotheses.

See Figure 71.

![Figure 71](image1.jpg)

76.) The ‘C1(Px), C2 (Px)’ box will open that allows you to set the number of unknown contributors. Use the arrows to set the number of unknown contributors in the hypotheses of the prosecution (C1) and then the defense (C2). Then click calculate to see the result.

See Figure 72.

![Figure 72](image2.jpg)

NOTE: Once the number of unknown contributors are set for one locus, the up and down arrows used to adjust the number are gone and the values are grayed out. This assures the same assumptions are used for the entire profile. Once they are set, it is possible to calculate the locus by simply double left clicking rather than right clicking to bring up the ‘C1(Px), C2 (Px)’ box.
77.) The calculations are displayed as follows:
   A. The Prosecution’s hypothesis result is in the column labeled ‘C1’.
   B. The Defense’s hypothesis result is in the column labeled ‘C2’.
   C. The combined likelihood ratio for each population group is displayed in the ‘1 Px/ blank/ 2 Px/ 1’ column.
   D. The conditional statement is listed in the ‘1 Px/ blank/ 2 Px/ 1’ column just above the three results for each population group.

See Figure 73

<table>
<thead>
<tr>
<th></th>
<th>1 Px</th>
<th>2 Px</th>
<th>1 Px/blank/2 Px/1</th>
<th>C1</th>
<th>C2</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>8.35</td>
<td></td>
<td></td>
<td>1</td>
<td>0.119809</td>
</tr>
<tr>
<td></td>
<td>16.7</td>
<td></td>
<td></td>
<td>1</td>
<td>0.059957</td>
</tr>
<tr>
<td></td>
<td>10.7</td>
<td></td>
<td></td>
<td>1</td>
<td>0.093047</td>
</tr>
</tbody>
</table>

**Figure 73**

78.) At the bottom of the page the likelihood ratios for the entire profile are displayed. This is separated out by the three subcategories and is displayed in both exponential form and in words.

NOTE: To remove any locus from further likelihood ratio calculations on this sample right click on the alleles of that particular locus to bring up the Frequency Calculations pane. Click on the name of the locus you would like to remove in the left ‘Show’ box, and click ‘Clear Locus’ from the right ‘Show’ box. This will remove the locus from further likelihood ratio calculations until the tab is closed and the sample is imported again.

To Set Aside Profiles for later comparisons:
78.) Right click on the sample ID of the sample you would like to set aside for later use. This will bring up the **Matching/Send for reference/Send profile/Other** pane.

79.) Under the ‘Send selection to’ box select the ‘Temp Data’ button and hit ‘OK’

See Figure 74.

80.) A new ‘Temp Data’ pane will appear at the bottom the screen. Navigate to this tab.

81.) The sample ID and profile will now appear in this tab; however, it can still be located in the previous, home folder. Right click on any of the alleles within the samples profile to bring up the **Get Data/Compare/Check/Fit/Misc** pane. This is the same pane as that used earlier while comparing data.
To view a table containing information on each of the samples contained within a Tab:

82.) Navigate to the ‘Analyst_Data’ tab right click on any of the sample ID’s listed within that tab. This will bring up the Matching/Send for reference/Send profile/Other pane.

Note: this can also be done with samples listed under the ‘Review_Data’ tab.

83.) Within the Matching/Send for reference/Send profile/Other pane under the ‘Send all data to’ box select the ‘Total data’ button. This will create a new ‘Total_data’ tab at the bottom of the screen

See Figure 75

Figure 75

84.) Navigate to the ‘Total_data’ tab. Within this tab multiple tables are created for each sample listed on the original tab. Each sample is separated by locus and the
allele call(s) for each locus is listed. The RFU and base pair values are also listed for each allele call at a particular locus.

See Figure 76
85.) To print this page left click anywhere within that page to bring up the Print/Select pages to view/Select user name pane. Towards the bottom of the pane select the ‘Page’ button, located within the ‘Print’ box.

See Figure 77

![Figure 77](image-url)

Mixture Interpretation Tool:

86.) Before using the mixture interpretation tool it may be necessary to designate a sample(s) as a reference. You may designate up to 6 samples as reference, but may Note: When using the 3 component mixture interpretation tool it is possible to apply up to 3 references.
87.) To designate a reference, double left click on the first locus of the sample to be designated ‘Reference 1’. This will bring up the **2 or 3 Contributor Mixture Interpretation** pane. On the left, within the box labeled ‘Set’ select the ‘Ref 1’ button. This will highlight both the ‘Ref 1’ and the sample name and allele calls found on the ‘Analyst Data’ tab. You may continue to set up to 6 references.

See Figure 78.

![Figure 78](image)

88.) After setting references, send the sample you would like interpret to the mixture interpretation tool by double left clicking on the first locus. This will bring up the **2 or 3 Contributor Mixture Interpretation** pane.

89.) In the left-hand corner there are two boxes, one displaying a ‘2’ and one displaying a ‘3’. This is where you define your mixture as either a 2 or 3 person mixture. The one that is active will be highlighted green.
90.) Apply the desired references by clicking the ‘Ref 1’ box (or corresponding box to the previous references set) located under the ‘apply’ area. The sample ID and allele calls at the selected locus will appear once the reference has been applied.

91.) Once all desired references have been applied look to the bottom of the pane for a display of all possible allele combinations at the selected locus. The only combinations that will display are those that contain the applied reference(s).

See Figure 79

92.) You may further limit the combinations by changing the required PHr (peak height ratio) and mP (minimum proportion). If the PHr is set at 0.5, only combinations were a heterozygote has 50% or better peak balance will be displayed. The mP can be used to ignore combinations where a contributor would be present.
only below the set value. If the mP is set at 0.1, than any combinations that would require a contributor to be less than 11% of the DNA will be hidden from view.

See Figure 80.

**Figure 80**

NOTE: The top line in the lower half of this pane states the conditions present that affect the displayed combinations, such as a required genotype and the peak height ratio. The displayed combinations list the two genotypes and their proportion of total DNA and peak height ratio (if a heterozygote).
To deconvolute the mixed profile, click the boxes for the desired alleles of the individual contributors on in the upper right side of the pane. For example, P1 may be the known victim or the major contributor, while P2 may be the deduced foreign or minor profile. An allele can be sent to both profiles as needed, or all alleles can be sent to one or both profiles. There is no “limit” on the number of times an allele can be used. The tool supports up to three profiles at a time.

See Figure 81.

**Figure 81**

NOTE: An allele can be sent to the user defined profiles independently as needed, or all alleles can be sent to one or both profiles. There is no “limit” on the number of times an allele can be used. The tool supports up to three profiles at a time. For example, if the known donor is a 29, 30, click the 29 and 30 boxes for P1. If a 28, 28 and 28, 29 and 28, 30 are all possible types for the other profile; you may click all three boxes for P2.
94.) The word “Any” can be added to a locus as well by double left clicking between the allele designation boxes. This can be used to designate any contributor that contains a 20 allele, for example.

95.) There are four icons at the top of the right of the pane that allow the user to interact with the user defined profiles and the Analyst, Review, and Temp_Data pages.

To create a record of the user defined profiles created during the deconvolution process, click on this icon:

To limit the view in the table (Analyst_Data, etc) to just the set references and the user deconvoluted samples, click this icon:

To show all samples again in the table, click this icon:

To remove all user deconvoluted profiles, click this icon:

CAUTION: Unless you have saved the table by using the save Page_Data function described below clicking the remove icon will undo all the work you did to deconvolute the sample!!!
96.) The deconvoluted profiles are added with the term “User defined 1(-3)” directly under the row for the original sample data. These new user defined samples are treated like any other sample for all functions. All matching and statistics functions will work on these new profiles as described for the original mixed sample.

See Figure 82

<table>
<thead>
<tr>
<th>Sample ID</th>
<th>DRS1179</th>
<th>D21S11</th>
<th>D3S1358</th>
<th>CSF1PO</th>
<th>D3S1801</th>
<th>TH01</th>
<th>D18S</th>
</tr>
</thead>
<tbody>
<tr>
<td>XX0156.1 99XXXX0999Q1(15)-2F1 Shirt Vct 06-06-20-D01</td>
<td>12, 13</td>
<td>28, 29, 30</td>
<td>9, 10</td>
<td>10, 11, 12</td>
<td>15, 16</td>
<td>6, 9, 3</td>
<td>8, 11,</td>
</tr>
<tr>
<td>User defined 1: XX0156.1 99XXXX0999Q1(15)-2 ...</td>
<td>12, 15</td>
<td>29, 30</td>
<td>10</td>
<td>10, 12</td>
<td>15, 16, Any</td>
<td></td>
<td></td>
</tr>
<tr>
<td>User defined 2: XX0156.1 99XXXX0999Q1(15)-2 ...</td>
<td>12</td>
<td>28</td>
<td>9, 10</td>
<td>10, 11, 12</td>
<td>15</td>
<td></td>
<td></td>
</tr>
<tr>
<td>XX0167 99XXXX0999K1(11) Blood Vct 06-06-20-C02</td>
<td>12, 13</td>
<td>29, 30</td>
<td>10</td>
<td>10, 12</td>
<td>15, 16</td>
<td>6, 9, 3</td>
<td>8, 12</td>
</tr>
<tr>
<td>XX0168 99XXXX0999K2 Blood Susp 06-06-20-H02</td>
<td>12</td>
<td>28</td>
<td>9, 10</td>
<td>10, 11</td>
<td>15</td>
<td>6, 9, 3</td>
<td>11, 12</td>
</tr>
</tbody>
</table>

Figure 82

NOTE: The new user defined entries can be renamed simple by typing the new name in the sample ID cell. However; if any changes are to be made, the software expects to see “User defined” in the sample name. If a different name is present, additional rows will be added to the table. There are times when the user wants to consider alternate deconvolution scenarios for the same sample. This can be done by changing the names of the first set of user defined profiles, then simply repeating it. The second set of user defined profiles will be inserted between the original mixed sample row and the now renamed first set.
97.) To recalculate for stutter effects on peak height ratios and proportions, simply double left click on a peak height value above the P1, P2, P3 area.

See Figure 83

![Figure 83](image-url)
The default value subtracts 100% of the maximum locus specific stutter. This may be reduced to 70%, 50% or other by using the left and right arrows that have now appeared.

See Figure 83

**Figure 83**

**NOTE:** Clicking the top right ‘Re-set’ button will go back to the original data where no consideration for stutter is made.
99.) If an allele(s) is not necessary for consideration it can be removed by double left clicking on the allele. The remaining alleles are now highlighted, and message appears in the lower half stating the calculations are not considering all alleles in the locus.

See Figure 84.

![Figure 84](image)

**Figure 84**

NOTE: Clicking the top right ‘Re-set’ button will go back to the original data where all alleles are considered. This may be useful if there is a 3 person mixture with one allele of a very minor heterozygote contributor dropping out. If the remaining allele is removed, it may be useful to switch to the 2 person calculator and then consider the remaining combinations.
100.) To navigate to a new locus click either the left or right arrows located in the left corner of the top middle pane. The current locus being viewed is displayed to the right of these arrows. Below the locus name the allele call(s), RFU value(s), and base pair size are displayed.

NOTE: It is also possible to navigate to the next locus by using the arrows in the top right corner, located next to the ‘reset’ button.

See Figure 85

![Figure 85](image-url)
101.) To send data to the ‘Mixture Interpretation Page’ (which will open as a new tab at the bottom of the page) there are two options. This page is a summary of the peak height ratios and proportions for the sample.

-To send only selected loci: Navigate through each locus and send only the desired loci to the ‘Mixture Interpretation Page’ by clicking the lighter, open arrow below the number ‘2’ button. This must be done locus by locus.

-To send the entire profile: Click the darker, filled arrow located under the number ‘3’ button.

NOTE: Only the combinations allowed by the selected PHr, mPH, and mP selections will be sent to the summary page. If references have been applied, only the combinations with the required genotype combinations will be sent.

102.) Once the data has been sent to the ‘Mixture Interpretation Page’ a new ‘Mix_Interp’ tab will appear at the bottom of the screen. Navigate to this tab.

103.) The ‘Mix_Interp’ tab separates the sample by locus. Each locus has an entry for each category of possible allele combinations under the conditions previously selected. However; not all categories will have entries. You can limit the view to only those categories with valid allele combinations by right clicking on any text, which brings up the ‘Print / Select pages to view / Select user name’ box. Under the ‘Chart’ area select ‘Condense View’.

See Figure 86.
104.) The allowable combinations are listed in the order they were sent and a statement that describes the required conditions and any reference profile(s).

See Figure 87.

NOTE: A locus can be sent to this summary page more than once. For example, the entire profile can be sent by clicking the dark arrow with a PHr of 50%. Then a particular locus or group of loci can be sent again with a PHr of 60%. When graphing the result, (see below) the graph will use the most recently sent data.

<table>
<thead>
<tr>
<th>Locus</th>
<th>Description</th>
<th>Conditions</th>
</tr>
</thead>
<tbody>
<tr>
<td>D2S119</td>
<td>For a 2-contributor 2-allele mixture of types AB &amp; AB: 1-combination: Alleles (RFU): 12 (1580); 13 (2245)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Only combinations including the following reference profiles are included: (12, 13); all peak height ratios are &gt;= (0.5);</td>
<td></td>
</tr>
<tr>
<td></td>
<td>12, 13 and 12, 13 (phr = 0.097)</td>
<td></td>
</tr>
<tr>
<td>D6S179</td>
<td>For a 2-contributor 2-allele mixture of types AA &amp; BB: (2-combinations for AB: phr = 1 or calc based on set phr): Alleles (RFUs): 12 (1580), 13 (2245)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Only combinations including the following reference profiles are included: (12, 13); all peak height ratios are &gt;= (0.5);</td>
<td></td>
</tr>
<tr>
<td></td>
<td>12, 13 (p = 0.03); 12, 13 (phr = 0.63; p = 0.97)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>13, 13 (p = 0.19); 12, 13 (phr = 1; p = 0.81)</td>
<td></td>
</tr>
<tr>
<td>D6S179</td>
<td>For a 2-contributor 2-allele mixture of types AB &amp; AB: 1-combination: Alleles (RFUs): 12 (1580), 13 (2245)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Only combinations including the following reference profiles are included: (12, 13); all peak height ratios are &gt;= (0.5);</td>
<td></td>
</tr>
<tr>
<td></td>
<td>12, 13 and 12, 13 (phr = 0.67)</td>
<td></td>
</tr>
<tr>
<td>D21S11</td>
<td>For a 2-contributor 3-allele mixture of types AA &amp; BB: 3-combinations: Alleles (RFUs): 28 (916), 29 (1144), 30 (994)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Only combinations including the following reference profiles are included: (29, 30); all peak height ratios are &gt;= (0.5);</td>
<td></td>
</tr>
<tr>
<td></td>
<td>28, 29 (phr = 0.7); 29, 30 (phr = 0.007; p = 0.7)</td>
<td></td>
</tr>
<tr>
<td>D21S11</td>
<td>For a 2-contributor 3-allele mixture of types BB &amp; BB: 3-combinations: Alleles (RFUs): 28 (916), 29 (1144), 30 (994)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Only combinations including the following reference profiles are included: (29, 30); all peak height ratios are &gt;= (0.5);</td>
<td></td>
</tr>
<tr>
<td></td>
<td>28, 29 (phr = 0.7); 29, 30 (phr = 0.007; p = 0.7)</td>
<td></td>
</tr>
<tr>
<td>D7S980</td>
<td>For a 2-contributor 2-allele mixture of types AA &amp; BB: 1-combination: Alleles (RFUs): 9 (594), 10 (2480)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Only combinations including the following reference profiles are included: (10, 10); all peak height ratios are &gt;= (0.5);</td>
<td></td>
</tr>
<tr>
<td></td>
<td>9, 9 (p = 0.19); 10, 10 (p = 0.81)</td>
<td></td>
</tr>
<tr>
<td>D7S980</td>
<td>For a 2-contributor 2-allele mixture of types AA &amp; BB: (2-combinations for AB: phr = 1 or calc based on set phr): Alleles (RFUs): 9 (594), 10 (2480)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Only combinations including the following reference profiles are included: (10, 10); all peak height ratios are &gt;= (0.5);</td>
<td></td>
</tr>
<tr>
<td></td>
<td>10, 10 (phr = 0.01); 9, 10 (phr = 1; p = 0.30)</td>
<td></td>
</tr>
</tbody>
</table>

**Figure 87**

105.) To print this page right click anywhere within the page to bring up the Print/Select pages to view/Select user name pane. At the bottom of the pane, under the ‘Print’ area, select the ‘Page’ button.
106.) To create a chart displaying the proportions of each profile within the selected sample right click anywhere within the data displayed on the ‘Mix_Interp’ tab. This will bring up the Print/Select pages to view/Select user name pane. Within this pane, on the right side under the ‘Chart’ area select the ‘Make Chart’ button.

See Figure 88.

NOTE: In order to generate a chart, all references must have been applied prior to sending to the Mix_Interp page.

IMPORTANT: Two references MUST have been applied to graph a 2-person mixture, and three references to graph a 3-person mixture. If the incorrect number of references are applied, nothing will happen.

Figure 88
107.) An excel bar graph will appear. The graph displays the proportions of each locus both visually on the graph and numerically in the chart displayed below the chart. Not all loci will chart. If both contributors have the same type, no proportion can be calculated. In a 3-person mixture, there are four situations where no proportions and/or peak height ratios are calculated. If one of these combinations is valid, it is designated as “Not excluded”, but no graphing can be done.

NOTE: The graph may need to be “stretched” to read proportions to 2 decimal places.

See Figure 89.

![Figure 89](image)

108.) Right clicking outside the graph brings up commands for clearing the chart and re-ordering the loci.

See Figure 90.

![Figure 90](image)
109). The ‘Locus Order’ function changes the graph from the order of the kit to an order that is arranged with the larger loci on the left, and the smaller loci on the right. This may be useful in situations where one contributor shows signs of degradation.

See Figure 91

![Figure 91](image1)

110.) Double clicking outside the graph rotates between a “stacked” graph and a side-by-side graph.

See Figure 92.

![Figure 92](image2)
111.) With DNA_DataAnalysis it is also possible to perform Least-Squares Deconvolution calculations on the selected sample. The LSD calculations only work for a 2-person mixture. This can be done by navigating back to the ‘Analyst_Data’ tab. Left click on the allele calls of the first locus of the selected sample to bring up the 2 or 3 Contributor Mixture Interpretation pane. Set and apply the references as described above.

112.) In the left-hand corner select the ‘LSD’ button. This will show all possible combinations given the selected contributors in the bottom half of the 2 or 3 Contributor Mixture Interpretation pane.

See Figure 93.

![Figure 93](image)

113.) To send data to the ‘Mixture Interpretation Page’ (which will open as a new tab at the bottom of the page) there are two options. This is similar to the approach described above for the 2- and 3-person default calculations.

- **To send only selected loci**: Navigate through each locus and send only the desired loci to the ‘Mixture Interpretation Page’ by clicking the lighter, open box below the ‘LSD’ button. This must be done locus by locus.

- **To send the entire profile**: Click the darker, filled box located under the ‘LSD’ button.

114.) This will send the selected data to the ‘Mix_Interp’ tab. It is set up in the same format as stated above. If reference(s) have been applied, only combinations with those required profiles will be available. The chart function does not apply for samples where LSD was used.
Saving Data

115.) Any single sample can be saved for later use. Also, any Analyst_Data, Review_Data or Temp_Data table can be saved, including all ‘User defined’ profiles that were generated using the mixture deconvolution tool.

116.) Right click on a sample ID cell. If a single profile is to be saved, you must click on the sample ID of that profile. If the entire page of data is to be saved, you may click on any sample ID. Select the appropriate choice at the bottom of the form, and then click OK.

See Figure 94.

Note: The ‘Page View’ function saves the page with all matching/highlighting/etc. for later reference. However; this function is analogous to a screen shot save, as the only thing saved is what you see. The underlying data (peak height, base pair size, etc.) is not saved. This saved Page View can be opened as any normal excel file to see matching, etc. but will have no functionality in DNA_DataAnalysis.

Figure 94
117.) A new form will appear. You may re-name the file anything you wish by typing over the default name that appears, then click ‘Saved Profiles’. This will then save the data in the DNA_DataAnalysis → Saved Profiles → Page_Data/Page_Views/Single Profiles folder as appropriate.

See Figure 95.

![Figure 95](image)

118.) The files may be saved in a new folder of your choosing if you set it up properly prior to saving. Right click at the very top of the page to bring up the ‘Print / Select pages to view / Select user name’ form. Click ‘Set new location’ and then type the name of the new folder. Click ‘Set new location’ again to create the folder in the DNA_DataAnalysis folder. Now the new location will appear in the ‘Enter a file name’ form above.

See Figure 96.

![Figure 96](image)

Printing a Page

119). Any page may be printed by hitting F4.

120). The DNA_DataAnalysis pull-down menu at the very top right of the page has ‘Show Special Keys’ option that will explain all keyboard shortcuts.
Export to CODIS:

121.) To export a set of samples into CODIS right click on the sample ID, this will bring up the Matching/Send for a reference/Send profile/Other box.

122.) In the bottom right hand corner, select the ‘CODIS’ button.

123.) This will change the options available on the Matching/Send for a reference/Send profile/Other box.

124.) Various checks can be performed on the samples prior to upload into CODIS. These can be located under the ‘CODIS checks’ area within the Matching/Send for a reference/Send profile/Other box.

125.) Once all of the necessary checks have been performed select the ‘Validate CMF’ button, located to the left of the ‘CODIS CMF’ area of the Matching/Send for a reference/Send profile/Other box.

126.) All samples which can not be uploaded into CODIS will be highlighted in pink.

127.) Within the drop-down menu select the type of sample about to uploaded into CODIS

128.) Select the ‘Send for CMF’ button located under the drop down menu. All samples that meet the specifications and will be uploaded into CODIS will be highlighted in green.

129.) Select the ‘Make CMF’ button. The button will automatically change to read ‘CMF name A:’; by clicking on this button once more it can read ‘CMF name H:’ Select either, based on the location you would like the file to be sent to.

130.) Type in the name of the file in the box next to the ‘CMF name A/H:’ button, and select ‘OK’

131.) A text file will open, this is the CODIS 1.0 CMF file.