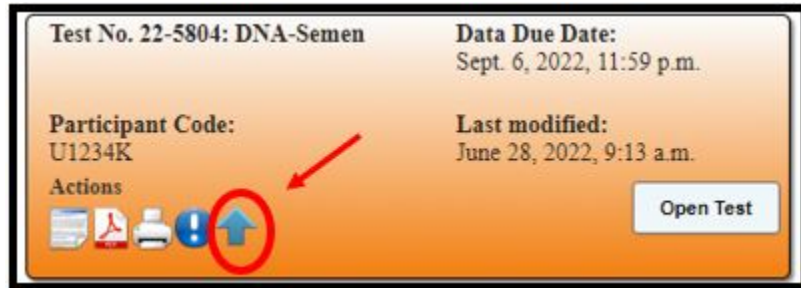


How to Upload DNA Data into Your Test

This guide explains how to upload DNA allelic data into your Forensic Biology, DNA Sample Specific, or Probabilistic Genotyping test. **Note:** *Uploading data through this process will override any data already entered in the applicable test section.*

Once the test is claimed, it will appear in the “My Data Entry” section. Click on the blue arrow icon under “Actions” and the “DNA File Upload” page will appear.



First, choose the “Software used” and “Sequence type” for the data being uploaded.

Note: *Ensure your data has been exported correctly depending on the software used. For uploading data via GeneMapper® ID/ID-X, additional instructions will appear on the bottom of the page.*

For STRMix, ensure the data from the software has been exported as a .txt file. Versions 2.4, 2.5, and 2.6 are currently supported.

For TrueAllele, ensure the data from the software has been exported as a .csv file.

Next, click on the “Choose Files” button to locate the file to upload and select a kit from the “Amplification Kit Arrangement.” This amplification kit will control the loci order. Multiple files may be chosen at once. (Supports ArmedXpert, GeneMapper® ID/ID-X, STRMix, and TrueAllele files).

DNA File Upload

Software Used:
STRmix

Sequence type:
 STR
 YSTR

File:
Choose Files No file chosen

Amplification Kit Arrangement:
 Default
 Identifiler®
 PowerPlex 16®
 PowerPlex® Fusion 5C
 PowerPlex® Fusion 6C
 GlobalFiler™
 Investigator® 24plex

Load File

Locate the file under the appropriate folder. Click on the file containing the data to be uploaded, then click “Open.”

After the file has been chosen, click on the “Load File” button on the bottom of the screen. Select the appropriate file for each item number on the top of the screen. Click the arrow to open the drop-down list above each necessary item number. You can select a file for all necessary items in your test at once.

Samples				
Name	Select	Select	Select	Select
Items	1	2	3	4

Once chosen, all alleles will appear for each locus.

The screenshot shows a web interface for selecting genetic loci. At the top, there are dropdown menus for 'Contributor 1' (set to 1) and 'Contributor 2' (set to 2). Below these are fields for 'Sample Name' and 'Sample File'. The main section is a table with four columns: 'CTS Locus', 'File Locus', and two 'Alleles' columns. The 'CTS Locus' column contains a list of dropdown menus for various loci, including D1S1656, D2S1338, D2S441, D3S1358, D5S818, D7S820, D8S1179, D10S1248, D12S391, D13S317, D16S539, D18S51, D19S433, D21S11, D22S1045, Amelogenin, CSF1PO, FGA, Penta D, Penta E, SE33, TH01, TPOX, vWA, DY3S91, DY5S70, DY5S76, and Y Indel. The 'File Locus' column contains corresponding text input fields. The 'Alleles' columns show the list of alleles for each locus, such as '15, 16' for D1S1656 and '14, Q, 15, 16, 17, 3' for D1S1656 in the second column.

Ensure to review this data. If the “CTS Locus” does not match the “File Locus,” click the arrow next to the “CTS Locus” to choose the correct locus.

This is a close-up of the 'CTS Locus' dropdown menu from the previous screenshot. A red arrow points to the 'D3S1358' option, which is currently selected. The dropdown list includes: D1S1656, D2S1338, D2S441, D3S1358, D5S818, D7S820, D8S1179, D10S1248, D12S391, D13S317, D16S539, D18S51, D19S433, D21S11, D22S1045, Amelogenin, CSF1PO, FGA, and Y Indel. The 'File Locus' column shows 'D3S1358' in the corresponding input field.

Next, review the “Substitution Options” at the bottom of the screen. This section allows you to substitute a character or blank space with something else.

Exclude	Character(s)	Substitute With
<input type="checkbox"/> Select All		
<input type="checkbox"/>	Q	<input type="text"/>
	BlankSpace	<input type="text"/>

In this section, you can also choose how to display homozygous alleles. By default, a homozygous allele will be represented by a single allele (i.e., “8”). Click on the box next to any character if you would like the homozygous allele to be shown as the two identical alleles (i.e., “8,8”).

Display as Homozygotes	Character(s)	Substitute With
<input type="checkbox"/> Select All		
<input type="checkbox"/>	16	<input type="text" value="16,16"/>
<input type="checkbox"/>	X	<input type="text" value="X,X"/>
<input type="checkbox"/>	11	<input type="text" value="11,11"/>
<input type="checkbox"/>	12	<input type="text" value="12,12"/>
<input type="checkbox"/>	28.2	<input type="text" value="28.2,28.2"/>

YSTR loci are excluded from this section where homozygotes are adjusted.

Once this section is complete, click the “Next” button at the bottom, right hand area of the screen.

The next window will show all changes to the data based on your chosen options for a final review. Click on the “Save” button to successfully transfer this data into the test.

The screenshot shows a 'Samples' configuration window. At the top, there are dropdown menus for 'Contributor 1' (set to 1), 'Contributor 2' (set to 2), and two 'Select' dropdowns (set to 3 and 4). Below this is a 'Sample Name' field and a 'Sample File' section. The main area is a grid of genetic markers. The first column lists 'CTS Locus' with dropdown menus for each. The second column lists 'File Locus' with text input fields. The third and fourth columns are labeled 'Alleles' and contain lists of possible allele values for each marker. At the bottom, a 'Summary of Selected Options' section states 'Special Alleles were excluded:' and 'Homozygotes were reviewed:' with a list of excluded alleles: 10 xxx 10, 10; 11 xxx X, X; 11 xxx 11, 11.

Your files have now been uploaded to the test! You will be sent back to the “My Data Entry” page. Click on the “Open Test” button to review the data that has been uploaded.

The card contains the following information:

- Test No. 22-5804: DNA-Semen**
- Data Due Date:** Sept. 6, 2022, 11:59 p.m.
- Participant Code:** U1234K
- Last modified:** June 28, 2022, 9:13 a.m.
- Actions:** A row of icons including a document, a red 'X', a printer, a warning sign, and an upward arrow.
- Open Test:** A button circled in red.

Appendix A

[ArmedXpert users can use the free CTS plugin to export table(s) directly, or create a genotypes export table using GeneMapper® ID/ID]

- Select an existing table setting or create a new table as described below.
- Click on the genotypes tab in GMID before selecting File > Export (Ctrl+E)
- The genotypes file generally has tab delimited columns such as: Sample File, Sample Name, Marker Allele 1, Size 1, Height 1, Allele 2, Size 2, Height 2, etc.
- "Sample File" and/or "Sample Name" columns are required in order to upload the STR genotypes.
- The "Marker" column is required.
- The "Allele" columns have to exist (at least one). The Allele column title format should look like this "Allele#" or "Allele #".
- Any additional columns, such as "Size" and "Height", are unnecessary, and will not affect the upload.

Note: *The file needs to be exported as a text file.*

The screenshot displays the GeneMapper ID v3.7.1 interface. The main window shows a data table with columns: Sample, Sample Name, Sample ID, Run Name, Marker, Dye, Allele 1, Size 1, Height 1, Peak Area, AE Comment, Allele 2, Size 2, Height 2. A red box highlights the 'Genotypes' tab in the 'Panels' section. A 'Table Setting Editor' dialog box is open, showing the 'Genotypes Table Settings' tab. The 'Column Settings' table is as follows:

Show	Column	Filtering	Content
<input checked="" type="checkbox"/>	Sample File	Show All Records	
<input checked="" type="checkbox"/>	Sample Name	Show All Records	
<input checked="" type="checkbox"/>	Sample ID	Show All Records	
<input checked="" type="checkbox"/>	Run Name	Show All Records	
<input type="checkbox"/>	Panel	Show All Records	
<input checked="" type="checkbox"/>	Marker	Show All Records	
<input checked="" type="checkbox"/>	Dye	Show All Records	N/A
<input checked="" type="checkbox"/>	Allele	Show All Records	
<input checked="" type="checkbox"/>	Size	Show All Records	
<input checked="" type="checkbox"/>	Height	Show All Records	
<input checked="" type="checkbox"/>	Peak Area	Show All Records	
<input type="checkbox"/>	Data Point	Show All Records	

The 'Font Settings' section shows 'Font: Arial' and 'Size: 11'. The 'Allele Settings' section shows 'Number of Alleles: 50' and a checked box for 'Keep Allele, Size, Height, Area, Data Point, Mutation and Comment together'.